

UniFrac: a New Phylogenetic Method for Comparing Mi

Applied and Environmental Microbiology

71, 8228-8235

DOI: [10.1128/aem.71.12.8228-8235.2005](https://doi.org/10.1128/aem.71.12.8228-8235.2005)

Citation Report

#	ARTICLE	IF	CITATIONS
4	Unexpected Diversity and Complexity of the Guerrero Negro Hypersaline Microbial Mat. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3685-3695.	1.4	435
5	Ecological and Evolutionary Forces Shaping Microbial Diversity in the Human Intestine. <i>Cell</i> , 2006, 124, 837-848.	13.5	2,744
6	Reciprocal Gut Microbiota Transplants from Zebrafish and Mice to Germ-free Recipients Reveal Host Habitat Selection. <i>Cell</i> , 2006, 127, 423-433.	13.5	808
7	UniFrac—an online tool for comparing microbial community diversity in a phylogenetic context. <i>BMC Bioinformatics</i> , 2006, 7, 371.	1.2	1,321
8	Introducing TreeClimber, a Test To Compare Microbial Community Structures. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2379-2384.	1.4	97
9	Introducing SONS, a Tool for Operational Taxonomic Unit-Based Comparisons of Microbial Community Memberships and Structures. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6773-6779.	1.4	239
10	Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5261-5267.	1.4	17,125
11	Molecular-phylogenetic characterization of microbial community imbalances in human inflammatory bowel diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13780-13785.	3.3	3,871
12	Microbial Community Biofabrics in a Geothermal Mine Adit. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6172-6180.	1.4	76
13	Long-term maintenance of species-specific bacterial microbiota in the basal metazoan <i>Hydra</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13146-13151.	3.3	320
14	No Evidence of an Impact on the Rhizosphere Diazotroph Community by the Expression of <i>Bacillus thuringiensis</i> Cry1Ab Toxin by Bt White Spruce. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6577-6583.	1.4	35
15	Alignment-Independent Comparisons of Human Gastrointestinal Tract Microbial Communities in a Multidimensional 16S rRNA Gene Evolutionary Space. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2727-2734.	1.4	28
16	Molecular identification of bacteria in bronchoalveolar lavage fluid from children with cystic fibrosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20529-20533.	3.3	339
17	Phylogenetic Composition of Rocky Mountain Endolithic Microbial Ecosystems. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3497-3504.	1.4	113
18	Short pyrosequencing reads suffice for accurate microbial community analysis. <i>Nucleic Acids Research</i> , 2007, 35, e120-e120.	6.5	638
19	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007, 8, R171.	13.9	170
20	Endolithic Microbial Ecosystems. <i>Annual Review of Microbiology</i> , 2007, 61, 331-347.	2.9	174
21	Quantitative and Qualitative $\hat{\pi}^2$ Diversity Measures Lead to Different Insights into Factors That Structure Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1576-1585.	1.4	2,418

#	ARTICLE	IF	CITATIONS
22	Database-Driven Grid Computing and Distributed Web Applications: A Comparison. , 0, , 247-266.		1
23	The Human Microbiome Project. <i>Nature</i> , 2007, 449, 804-810.	13.7	4,750
24	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.	2.0	64
25	Bacterial and fungal community structure in Arctic tundra tussock and shrub soils. <i>FEMS Microbiology Ecology</i> , 2007, 59, 428-435.	1.3	221
26	Molecular bacterial community analysis of clean rooms where spacecraft are assembled. <i>FEMS Microbiology Ecology</i> , 2007, 61, 509-521.	1.3	113
27	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7059-7066.	1.4	480
28	Global patterns in bacterial diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11436-11440.	3.3	1,461
29	Effect of long-term nitrogen fertilization on mycorrhizal fungi associated with a dominant grass in a semiarid grassland. <i>Plant and Soil</i> , 2007, 296, 65-75.	1.8	101
30	Biostimulation of Estuarine Microbiota on Substrate Coated Agar Slides: A Novel Approach to Study Diversity of Autochthonous <i>Bdellovibrio</i> - and Like Organisms. <i>Microbial Ecology</i> , 2008, 55, 640-650.	1.4	17
31	Correlating viral phenotypes with phylogeny: Accounting for phylogenetic uncertainty. <i>Infection, Genetics and Evolution</i> , 2008, 8, 239-246.	1.0	408
32	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 109-114.	2.8	104
33	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	6.0	3,171
34	The influence of sex, handedness, and washing on the diversity of hand surface bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17994-17999.	3.3	980
35	Species divergence and the measurement of microbial diversity. <i>FEMS Microbiology Reviews</i> , 2008, 32, 557-578.	3.9	400
36	Diversity and abundance of glycosyl hydrolase family 5 in the North Atlantic Ocean. <i>FEMS Microbiology Ecology</i> , 2008, 63, 316-327.	1.3	26
37	Change of bacterial communities in sediments along Songhua River in Northeastern China after a nitrobenzene pollution event. <i>FEMS Microbiology Ecology</i> , 2008, 65, 494-503.	1.3	41
38	Molecular-phylogenetic characterization of microbial communities imbalances in the small intestine of dogs with inflammatory bowel disease. <i>FEMS Microbiology Ecology</i> , 2008, 66, 579-589.	1.3	197
39	Evaluating different approaches that test whether microbial communities have the same structure. <i>ISME Journal</i> , 2008, 2, 265-275.	4.4	164

#	ARTICLE	IF	CITATIONS
40	Innate immunity and intestinal microbiota in the development of Type 1 diabetes. <i>Nature</i> , 2008, 455, 1109-1113.	13.7	1,745
41	Error-correcting barcoded primers for pyrosequencing hundreds of samples in multiplex. <i>Nature Methods</i> , 2008, 5, 235-237.	9.0	1,190
42	Worlds within worlds: evolution of the vertebrate gut microbiota. <i>Nature Reviews Microbiology</i> , 2008, 6, 776-788.	13.6	1,342
43	Strong host preference of ectomycorrhizal fungi in a Tasmanian wet sclerophyll forest as revealed by DNA barcoding and taxon-specific primers. <i>New Phytologist</i> , 2008, 180, 479-490.	3.5	362
44	Elevated atmospheric CO ₂ affects soil microbial diversity associated with trembling aspen. <i>Environmental Microbiology</i> , 2008, 10, 926-941.	1.8	235
45	Microbial community analysis of two field-scale sulfate-reducing bioreactors treating mine drainage. <i>Environmental Microbiology</i> , 2008, 10, 2087-2097.	1.8	50
46	Viral communities associated with healthy and bleaching corals. <i>Environmental Microbiology</i> , 2008, 10, 2277-2286.	1.8	125
47	Environmental distribution and population biology of <i>Candidatus</i> <i>Accumulibacter</i> , a primary agent of biological phosphorus removal. <i>Environmental Microbiology</i> , 2008, 10, 2692-2703.	1.8	102
48	Portal protein diversity and phage ecology. <i>Environmental Microbiology</i> , 2008, 10, 2810-2823.	1.8	100
49	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.	1.8	252
50	Fruiting body and soil rDNA sampling detects complementary assemblage of Agaricomycotina (Basidiomycota, Fungi) in a hemlock-dominated forest plot in southern Ontario. <i>Molecular Ecology</i> , 2008, 17, 3037-3050.	2.0	78
51	XplorSeq: A software environment for integrated management and phylogenetic analysis of metagenomic sequence data. <i>BMC Bioinformatics</i> , 2008, 9, 420.	1.2	47
52	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. <i>BMC Evolutionary Biology</i> , 2008, 8, 327.	3.2	25
53	Insights and inferences about integron evolution from genomic data. <i>BMC Genomics</i> , 2008, 9, 261.	1.2	51
54	Diversity and seasonal dynamics of bacterial community in indoor environment. <i>BMC Microbiology</i> , 2008, 8, 56.	1.3	235
55	The Origins of Ecological Diversity in Prokaryotes. <i>Current Biology</i> , 2008, 18, R1024-R1034.	1.8	159
56	The influence of soil properties on the structure of bacterial and fungal communities across land-use types. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2407-2415.	4.2	1,688
57	Comparative Analysis of Human Gut Microbiota by Barcoded Pyrosequencing. <i>PLoS ONE</i> , 2008, 3, e2836.	1.1	901

#	ARTICLE	IF	CITATIONS
58	Rules of Engagement: Interspecies Interactions that Regulate Microbial Communities. Annual Review of Microbiology, 2008, 62, 375-401.	2.9	362
59	DNA variation and symbiotic associations in phenotypically diverse sea urchin <i>Strongylocentrotus intermedius</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16218-16223.	3.3	36
60	Bioinformatics for DNA Sequence-based Microbiota Analyses. , 2008, , 245-254.		1
62	A renaissance for the pioneering 16S rRNA gene. Current Opinion in Microbiology, 2008, 11, 442-446.	2.3	418
63	Supplemental programs for enhanced recovery of data from the DOTUR application. Journal of Microbiological Methods, 2008, 75, 572-575.	0.7	4
64	Metagenomic Approaches for Defining the Pathogenesis of Inflammatory Bowel Diseases. Cell Host and Microbe, 2008, 3, 417-427.	5.1	423
65	Microbial burden and diversity of commercial airline cabin air during short and long durations of travel. ISME Journal, 2008, 2, 482-497.	4.4	51
66	Increasing ecological inference from high throughput sequencing of fungi in the environment through a tagging approach. Molecular Ecology Resources, 2008, 8, 742-752.	2.2	45
67	Short-Term Temporal Variability in Airborne Bacterial and Fungal Populations. Applied and Environmental Microbiology, 2008, 74, 200-207.	1.4	250
68	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. Nucleic Acids Research, 2008, 36, e120-e120.	6.5	508
69	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.	0.7	146
70	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.	0.9	19
71	Symbiotic gut microbes modulate human metabolic phenotypes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2117-2122.	3.3	994
72	A diversity profile of the human skin microbiota. Genome Research, 2008, 18, 1043-1050.	2.4	818
73	Microbes on mountainsides: Contrasting elevational patterns of bacterial and plant diversity. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11505-11511.	3.3	758
74	The convergence of carbohydrate active gene repertoires in human gut microbes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15076-15081.	3.3	120
75	Bacterial Community in the Crop of the Hoatzin, a Neotropical Folivorous Flying Bird. Applied and Environmental Microbiology, 2008, 74, 5905-5912.	1.4	61
76	The Macaque Gut Microbiome in Health, Lentiviral Infection, and Chronic Enterocolitis. PLoS Pathogens, 2008, 4, e20.	2.1	371

#	ARTICLE	IF	CITATIONS
77	Environmental and anthropogenic controls over bacterial communities in wetland soils. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17842-17847.	3.3	387
78	Influence of Particle Size on Bacterial Community Structure in Aquatic Sediments as Revealed by 16S rRNA Gene Sequence Analysis. Applied and Environmental Microbiology, 2008, 74, 5237-5240.	1.4	48
79	Subsurface Microbial Diversity in Deep-Granitic-Fracture Water in Colorado. Applied and Environmental Microbiology, 2008, 74, 143-152.	1.4	122
80	A bush, not a tree: The extraordinary diversity of cold-water basal foraminiferans extends to warm-water environments. Limnology and Oceanography, 2008, 53, 1339-1351.	1.6	54
81	Global Sequencing: A Review of Current Molecular Data and New Methods Available to Assess Microbial Diversity. Microbes and Environments, 2008, 23, 253-268.	0.7	64
82	Influenza A H5N1 Immigration Is Filtered Out at Some International Borders. PLoS ONE, 2008, 3, e1697.	1.1	51
83	Regulation of myocardial ketone body metabolism by the gut microbiota during nutrient deprivation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11276-11281.	3.3	224
84	Impact of sideways and bottom-up control factors on bacterial community succession over a tidal cycle. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4301-4306.	3.3	78
85	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.	1.4	94
86	Dominant Bacteria and Biomass in the Kuytun 51 Glacier. Applied and Environmental Microbiology, 2009, 75, 7287-7290.	1.4	41
87	Variations in Archaeal and Bacterial Diversity Associated with the Sulfate-Methane Transition Zone in Continental Margin Sediments (Santa Barbara Basin, California). Applied and Environmental Microbiology, 2009, 75, 1487-1499.	1.4	145
88	Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. PLoS Computational Biology, 2009, 5, e1000352.	1.5	1,495
89	The Cladistic Basis for the Phylogenetic Diversity (PD) Measure Links Evolutionary Features to Environmental Gradients and Supports Broad Applications of Microbial Ecology's "Phylogenetic Beta Diversity" Framework. International Journal of Molecular Sciences, 2009, 10, 4723-4741.	1.8	80
90	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.	1.4	47
91	GenGIS: A geospatial information system for genomic data. Genome Research, 2009, 19, 1896-1904.	2.4	119
92	Molecular diversity of bacterial chitinases in arable soils and the effects of environmental factors on the chitinolytic bacterial community. Soil Biology and Biochemistry, 2009, 41, 473-480.	4.2	44
93	Assessment of 10 years of CO ₂ fumigation on soil microbial communities and function in a sweetgum plantation. Soil Biology and Biochemistry, 2009, 41, 514-520.	4.2	84
94	Temporal changes in diversity and expression patterns of fungal laccase genes within the organic horizon of a brown forest soil. Soil Biology and Biochemistry, 2009, 41, 1380-1389.	4.2	51

#	ARTICLE	IF	CITATIONS
95	Photoacceleration of plant litter decomposition in an arid environment. <i>Soil Biology and Biochemistry</i> , 2009, 41, 1433-1441.	4.2	127
96	Distribution and diversity of autotrophic bacteria in groundwater systems based on the analysis of RubisCO genotypes. <i>Systematic and Applied Microbiology</i> , 2009, 32, 140-150.	1.2	59
97	The oligonucleotide frequency derived error gradient and its application to the binning of metagenome fragments. <i>BMC Genomics</i> , 2009, 10, S10.	1.2	20
98	The effect of the macrolide antibiotic tylosin on microbial diversity in the canine small intestine as demonstrated by massive parallel 16S rRNA gene sequencing. <i>BMC Microbiology</i> , 2009, 9, 210.	1.3	165
99	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. <i>Anaerobe</i> , 2009, 15, 145-154.	1.0	15
100	Study of the diversity of culturable actinomycetes in the North Pacific and Caribbean coasts of Costa Rica. <i>Antonie Van Leeuwenhoek</i> , 2009, 96, 71-78.	0.7	18
101	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.	0.5	65
102	Laccase Gene Composition and Relative Abundance in Oak Forest Soil is not Affected by Short-Term Nitrogen Fertilization. <i>Microbial Ecology</i> , 2009, 57, 50-57.	1.4	31
103	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.	1.4	82
104	Bacterial Succession on the Leaf Surface: A Novel System for Studying Successional Dynamics. <i>Microbial Ecology</i> , 2009, 58, 189-198.	1.4	223
105	The Biogeography of Ammonia-Oxidizing Bacterial Communities in Soil. <i>Microbial Ecology</i> , 2009, 58, 435-445.	1.4	128
106	Multiple Antimicrobial Resistance of Gram-Negative Bacteria from Natural Oligotrophic Lakes Under Distinct Anthropogenic Influence in a Tropical Region. <i>Microbial Ecology</i> , 2009, 58, 762-772.	1.4	42
107	Increased Diversity of Predacious <i>Bdellovibrio</i> -Like Organisms (BLOs) as a Function of Eutrophication in Kumaon Lakes of India. <i>Current Microbiology</i> , 2009, 59, 1-8.	1.0	14
108	Litter quality is in the eye of the beholder: initial decomposition rates as a function of inoculum characteristics. <i>Functional Ecology</i> , 2009, 23, 627-636.	1.7	264
109	Molecular phylogenetic biodiversity assessment of arctic and boreal ectomycorrhizal <i>Lactarius</i> Pers. (Russulales; Basidiomycota) in Alaska, based on soil and sporocarp DNA. <i>Molecular Ecology</i> , 2009, 18, 2213-2227.	2.0	59
110	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , 2009, 3, 442-453.	4.4	984
111	Evidence for the functional significance of diazotroph community structure in soil. <i>ISME Journal</i> , 2009, 3, 124-136.	4.4	224
112	Biogeography of two cold-adapted genera: <i>Psychrobacter</i> and <i>Exiguobacterium</i> . <i>ISME Journal</i> , 2009, 3, 658-665.	4.4	78

#	ARTICLE	IF	CITATIONS
113	16S rRNA gene-based analysis of fecal microbiota from preterm infants with and without necrotizing enterocolitis. <i>ISME Journal</i> , 2009, 3, 944-954.	4.4	508
114	Accurate determination of microbial diversity from 454 pyrosequencing data. <i>Nature Methods</i> , 2009, 6, 639-641.	9.0	895
115	Temporal and spatial variability in nearshore bacterioplankton communities of Lake Michigan. <i>FEMS Microbiology Ecology</i> , 2009, 67, 511-522.	1.3	86
116	Subseafloor microbial communities associated with rapid turbidite deposition in the Gulf of Mexico continental slope (IODP Expedition 308). <i>FEMS Microbiology Ecology</i> , 2009, 69, 410-424.	1.3	55
117	Deposition and postdeposition mechanisms as possible drivers of microbial population variability in glacier ice. <i>FEMS Microbiology Ecology</i> , 2009, 70, 165-176.	1.3	66
118	Bacterial diversity of water and sediment in the Changjiang estuary and coastal area of the East China Sea. <i>FEMS Microbiology Ecology</i> , 2009, 70, 236-248.	1.3	185
119	Characterizing microbial diversity in production water from an Alaskan mesothermic petroleum reservoir with two independent molecular methods. <i>Environmental Microbiology</i> , 2009, 11, 176-187.	1.8	155
120	The phylogeography of Adelie penguin faecal flora. <i>Environmental Microbiology</i> , 2009, 11, 577-588.	1.8	69
121	Disturbing epithelial homeostasis in the metazoan <i>Hydra</i> leads to drastic changes in associated microbiota. <i>Environmental Microbiology</i> , 2009, 11, 2361-2369.	1.8	64
122	Evidence for structuring of bacterial community composition by organic carbon source in temperate lakes. <i>Environmental Microbiology</i> , 2009, 11, 2463-2472.	1.8	123
123	Microbial diversity in modern marine stromatolites, Highborne Cay, Bahamas. <i>Environmental Microbiology</i> , 2009, 11, 2710-2719.	1.8	95
124	Effects of salinity and nutrients on microbial assemblages in Louisiana wetland sediments. <i>Wetlands</i> , 2009, 29, 277-287.	0.7	79
125	Fumarole-Supported Islands of Biodiversity within a Hyperarid, High-Elevation Landscape on Socompa Volcano, Puna de Atacama, Andes. <i>Applied and Environmental Microbiology</i> , 2009, 75, 735-747.	1.4	133
126	The Effect of Diet on the Human Gut Microbiome: A Metagenomic Analysis in Humanized Gnotobiotic Mice. <i>Science Translational Medicine</i> , 2009, 1, 6ra14.	5.8	2,492
127	Pyrosequencing-Based Assessment of Soil pH as a Predictor of Soil Bacterial Community Structure at the Continental Scale. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5111-5120.	1.4	3,268
128	The Human Intestinal Microbiome: A New Frontier of Human Biology. <i>DNA Research</i> , 2009, 16, 1-12.	1.5	227
129	Global diversity in the human salivary microbiome. <i>Genome Research</i> , 2009, 19, 636-643.	2.4	395
130	Infrequent marine-freshwater transitions in the microbial world. <i>Trends in Microbiology</i> , 2009, 17, 414-422.	3.5	311

#	ARTICLE	IF	CITATIONS
131	Characterization of Airborne Microbial Communities at a High-Elevation Site and Their Potential To Act as Atmospheric Ice Nuclei. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5121-5130.	1.4	273
132	Phylogenetic structure in tropical hummingbird communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19673-19678.	3.3	341
133	Bacterial Community Variation in Human Body Habitats Across Space and Time. <i>Science</i> , 2009, 326, 1694-1697.	6.0	2,713
134	Microbial community profiling for human microbiome projects: Tools, techniques, and challenges. <i>Genome Research</i> , 2009, 19, 1141-1152.	2.4	805
135	The occupant as a source of house dust bacteria. <i>Journal of Allergy and Clinical Immunology</i> , 2009, 124, 834-840.e47.	1.5	180
136	High-Fat Diet Determines the Composition of the Murine Gut Microbiome Independently of Obesity. <i>Gastroenterology</i> , 2009, 137, 1716-1724.e2.	0.6	1,344
137	Microbial Species Richness and Metabolic Activities in Hypersaline Microbial Mats: Insight into Biosignature Formation Through Lithification. <i>Astrobiology</i> , 2009, 9, 861-874.	1.5	43
138	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.	1.4	18,390
139	Community-Wide Response of the Gut Microbiota to Enteropathogenic <i>Citrobacter rodentium</i> Infection Revealed by Deep Sequencing. <i>Infection and Immunity</i> , 2009, 77, 4668-4678.	1.0	121
140	Molecular Characterization of Bacteriophages for Microbial Source Tracking in Korea. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7107-7114.	1.4	36
141	Changes in diversity and biomass of bacteria along a shallow snow pit from Kuytun 51 Glacier, Tianshan Mountains, China. <i>Journal of Geophysical Research</i> , 2009, 114, .	3.3	15
142	The gut microbiota of tollâ€like receptor 2â€deficient mice exhibits lineageâ€specific modifications. <i>Environmental Microbiology Reports</i> , 2009, 1, 65-70.	1.0	13
143	Contrasting the influences of stream inputs and landscape position on bacterioplankton community structure and dissolved organic matter composition in highâ€elevation lake chains. <i>Limnology and Oceanography</i> , 2009, 54, 1292-1305.	1.6	56
144	Altitudinal Changes in a Bacterial Community on Gulkana Glacier in Alaska. <i>Microbes and Environments</i> , 2010, 25, 171-182.	0.7	33
145	Factors promoting microbial diversity in the McMurdo Dry Valleys, Antarctica. , 2010, , 221-257.		27
146	Relationship Between Soil Properties and Patterns of Bacterial Î²-diversity Across Reclaimed and Natural Boreal Forest Soils. <i>Microbial Ecology</i> , 2010, 59, 563-573.	1.4	93
147	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.	1.4	102
148	Pyrosequencing Reveals a Highly Diverse and Cultivar-Specific Bacterial Endophyte Community in Potato Roots. <i>Microbial Ecology</i> , 2010, 60, 157-166.	1.4	256

#	ARTICLE	IF	CITATIONS
149	Microbial community shifts influence patterns in tropical forest nitrogen fixation. <i>Oecologia</i> , 2010, 164, 521-531.	0.9	120
150	Slowed decomposition is biotically mediated in an ectomycorrhizal, tropical rain forest. <i>Oecologia</i> , 2010, 164, 785-795.	0.9	84
151	Metagenomics: Facts and Artifacts, and Computational Challenges. <i>Journal of Computer Science and Technology</i> , 2010, 25, 71-81.	0.9	132
152	Microbial consumption and production of volatile organic compounds at the soil-litter interface. <i>Biogeochemistry</i> , 2010, 99, 97-107.	1.7	110
153	Intestinal Microbial Ecology in Premature Infants Assessed with Non-“Culture-Based Techniques. <i>Journal of Pediatrics</i> , 2010, 156, 20-25.	0.9	335
154	Indirect host effect on ectomycorrhizal fungi: Leaf fall and litter quality explain changes in fungal communities on the roots of co-occurring Mediterranean oaks. <i>Soil Biology and Biochemistry</i> , 2010, 42, 788-796.	4.2	96
155	Shifts in bacterial community structure associated with inputs of low molecular weight carbon compounds to soil. <i>Soil Biology and Biochemistry</i> , 2010, 42, 896-903.	4.2	436
156	Bacterial diversity and occurrence of ammonia-oxidizing bacteria in the Atacama Desert soil during a “desert bloom” event. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1183-1188.	4.2	50
157	Plot-scale manipulations of organic matter inputs to soils correlate with shifts in microbial community composition in a lowland tropical rain forest. <i>Soil Biology and Biochemistry</i> , 2010, 42, 2153-2160.	4.2	223
158	Investigation of catechol 2,3-dioxygenase and 16S rRNA gene diversity in hypoxic, petroleum hydrocarbon contaminated groundwater. <i>Systematic and Applied Microbiology</i> , 2010, 33, 398-406.	1.2	51
159	Introducing W.A.T.E.R.S.: a Workflow for the Alignment, Taxonomy, and Ecology of Ribosomal Sequences. <i>BMC Bioinformatics</i> , 2010, 11, 317.	1.2	29
160	VITCOMIC: visualization tool for taxonomic compositions of microbial communities based on 16S rRNA gene sequences. <i>BMC Bioinformatics</i> , 2010, 11, 332.	1.2	25
161	pplacer: linear time maximum-likelihood and Bayesian phylogenetic placement of sequences onto a fixed reference tree. <i>BMC Bioinformatics</i> , 2010, 11, 538.	1.2	901
162	Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. <i>BMC Microbiology</i> , 2010, 10, 206.	1.3	335
163	Bacterial diversity at different stages of the composting process. <i>BMC Microbiology</i> , 2010, 10, 94.	1.3	337
164	Molecular analysis of the bacterial microbiota in duodenal biopsies from dogs with idiopathic inflammatory bowel disease. <i>Veterinary Microbiology</i> , 2010, 142, 394-400.	0.8	155
165	Molecular characterization of the cloacal microbiota of wild and captive parrots. <i>Veterinary Microbiology</i> , 2010, 146, 320-325.	0.8	102
166	Analysis of Multitag Pyrosequence Data from Human Cervical Lavage Samples. <i>Chemistry and Biodiversity</i> , 2010, 7, 1076-1085.	1.0	8

#	ARTICLE	IF	CITATIONS
167	Resemblance in phylogenetic diversity among ecological assemblages. <i>Journal of Vegetation Science</i> , 2010, 21, 809-820.	1.1	45
168	Spatio-temporal variations in protistan communities along an O ₂ /H ₂ S gradient in the anoxic Framvaren Fjord (Norway). <i>FEMS Microbiology Ecology</i> , 2010, 72, 89-102.	1.3	67
169	Comparative analysis of bacterioplankton assemblages from <i>Karenia brevis</i> bloom and nonbloom water on the west Florida shelf (Gulf of Mexico, USA) using 16S rRNA gene clone libraries. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	51
170	Effect of storage conditions on the assessment of bacterial community structure in soil and human-associated samples. <i>FEMS Microbiology Letters</i> , 2010, 307, 80-86.	0.7	341
171	Phylogenetic similarity and structure of Agaricomycotina communities across a forested landscape. <i>Molecular Ecology</i> , 2010, 19, 1469-1482.	2.0	43
172	Quantifying microbial communities with 454 pyrosequencing: does read abundance count?. <i>Molecular Ecology</i> , 2010, 19, 5555-5565.	2.0	468
173	Bacterial communities of disease vectors sampled across time, space, and species. <i>ISME Journal</i> , 2010, 4, 223-231.	4.4	43
174	Community shifts of soybean stem-associated bacteria responding to different nodulation phenotypes and N levels. <i>ISME Journal</i> , 2010, 4, 315-326.	4.4	63
175	Evolutionary divergence and biogeography of sympatric niche-differentiated bacterial populations. <i>ISME Journal</i> , 2010, 4, 488-497.	4.4	61
176	Developmental microbial ecology of the crop of the folivorous hoatzin. <i>ISME Journal</i> , 2010, 4, 611-620.	4.4	55
177	Ecological and evolutionary factors underlying global and local assembly of denitrifier communities. <i>ISME Journal</i> , 2010, 4, 633-641.	4.4	217
178	Fast UniFrac: facilitating high-throughput phylogenetic analyses of microbial communities including analysis of pyrosequencing and PhyloChip data. <i>ISME Journal</i> , 2010, 4, 17-27.	4.4	1,025
179	Viral and microbial community dynamics in four aquatic environments. <i>ISME Journal</i> , 2010, 4, 739-751.	4.4	387
180	Freshwater <i>Perkinsea</i> and marine-freshwater colonizations revealed by pyrosequencing and phylogeny of environmental rDNA. <i>ISME Journal</i> , 2010, 4, 1144-1153.	4.4	208
181	Soil bacterial and fungal communities across a pH gradient in an arable soil. <i>ISME Journal</i> , 2010, 4, 1340-1351.	4.4	3,154
182	Postprandial remodeling of the gut microbiota in Burmese pythons. <i>ISME Journal</i> , 2010, 4, 1375-1385.	4.4	229
183	Bacterial community shifts in taxa and diversity in response to localized organic loading in the deep sea. <i>Environmental Microbiology</i> , 2010, 12, 344-363.	1.8	90
184	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. <i>Environmental Microbiology</i> , 2010, 12, 2998-3006.	1.8	551

#	ARTICLE	IF	CITATIONS
185	Differences in community composition of bacteria in four glaciers in western China. <i>Biogeosciences</i> , 2010, 7, 1937-1952.	1.3	24
186	Robust Computational Analysis of rRNA Hypervariable Tag Datasets. <i>PLoS ONE</i> , 2010, 5, e15220.	1.1	15
187	Environmental Shaping of Sponge Associated Archaeal Communities. <i>PLoS ONE</i> , 2010, 5, e15774.	1.1	84
188	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.	1.1	223
189	Simulated Atmospheric Nitrogen Deposition Alters Actinobacterial Community Composition in Forest Soils. <i>Soil Science Society of America Journal</i> , 2010, 74, 1157-1166.	1.2	81
190	Infrequent Transitions between Saline and Fresh Waters in One of the Most Abundant Microbial Lineages (SAR11). <i>Molecular Biology and Evolution</i> , 2010, 27, 347-357.	3.5	66
191	Forensic identification using skin bacterial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6477-6481.	3.3	507
192	Stable tRNA-based phylogenies using only 76 nucleotides. <i>Rna</i> , 2010, 16, 1469-1477.	1.6	36
193	Biogeography and Biodiversity in Sulfide Structures of Active and Inactive Vents at Deep-Sea Hydrothermal Fields of the Southern Mariana Trough. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2968-2979.	1.4	88
194	The bacterial microbiota in the oral mucosa of rural Amerindians. <i>Microbiology (United Kingdom)</i> , 2010, 156, 3282-3287.	0.7	65
195	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. <i>Genome Research</i> , 2010, 20, 1411-1419.	2.4	284
196	Characterization of Bacterial Community Structure in a Drinking Water Distribution System during an Occurrence of Red Water. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7171-7180.	1.4	111
197	Nested PCR and New Primers for Analysis of Sulfate-Reducing Bacteria in Low-Cell-Biomass Environments. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2856-2865.	1.4	48
198	In an early branching metazoan, bacterial colonization of the embryo is controlled by maternal antimicrobial peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18067-18072.	3.3	143
199	Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers. <i>Applied and Environmental Microbiology</i> , 2010, 76, 999-1007.	1.4	690
200	Diversity of Anaerobic Microbes in Spacecraft Assembly Clean Rooms. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2837-2845.	1.4	50
201	High-Density 16S Microarray and Clone Library-Based Microbial Community Composition of the Phoenix Spacecraft Assembly Clean Room. <i>Astrobiology</i> , 2010, 10, 499-508.	1.5	37
202	Application of Molecular Techniques To Elucidate the Influence of Cellulosic Waste on the Bacterial Community Structure at a Simulated Low-Level-Radioactive-Waste Site. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3106-3115.	1.4	39

#	ARTICLE	IF	CITATIONS
203	Microbial Community Changes in Response to Ethanol or Methanol Amendments for U(VI) Reduction. Applied and Environmental Microbiology, 2010, 76, 5728-5735.	1.4	38
204	Characterization of the Oral Fungal Microbiome (Mycobiome) in Healthy Individuals. PLoS Pathogens, 2010, 6, e1000713.	2.1	869
205	Molecular Source Tracking of Bioaerosols in the Quarantined Katrina Flood Zone. Aerosol Science and Technology, 2010, 44, 230-239.	1.5	8
206	A Primer on Metagenomics. PLoS Computational Biology, 2010, 6, e1000667.	1.5	523
207	Cyanobacterial communities on Qiyi glacier, Qilian Shan, China. Annals of Glaciology, 2010, 51, 135-144.	2.8	26
208	Comparative Analyses of the Bacterial Microbiota of the Human Nostril and Oropharynx. MBio, 2010, 1, .	1.8	266
209	Picante: R tools for integrating phylogenies and ecology. Bioinformatics, 2010, 26, 1463-1464.	1.8	4,517
210	Which Microbial Communities Are Present? Sequence-Based Metagenomics. , 2010, , 63-76.		1
211	Biogeography and habitat modelling of high-alpine bacteria. Nature Communications, 2010, 1, 53.	5.8	141
212	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.	3.3	335
213	Phylogenetic Metrics of Community Similarity. American Naturalist, 2010, 176, E128-E142.	1.0	85
214	Change of microbial communities in glaciers along a transition of air masses in western China. Journal of Geophysical Research, 2010, 115, .	3.3	4
215	Next-Generation Sequencing in the Analysis of Human Microbiota. Molecular Diagnosis and Therapy, 2010, 14, 343-350.	1.6	35
216	Comparative analysis of the composition of bacterial communities from two constructed wetlands for municipal and swine wastewater treatment. Journal of Water and Health, 2010, 8, 147-157.	1.1	11
217	Metabolic Syndrome and Altered Gut Microbiota in Mice Lacking Toll-Like Receptor 5. Science, 2010, 328, 228-231.	6.0	1,804
218	Characterization of Enterococcus spp. from Human and Animal Feces Using 16S rRNA Sequences, the <i>espA</i> Gene, and PFGE for Microbial Source Tracking in Korea. Environmental Science & Technology, 2010, 44, 3423-3428.	4.6	14
219	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.	1.2	103
220	Structural differentiation of bacterial communities in indole-degrading bioreactors under denitrifying and sulfate-reducing conditions. Research in Microbiology, 2010, 161, 687-693.	1.0	44

#	ARTICLE	IF	CITATIONS
221	Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11971-11975.	3.3	3,738
222	Marine Hypersaline Microcoleus-Dominated Cyanobacterial Mats in the Saltern at Guerrero Negro, Baja California Sur, Mexico: A System-Level Perspective. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , 401-420.	0.3	6
223	The ecology of the phyllosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. <i>Environmental Microbiology</i> , 2010, 12, 2885-2893.	1.8	574
224	Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. <i>Ecology</i> , 2010, 91, 3463-3470.	1.5	475
225	Identifying biologically relevant differences between metagenomic communities. <i>Bioinformatics</i> , 2010, 26, 715-721.	1.8	916
226	Microbes at Work. , 2010, , .		34
227	Microbial Mats. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , .	0.3	36
228	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , 2010, 11, 210.	13.9	134
229	Metagenomic analyses reveal antibiotic-induced temporal and spatial changes in intestinal microbiota with associated alterations in immune cell homeostasis. <i>Mucosal Immunology</i> , 2010, 3, 148-158.	2.7	355
230	Pyrosequencing Assessment of Soil Microbial Communities in Organic and Conventional Potato Farms. <i>Plant Disease</i> , 2010, 94, 1329-1335.	0.7	109
231	The human gut virome: Inter-individual variation and dynamic response to diet. <i>Genome Research</i> , 2011, 21, 1616-1625.	2.4	825
232	Visual exploration of microbial populations. , 2011, , .		6
233	Effect of Organic Substrate on the Microbial Community Structure in Pilot-Scale Sulfate-Reducing Biochemical Reactors Treating Mine Drainage. <i>Environmental Engineering Science</i> , 2011, 28, 563-572.	0.8	66
234	Responses of Aerobic and Anaerobic Ammonia/Ammonium-Oxidizing Microorganisms to Anthropogenic Pollution in Coastal Marine Environments. <i>Methods in Enzymology</i> , 2011, 496, 35-62.	0.4	33
235	Colonic mucosa-associated microbiota is influenced by an interaction of Crohn disease and <i>FUT2</i> (<i>Secretor</i>) genotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19030-19035.	3.3	304
236	Topographical Continuity of Bacterial Populations in the Healthy Human Respiratory Tract. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 184, 957-963.	2.5	912
237	The Human Microbiota as a Marker for Migrations of Individuals and Populations. <i>Annual Review of Anthropology</i> , 2011, 40, 451-474.	0.4	46
241	Distribution and diversity of oligotrich and choreotrich ciliates across an environmental gradient in a large temperate estuary. <i>Aquatic Microbial Ecology</i> , 2011, 64, 51-67.	0.9	25

#	ARTICLE	IF	CITATIONS
242	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	6.0	1,712
243	Evaluation of short read metagenomic assembly. <i>BMC Genomics</i> , 2011, 12, S8.	1.2	46
244	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4516-4522.	3.3	7,425
245	A Bioinformatics Pipeline for Sequence-Based Analyses of Fungal Biodiversity. <i>Methods in Molecular Biology</i> , 2011, 722, 141-155.	0.4	22
246	Metagenomic biomarker discovery and explanation. <i>Genome Biology</i> , 2011, 12, R60.	13.9	11,192
247	Association Between Composition of the Human Gastrointestinal Microbiome and Development of Fatty Liver With Choline Deficiency. <i>Gastroenterology</i> , 2011, 140, 976-986.	0.6	512
248	Long-term land use effects on soil microbial community structure and function. <i>Applied Soil Ecology</i> , 2011, 51, 66-78.	2.1	163
249	NLRP6 Inflammasome Regulates Colonic Microbial Ecology and Risk for Colitis. <i>Cell</i> , 2011, 145, 745-757.	13.5	1,716
250	A review of molecular methods to study the microbiota of soil and the mycosphere. <i>European Journal of Soil Biology</i> , 2011, 47, 77-87.	1.4	98
251	Evaluation of different partial 16S rRNA gene sequence regions for phylogenetic analysis of microbiomes. <i>Journal of Microbiological Methods</i> , 2011, 84, 81-87.	0.7	274
252	Rethinking microbial diversity analysis in the high throughput sequencing era. <i>Journal of Microbiological Methods</i> , 2011, 86, 42-51.	0.7	262
253	Skin microbiome: genomics-based insights into the diversity and role of skin microbes. <i>Trends in Molecular Medicine</i> , 2011, 17, 320-328.	3.5	222
254	Bacterial community characteristics under long-term antibiotic selection pressures. <i>Water Research</i> , 2011, 45, 6063-6073.	5.3	116
255	A novel method for determining microflora composition using dynamic phylogenetic analysis of 16S ribosomal RNA deep sequencing data. <i>Genomics</i> , 2011, 98, 253-259.	1.3	11
256	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. <i>Trends in Microbiology</i> , 2011, 19, 472-482.	3.5	23
257	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 2011, , .	0.1	5
258	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 2011, , .	0.1	0
259	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.0. <i>Nature Precedings</i> , 2011, , .	0.1	3

#	ARTICLE	IF	CITATIONS
260	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing " standard operating procedure, version 1.1. Nature Precedings, 0, , .	0.1	2
261	Land-use systems affect Archaeal community structure and functional diversity in western Amazon soils. Revista Brasileira De Ciencia Do Solo, 2011, 35, 1527-1540.	0.5	31
262	Exploring the Diversity of Gardnerella vaginalis in the Genitourinary Tract Microbiota of Monogamous Couples Through Subtle Nucleotide Variation. PLoS ONE, 2011, 6, e26732.	1.1	172
263	Potential Accumulative Effect of the Herbicide Glyphosate on Glyphosate-Tolerant Maize Rhizobacterial Communities over a Three-Year Cultivation Period. PLoS ONE, 2011, 6, e27558.	1.1	25
264	Degradation of Potassium Rock by Earthworms and Responses of Bacterial Communities in Its Gut and Surrounding Substrates after Being Fed with Mineral. PLoS ONE, 2011, 6, e28803.	1.1	35
265	COMPARISONS OF DISTANCE METHODS FOR COMBINING COVARIATES AND ABUNDANCES IN MICROBIOME STUDIES. , 2011, , .		29
266	The effect of UV pre-treatment on biofouling of BWRO membranes: A field study. Desalination and Water Treatment, 2011, 31, 151-163.	1.0	24
267	Distribution and Diversity of Anaerobic Ammonium Oxidation (Anammox) Bacteria in the Sediment of a Eutrophic Freshwater Lake, Lake Kitaura, Japan. Microbes and Environments, 2011, 26, 189-197.	0.7	113
268	Epibacterial community patterns on marine macroalgae are host-specific but temporally variable. Environmental Microbiology, 2011, 13, 655-665.	1.8	328
269	Phylogenetic beta diversity reveals historical effects in the assemblage of the tree florae of the Ryukyu Archipelago. Journal of Biogeography, 2011, 38, 1006-1008.	1.4	21
270	Characterization of the skin fungal microbiota in patients with atopic dermatitis and in healthy subjects. Microbiology and Immunology, 2011, 55, 625-632.	0.7	169
271	Fungal community composition and function after long-term exposure of northern forests to elevated atmospheric CO ₂ and tropospheric O ₃ . Global Change Biology, 2011, 17, 2184-2195.	4.2	45
272	Phylogenetic ecology of widespread uncultured clades of the Kingdom Euryarchaeota. Molecular Ecology, 2011, 20, 1988-1996.	2.0	36
273	Supervised classification of human microbiota. FEMS Microbiology Reviews, 2011, 35, 343-359.	3.9	377
274	Impact of endochitinase-transformed white spruce on soil fungal communities under greenhouse conditions. FEMS Microbiology Ecology, 2011, 76, 199-208.	1.3	17
275	Spatial and temporal changes of cyanophage communities in paddy field soils as revealed by the capsid assembly protein gene g20. FEMS Microbiology Ecology, 2011, 76, 352-359.	1.3	29
276	Prokaryotic abundance and 16S rRNA gene sequences detected in marine aerosols on the East Sea (Korea). FEMS Microbiology Ecology, 2011, 76, 327-341.	1.3	81
277	Diversity and dynamics of free-living and particle-associated <i>Betaproteobacteria</i> and <i>Actinobacteria</i> in relation to phytoplankton and zooplankton communities. FEMS Microbiology Ecology, 2011, 77, 461-476.	1.3	56

#	ARTICLE	IF	CITATIONS
278	Effect of a multi-species synbiotic formulation on fecal bacterial microbiota of healthy cats and dogs as evaluated by pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2011, 78, 542-554.	1.3	116
279	The impact of reduced pH on the microbial community of the coral <i>Acropora eurystroma</i> . <i>ISME Journal</i> , 2011, 5, 51-60.	4.4	217
280	Vertical stratification of microbial communities in the Red Sea revealed by 16S rDNA pyrosequencing. <i>ISME Journal</i> , 2011, 5, 507-518.	4.4	151
281	Analysis of human and animal fecal microbiota for microbial source tracking. <i>ISME Journal</i> , 2011, 5, 362-365.	4.4	87
282	Unveiling an abundant core microbiota in the human adult colon by a phylogroup-independent searching approach. <i>ISME Journal</i> , 2011, 5, 519-531.	4.4	77
283	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172.	4.4	2,280
284	Patterns of fungal diversity and composition along a salinity gradient. <i>ISME Journal</i> , 2011, 5, 379-388.	4.4	160
285	Capturing diversity of marine heterotrophic protists: one cell at a time. <i>ISME Journal</i> , 2011, 5, 674-684.	4.4	86
286	Pyrosequencing reveals highly diverse and species-specific microbial communities in sponges from the Red Sea. <i>ISME Journal</i> , 2011, 5, 650-664.	4.4	265
287	Response of <i>Prochlorococcus</i> ecotypes to co-culture with diverse marine bacteria. <i>ISME Journal</i> , 2011, 5, 1125-1132.	4.4	142
288	Ovine pedomics: the first study of the ovine foot 16S rRNA-based microbiome. <i>ISME Journal</i> , 2011, 5, 1426-1437.	4.4	46
289	Specific assemblages of major capsid genes (g23) of T4-type bacteriophages isolated from upland black soils in Northeast China. <i>Soil Biology and Biochemistry</i> , 2011, 43, 1980-1984.	4.2	20
290	F+ RNA coliphage-based microbial source tracking in water resources of South Korea. <i>Science of the Total Environment</i> , 2011, 412-413, 127-131.	3.9	29
291	Molecular analysis of bacterial communities in raw cow milk and the impact of refrigeration on its structure and dynamics. <i>Food Microbiology</i> , 2011, 28, 465-471.	2.1	101
292	Influence of Plant Polymers on the Distribution and Cultivation of Bacteria in the Phylum <i>Acidobacteria</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 586-596.	1.4	227
293	Comparative analysis of microbial diversity in Longitarsus flea beetles (Coleoptera: Chrysomelidae). <i>Genetica</i> , 2011, 139, 541-550.	0.5	39
294	Seasonal changes and diversity of bacteria in Bohai Bay by RFLP analysis of PCR-amplified 16S rDNA gene fragments. <i>World Journal of Microbiology and Biotechnology</i> , 2011, 27, 275-284.	1.7	12
295	Ectomycorrhizal fungal diversity in orchards of cultivated pecan (<i>Carya illinoensis</i> ; Juglandaceae). <i>Mycorrhiza</i> , 2011, 21, 601-612.	1.3	56

#	ARTICLE	IF	CITATIONS
296	Promiscuity in mice is associated with increased vaginal bacterial diversity. <i>Die Naturwissenschaften</i> , 2011, 98, 951-960.	0.6	20
297	Annual and Seasonal Variation in the Phyllosphere Bacterial Community Associated with Leaves of the Southern Magnolia (<i>Magnolia grandiflora</i>). <i>Microbial Ecology</i> , 2011, 61, 113-122.	1.4	75
298	Land Use Intensity Controls Actinobacterial Community Structure. <i>Microbial Ecology</i> , 2011, 61, 286-302.	1.4	52
299	Euxinic Freshwater Hypolimnia Promote Bacterial Endemicity in Continental Areas. <i>Microbial Ecology</i> , 2011, 61, 465-472.	1.4	46
300	Presence and Diversity of <i>Streptomyces</i> in <i>Dendroctonus</i> and Sympatric Bark Beetle Galleries Across North America. <i>Microbial Ecology</i> , 2011, 61, 759-768.	1.4	63
301	The Microbial Phylogeography of the Carnivorous Plant <i>Sarracenia alata</i> . <i>Microbial Ecology</i> , 2011, 61, 750-758.	1.4	34
302	Influence of Deglaciation on Microbial Communities in Marine Sediments Off the Coast of Svalbard, Arctic Circle. <i>Microbial Ecology</i> , 2011, 62, 537-548.	1.4	23
303	Phylogenetic diversity of bacterial communities in bovine rumen as affected by diets and microenvironments. <i>Folia Microbiologica</i> , 2011, 56, 453-458.	1.1	41
304	Diversity and novelty of the gut microbial community of an herbivorous rodent (<i>Neotoma bryanti</i>). <i>Symbiosis</i> , 2011, 54, 47-54.	1.2	44
305	Preliminary characterization of the oral microbiota of Chinese adults with and without gingivitis. <i>BMC Oral Health</i> , 2011, 11, 33.	0.8	104
306	Variance adjusted weighted UniFrac: a powerful beta diversity measure for comparing communities based on phylogeny. <i>BMC Bioinformatics</i> , 2011, 12, 118.	1.2	126
307	Flexible taxonomic assignment of ambiguous sequencing reads. <i>BMC Bioinformatics</i> , 2011, 12, 8.	1.2	26
308	Comparative genomics of four closely related <i>Clostridium perfringens</i> bacteriophages reveals variable evolution among core genes with therapeutic potential. <i>BMC Genomics</i> , 2011, 12, 282.	1.2	23
309	Differences between the normal vaginal bacterial community of baboons and that of humans. <i>American Journal of Primatology</i> , 2011, 73, 119-126.	0.8	27
310	Enteric dysbiosis associated with a mouse model of alcoholic liver disease. <i>Hepatology</i> , 2011, 53, 96-105.	3.6	636
311	Disease phenotype and genotype are associated with shifts in intestinal-associated microbiota in inflammatory bowel diseases. <i>Inflammatory Bowel Diseases</i> , 2011, 17, 179-184.	0.9	505
312	Microbial Life in a Liquid Asphalt Desert. <i>Astrobiology</i> , 2011, 11, 241-258.	1.5	49
313	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011, 8, 761-763.	9.0	1,284

#	ARTICLE	IF	CITATIONS
314	Human oral, gut, and plaque microbiota in patients with atherosclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4592-4598.	3.3	943
315	Molecular Definition of Vaginal Microbiota in East African Commercial Sex Workers. Applied and Environmental Microbiology, 2011, 77, 4066-4074.	1.4	71
316	Enteral Tube Feeding Alters the Oral Indigenous Microbiota in Elderly Adults. Applied and Environmental Microbiology, 2011, 77, 6739-6745.	1.4	37
317	Biodiversity and Emerging Biogeography of the Neutrophilic Iron-Oxidizing Zetaproteobacteria. Applied and Environmental Microbiology, 2011, 77, 5445-5457.	1.4	125
318	Electroactivity of Phototrophic River Biofilms and Constitutive Cultivable Bacteria. Applied and Environmental Microbiology, 2011, 77, 5394-5401.	1.4	28
319	Army Ants Harbor a Host-Specific Clade of <i>Entomoplasmatales</i> Bacteria. Applied and Environmental Microbiology, 2011, 77, 346-350.	1.4	68
320	Global Phylogeography of Chitinase Genes in Aquatic Metagenomes. Applied and Environmental Microbiology, 2011, 77, 1101-1106.	1.4	21
321	Phylogenetic Beta Diversity Metrics, Trait Evolution and Inferring the Functional Beta Diversity of Communities. PLoS ONE, 2011, 6, e21264.	1.1	200
322	Bacterial Communities of Two Parthenogenetic Aphid Species Cocolonizing Two Host Plants across the Hawaiian Islands. Applied and Environmental Microbiology, 2011, 77, 8345-8349.	1.4	57
323	Lack of Correlation between Turnover of Low-Molecular-Weight Dissolved Organic Carbon and Differences in Microbial Community Composition or Growth across a Soil pH Gradient. Applied and Environmental Microbiology, 2011, 77, 2791-2795.	1.4	38
324	Evaluation of Subsampling-Based Normalization Strategies for Tagged High-Throughput Sequencing Data Sets from Gut Microbiomes. Applied and Environmental Microbiology, 2011, 77, 8795-8798.	1.4	125
325	Soil rotifer communities are extremely diverse globally but spatially autocorrelated locally. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4406-4410.	3.3	90
326	Beneficial Microorganisms in Multicellular Life Forms. , 2011, , .		16
327	Bacterial community comparisons by taxonomy-supervised analysis independent of sequence alignment and clustering. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14637-14642.	3.3	87
328	The Genotype of the Calcium/Calmodulin-Dependent Protein Kinase Gene (<i>CCaMK</i>) Determines Bacterial Community Diversity in Rice Roots under Paddy and Upland Field Conditions. Applied and Environmental Microbiology, 2011, 77, 4399-4405.	1.4	30
329	Autoregulation of Nodulation Interferes with Impacts of Nitrogen Fertilization Levels on the Leaf-Associated Bacterial Community in Soybeans. Applied and Environmental Microbiology, 2011, 77, 1973-1980.	1.4	50
330	Diversity and distribution of soil fungal communities in a semiarid grassland. Mycologia, 2011, 103, 10-21.	0.8	153
331	Bacterial community structures are unique and resilient in full-scale bioenergy systems. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4158-4163.	3.3	412

#	ARTICLE	IF	CITATIONS
332	Succession of microbial consortia in the developing infant gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4578-4585.	3.3	2,108
334	Sparse distance-based learning for simultaneous multiclass classification and feature selection of metagenomic data. Bioinformatics, 2011, 27, 3242-3249.	1.8	50
335	<i>Frankia</i> Assemblages Associated with <i>Alnus rubra</i> and <i>Alnus viridis</i> Are Strongly Influenced by Host Species Identity. International Journal of Plant Sciences, 2011, 172, 403-410.	0.6	7
336	Performance, Accuracy, and Web Server for Evolutionary Placement of Short Sequence Reads under Maximum Likelihood. Systematic Biology, 2011, 60, 291-302.	2.7	476
337	Concentration and Diversity of Uncultured <i>Legionella</i> spp. in Two Unchlorinated Drinking Water Supplies with Different Concentrations of Natural Organic Matter. Applied and Environmental Microbiology, 2011, 77, 634-641.	1.4	76
338	Phylogenetic Diversity Theory Sheds Light on the Structure of Microbial Communities. PLoS Computational Biology, 2012, 8, e1002832.	1.5	56
339	The Spatial and Temporal Dynamics of Rabies in China. PLoS Neglected Tropical Diseases, 2012, 6, e1640.	1.3	45
340	Phylogenetic and functional alpha and beta diversity in temperate and tropical tree communities. Ecology, 2012, 93, S112.	1.5	193
341	Meta-Storms: efficient search for similar microbial communities based on a novel indexing scheme and similarity score for metagenomic data. Bioinformatics, 2012, 28, 2493-2501.	1.8	44
342	Chapter 12: Human Microbiome Analysis. PLoS Computational Biology, 2012, 8, e1002808.	1.5	408
343	Spatial Distribution of Viruses Associated with Planktonic and Attached Microbial Communities in Hydrothermal Environments. Applied and Environmental Microbiology, 2012, 78, 1311-1320.	1.4	42
344	Analysis of the community structure of abyssal kinetoplastids revealed similar communities at larger spatial scales. ISME Journal, 2012, 6, 713-723.	4.4	25
345	PhyloTempo: A Set of R Scripts for Assessing and Visualizing Temporal Clustering in Genealogies Inferred from Serially Sampled Viral Sequences. Evolutionary Bioinformatics, 2012, 8, EBO.S9738.	0.6	24
346	Structural Changes of Gut Microbiota during Berberine-Mediated Prevention of Obesity and Insulin Resistance in High-Fat Diet-Fed Rats. PLoS ONE, 2012, 7, e42529.	1.1	435
347	Profound Alterations of Intestinal Microbiota following a Single Dose of Clindamycin Results in Sustained Susceptibility to Clostridium difficile-Induced Colitis. Infection and Immunity, 2012, 80, 62-73.	1.0	473
348	Human Intestinal Lumen and Mucosa-Associated Microbiota in Patients with Colorectal Cancer. PLoS ONE, 2012, 7, e39743.	1.1	821
349	Factors That Affect Large Subunit Ribosomal DNA Amplicon Sequencing Studies of Fungal Communities: Classification Method, Primer Choice, and Error. PLoS ONE, 2012, 7, e35749.	1.1	52
350	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. Genome Research, 2012, 22, 1974-1984.	2.4	120

#	ARTICLE	IF	CITATIONS
351	Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. <i>Genome Research</i> , 2012, 22, 2146-2152.	2.4	167
352	Denitrifying Bacteria from the Genus <i>Rhodanobacter</i> Dominate Bacterial Communities in the Highly Contaminated Subsurface of a Nuclear Legacy Waste Site. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1039-1047.	1.4	184
353	The Human Microbiome and Its Potential Importance to Pediatrics. <i>Pediatrics</i> , 2012, 129, 950-960.	1.0	252
354	Interleukin-1 β (IL-1 β) promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. <i>Gut</i> , 2012, 61, 373-384.	6.1	68
355	454 Pyrosequencing reveals bacterial diversity of activated sludge from 14 sewage treatment plants. <i>ISME Journal</i> , 2012, 6, 1137-1147.	4.4	957
356	Evidence for Cascades of Perturbation and Adaptation in the Metabolic Genes of Higher Termite Gut Symbionts. <i>MBio</i> , 2012, 3, .	1.8	13
357	Forensic identification with environmental samples. , 2012, , .		5
358	Colonic mucosal microbiome differs from stool microbiome in cirrhosis and hepatic encephalopathy and is linked to cognition and inflammation. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 303, G675-G685.	1.6	462
359	Consumption of different soymilk formulations differentially affects the gut microbiomes of overweight and obese men. <i>Gut Microbes</i> , 2012, 3, 490-500.	4.3	58
360	Abiotic Factors Shape Microbial Diversity in Sonoran Desert Soils. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7527-7537.	1.4	195
361	Abundance and Genetic Diversity of Aerobic Anoxygenic Phototrophic Bacteria of Coastal Regions of the Pacific Ocean. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2858-2866.	1.4	53
362	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <i>ISME Journal</i> , 2012, 6, 94-103.	4.4	537
363	Contrasting patterns of niche partitioning between two anaerobic terminal oxidizers of organic matter. <i>ISME Journal</i> , 2012, 6, 905-914.	4.4	20
364	Actinobacterial Diversity in Microbial Mats of Five Hot Springs in Central and Central-Eastern Tibet, China. <i>Geomicrobiology Journal</i> , 2012, 29, 520-527.	1.0	17
365	Pyrosequencing as a tool for better understanding of human microbiomes. <i>Journal of Oral Microbiology</i> , 2012, 4, 10743.	1.2	121
366	Pulmonary Bacterial Communities in Surgically Resected Noncystic Fibrosis Bronchiectasis Lungs Are Similar to Those in Cystic Fibrosis. <i>Pulmonary Medicine</i> , 2012, 2012, 1-9.	0.5	19
367	Recruitment of Members from the Rare Biosphere of Marine Bacterioplankton Communities after an Environmental Disturbance. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1361-1369.	1.4	102
368	A Crypt-Specific Core Microbiota Resides in the Mouse Colon. <i>MBio</i> , 2012, 3, .	1.8	172

#	ARTICLE	IF	CITATIONS
369	Discrimination of the oral microbiota associated with high hydrogen sulfide and methyl mercaptan production. <i>Scientific Reports</i> , 2012, 2, 215.	1.6	68
370	Use of Direct Gradient Analysis to Uncover Biological Hypotheses in 16S Survey Data and Beyond. <i>Scientific Reports</i> , 2012, 2, 774.	1.6	18
371	Disturbance of deep-sea environments induced by the M9.0 Tohoku Earthquake. <i>Scientific Reports</i> , 2012, 2, 270.	1.6	55
372	Microbes en masse: The sequencing machine. <i>Nature</i> , 2012, 487, 156-158.	13.7	4
373	Phylogenetic diversity and assemblage of major capsid genes (<i>g23</i>) of T4-type bacteriophages in paddy field soils during rice growth season in Northeast China. <i>Soil Science and Plant Nutrition</i> , 2012, 58, 435-444.	0.8	21
374	Compositional and phylogenetic dissimilarity of host communities drives dissimilarity of ectoparasite assemblages: geographical variation and scale-dependence. <i>Parasitology</i> , 2012, 139, 338-347.	0.7	21
375	Comparative Survey of Rumen Microbial Communities and Metabolites across One Caprine and Three Bovine Groups, Using Bar-Coded Pyrosequencing and ¹ H Nuclear Magnetic Resonance Spectroscopy. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5983-5993.	1.4	120
376	Defining the human microbiome. <i>Nutrition Reviews</i> , 2012, 70, S38-S44.	2.6	789
377	Central Role of Dynamic Tidal Biofilms Dominated by Aerobic Hydrocarbonoclastic Bacteria and Diatoms in the Biodegradation of Hydrocarbons in Coastal Mudflats. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3638-3648.	1.4	90
378	Comparative faecal microbiota of dogs with and without calcium oxalate stones. <i>Journal of Applied Microbiology</i> , 2012, 113, 745-756.	1.4	18
379	Do diet and taxonomy influence insect gut bacterial communities?. <i>Molecular Ecology</i> , 2012, 21, 5124-5137.	2.0	467
380	Deep sequencing reveals extensive variation in the gut microbiota of wild mosquitoes from Kenya. <i>Molecular Ecology</i> , 2012, 21, 5138-5150.	2.0	256
381	Effect of Rainfall-Induced Soil Geochemistry Dynamics on Grassland Soil Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7587-7595.	1.4	55
382	Intestinal microbiota associated with differential feed conversion efficiency in chickens. <i>Applied Microbiology and Biotechnology</i> , 2012, 96, 1361-1369.	1.7	229
383	Familial transmission rather than defective innate immunity shapes the distinct intestinal microbiota of TLR-deficient mice. <i>Journal of Experimental Medicine</i> , 2012, 209, 1445-1456.	4.2	295
384	Water-sediment niche differentiation in ancient marine lineages of <i>Exiguobacterium</i> endemic to the Cuatro Ciénegas Basin. <i>Environmental Microbiology</i> , 2012, 14, 2323-2333.	1.8	48
385	Distinct approaches for the detection and removal of chimeric 16S rRNA sequences can significantly affect the outcome of between-site comparisons. <i>Aquatic Microbial Ecology</i> , 2012, 66, 13-21.	0.9	3
386	Molecular Characterisation of Gastrointestinal Microbiota of Children With Autism (With and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1 419-427.	2.1	166

#	ARTICLE	IF	CITATIONS
387	Taxonomic and functional characterization of microbial communities in Technosols constructed for remediation of a contaminated industrial wasteland. <i>Journal of Soils and Sediments</i> , 2012, 12, 1396-1406.	1.5	23
388	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. <i>Cell</i> , 2012, 150, 470-480.	13.5	1,603
389	Transient Inability to Manage Proteobacteria Promotes Chronic Gut Inflammation in TLR5-Deficient Mice. <i>Cell Host and Microbe</i> , 2012, 12, 139-152.	5.1	459
390	Advances in the methods for studying gut microbiota and their relevance to the research of dietary fiber functions. <i>Food Research International</i> , 2012, 48, 916-929.	2.9	49
391	Dysbiosis in Epizootic Shell Disease of the American Lobster (<i>Homarus americanus</i>). <i>Journal of Shellfish Research</i> , 2012, 31, 463-472.	0.3	56
392	Abundance and Diversity of Microbial Inhabitants in European Spacecraft-Associated Clean Rooms. <i>Astrobiology</i> , 2012, 12, 572-585.	1.5	28
393	Bacterial Community Structure in the Drinking Water Microbiome Is Governed by Filtration Processes. <i>Environmental Science & Technology</i> , 2012, 46, 8851-8859.	4.6	366
394	Next-generation Sequencing Approaches to Understanding the Oral Microbiome. <i>Advances in Dental Research</i> , 2012, 24, 81-85.	3.6	62
395	Spatial and Species Variations in Bacterial Communities Associated with Corals from the Red Sea as Revealed by Pyrosequencing. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7173-7184.	1.4	97
396	Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene. <i>ISME Journal</i> , 2012, 6, 11-20.	4.4	175
397	Comparative Ocular Microbial Communities in Humans with and without Blepharitis. , 2012, 53, 5585.		153
398	An irritable bowel syndrome subtype defined by species-specific alterations in faecal microbiota. <i>Gut</i> , 2012, 61, 997-1006.	6.1	742
399	Biodiversity characterization of cellulolytic bacteria present on native Chaco soil by comparison of ribosomal RNA genes. <i>Research in Microbiology</i> , 2012, 163, 221-232.	1.0	59
400	Differences in crop bacterial community structure between hoatzins from different geographical locations. <i>Research in Microbiology</i> , 2012, 163, 211-220.	1.0	23
401	Saliva microbiomes distinguish caries-active from healthy human populations. <i>ISME Journal</i> , 2012, 6, 1-10.	4.4	320
402	Antibiotics in early life alter the murine colonic microbiome and adiposity. <i>Nature</i> , 2012, 488, 621-626.	13.7	1,358
403	Abundance and Composition of Epiphytic Bacterial and Archaeal Ammonia Oxidizers of Marine Red and Brown Macroalgae. <i>Applied and Environmental Microbiology</i> , 2012, 78, 318-325.	1.4	47
404	Associating microbiome composition with environmental covariates using generalized UniFrac distances. <i>Bioinformatics</i> , 2012, 28, 2106-2113.	1.8	780

#	ARTICLE	IF	CITATIONS
405	Lung-enriched Organisms and Aberrant Bacterial and Fungal Respiratory Microbiota after Lung Transplant. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 536-545.	2.5	275
406	Targeting the Human Genome's Microbiome Axis for Drug Discovery: Inspirations from Global Systems Biology and Traditional Chinese Medicine. <i>Journal of Proteome Research</i> , 2012, 11, 3509-3519.	1.8	57
407	Measuring Community Similarity with Phylogenetic Networks. <i>Molecular Biology and Evolution</i> , 2012, 29, 3947-3958.	3.5	21
408	Glyphosate affects the rhizobacterial communities in glyphosate-tolerant cotton. <i>Applied Soil Ecology</i> , 2012, 55, 20-26.	2.1	12
409	High abundance of genetic Bacteroidetes markers for total fecal pollution in pristine alpine soils suggests lack in specificity for feces. <i>Journal of Microbiological Methods</i> , 2012, 88, 433-435.	0.7	28
410	Gut Immune Maturation Depends on Colonization with a Host-Specific Microbiota. <i>Cell</i> , 2012, 149, 1578-1593.	13.5	1,050
411	Evidence against fluvial seeding of recurrent toxic blooms of <i>Microcystis</i> spp. in Lake Erie's western basin. <i>Harmful Algae</i> , 2012, 15, 71-77.	2.2	37
412	Stochastic and deterministic assembly processes in subsurface microbial communities. <i>ISME Journal</i> , 2012, 6, 1653-1664.	4.4	1,203
413	Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel (<i>Petaurista alborufus lena</i>). <i>BMC Genomics</i> , 2012, 13, 466.	1.2	27
414	Comparison of metagenomic samples using sequence signatures. <i>BMC Genomics</i> , 2012, 13, 730.	1.2	74
415	Comparative molecular analysis of chemolithoautotrophic bacterial diversity and community structure from coastal saline soils, Gujarat, India. <i>BMC Microbiology</i> , 2012, 12, 150.	1.3	45
416	Short-term responses of unicellular planktonic eukaryotes to increases in temperature and UVB radiation. <i>BMC Microbiology</i> , 2012, 12, 202.	1.3	5
417	Influence of wet distillers grains diets on beef cattle fecal bacterial community structure. <i>BMC Microbiology</i> , 2012, 12, 25.	1.3	51
418	Huanglongbing alters the structure and functional diversity of microbial communities associated with citrus rhizosphere. <i>ISME Journal</i> , 2012, 6, 363-383.	4.4	162
419	Major histocompatibility complex class II compatibility, but not class I, predicts mate choice in a bird with highly developed olfaction. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4457-4463.	1.2	87
420	Bacterial Community Composition and Diversity in Methane Charged Sediments Revealed by Multitag Pyrosequencing. <i>Geomicrobiology Journal</i> , 2012, 29, 340-351.	1.0	8
421	Changes in coral microbial communities in response to a natural pH gradient. <i>ISME Journal</i> , 2012, 6, 1775-1785.	4.4	98
422	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , 2012, 488, 86-90.	13.7	2,475

#	ARTICLE	IF	CITATIONS
423	Metabolic stratification driven by surface and subsurface interactions in a terrestrial mud volcano. ISME Journal, 2012, 6, 2280-2290.	4.4	54
424	Millimeter-scale patterns of phylogenetic and trait diversity in a salt marsh microbial mat. Frontiers in Microbiology, 2012, 3, 293.	1.5	52
425	Microbial Community Changes Along a Land-Use Gradient of Desert Soil Origin. Pedosphere, 2012, 22, 593-603.	2.1	34
426	The potential for microbial life in the highest elevation (>6000 m.a.s.l.) mineral soils of the Atacama region. Journal of Geophysical Research, 2012, 117, .	3.3	67
427	The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites. Journal of Allergy and Clinical Immunology, 2012, 129, 1204-1208.	1.5	266
428	Integrated and novel survey methods for rhinoceros populations confirm the extinction of Rhinoceros sondaicus annamiticus from Vietnam. Biological Conservation, 2012, 155, 59-67.	1.9	35
429	Fungal communities at the edge: Ecological lessons from high alpine fungi. Fungal Ecology, 2012, 5, 443-452.	0.7	70
430	Microbial 16S rRNA Ion Tag and community metagenome sequencing using the Ion Torrent (PGM) Platform. Journal of Microbiological Methods, 2012, 91, 80-88.	0.7	187
431	Effect of Cry1Ab Protein on Rhizobacterial Communities of Bt-Maize over a Four-Year Cultivation Period. PLoS ONE, 2012, 7, e35481.	1.1	40
432	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. Gut, 2012, 61, 1124-1131.	6.1	321
433	High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57.		0
434	Molecular analysis of gut microbiota in obesity among Indian individuals. Journal of Biosciences, 2012, 37, 647-657.	0.5	142
435	High throughput sequencing methods for microbiome profiling: application to food animal systems. Animal Health Research Reviews, 2012, 13, 40-53.	1.4	27
436	Culture-Free Survey Reveals Diverse and Distinctive Fungal Communities Associated with Developing Figs (Ficus spp.) in Panama. Microbial Ecology, 2012, 64, 1073-1084.	1.4	28
437	Microbial and Geochemical Assessment of Bauxitic Un-mined and Post-mined Chronosequence Soils from Mocho Mountains, Jamaica. Microbial Ecology, 2012, 64, 738-749.	1.4	17
438	Composition of Methane-Oxidizing Bacterial Communities as a Function of Nutrient Loading in the Florida Everglades. Microbial Ecology, 2012, 64, 750-759.	1.4	14
439	Mycangia of Ambrosia Beetles Host Communities of Bacteria. Microbial Ecology, 2012, 64, 784-793.	1.4	60
440	Quantification of Subfamily I.2.C Catechol 2,3-Dioxygenase mRNA Transcripts in Groundwater Samples of an Oxygen-Limited BTEX-Contaminated Site. Environmental Science & Technology, 2012, 46, 232-240.	4.6	40

#	ARTICLE	IF	CITATIONS
441	The Genboree Microbiome Toolset and the analysis of 16S rRNA microbial sequences. BMC Bioinformatics, 2012, 13, S11.	1.2	44
442	Insight into the bacterial gut microbiome of the North American moose (<i>Alces alces</i>). BMC Microbiology, 2012, 12, 212.	1.3	51
443	Effect of <i>Lactobacillus salivarius</i> Bacteriocin Abp118 on the Mouse and Pig Intestinal Microbiota. PLoS ONE, 2012, 7, e31113.	1.1	136
444	Deep Sequencing Analyses of Low Density Microbial Communities: Working at the Boundary of Accurate Microbiota Detection. PLoS ONE, 2012, 7, e32942.	1.1	160
445	Comparison of Storage Conditions for Human Vaginal Microbiome Studies. PLoS ONE, 2012, 7, e36934.	1.1	59
446	Fungal Diversity Associated with Hawaiian <i>Drosophila</i> Host Plants. PLoS ONE, 2012, 7, e40550.	1.1	22
447	Estimation of Distribution Overlap of Urn Models. PLoS ONE, 2012, 7, e42368.	1.1	7
448	Elevational Patterns in Archaeal Diversity on Mt. Fuji. PLoS ONE, 2012, 7, e44494.	1.1	54
449	Characterization of the Active Microbiotas Associated with Honey Bees Reveals Healthier and Broader Communities when Colonies are Genetically Diverse. PLoS ONE, 2012, 7, e32962.	1.1	143
450	Brewhouse-Resident Microbiota Are Responsible for Multi-Stage Fermentation of American Coolship Ale. PLoS ONE, 2012, 7, e35507.	1.1	161
451	Symbiotic Associations in the Phenotypically-Diverse Brown Alga <i>Saccharina japonica</i> . PLoS ONE, 2012, 7, e39587.	1.1	34
452	Quantifying Phylogenetic Beta Diversity: Distinguishing between $\hat{\alpha}$ Turnover of Lineages and Phylogenetic Diversity Gradients. PLoS ONE, 2012, 7, e42760.	1.1	169
453	A Direct PCR Approach to Accelerate Analyses of Human-Associated Microbial Communities. PLoS ONE, 2012, 7, e44563.	1.1	60
454	Next-Generation Sequencing Reveals Significant Bacterial Diversity of Botrytized Wine. PLoS ONE, 2012, 7, e36357.	1.1	196
455	Succession in the Gut Microbiome following Antibiotic and Antibody Therapies for <i>Clostridium difficile</i> . PLoS ONE, 2012, 7, e46966.	1.1	80
456	Statistical Object Data Analysis of Taxonomic Trees from Human Microbiome Data. PLoS ONE, 2012, 7, e48996.	1.1	15
457	Combined Analyses of the ITS Loci and the Corresponding 16S rRNA Genes Reveal High Micro- and Macrodiversity of SAR11 Populations in the Red Sea. PLoS ONE, 2012, 7, e50274.	1.1	35
458	The Bacterial Composition within the <i>Sarracenia purpurea</i> Model System: Local Scale Differences and the Relationship with the Other Members of the Food Web. PLoS ONE, 2012, 7, e50969.	1.1	22

#	ARTICLE	IF	CITATIONS
459	Hypothesis Testing and Power Calculations for Taxonomic-Based Human Microbiome Data. PLoS ONE, 2012, 7, e52078.	1.1	289
460	Climate Change Impacts on the Tree of Life: Changes in Phylogenetic Diversity Illustrated for Acropora Corals. Biology, 2012, 1, 906-932.	1.3	31
461	Pyrosequencing Reveals Bacteria Carried in Different Wind-Eroded Sediments. Journal of Environmental Quality, 2012, 41, 744-753.	1.0	27
462	Carbon, Metals, and Grain Size Correlate with Bacterial Community Structure in Sediments of a High Arsenic Aquifer. Frontiers in Microbiology, 2012, 3, 82.	1.5	27
463	Microbial communities associated with wet flue gas desulfurization systems. Frontiers in Microbiology, 2012, 3, 412.	1.5	10
464	Pyrosequencing analysis of the protist communities in a High Arctic meromictic lake: DNA preservation and change. Frontiers in Microbiology, 2012, 3, 422.	1.5	61
465	Diversity of cultured photosynthetic flagellates in the northeast Pacific and Arctic Oceans in summer. Biogeosciences, 2012, 9, 4553-4571.	1.3	53
466	Metagenomics in Polluted Aquatic Environments. , 0, , .		1
467	Computational methods for the analysis of tag sequences in metagenomics studies. Frontiers in Bioscience - Scholar, 2012, S4, 1333-1343.	0.8	2
468	Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temperatures. Biogeosciences, 2012, 9, 4645-4659.	1.3	59
469	Human gut microbiome viewed across age and geography. Nature, 2012, 486, 222-227.	13.7	6,247
470	Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. ISME Journal, 2012, 6, 2091-2106.	4.4	291
471	Patterns in the distribution of soil bacterial 16S rRNA gene sequences from different regions of Antarctica. Geoderma, 2012, 181-182, 45-55.	2.3	50
472	Gut microbiota composition correlates with diet and health in the elderly. Nature, 2012, 488, 178-184.	13.7	2,618
473	Characterization of Soil Bacterial Assemblies in Brazilian Savanna-Like Vegetation Reveals Acidobacteria Dominance. Microbial Ecology, 2012, 64, 760-770.	1.4	76
474	Contrasting denitrifier communities relate to contrasting N2O emission patterns from acidic peat soils in arctic tundra. ISME Journal, 2012, 6, 1058-1077.	4.4	152
475	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. ISME Journal, 2012, 6, 1273-1276.	4.4	102
476	Coral-associated marine fungi form novel lineages and heterogeneous assemblages. ISME Journal, 2012, 6, 1291-1301.	4.4	154

#	ARTICLE	IF	CITATIONS
477	Red Waters of <i>Myrionecta rubra</i> are Biogeochemical Hotspots for the Columbia River Estuary with Impacts on Primary/Secondary Productions and Nutrient Cycles. <i>Estuaries and Coasts</i> , 2012, 35, 878-891.	1.0	36
478	Phylogenetic Analysis Suggests That Habitat Filtering Is Structuring Marine Bacterial Communities Across the Globe. <i>Microbial Ecology</i> , 2012, 64, 8-17.	1.4	68
479	Chrysophytes and other protists in High Arctic lakes: molecular gene surveys, pigment signatures and microscopy. <i>Polar Biology</i> , 2012, 35, 733-748.	0.5	72
480	The Effects of Soil Bacterial Community Structure on Decomposition in a Tropical Rain Forest. <i>Ecosystems</i> , 2012, 15, 284-298.	1.6	59
481	Soil microbial community response to drying and rewetting stress: does historical precipitation regime matter?. <i>Biogeochemistry</i> , 2012, 109, 101-116.	1.7	360
482	Methanogen diversity and community composition in peatlands of the central to northern Appalachian Mountain region, North America. <i>Biogeochemistry</i> , 2012, 109, 117-131.	1.7	56
483	Comparative microbial diversity analyses of modern marine thrombolitic mats by barcoded pyrosequencing. <i>Environmental Microbiology</i> , 2012, 14, 82-100.	1.8	56
484	Photoautotrophic symbiont and geography are major factors affecting highly structured and diverse bacterial communities in the lichen microbiome. <i>Environmental Microbiology</i> , 2012, 14, 147-161.	1.8	176
485	Biogeography of pelagic bacterioplankton across an antagonistic temperature-salinity gradient in the Red Sea. <i>Molecular Ecology</i> , 2012, 21, 388-405.	2.0	98
486	Consistent effects of nitrogen amendments on soil microbial communities and processes across biomes. <i>Global Change Biology</i> , 2012, 18, 1918-1927.	4.2	936
487	Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2012, 13, 47-58.	7.7	601
488	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. <i>Obesity</i> , 2012, 20, 738-747.	1.5	352
489	Genetic characterization of denitrifier communities with contrasting intrinsic functional traits. <i>FEMS Microbiology Ecology</i> , 2012, 79, 542-554.	1.3	56
490	Genetic difference but functional similarity among fish gut bacterial communities through molecular and biochemical fingerprints. <i>FEMS Microbiology Ecology</i> , 2012, 79, 568-580.	1.3	69
491	Gender-specific bacterial composition of black flies (Diptera: Simuliidae). <i>FEMS Microbiology Ecology</i> , 2012, 80, 659-670.	1.3	27
492	Advancing analytical algorithms and pipelines for billions of microbial sequences. <i>Current Opinion in Biotechnology</i> , 2012, 23, 64-71.	3.3	57
493	Phylogenetic diversity of microbial communities associated with the crude-oil, large-insoluble-particle and formation-water components of the reservoir fluid from a non-flooded high-temperature petroleum reservoir. <i>Journal of Bioscience and Bioengineering</i> , 2012, 113, 204-210.	1.1	69
494	A fast, highly sensitive double-nested PCR-based method to screen fish immunobiomes. <i>Molecular Ecology Resources</i> , 2012, 12, 1027-1039.	2.2	11

#	ARTICLE	IF	CITATIONS
495	Lineage-dependent ecological coherence in bacteria. <i>FEMS Microbiology Ecology</i> , 2012, 81, 574-582.	1.3	28
496	Effects of season and experimental warming on the bacterial community in a temperate mountain forest soil assessed by 16S rRNA gene pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2012, 82, 551-562.	1.3	128
497	Towards diagnostic guidelines for biofilm-associated infections. <i>FEMS Immunology and Medical Microbiology</i> , 2012, 65, 127-145.	2.7	288
498	Molecular methods for pathogen and microbial community detection and characterization: Current and potential application in diagnostic microbiology. <i>Infection, Genetics and Evolution</i> , 2012, 12, 505-521.	1.0	123
499	Pyrosequencing and mid-infrared spectroscopy reveal distinct aggregate stratification of soil bacterial communities and organic matter composition. <i>Soil Biology and Biochemistry</i> , 2012, 46, 63-72.	4.2	228
500	Digging deeper to find unique microbial communities: The strong effect of depth on the structure of bacterial and archaeal communities in soil. <i>Soil Biology and Biochemistry</i> , 2012, 50, 58-65.	4.2	614
501	Bacterial community structure of contrasting soils underlying Bornean rain forests: Inferences from microarray and next-generation sequencing methods. <i>Soil Biology and Biochemistry</i> , 2012, 55, 48-59.	4.2	41
502	Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. <i>Molecular Ecology</i> , 2012, 21, 3363-3378.	2.0	814
503	Microbiome analysis among bats describes influences of host phylogeny, life history, physiology and geography. <i>Molecular Ecology</i> , 2012, 21, 2617-2627.	2.0	195
504	Alterations in composition and diversity of the intestinal microbiota in patients with diarrhoea-predominant irritable bowel syndrome. <i>Neurogastroenterology and Motility</i> , 2012, 24, 521.	1.6	350
505	Intestinal aganglionosis is associated with early and sustained disruption of the colonic microbiome. <i>Neurogastroenterology and Motility</i> , 2012, 24, 874.	1.6	74
506	The Phylogenetic Kantorovich-Rubinstein Metric for Environmental Sequence Samples. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012, 74, 569-592.	1.1	97
507	Multi-locus sequence analysis, taxonomic resolution and biogeography of marine <i>Synechococcus</i> . <i>Environmental Microbiology</i> , 2012, 14, 372-386.	1.8	123
508	Microbial methane cycling in a terrestrial mud volcano in eastern Taiwan. <i>Environmental Microbiology</i> , 2012, 14, 895-908.	1.8	67
509	Phylogenomics of T4 cyanophages: lateral gene transfer in the "core"™ and origins of host genes. <i>Environmental Microbiology</i> , 2012, 14, 2113-2126.	1.8	114
510	Temporal variability in the diversity and composition of stream bacterioplankton communities. <i>Environmental Microbiology</i> , 2012, 14, 2417-2428.	1.8	83
511	Geographic distance and pH drive bacterial distribution in alkaline lake sediments across Tibetan Plateau. <i>Environmental Microbiology</i> , 2012, 14, 2457-2466.	1.8	484
512	Using high throughput sequencing to explore the biodiversity in oral bacterial communities. <i>Molecular Oral Microbiology</i> , 2012, 27, 182-201.	1.3	112

#	ARTICLE	IF	CITATIONS
513	A Hump-Backed Trend in Bacterial Diversity with Elevation on Mount Fuji, Japan. <i>Microbial Ecology</i> , 2012, 63, 429-437.	1.4	166
514	A Molecular Enrichment Strategy Based on <i>cpn60</i> for Detection of Epsilon-Proteobacteria in the Dog Fecal Microbiome. <i>Microbial Ecology</i> , 2012, 63, 348-357.	1.4	32
515	Distinctive Phyllosphere Bacterial Communities in Tropical Trees. <i>Microbial Ecology</i> , 2012, 63, 674-681.	1.4	154
516	Compositions of microbial communities associated with oil and water in a mesothermic oil field. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 493-506.	0.7	75
517	Cultivable bacteria from ancient algal mats from the McMurdo Dry Valleys, Antarctica. <i>Extremophiles</i> , 2012, 16, 105-114.	0.9	30
518	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.	1.8	169
519	Culture-independent analysis of <i>Pseudomonas</i> community structures in fertilized and unfertilized agricultural soils. <i>Annals of Microbiology</i> , 2013, 63, 323-333.	1.1	4
520	Comparative analysis of basidiomycetous laccase genes in forest soils reveals differences at the cDNA and DNA levels. <i>Plant and Soil</i> , 2013, 366, 321-331.	1.8	5
521	Community Composition of NirS-Type Denitrifier in a Shallow Eutrophic Lake. <i>Microbial Ecology</i> , 2013, 66, 796-805.	1.4	12
522	Feedstocks Affect the Diversity and Distribution of Propionate CoA-Transferase Genes (<i>pct</i>) in Anaerobic Digesters. <i>Microbial Ecology</i> , 2013, 66, 351-362.	1.4	8
523	Microbial Communities Involved in Biological Ammonium Removal from Coal Combustion Wastewaters. <i>Microbial Ecology</i> , 2013, 66, 49-59.	1.4	17
524	Comparison of Soil Bacterial Communities of <i>Pinus patula</i> of Nilgiris, Western Ghats with Other Biogeographically Distant Pine Forest Clone Libraries. <i>Microbial Ecology</i> , 2013, 66, 132-144.	1.4	8
525	Characterization of the Major Capsid Genes (<i>g23</i>) of T4-Type Bacteriophages in the Wetlands of Northeast China. <i>Microbial Ecology</i> , 2013, 65, 616-625.	1.4	27
526	Deep Sequencing of <i>Myxilla</i> (<i>Ectyomyxilla</i>) <i>methanophila</i> , an Epibiotic Sponge on Cold-Seep Tubeworms, Reveals Methylophilic, Thiotrophic, and Putative Hydrocarbon-Degrading Microbial Associations. <i>Microbial Ecology</i> , 2013, 65, 450-461.	1.4	25
527	Diversity, distribution and sources of bacteria in residential kitchens. <i>Environmental Microbiology</i> , 2013, 15, 588-596.	1.8	170
528	Pyrosequencing analysis of the human microbiota of healthy Chinese undergraduates. <i>BMC Genomics</i> , 2013, 14, 390.	1.2	105
529	Comparative analysis of oral treponemes associated with periodontal health and disease. <i>BMC Infectious Diseases</i> , 2013, 13, 174.	1.3	32
530	Influence of <i>Salmonella enterica</i> serovar <i>Enteritidis</i> infection on the composition of chicken cecal microbiota. <i>BMC Veterinary Research</i> , 2013, 9, 140.	0.7	91

#	ARTICLE	IF	CITATIONS
531	Chicken faecal microbiota and disturbances induced by single or repeated therapy with tetracycline and streptomycin. <i>BMC Veterinary Research</i> , 2013, 9, 30.	0.7	96
532	Specificity and temporal dynamics of complex bacteria-sponge symbiotic interactions. <i>Ecology</i> , 2013, 94, 2781-2791.	1.5	33
533	Culture-independent molecular approaches reveal a mostly unknown high diversity of active nitrogen-fixing bacteria associated with <i>Pennisetum purpureum</i> a bioenergy crop. <i>Plant and Soil</i> , 2013, 373, 737-754.	1.8	29
534	Detection of photoactive siderophore biosynthetic genes in the marine environment. <i>BioMetals</i> , 2013, 26, 507-516.	1.8	17
535	Bacterial and fungal diversity in the starter production process of Fen liquor, a traditional Chinese liquor. <i>Journal of Microbiology</i> , 2013, 51, 430-438.	1.3	61
536	Characterization of bacterial and archaeal communities in air-cathode microbial fuel cells, open circuit and sealed-off reactors. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9885-9895.	1.7	84
537	More refined diversity of anammox bacteria recovered and distribution in different ecosystems. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 3653-3663.	1.7	47
538	Investigating the Diversity of <i>Pseudomonas</i> spp. in Soil Using Culture Dependent and Independent Techniques. <i>Current Microbiology</i> , 2013, 67, 423-430.	1.0	20
539	Use of Pyrosequencing to Characterize the Microbiota in the Ileum of Goats Fed with Increasing Proportion of Dietary Grain. <i>Current Microbiology</i> , 2013, 67, 341-350.	1.0	42
540	Diversity of Chemotactic Heterotrophic Bacteria Associated with Arctic Cyanobacteria. <i>Current Microbiology</i> , 2013, 66, 64-71.	1.0	12
541	Analysis of the bacterial communities associated with different drinking water treatment processes. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 1573-1584.	1.7	48
542	Enrichment of lung microbiome with supraglottic taxa is associated with increased pulmonary inflammation. <i>Microbiome</i> , 2013, 1, 19.	4.9	355
543	Spatial pattern in Antarctica: what can we learn from Antarctic bacterial isolates?. <i>Extremophiles</i> , 2013, 17, 733-745.	0.9	17
544	Anammox bacterial populations in deep marine hypersaline gradient systems. <i>Extremophiles</i> , 2013, 17, 289-299.	0.9	41
545	Phoenix 2: A locally installable large-scale 16S rRNA gene sequence analysis pipeline with Web interface. <i>Journal of Biotechnology</i> , 2013, 167, 393-403.	1.9	53
546	Characterizing the microbiota across the gastrointestinal tract of a Brazilian Nelore steer. <i>Veterinary Microbiology</i> , 2013, 164, 307-314.	0.8	176
547	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU. , 2013, , .		1
548	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. <i>Letters in Applied Microbiology</i> , 2013, 57, 492-501.	1.0	90

#	ARTICLE	IF	CITATIONS
549	Temporal Bacterial Community Dynamics Vary Among Ulcerative Colitis Patients After Fecal Microbiota Transplantation. <i>American Journal of Gastroenterology</i> , 2013, 108, 1620-1630.	0.2	298
550	A Dried Yeast Fermentate Selectively Modulates both the Luminal and Mucosal Gut Microbiota and Protects against Inflammation, As Studied in an Integrated in Vitro Approach. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 9380-9392.	2.4	49
551	A non-phylogenetic alpha diversity approach on prokaryotic community structure in aquatic systems. <i>Ecological Indicators</i> , 2013, 29, 361-366.	2.6	9
552	Prevalence of Viral Photosynthetic and Capsid Protein Genes from Cyanophages in Two Large and Deep Perialpine Lakes. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7169-7178.	1.4	23
553	Histone deacetylase 3 coordinates commensal-bacteria-dependent intestinal homeostasis. <i>Nature</i> , 2013, 504, 153-157.	13.7	212
554	A newly designed degenerate PCR primer based on pmoA gene for detection of nitrite-dependent anaerobic methane-oxidizing bacteria from different ecological niches. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 10155-10162.	1.7	54
555	Nasal Microenvironments and Interspecific Interactions Influence Nasal Microbiota Complexity and <i>S.Âureus</i> Carriage. <i>Cell Host and Microbe</i> , 2013, 14, 631-640.	5.1	294
556	Biases in community structures of ammonia/ammonium-oxidizing microorganisms caused by insufficient DNA extractions from Baijiang soil revealed by comparative analysis of coastal wetland sediment and rice paddy soil. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8741-8756.	1.7	18
557	Structure-constrained sparse canonical correlation analysis with an application to microbiome data analysis. <i>Biostatistics</i> , 2013, 14, 244-258.	0.9	128
558	Cell Size Distributions of Soil Bacterial and Archaeal Taxa. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7610-7617.	1.4	98
559	Microbiota Modulate Behavioral and Physiological Abnormalities Associated with Neurodevelopmental Disorders. <i>Cell</i> , 2013, 155, 1451-1463.	13.5	2,596
560	Gut Microbiota from Twins Discordant for Obesity Modulate Metabolism in Mice. <i>Science</i> , 2013, 341, 1241214.	6.0	3,006
561	Microbial communities associated with the degradation of oak wood in the Blanes submarine canyon and its adjacent open slope (NW Mediterranean). <i>Progress in Oceanography</i> , 2013, 118, 137-143.	1.5	26
562	Topics in Applied Statistics. <i>Springer Proceedings in Mathematics and Statistics</i> , 2013, , .	0.1	2
563	<i>Rhodobacteraceae</i> are the key members of the microbial community of the initial biofilm formed in Eastern Mediterranean coastal seawater. <i>FEMS Microbiology Ecology</i> , 2013, 85, 348-357.	1.3	229
564	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013, 23, 1704-1714.	2.4	352
565	mPUMA: a computational approach to microbiota analysis by de novo assembly of operational taxonomic units based on protein-coding barcode sequences. <i>Microbiome</i> , 2013, 1, 23.	4.9	29
566	Molecular diversity of rumen bacterial communities from tannin-rich and fiber-rich forage fed domestic Sika deer (<i>Cervus nippon</i>) in China. <i>BMC Microbiology</i> , 2013, 13, 151.	1.3	81

#	ARTICLE	IF	CITATIONS
567	Community differentiation of the cutaneous microbiota in psoriasis. <i>Microbiome</i> , 2013, 1, 31.	4.9	353
568	Culture dependent and independent analysis of bacterial communities associated with commercial salad leaf vegetables. <i>BMC Microbiology</i> , 2013, 13, 274.	1.3	176
569	Utilizing novel diversity estimators to quantify multiple dimensions of microbial biodiversity across domains. <i>BMC Microbiology</i> , 2013, 13, 259.	1.3	9
570	Genome-wide mapping of gene-microbiota interactions in susceptibility to autoimmune skin blistering. <i>Nature Communications</i> , 2013, 4, 2462.	5.8	87
571	Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. <i>Journal of Applied Microbiology</i> , 2013, 115, 1147-1158.	1.4	209
572	Human gut microbiota community structures in urban and rural populations in Russia. <i>Nature Communications</i> , 2013, 4, 2469.	5.8	233
573	The nonfermentable dietary fiber hydroxypropyl methylcellulose modulates intestinal microbiota. <i>FASEB Journal</i> , 2013, 27, 692-702.	0.2	78
574	Alterations in the Gut Microbiota Associated with HIV-1 Infection. <i>Cell Host and Microbe</i> , 2013, 14, 329-339.	5.1	387
575	A meta-analysis of changes in bacterial and archaeal communities with time. <i>ISME Journal</i> , 2013, 7, 1493-1506.	4.4	322
576	Microbial characterization of basalt formation waters targeted for geological carbon sequestration. <i>FEMS Microbiology Ecology</i> , 2013, 85, 62-73.	1.3	28
577	Differential abundance analysis for microbial marker-gene surveys. <i>Nature Methods</i> , 2013, 10, 1200-1202.	9.0	1,921
578	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
579	Changes in Soil Bacterial Community Structure with Increasing Disturbance Frequency. <i>Microbial Ecology</i> , 2013, 66, 171-181.	1.4	57
580	Microbial community composition and endolith colonization at an active rctic thermal spring are driven by calcite precipitation. <i>Environmental Microbiology Reports</i> , 2013, 5, 648-659.	1.0	14
581	Diversity and heritability of the maize rhizosphere microbiome under field conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6548-6553.	3.3	1,594
582	The Gut Microbiome Modulates Colon Tumorigenesis. <i>MBio</i> , 2013, 4, e00692-13.	1.8	582
583	Water mass and depth determine the distribution and diversity of Rhodobacterales in an Arctic marine system. <i>FEMS Microbiology Ecology</i> , 2013, 84, 564-576.	1.3	20
584	Higher seasonal variation of actinobacterial communities than spatial heterogeneity in the surface sediments of Taihu Lake, China. <i>Canadian Journal of Microbiology</i> , 2013, 59, 353-358.	0.8	3

#	ARTICLE	IF	CITATIONS
585	Human Analysts at Superhuman Scales: What Has Friendly Software To Do?. <i>Big Data</i> , 2013, 1, 227-236.	2.1	1
586	Studying the microbiology of the indoor environment. <i>Genome Biology</i> , 2013, 14, 202.	13.9	129
587	Olfactory receptor responding to gut microbiota-derived signals plays a role in renin secretion and blood pressure regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4410-4415.	3.3	893
588	Reactor performance in terms of COD and nitrogen removal and bacterial community structure of a three-stage rotating bioelectrochemical contactor. <i>Water Research</i> , 2013, 47, 881-894.	5.3	82
589	Surveying the Microbiome of Ants: Comparing 454 Pyrosequencing with Traditional Methods To Uncover Bacterial Diversity. <i>Applied and Environmental Microbiology</i> , 2013, 79, 525-534.	1.4	122
590	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 57-59.	9.0	3,402
591	Global biogeography of highly diverse protistan communities in soil. <i>ISME Journal</i> , 2013, 7, 652-659.	4.4	412
592	Distinct cutaneous bacterial assemblages in a sampling of South American Amerindians and US residents. <i>ISME Journal</i> , 2013, 7, 85-95.	4.4	101
593	Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. <i>ISME Journal</i> , 2013, 7, 173-183.	4.4	41
594	Biogeography of bacterial communities exposed to progressive long-term environmental change. <i>ISME Journal</i> , 2013, 7, 937-948.	4.4	330
595	The gut microbiota, obesity and insulin resistance. <i>Molecular Aspects of Medicine</i> , 2013, 34, 39-58.	2.7	506
596	Bacteria and diatom co-occurrence patterns in microbial mats from polar desert streams. <i>Environmental Microbiology</i> , 2013, 15, 1115-1131.	1.8	44
597	Temporal dynamics and phylogenetic diversity of free-living and particle-associated <i>Verrucomicrobia</i> communities in relation to environmental variables in a mesotrophic lake. <i>FEMS Microbiology Ecology</i> , 2013, 83, 189-201.	1.3	50
598	Emission of nitrous oxide and dinitrogen by diverse earthworm families from Brazil and resolution of associated denitrifying and nitrate-dissimilating taxa. <i>FEMS Microbiology Ecology</i> , 2013, 83, 375-391.	1.3	45
599	Prevalence and diversity of <i>Synergistetes</i> taxa in periodontal health and disease. <i>Journal of Periodontal Research</i> , 2013, 48, 159-168.	1.4	37
600	The role of biogeography in shaping diversity of the intestinal microbiota in house mice. <i>Molecular Ecology</i> , 2013, 22, 1904-1916.	2.0	171
601	Substrate induced emergence of different active bacterial and archaeal assemblages during biomethane production. <i>Bioresource Technology</i> , 2013, 148, 517-524.	4.8	29
602	Microbial community changes with decaying chloramine residuals in a lab-scale system. <i>Water Research</i> , 2013, 47, 4666-4679.	5.3	69

#	ARTICLE	IF	CITATIONS
603	Patterns and Processes of Microbial Community Assembly. <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 342-356.	2.9	1,325
604	Phylogenetic detection of novel <i>Cryptomycota</i> in an <i>Isoetes</i> (<i>Utricularia</i>) Tj ETQq1 1 0.784314 rgBT / Dv high-throughput sequencing sets. <i>Environmental Microbiology</i> , 2013, 15, 2333-2341.	1.8	37
605	The effect of coal oxidation on methane production and microbial community structure in Powder River Basin coal. <i>International Journal of Coal Geology</i> , 2013, 115, 71-78.	1.9	55
606	Spatial patterns of bacterial community composition within Lake Erie sediments. <i>Journal of Great Lakes Research</i> , 2013, 39, 344-351.	0.8	24
607	Microbial effects on the release and attenuation of arsenic in the shallow subsurface of a natural geochemical anomaly. <i>Environmental Pollution</i> , 2013, 180, 84-91.	3.7	21
608	Establishing a relationship between bacteria in the human gut and Complex Regional Pain Syndrome. <i>Brain, Behavior, and Immunity</i> , 2013, 29, 62-69.	2.0	18
609	Fecal Microbiome and Volatile Organic Compound Metabolome in Obese Humans With Nonalcoholic Fatty Liver Disease. <i>Clinical Gastroenterology and Hepatology</i> , 2013, 11, 868-875.e3.	2.4	564
610	Spatial uniformity of microbial diversity in a continuous bioelectrochemical system. <i>Bioresource Technology</i> , 2013, 129, 599-605.	4.8	35
611	A comparison of microbial communities in deep-sea polymetallic nodules and the surrounding sediments in the Pacific Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2013, 79, 40-49.	0.6	54
612	Bacterial census of poultry intestinal microbiome. <i>Poultry Science</i> , 2013, 92, 671-683.	1.5	375
613	Stool substitute transplant therapy for the eradication of <i>Clostridium difficile</i> infection: â€œRePOOPulatingâ€™ the gut. <i>Microbiome</i> , 2013, 1, 3.	4.9	621
614	Geographic distance and ecosystem size determine the distribution of smallest protists in lacustrine ecosystems. <i>FEMS Microbiology Ecology</i> , 2013, 85, 85-94.	1.3	51
615	Microbial composition affects the functioning of estuarine sediments. <i>ISME Journal</i> , 2013, 7, 868-879.	4.4	130
616	Genetic Control of Obesity and Gut Microbiota Composition in Response to High-Fat, High-Sucrose Diet in Mice. <i>Cell Metabolism</i> , 2013, 17, 141-152.	7.2	464
617	Fecal microbiota diversity in survivors of adolescent/young adult Hodgkin lymphoma: a study of twins. <i>British Journal of Cancer</i> , 2013, 108, 1163-1167.	2.9	45
618	Variations in Diversity and Richness of Gut Bacterial Communities of Termites (<i>Reticulitermes flavipes</i>) Fed with Grassy and Woody Plant Substrates. <i>Microbial Ecology</i> , 2013, 65, 531-536.	1.4	61
619	Distinct but Closely Related Sebaciniales form Mycorrhizae with Coexisting Ericaceae and Orchidaceae in a Neotropical Mountain Area. <i>Soil Biology</i> , 2013, , 81-105.	0.6	8
620	Loss in microbial diversity affects nitrogen cycling in soil. <i>ISME Journal</i> , 2013, 7, 1609-1619.	4.4	603

#	ARTICLE	IF	CITATIONS
621	Temporal variability in soil microbial communities across land-use types. <i>ISME Journal</i> , 2013, 7, 1641-1650.	4.4	408
622	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.	1.4	22
623	Compression-based distance (CBD): a simple, rapid, and accurate method for microbiota composition comparison. <i>BMC Bioinformatics</i> , 2013, 14, 136.	1.2	5
624	Phylogenetic beta diversity in bacterial assemblages across ecosystems: deterministic versus stochastic processes. <i>ISME Journal</i> , 2013, 7, 1310-1321.	4.4	515
625	Pyrosequencing Analysis of the Salivary Microbiota of Healthy Chinese Children and Adults. <i>Microbial Ecology</i> , 2013, 65, 487-495.	1.4	55
626	Arbuscular mycorrhizal fungi associated with a single agronomic plant host across the landscape: Community differentiation along a soil textural gradient. <i>Soil Biology and Biochemistry</i> , 2013, 64, 191-199.	4.2	41
627	Dynamics of ammonia-oxidizing Archaea and Bacteria in contrasted freshwater ecosystems. <i>Research in Microbiology</i> , 2013, 164, 360-370.	1.0	47
628	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.	1.4	90
629	Alpine and Arctic Soil Microbial Communities. , 2013, , 43-55.		9
630	Changes in assembly processes in soil bacterial communities following a wildfire disturbance. <i>ISME Journal</i> , 2013, 7, 1102-1111.	4.4	354
631	Phylogenetic beta diversity of angiosperms in North America. <i>Global Ecology and Biogeography</i> , 2013, 22, 1152-1161.	2.7	56
632	Biodiversity and evolutionary history: useful extensions of the PD phylogenetic diversity assessment framework. <i>Annals of the New York Academy of Sciences</i> , 2013, 1289, 69-89.	1.8	56
633	<i>In situ</i> chemistry and microbial community compositions in five deep-sea hydrothermal fluid samples from Iriana in the Logatchev field. <i>Environmental Microbiology</i> , 2013, 15, 1551-1560.	1.8	47
635	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <i>ISME Journal</i> , 2013, 7, 50-60.	4.4	198
636	Influence of oxic/anoxic fluctuations on ammonia oxidizers and nitrification potential in a wet tropical soil. <i>FEMS Microbiology Ecology</i> , 2013, 85, 179-194.	1.3	62
637	Methyl Coenzyme M Reductase A (mcrA) Gene-Based Investigation of Methanogens in the Mudflat Sediments of Yangtze River Estuary, China. <i>Microbial Ecology</i> , 2013, 66, 257-267.	1.4	49
638	A Guide to Enterotypes across the Human Body: Meta-Analysis of Microbial Community Structures in Human Microbiome Datasets. <i>PLoS Computational Biology</i> , 2013, 9, e1002863.	1.5	446
639	Early Diet Impacts Infant Rhesus Gut Microbiome, Immunity, and Metabolism. <i>Journal of Proteome Research</i> , 2013, 12, 2833-2845.	1.8	90

#	ARTICLE	IF	CITATIONS
640	Microbial community analysis of deeply buried marine sediments of the New Jersey shallow shelf (IODP Tj ETQq0 0,0rgBT /Overlock 10	1.3	41
641	Measuring and Estimating Species Richness, Species Diversity, and Biotic Similarity from Sampling Data. , 2013, , 195-211.		307
642	Integrating niche-based process and spatial process in biogeography of magnetotactic bacteria. Scientific Reports, 2013, 3, 1643.	1.6	68
643	A global perspective on marine photosynthetic picoeukaryote community structure. ISME Journal, 2013, 7, 922-936.	4.4	75
644	Association of gut microbiota with post-operative clinical course in Crohn's disease. BMC Gastroenterology, 2013, 13, 131.	0.8	95
645	Diversity, dynamic and abundance of Geobacteraceae species in paddy soil following slurry incubation. European Journal of Soil Biology, 2013, 56, 11-18.	1.4	32
646	Contemporary environmental variation determines microbial diversity patterns in acid mine drainage. ISME Journal, 2013, 7, 1038-1050.	4.4	348
647	Probiotic Dosing of Ruminococcus flavefaciens Affects Rumen Microbiome Structure and Function in Reindeer. Microbial Ecology, 2013, 66, 840-849.	1.4	15
648	Gut Microbiome Perturbations Induced by Bacterial Infection Affect Arsenic Biotransformation. Chemical Research in Toxicology, 2013, 26, 1893-1903.	1.7	73
649	Standard methods for research on <i>Apis mellifera</i> gut symbionts. Journal of Apicultural Research, 2013, 52, 1-24.	0.7	98
650	Widespread Colonization of the Lung by <i>Tropheryma whippelii</i> in HIV Infection. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1110-1117.	2.5	175
651	Impact of <i>Azospirillum</i> sp. B510 Inoculation on Rice-Associated Bacterial Communities in a Paddy Field. Microbes and Environments, 2013, 28, 487-490.	0.7	29
652	Elevated ground-level O ₃ negatively influences paddy methanogenic archaeal community. Scientific Reports, 2013, 3, 3193.	1.6	34
653	The bacterial community structure in an alkaline saline soil spiked with anthracene. Electronic Journal of Biotechnology, 2013, 16, .	1.2	10
654	Seasonal restructuring of the ground squirrel gut microbiota over the annual hibernation cycle. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2013, 304, R33-R42.	0.9	159
655	Probabilistic Inference of Biochemical Reactions in Microbial Communities from Metagenomic Sequences. PLoS Computational Biology, 2013, 9, e1002981.	1.5	17
656	Potentiostatically Poised Electrodes Mimic Iron Oxide and Interact with Soil Microbial Communities to Alter the Biogeochemistry of Arctic Peat Soils. Minerals (Basel, Switzerland), 2013, 3, 318-336.	0.8	10
657	Upper Arctic Ocean water masses harbor distinct communities of heterotrophic flagellates. Biogeosciences, 2013, 10, 4273-4286.	1.3	33

#	ARTICLE	IF	CITATIONS
658	The Role of Microbial Communities in Parturition: Is There Evidence of Association with Preterm Birth and Perinatal Morbidity and Mortality?. <i>American Journal of Perinatology</i> , 2013, 30, 613-624.	0.6	34
659	Surface Microbes in the Neonatal Intensive Care Unit: Changes with Routine Cleaning and over Time. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2617-2624.	1.8	73
660	Quantitation and Composition of Cutaneous Microbiota in Diabetic and Nondiabetic Men. <i>Journal of Infectious Diseases</i> , 2013, 207, 1105-1114.	1.9	90
661	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. <i>Journal of Experimental Medicine</i> , 2013, 210, 2011-2024.	4.2	144
662	Data report: microbial diversity in sediment near Grizzly Bare Seamount in Holes U1363B and U1363G. <i>Proceedings of the Integrated Ocean Drilling Program Integrated Ocean Drilling Program</i> , 0, , .	1.0	1
663	Microbial Diversity and Structure Are Drivers of the Biological Barrier Effect against <i>Listeria monocytogenes</i> in Soil. <i>PLoS ONE</i> , 2013, 8, e76991.	1.1	94
664	Distinct Distal Gut Microbiome Diversity and Composition in Healthy Children from Bangladesh and the United States. <i>PLoS ONE</i> , 2013, 8, e53838.	1.1	278
665	Fungi of the Murine Gut: Episodic Variation and Proliferation during Antibiotic Treatment. <i>PLoS ONE</i> , 2013, 8, e71806.	1.1	201
666	Facility-Specific "House" Microbiome Drives Microbial Landscapes of Artisan Cheesemaking Plants. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5214-5223.	1.4	232
667	Mineralogical Study of a Biologically-Based Treatment System That Removes Arsenic, Zinc and Copper from Landfill Leachate. <i>Minerals (Basel, Switzerland)</i> , 2013, 3, 427-449.	0.8	11
668	Unique Vaginal Microbiota That Includes an Unknown Mycoplasma-Like Organism Is Associated With <i>Trichomonas vaginalis</i> Infection. <i>Journal of Infectious Diseases</i> , 2013, 207, 1922-1931.	1.9	81
669	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.	1.2	38
670	Altered enteric microbiota ecology in interleukin 10-deficient mice during development and progression of intestinal inflammation. <i>Gut Microbes</i> , 2013, 4, 316-324.	4.3	126
671	Parallel changes of taxonomic interaction networks in lacustrine bacterial communities induced by a polymetallic perturbation. <i>Evolutionary Applications</i> , 2013, 6, 643-659.	1.5	30
672	Spatial patterns of bacterial and archaeal communities along the Romanche Fracture Zone (tropical) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.3	16
673	Complement modulates the cutaneous microbiome and inflammatory milieu. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15061-15066.	3.3	138
674	Exploring the maize rhizosphere microbiome in the field: A glimpse into a highly complex system. <i>Communicative and Integrative Biology</i> , 2013, 6, e25177.	0.6	31
675	Molecular Analysis of Bacterial and Circovirus Bioaerosols in Concentrated Animal Feeding Operations. <i>Aerosol Science and Technology</i> , 2013, 47, 755-766.	1.5	6

#	ARTICLE	IF	CITATIONS
676	Surprisingly extensive mixed phylogenetic and ecological signals among bacterial Operational Taxonomic Units. <i>Nucleic Acids Research</i> , 2013, 41, 5175-5188.	6.5	121
677	Collaborative cloud-enabled tools allow rapid, reproducible biological insights. <i>ISME Journal</i> , 2013, 7, 461-464.	4.4	19
678	Factors that drive variation among gut microbial communities. <i>Gut Microbes</i> , 2013, 4, 403-408.	4.3	24
679	Biphasic assembly of the murine intestinal microbiota during early development. <i>ISME Journal</i> , 2013, 7, 1112-1115.	4.4	142
680	High-resolution microbial community reconstruction by integrating short reads from multiple 16S rRNA regions. <i>Nucleic Acids Research</i> , 2013, 41, e205-e205.	6.5	46
681	Microbiome Assembly across Multiple Body Sites in Low-Birthweight Infants. <i>MBio</i> , 2013, 4, e00782-13.	1.8	147
682	<i>De novo</i> Semi-alignment of 16S rRNA Gene Sequences for Deep Phylogenetic Characterization of Next Generation Sequencing Data. <i>Microbes and Environments</i> , 2013, 28, 211-216.	0.7	76
683	Bacterial and Archaeal Diversity in an Iron-Rich Coastal Hydrothermal Field in Yamagawa, Kagoshima, Japan. <i>Microbes and Environments</i> , 2013, 28, 405-413.	0.7	10
684	Reduced diversity and changed bacterioplankton community composition do not affect utilization of dissolved organic matter in the Adriatic Sea. <i>Aquatic Microbial Ecology</i> , 2013, 71, 15-24.	0.9	13
685	Alteration of Intestinal Dysbiosis by Fecal Microbiota Transplantation Does not Induce Remission in Patients with Chronic Active Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 2155-2165.	0.9	216
686	Comparative molecular analysis of the prokaryotic diversity of two salt mine soils in southwest China. <i>Journal of Basic Microbiology</i> , 2013, 53, 942-952.	1.8	26
687	Histamineâ€2 Receptor Blockers Alter the Fecal Microbiota in Premature Infants. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2013, 56, 397-400.	0.9	94
688	Impact of Ethnicity, Geography, and Disease on the Microbiota in Health and Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 2906-2918.	0.9	79
689	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature <i>Populus deltoides</i> Trees. <i>PLoS ONE</i> , 2013, 8, e76382.	1.1	315
690	Molecular Characterization of the Bacterial Community in a Potato Phytosphere. <i>Microbes and Environments</i> , 2013, 28, 295-305.	0.7	19
691	Long-Term Experimental Nitrogen Deposition Alters the Composition of the Active Fungal Community in the Forest Floor. <i>Soil Science Society of America Journal</i> , 2013, 77, 1648-1658.	1.2	45
692	DNA from lake sediments reveals the long-term dynamics and diversity of <i>Synechococcus</i> assemblages. <i>Biogeosciences</i> , 2013, 10, 3817-3838.	1.3	42
693	Sputum Microbiota in Tuberculosis as Revealed by 16S rRNA Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e54574.	1.1	85

#	ARTICLE	IF	CITATIONS
694	Bacterial Diversity in Two Neonatal Intensive Care Units (NICUs). PLoS ONE, 2013, 8, e54703.	1.1	120
695	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.	1.1	76
696	Bacterial Communities Associated with the Surfaces of Fresh Fruits and Vegetables. PLoS ONE, 2013, 8, e59310.	1.1	366
697	phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. PLoS ONE, 2013, 8, e61217.	1.1	13,960
698	A Cross-Taxon Analysis of Insect-Associated Bacterial Diversity. PLoS ONE, 2013, 8, e61218.	1.1	157
699	Bacterial Community Profiling of Milk Samples as a Means to Understand Culture-Negative Bovine Clinical Mastitis. PLoS ONE, 2013, 8, e61959.	1.1	132
700	Phylogeny of Bacterial and Archaeal Genomes Using Conserved Genes: Supertrees and Supermatrices. PLoS ONE, 2013, 8, e62510.	1.1	138
701	Analyses of the Stability and Core Taxonomic Memberships of the Human Microbiome. PLoS ONE, 2013, 8, e63139.	1.1	184
702	Home Life: Factors Structuring the Bacterial Diversity Found within and between Homes. PLoS ONE, 2013, 8, e64133.	1.1	277
703	Monitoring Seasonal Changes in Winery-Resident Microbiota. PLoS ONE, 2013, 8, e66437.	1.1	167
704	Prospecting Environmental Mycobacteria: Combined Molecular Approaches Reveal Unprecedented Diversity. PLoS ONE, 2013, 8, e68648.	1.1	34
705	Exploring the Sources of Bacterial Spoilers in Beefsteaks by Culture-Independent High-Throughput Sequencing. PLoS ONE, 2013, 8, e70222.	1.1	176
706	Impact of Ileocecal Resection and Concomitant Antibiotics on the Microbiome of the Murine Jejunum and Colon. PLoS ONE, 2013, 8, e73140.	1.1	54
707	Tropical Aquatic Archaea Show Environment-Specific Community Composition. PLoS ONE, 2013, 8, e76321.	1.1	10
708	Diverse Vaginal Microbiomes in Reproductive-Age Women with Vulvovaginal Candidiasis. PLoS ONE, 2013, 8, e79812.	1.1	108
709	Reduced Incidence of Prevotella and Other Fermenters in Intestinal Microflora of Autistic Children. PLoS ONE, 2013, 8, e68322.	1.1	709
710	Microbial communities associated with ferromanganese nodules and the surrounding sediments. Frontiers in Microbiology, 2013, 4, 161.	1.5	46
711	The effects of high-tannin leaf litter from transgenic poplars on microbial communities in microcosm soils. Frontiers in Microbiology, 2013, 4, 290.	1.5	31

#	ARTICLE	IF	CITATIONS
712	Effect of Different Feed Structures and Bedding on the Horizontal Spread of <i>Campylobacter jejuni</i> within Broiler Flocks. <i>Agriculture (Switzerland)</i> , 2013, 3, 741-760.	1.4	11
713	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013, 2, e00458.	2.8	801
714	Analysis of Oropharyngeal Microbiota between the Patients with Bronchial Asthma and the Non-Asthmatic Persons. <i>Journal of Bacteriology and Virology</i> , 2013, 43, 270.	0.0	14
715	Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms. <i>Biogeosciences</i> , 2013, 10, 555-566.	1.3	60
716	Changes in Abundance of Oral Microbiota Associated with Oral Cancer. <i>PLoS ONE</i> , 2014, 9, e98741.	1.1	295
717	Structure, Composition and Metagenomic Profile of Soil Microbiomes Associated to Agricultural Land Use and Tillage Systems in Argentine Pampas. <i>PLoS ONE</i> , 2014, 9, e99949.	1.1	191
718	Phylogenetic Distribution of the Capsid Assembly Protein Gene (g20) of Cyanophages in Paddy Floodwaters in Northeast China. <i>PLoS ONE</i> , 2014, 9, e88634.	1.1	9
719	Diversity of Rumen Bacteria in Canadian Cervids. <i>PLoS ONE</i> , 2014, 9, e89682.	1.1	77
720	Fecal Microbial Composition of Ulcerative Colitis and Crohn's Disease Patients in Remission and Subsequent Exacerbation. <i>PLoS ONE</i> , 2014, 9, e90981.	1.1	100
721	Airborne Bacterial Communities in Residences: Similarities and Differences with Fungi. <i>PLoS ONE</i> , 2014, 9, e91283.	1.1	120
722	Persistence, Seasonal Dynamics and Pathogenic Potential of <i>Vibrio</i> Communities from Pacific Oyster Hemolymph. <i>PLoS ONE</i> , 2014, 9, e94256.	1.1	75
723	Toward Understanding the Dynamics of Microbial Communities in an Estuarine System. <i>PLoS ONE</i> , 2014, 9, e94449.	1.1	24
724	Analysis of Plant-Bacteria Interactions in Their Native Habitat: Bacterial Communities Associated with Wild Tobacco Are Independent of Endogenous Jasmonic Acid Levels and Developmental Stages. <i>PLoS ONE</i> , 2014, 9, e94710.	1.1	43
725	The Gut Microbial Community of Midas Cichlid Fish in Repeatedly Evolved Limnetic-Benthic Species Pairs. <i>PLoS ONE</i> , 2014, 9, e95027.	1.1	68
726	Short-Term Effect of Antibiotics on Human Gut Microbiota. <i>PLoS ONE</i> , 2014, 9, e95476.	1.1	272
727	Understanding Cultivar-Specificity and Soil Determinants of the Cannabis Microbiome. <i>PLoS ONE</i> , 2014, 9, e99641.	1.1	73
728	The Bias Associated with Amplicon Sequencing Does Not Affect the Quantitative Assessment of Bacterial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e99722.	1.1	45
729	Coupling Genetic and Chemical Microbiome Profiling Reveals Heterogeneity of Archaeome and Bacteriome in Subsurface Biofilms That Are Dominated by the Same Archaeal Species. <i>PLoS ONE</i> , 2014, 9, e99801.	1.1	28

#	ARTICLE	IF	CITATIONS
730	Bacterial Community Composition in the Gut Content and Ambient Sediment of Sea Cucumber <i>Apostichopus japonicus</i> Revealed by 16S rRNA Gene Pyrosequencing. PLoS ONE, 2014, 9, e100092.	1.1	79
731	Oral Microbiota Distinguishes Acute Lymphoblastic Leukemia Pediatric Hosts from Healthy Populations. PLoS ONE, 2014, 9, e102116.	1.1	61
732	Identification of the Microbiota in Carious Dentin Lesions Using 16S rRNA Gene Sequencing. PLoS ONE, 2014, 9, e103712.	1.1	75
733	Characterization of Microbiota Composition and Presence of Selected Antibiotic Resistance Genes in Carriage Water of Ornamental Fish. PLoS ONE, 2014, 9, e103865.	1.1	37
734	HLA-B27 and Human β 2-Microglobulin Affect the Gut Microbiota of Transgenic Rats. PLoS ONE, 2014, 9, e105684.	1.1	209
735	Microbial Communities in the Upper Respiratory Tract of Patients with Asthma and Chronic Obstructive Pulmonary Disease. PLoS ONE, 2014, 9, e109710.	1.1	74
736	Maternal Obesity Is Associated with Alterations in the Gut Microbiome in Toddlers. PLoS ONE, 2014, 9, e113026.	1.1	149
737	Succession and Replacement of Bacterial Populations in the Caecum of Egg Laying Hens over Their Whole Life. PLoS ONE, 2014, 9, e115142.	1.1	151
738	The Antipsychotic Olanzapine Interacts with the Gut Microbiome to Cause Weight Gain in Mouse. PLoS ONE, 2014, 9, e115225.	1.1	147
739	Investigation of bacterial diversity in the feces of cattle fed different diets ¹ . Journal of Animal Science, 2014, 92, 683-694.	0.2	134
740	Temporal dynamics in the ruminal microbiome of dairy cows during the transition period. Journal of Animal Science, 2014, 92, 4014-4022.	0.2	101
741	Early Methanogenic Colonisation in the Faeces of Meishan and Yorkshire Piglets as Determined by Pyrosequencing Analysis. Archaea, 2014, 2014, 1-10.	2.3	48
742	An Antimethanogenic Nutritional Intervention in Early Life of Ruminants Modifies Ruminal Colonization by Archaea. Archaea, 2014, 2014, 1-12.	2.3	78
743	Zooplankton diversity across three Red Sea reefs using pyrosequencing. Frontiers in Marine Science, 2014, 1, .	1.2	37
744	Spatial variations of community structures and methane cycling across a transect of Lei-Gong-Hou mud volcanoes in eastern Taiwan. Frontiers in Microbiology, 2014, 5, 121.	1.5	13
745	Two distinct microbial communities revealed in the sponge <i>Cinachyrella</i> . Frontiers in Microbiology, 2014, 5, 581.	1.5	42
746	MEAT SCIENCE AND MUSCLE BIOLOGY SYMPOSIUM: <i>Escherichia coli</i> O157:H7, diet, and fecal microbiome in beef cattle ¹² . Journal of Animal Science, 2014, 92, 1345-1355.	0.2	19
747	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. PeerJ, 2014, 2, e545.	0.9	535

#	ARTICLE	IF	CITATIONS
748	Tipping elements in the human intestinal ecosystem. <i>Nature Communications</i> , 2014, 5, 4344.	5.8	217
750	Meta-analyses of human gut microbes associated with obesity and IBD. <i>FEBS Letters</i> , 2014, 588, 4223-4233.	1.3	697
751	A high-throughput sequencing ecotoxicology study of freshwater bacterial communities and their responses to tebuconazole. <i>FEMS Microbiology Ecology</i> , 2014, 90, 563-574.	1.3	35
752	Probiotics and virulent human rotavirus modulate the transplanted human gut microbiota in gnotobiotic pigs. <i>Gut Pathogens</i> , 2014, 6, 39.	1.6	49
753	Diversity of Desulfobacteriaceae and Overall Activity of Sulfate-Reducing Microorganisms in and Around a Salt pan in a Southern California Coastal Wetland. <i>Wetlands</i> , 2014, 34, 969-977.	0.7	17
754	Effects of straw amendment and moisture on microbial communities in Chinese fluvo-aquic soil. <i>Journal of Soils and Sediments</i> , 2014, 14, 1829-1840.	1.5	91
755	The gut microbiota of Colombians differs from that of Americans, Europeans and Asians. <i>BMC Microbiology</i> , 2014, 14, 311.	1.3	178
756	Accelerating microbiomic big data analysis by spectral interpolation. , 2014, , .		0
757	Metagenomic analysis of size-fractionated picoplankton in a marine oxygen minimum zone. <i>ISME Journal</i> , 2014, 8, 187-211.	4.4	281
758	Indoor-Air Microbiome in an Urban Subway Network: Diversity and Dynamics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6760-6770.	1.4	141
759	A review of software for analyzing molecular sequences. <i>BMC Research Notes</i> , 2014, 7, 830.	0.6	63
760	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , 2014, 2, 30.	4.9	233
761	Reproducibility of pyrosequencing data for biodiversity assessment in complex communities. <i>Methods in Ecology and Evolution</i> , 2014, 5, 881-890.	2.2	40
762	Differences in Gastric Mucosal Microbiota Profiling in Patients with Chronic Gastritis, Intestinal Metaplasia, and Gastric Cancer Using Pyrosequencing Methods. <i>Helicobacter</i> , 2014, 19, 407-416.	1.6	253
763	Microbial cargo: do bacteria on symbiotic propagules reinforce the microbiome of lichens?. <i>Environmental Microbiology</i> , 2014, 16, 3743-3752.	1.8	78
764	In-depth analyses of deep subsurface sediments using 454-pyrosequencing reveals a reservoir of buried fungal communities at record-breaking depths. <i>FEMS Microbiology Ecology</i> , 2014, 90, 908-921.	1.3	40
765	Removal of Pharmaceuticals and Personal Care Products during Water Recycling: Microbial Community Structure and Effects of Substrate Concentration. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2440-2450.	1.4	37
766	Methanogen prevalence throughout the gastrointestinal tract of pre-weaned dairy calves. <i>Gut Microbes</i> , 2014, 5, 628-638.	4.3	32

#	ARTICLE	IF	CITATIONS
767	Waste Not, Want Not: Why Rarefying Microbiome Data Is Inadmissible. PLoS Computational Biology, 2014, 10, e1003531.	1.5	2,343
768	Interactions between Bacillus anthracis and Plants May Promote Anthrax Transmission. PLoS Neglected Tropical Diseases, 2014, 8, e2903.	1.3	40
769	Evaluation of Hand Bacteria as a Human Biometric Identifier. , 2014, , .		0
770	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. Frontiers in Microbiology, 2014, 5, 298.	1.5	130
771	Biogeography of anaerobic ammonia-oxidizing (anammox) bacteria. Frontiers in Microbiology, 2014, 5, 399.	1.5	160
772	Characterizing the avian gut microbiota: membership, driving influences, and potential function. Frontiers in Microbiology, 2014, 5, 223.	1.5	328
773	Soil bacterial community structure remains stable over a 5-year chronosequence of insect-induced tree mortality. Frontiers in Microbiology, 2014, 5, 681.	1.5	26
774	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. Frontiers in Microbiology, 2014, 5, 524.	1.5	70
775	Microbial eukaryote diversity in the marine oxygen minimum zone off northern Chile. Frontiers in Microbiology, 2014, 5, 543.	1.5	47
776	Biogeography rather than association with cyanobacteria structures symbiotic microbial communities in the marine sponge Petrosia ficiformis. Frontiers in Microbiology, 2014, 5, 529.	1.5	68
777	Site- and horizon-specific patterns of microbial community structure and enzyme activities in permafrost-affected soils of Greenland. Frontiers in Microbiology, 2014, 5, 541.	1.5	73
778	Bacterial communities in the rumen of Holstein heifers differ when fed orchardgrass as pasture vs. hay. Frontiers in Microbiology, 2014, 5, 689.	1.5	36
779	Captivity results in disparate loss of gut microbial diversity in closely related hosts. , 2014, 2, cou009-cou009.		132
780	GPU-Meta-Storms: computing the structure similarities among massive amount of microbial community samples using GPU. Bioinformatics, 2014, 30, 1031-1033.	1.8	20
781	Oligotyping reveals differences between gut microbiomes of free-ranging sympatric Namibian carnivores (Acinonyx jubatus, Canis mesomelas) on a bacterial species-like level. Frontiers in Microbiology, 2014, 5, 526.	1.5	43
782	Comparisons of the composition and biogeographic distribution of the bacterial communities occupying South African thermal springs with those inhabiting deep subsurface fracture water. Frontiers in Microbiology, 2014, 5, 679.	1.5	72
783	Effects of bacterial inoculants on the indigenous microbiome and secondary metabolites of chamomile plants. Frontiers in Microbiology, 2014, 5, 64.	1.5	123
784	A Compositional Look at the Human Gastrointestinal Microbiome and Immune Activation Parameters in HIV Infected Subjects. PLoS Pathogens, 2014, 10, e1003829.	2.1	343

#	ARTICLE	IF	CITATIONS
785	Late winter under ice pelagic microbial communities in the high Arctic Ocean and the impact of short-term exposure to elevated CO ₂ levels. <i>Frontiers in Microbiology</i> , 2014, 5, 490.	1.5	21
786	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. <i>BMC Microbiology</i> , 2014, 14, 189.	1.3	292
787	Linking Geology and Microbiology: Inactive Pockmarks Affect Sediment Microbial Community Structure. <i>PLoS ONE</i> , 2014, 9, e85990.	1.1	14
788	Seven-Valent Pneumococcal Conjugate Vaccine and Nasopharyngeal Microbiota in Healthy Children. <i>Emerging Infectious Diseases</i> , 2014, 20, 201-210.	2.0	88
789	Microbial diversity and community structure across environmental gradients in Bransfield Strait, Western Antarctic Peninsula. <i>Frontiers in Microbiology</i> , 2014, 5, 647.	1.5	63
790	Microbiome Composition by Pyrosequencing in Mesenteric Lymph Nodes of Rats with CCl ₄ -Induced Cirrhosis. <i>Journal of Innate Immunity</i> , 2014, 6, 263-271.	1.8	19
791	Temporal changes and the effect of subtherapeutic concentrations of antibiotics in the gut microbiota of swine. <i>FEMS Microbiology Ecology</i> , 2014, 90, 599-608.	1.3	75
792	Differing assemblage composition and dynamics in <i>T</i> -like myophages of two neighbouring subalpine lakes. <i>Freshwater Biology</i> , 2014, 59, 1577-1595.	1.2	14
793	A phylogenetic perspective on species diversity, β -diversity and biogeography for the microbial world. <i>Molecular Ecology</i> , 2014, 23, 5868-5876.	2.0	20
794	Correlates of gut community composition across an ant species (<i>Cephalotes</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 1284-1300.	2.0	82
795	Bacterial Communities of Traditional Salted and Fermented Seafoods from Jeju Island of Korea Using 16S rRNA Gene Clone Library Analysis. <i>Journal of Food Science</i> , 2014, 79, M927-34.	1.5	37
796	Altered Duodenal Microbiota Composition in Celiac Disease Patients Suffering From Persistent Symptoms on a Long-Term Gluten-Free Diet. <i>American Journal of Gastroenterology</i> , 2014, 109, 1933-1941.	0.2	156
797	Endolithic bacterial communities in rock coatings from K�rkevagge, Swedish Lapland. <i>FEMS Microbiology Ecology</i> , 2014, 90, n/a-n/a.	1.3	14
798	Intertidal epilithic bacteria diversity changes along a naturally occurring carbon dioxide and pH gradient. <i>FEMS Microbiology Ecology</i> , 2014, 89, 670-678.	1.3	41
799	Molecular Characterization of Prokaryotic Communities Associated with Lonar Crater Basalts. <i>Geomicrobiology Journal</i> , 2014, 31, 519-528.	1.0	20
800	Shifts in microbial community structure and function in light- and dark-grown biofilms driven by warming. <i>Environmental Microbiology</i> , 2014, 16, 2550-2567.	1.8	38
801	Major faecal microbiota shifts in composition and diversity with age in a geographically restricted cohort of mothers and their children. <i>FEMS Microbiology Ecology</i> , 2014, 87, 280-290.	1.3	144
802	Deodorization of pig slurry and characterization of bacterial diversity using 16S rDNA sequence analysis. <i>Journal of Microbiology</i> , 2014, 52, 918-929.	1.3	8

#	ARTICLE	IF	CITATIONS
803	Does urbanization shape bacterial community composition in urban park soils? A case study in 16 representative Chinese cities based on the pyrosequencing method. <i>FEMS Microbiology Ecology</i> , 2014, 87, 182-192.	1.3	80
804	Intestinal Epithelial Cell Toll-like Receptor 5 Regulates the Intestinal Microbiota to Prevent Low-Grade Inflammation and Metabolic Syndrome in Mice. <i>Gastroenterology</i> , 2014, 147, 1363-1377.e17.	0.6	231
805	Analysis of [FeFe]-hydrogenase genes for the elucidation of a hydrogen-producing bacterial community in paddy field soil. <i>FEMS Microbiology Letters</i> , 2014, 350, 249-256.	0.7	11
806	Characterization of growing bacterial populations in McMurdo Dry Valley soils through stable isotope probing with ¹⁸ O-water. <i>FEMS Microbiology Ecology</i> , 2014, 89, 415-425.	1.3	49
807	Algae-bacteria association inferred by 16S rDNA similarity in established microalgae cultures. <i>MicrobiologyOpen</i> , 2014, 3, 356-368.	1.2	30
808	Analysis of the factors affecting the formation of the microbiome associated with chronic osteomyelitis of the jaw. <i>Clinical Microbiology and Infection</i> , 2014, 20, O309-O317.	2.8	21
809	Effect of dietary forage sources on rumen microbiota, rumen fermentation and biogenic amines in dairy cows. <i>Journal of the Science of Food and Agriculture</i> , 2014, 94, 1886-1895.	1.7	74
810	Dietary Î±-mangostin, a xanthone from mangosteen fruit, exacerbates experimental colitis and promotes dysbiosis in mice. <i>Molecular Nutrition and Food Research</i> , 2014, 58, 1226-1238.	1.5	37
811	Marek's disease virus influences the core gut microbiome of the chicken during the early and late phases of viral replication. <i>FEMS Microbiology Ecology</i> , 2014, 90, 300-312.	1.3	38
812	Land-use influences the distribution and activity of high affinity CO-oxidizing bacteria associated to type I-coxL genotype in soil. <i>Frontiers in Microbiology</i> , 2014, 5, 271.	1.5	36
813	Changes in the Bacterial Community Structure in Stored Wormbed Leachate. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2014, 24, 105-113.	1.0	10
814	Community Dynamics and Activity of Ammonia-Oxidizing Prokaryotes in Intertidal Sediments of the Yangtze Estuary. <i>Applied and Environmental Microbiology</i> , 2014, 80, 408-419.	1.4	140
815	Microbiota of Human Breast Tissue. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3007-3014.	1.4	376
816	Bacterial community composition of chronic periodontitis and novel oral sampling sites for detecting disease indicators. <i>Microbiome</i> , 2014, 2, 32.	4.9	77
817	Bacterial associates of seed-parasitic wasps (Hymenoptera: Megastigmus). <i>BMC Microbiology</i> , 2014, 14, 224.	1.3	20
818	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014, 15, 531.	3.8	355
819	Altered microbiota associated with abnormal humoral immune responses to commensal organisms in enthesitis-related arthritis. <i>Arthritis Research and Therapy</i> , 2014, 16, 486.	1.6	176
820	Microbial shifts in the aging mouse gut. <i>Microbiome</i> , 2014, 2, 50.	4.9	354

#	ARTICLE	IF	CITATIONS
821	Randomized Open-Label Pilot Study of the Influence of Probiotics and the Gut Microbiome on Toxic Metal Levels in Tanzanian Pregnant Women and School Children. <i>MBio</i> , 2014, 5, e01580-14.	1.8	163
822	High-grain feeding alters caecal bacterial microbiota composition and fermentation and results in caecal mucosal injury in goats. <i>British Journal of Nutrition</i> , 2014, 112, 416-427.	1.2	95
823	Gut Microbial Community Structure and Complications After Kidney Transplantation. <i>Transplantation</i> , 2014, 98, 697-705.	0.5	131
824	Advances in Machine Learning for Processing and Comparison of Metagenomic Data. , 2014, , 295-329.		7
825	Microbial Community Stratification Controlled by the Subseafloor Fluid Flow and Geothermal Gradient at the Iheya North Hydrothermal Field in the Mid-Okinawa Trough (Integrated Ocean Drilling) <i>Tj ETQq0 0 Q.rgBT /Ovz</i> 10 T		
826	Human and Environmental Impacts on River Sediment Microbial Communities. <i>PLoS ONE</i> , 2014, 9, e97435.	1.1	115
827	Sampling locality is more detectable than taxonomy or ecology in the gut microbiota of the brood-parasitic Brown-headed Cowbird (<i>Molothrus ater</i>). <i>PeerJ</i> , 2014, 2, e321.	0.9	126
828	The Effect of Malnutrition on Norovirus Infection. <i>MBio</i> , 2014, 5, e01032-13.	1.8	50
829	Early life establishment of site-specific microbial communities in the gut. <i>Gut Microbes</i> , 2014, 5, 192-201.	4.3	55
830	Intravenous lipopolysaccharide challenge alters ruminal bacterial microbiota and disrupts ruminal metabolism in dairy cattle. <i>British Journal of Nutrition</i> , 2014, 112, 170-182.	1.2	25
831	Extraction of Moving Objects Using Frame Differencing, Ghost and Shadow Removal. , 2014, , .		7
832	The microbial contribution to macroecology. <i>Frontiers in Microbiology</i> , 2014, 5, 203.	1.5	106
833	Spatial Diversity of Bacterioplankton Communities in Surface Water of Northern South China Sea. <i>PLoS ONE</i> , 2014, 9, e113014.	1.1	17
834	Application of Bioinformatics in Microbial Ecology. <i>Advanced Materials Research</i> , 0, 955-959, 276-280.	0.3	0
835	Validation of IMP Dehydrogenase Inhibitors in a Mouse Model of Cryptosporidiosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 1603-1614.	1.4	56
836	Characterization of bacterial community shift in human Ulcerative Colitis patients revealed by Illumina based 16S rRNA gene amplicon sequencing. <i>Gut Pathogens</i> , 2014, 6, 22.	1.6	84
837	Indoor-Biofilter Growth and Exposure to Airborne Chemicals Drive Similar Changes in Plant Root Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4805-4813.	1.4	28
838	The amphibian skin-associated microbiome across species, space and life history stages. <i>Molecular Ecology</i> , 2014, 23, 1238-1250.	2.0	360

#	ARTICLE	IF	CITATIONS
839	Altered gut microbiota and activity in a murine model of autism spectrum disorders. <i>Brain, Behavior, and Immunity</i> , 2014, 37, 197-206.	2.0	366
840	Bacterial Communities in Soil Under Moss and Lichen-Moss Crusts. <i>Geomicrobiology Journal</i> , 2014, 31, 152-160.	1.0	28
841	Phylogenetic generalised dissimilarity modelling: a new approach to analysing and predicting spatial turnover in the phylogenetic composition of communities. <i>Ecography</i> , 2014, 37, 21-32.	2.1	51
842	Contrasting diversity of phycodnavirus signature genes in two large and deep western European lakes. <i>Environmental Microbiology</i> , 2014, 16, 759-773.	1.8	15
843	Community differentiation and population enrichment of <i>Sargasso Sea</i> bacterioplankton in the euphotic zone of a mesoscale mode-2 water eddy. <i>Environmental Microbiology</i> , 2014, 16, 871-887.	1.8	66
844	Seasonal variations in bacterial communities and antibiotic-resistant strains associated with green bottle flies (Diptera: Calliphoridae). <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4197-4208.	1.7	30
845	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.	1.4	28
846	16S rRNA Gene Pyrosequencing Reveals Shift in Patient Faecal Microbiota During High-Dose Chemotherapy as Conditioning Regimen for Bone Marrow Transplantation. <i>Microbial Ecology</i> , 2014, 67, 690-699.	1.4	120
847	Litter quality versus soil microbial community controls over decomposition: a quantitative analysis. <i>Oecologia</i> , 2014, 174, 283-294.	0.9	169
848	Microscale evidence for a high decrease of soil bacterial density and diversity by cropping. <i>Agronomy for Sustainable Development</i> , 2014, 34, 831-840.	2.2	41
849	Conversion from natural wetlands to paddy field alters the composition of soil bacterial communities in Sanjiang Plain, Northeast China. <i>Annals of Microbiology</i> , 2014, 64, 1395-1403.	1.1	15
850	How distinct are arbuscular mycorrhizal fungal communities associating with grapevines?. <i>Biology and Fertility of Soils</i> , 2014, 50, 667-674.	2.3	43
851	Use of Whole Genome Shotgun Metagenomics: A Practical Guide for the Microbiome-Minded Physician Scientist. <i>Seminars in Reproductive Medicine</i> , 2014, 32, 005-013.	0.5	19
852	Metagenomics Using Next-Generation Sequencing. <i>Methods in Molecular Biology</i> , 2014, 1096, 183-201.	0.4	77
853	Functional and phylogenetic similarity among communities. <i>Methods in Ecology and Evolution</i> , 2014, 5, 666-675.	2.2	53
854	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317.	2.0	311
855	<i>Environmental Microbiology</i> . <i>Methods in Molecular Biology</i> , 2014, , .	0.4	14
856	Effect of intermittent aeration cycle on nutrient removal and microbial community in a fluidized bed reactor-membrane bioreactor combo system. <i>Bioresource Technology</i> , 2014, 156, 195-205.	4.8	63

#	ARTICLE	IF	CITATIONS
857	Functional and Phylogenetic Ecology in R. Use R!, 2014, , .	0.3	374
858	Dynamics of ammonia-oxidizing archaea and bacteria in relation to nitrification along simulated dissolved oxygen gradient in sedimentâ€“water interface of the Jiulong river estuarine wetland, China. Environmental Earth Sciences, 2014, 72, 2225-2237.	1.3	20
859	Niche Differentiation of Ammonia-Oxidising Archaea (AOA) and Bacteria (AOB) in Response to Paper and Pulp Mill Effluent. Microbial Ecology, 2014, 67, 758-768.	1.4	8
860	Divergent Responses of Soil Fungi Functional Groups to Short-term Warming. Microbial Ecology, 2014, 68, 708-715.	1.4	85
861	Distinct Bacterial Communities Dominate Tropical and Temperate Zone Leaf Litter. Microbial Ecology, 2014, 67, 837-848.	1.4	50
862	Diversity and abundance of Bacteria and nirS-encoding denitrifiers associated with the Juan de Fuca Ridge hydrothermal system. Annals of Microbiology, 2014, 64, 1691-1705.	1.1	20
863	tree<scp>NODF</scp>: nestedness to phylogenetic, functional and other treeâ€“based diversity metrics. Methods in Ecology and Evolution, 2014, 5, 563-572.	2.2	27
864	Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. Journal of Biogeography, 2014, 41, 749-761.	1.4	162
865	Genetic host specificity of hepatitis E virus. Infection, Genetics and Evolution, 2014, 24, 127-139.	1.0	14
866	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. ISME Journal, 2014, 8, 493-503.	4.4	40
867	Respiratory Microbiota Dynamics following Streptococcus pneumoniae Acquisition in Young and Elderly Mice. Infection and Immunity, 2014, 82, 1725-1731.	1.0	26
868	Rumen bacterial community evaluated by 454 pyrosequencing and terminal restriction fragment length polymorphism analyses in dairy sheep fed marine algae. Journal of Dairy Science, 2014, 97, 1661-1669.	1.4	60
869	Life with compass: diversity and biogeography of magnetotactic bacteria. Environmental Microbiology, 2014, 16, 2646-2658.	1.8	99
870	Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. Journal of Biotechnology, 2014, 190, 30-39.	1.9	34
871	FXR is a molecular target for the effects of vertical sleeve gastrectomy. Nature, 2014, 509, 183-188.	13.7	810
872	Kefir fermented milk and kefiran promote growth of Bifidobacterium bifidum PRL2010 and modulate its gene expression. International Journal of Food Microbiology, 2014, 178, 50-59.	2.1	59
873	High throughput sequencing analysis of biogeographical distribution of bacterial communities in the black soils of northeast China. Soil Biology and Biochemistry, 2014, 70, 113-122.	4.2	450
874	Quantitative divergence of the bacterial root microbiota in <i>Arabidopsis thaliana</i> relatives. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 585-592.	3.3	539

#	ARTICLE	IF	CITATIONS
875	Mosquitoes rely on their gut microbiota for development. <i>Molecular Ecology</i> , 2014, 23, 2727-2739.	2.0	429
876	Microbial Community Dynamics and Stability during an Ammonia-Induced Shift to Syntrophic Acetate Oxidation. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3375-3383.	1.4	118
877	Methane emission and dynamics of methanotrophic and methanogenic communities in a flooded rice field ecosystem. <i>FEMS Microbiology Ecology</i> , 2014, 88, 195-212.	1.3	110
878	Atmospheric N Deposition Increases Bacterial Laccase-Like Multicopper Oxidases: Implications for Organic Matter Decay. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4460-4468.	1.4	46
879	River organic matter shapes microbial communities in the sediment of the Rhône prodelta. <i>ISME Journal</i> , 2014, 8, 2327-2338.	4.4	64
880	Spatial and temporal variations of microbial community in a mixed plug-flow loop reactor fed with dairy manure. <i>Microbial Biotechnology</i> , 2014, 7, 332-346.	2.0	60
881	Diversity and structure of bacterial communities associated with <i>Plectonochaete chrysosporium</i> during wood decay. <i>Environmental Microbiology</i> , 2014, 16, 2238-2252.	1.8	51
882	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. <i>Ecology</i> , 2014, 95, 3190-3202.	1.5	174
883	Response of Free-Living Nitrogen-Fixing Microorganisms to Land Use Change in the Amazon Rainforest. <i>Applied and Environmental Microbiology</i> , 2014, 80, 281-288.	1.4	104
884	AIEC pathobiont instigates chronic colitis in susceptible hosts by altering microbiota composition. <i>Gut</i> , 2014, 63, 1069-1080.	6.1	182
885	Specificity and transcriptional activity of microbiota associated with low and high microbial abundance sponges from the Red Sea. <i>Molecular Ecology</i> , 2014, 23, 1348-1363.	2.0	139
886	Exploring links between pH and bacterial community composition in soils from the Craibstone Experimental Farm. <i>FEMS Microbiology Ecology</i> , 2014, 87, 403-415.	1.3	154
887	Metaproteomics Analysis Reveals the Adaptation Process for the Chicken Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 478-485.	1.4	65
888	Conventional CD4+ T cells regulate IL-22-producing intestinal innate lymphoid cells. <i>Mucosal Immunology</i> , 2014, 7, 1045-1057.	2.7	64
889	Potato-associated arbuscular mycorrhizal fungal communities in the Peruvian Andes. <i>Mycorrhiza</i> , 2014, 24, 405-417.	1.3	56
890	Microbial mechanisms coupling carbon and phosphorus cycles in phosphorus-limited northern Adriatic Sea. <i>Science of the Total Environment</i> , 2014, 470-471, 1173-1183.	3.9	13
891	Microbiota-Generated Metabolites Promote Metabolic Benefits via Gut-Brain Neural Circuits. <i>Cell</i> , 2014, 156, 84-96.	13.5	1,615
892	Phylogenetic diversity of eukaryotic marine microbial plankton on the Scotian Shelf Northwestern Atlantic Ocean. <i>Journal of Plankton Research</i> , 2014, 36, 344-363.	0.8	29

#	ARTICLE	IF	CITATIONS
893	Phylogeny-based classification of microbial communities. <i>Bioinformatics</i> , 2014, 30, 449-456.	1.8	29
894	Planctomycetes in Lakes: Poor or Strong Competitors for Phosphorus?. <i>Applied and Environmental Microbiology</i> , 2014, 80, 819-828.	1.4	21
895	Community structure and distribution of planktonic ammonia-oxidizing archaea and bacteria in the Dongjiang River, China. <i>Research in Microbiology</i> , 2014, 165, 657-670.	1.0	15
896	Impact of a hormone-releasing intrauterine system on the vaginal microbiome: a prospective baboon model. <i>Journal of Medical Primatology</i> , 2014, 43, 89-99.	0.3	21
897	Changes in free-living bacterial community diversity reflect the magnitude of environmental variability. <i>FEMS Microbiology Ecology</i> , 2014, 87, 291-301.	1.3	40
898	GeoChip-based insights into the microbial functional gene repertoire of marine sponges (high) Tj ETQq1 1 0.784314 rgBT /Overlock 1011 832-843.	1.3	55
899	Faecal microbiota composition and host-microbe cross-talk following gastroenteritis and in postinfectious irritable bowel syndrome. <i>Gut</i> , 2014, 63, 1737-1745.	6.1	282
900	Evaluation of photo-reactive siderophore producing bacteria before, during and after a bloom of the dinoflagellate <i>Lingulodinium polyedrum</i> . <i>Metallomics</i> , 2014, 6, 1156-1163.	1.0	13
901	Type I interferon signalling in the intestinal epithelium affects Paneth cells, microbial ecology and epithelial regeneration. <i>Gut</i> , 2014, 63, 1921-1931.	6.1	84
902	Technology and Techniques for Microbial Ecology via DNA Sequencing. <i>Annals of the American Thoracic Society</i> , 2014, 11, S16-S20.	1.5	8
903	Biofouling and Microbial Communities in Membrane Distillation and Reverse Osmosis. <i>Environmental Science & Technology</i> , 2014, 48, 13155-13164.	4.6	75
904	New insights into <i>Oculina patagonica</i> coral diseases and their associated <i>Vibrio</i> spp. communities. <i>ISME Journal</i> , 2014, 8, 1794-1807.	4.4	54
905	Soil Microbial Responses to Increased Moisture and Organic Resources along a Salinity Gradient in a Polar Desert. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3034-3043.	1.4	171
906	Impacts of freshwater flushing on anammox community structure and activities in the New River Estuary, USA. <i>Aquatic Microbial Ecology</i> , 2014, 72, 17-31.	0.9	51
907	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E139-48.	3.3	791
908	The pathogen <i>Batrachochytrium dendrobatidis</i> disturbs the frog skin microbiome during a natural epidemic and experimental infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5049-58.	3.3	264
909	Assessing the impact of water treatment on bacterial biofilms in drinking water distribution systems using high-throughput DNA sequencing. <i>Chemosphere</i> , 2014, 117, 185-192.	4.2	35
910	Structural changes in the gut microbiome of constipated patients. <i>Physiological Genomics</i> , 2014, 46, 679-686.	1.0	271

#	ARTICLE	IF	CITATIONS
911	Vertebrate Decomposition Is Accelerated by Soil Microbes. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4920-4929.	1.4	84
912	Effect of postextraction algal residue supplementation on the ruminal microbiome of steers consuming low-quality forage ¹ . <i>Journal of Animal Science</i> , 2014, 92, 5063-5075.	0.2	20
913	Dynamics of Gut Microbiota in Autoimmune Lupus. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7551-7560.	1.4	250
914	Bacteria from Diverse Habitats Colonize and Compete in the Mouse Gut. <i>Cell</i> , 2014, 159, 253-266.	13.5	324
915	Investigation of bacterial and fungal diversity in tarag using high-throughput sequencing. <i>Journal of Dairy Science</i> , 2014, 97, 6085-6096.	1.4	61
916	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	6.0	751
917	Responsiveness of cardiometabolic-related microbiota to diet is influenced by host genetics. <i>Mammalian Genome</i> , 2014, 25, 583-599.	1.0	66
918	Effects of a nutrient additive on the density of functional bacteria and the microbial community structure of bioorganic fertilizer. <i>Bioresource Technology</i> , 2014, 172, 328-334.	4.8	13
919	Who's for dinner? High-throughput sequencing reveals bat dietary differentiation in a biodiversity hotspot where prey taxonomy is largely undescribed. <i>Molecular Ecology</i> , 2014, 23, 3605-3617.	2.0	71
920	<i>Lactobacillus rhamnosus</i> HN001 decreases the severity of necrotizing enterocolitis in neonatal mice and preterm piglets: evidence in mice for a role of TLR9. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 306, G1021-G1032.	1.6	103
921	Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2014, 45, 297-324.	3.8	592
922	Spatial heterogeneity and stability of bacterial community in the gastrointestinal tracts of broiler chickens. <i>Poultry Science</i> , 2014, 93, 1942-1950.	1.5	106
923	Temporal Dynamics of the Cecal Gut Microbiota of Juvenile Arctic Ground Squirrels: a Strong Litter Effect across the First Active Season. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4260-4268.	1.4	15
924	Investigation of ruminal bacterial diversity in dairy cattle fed supplementary monensin alone and in combination with fat, using pyrosequencing analysis. <i>Canadian Journal of Microbiology</i> , 2014, 60, 65-71.	0.8	22
925	Diet-Induced Alterations in Gut Microflora Contribute to Lethal Pulmonary Damage in TLR2/TLR4-Deficient Mice. <i>Cell Reports</i> , 2014, 8, 137-149.	2.9	43
927	Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology. , 2014, , .		241
928	Metrics and Models of Community Phylogenetics. , 2014, , 451-464.		23
929	SnapShot: The Human Microbiome. <i>Cell</i> , 2014, 158, 690-690.e1.	13.5	26

#	ARTICLE	IF	CITATIONS
930	Recovery of novel alkaline phosphatase-encoding genes (<i>phoX</i>) from eutrophic Lake Taihu. Canadian Journal of Microbiology, 2014, 60, 167-171.	0.8	21
931	Influence of Hand Rearing and Bird Age on the Fecal Microbiota of the Critically Endangered Kakapo. Applied and Environmental Microbiology, 2014, 80, 4650-4658.	1.4	42
932	Correlation between viral production and carbon mineralization under nitrate-reducing conditions in aquifer sediment. ISME Journal, 2014, 8, 1691-1703.	4.4	46
933	Endophytic fungal symbionts associated with gypsophilous plants. Botany, 2014, 92, 295-301.	0.5	26
934	Individual diet has sex-dependent effects on vertebrate gut microbiota. Nature Communications, 2014, 5, 4500.	5.8	464
935	Archaeal diversity patterns under the seafloor along geochemical gradients. Journal of Geophysical Research C: Biogeosciences, 2014, 119, 1770-1788.	1.3	4
937	Gastrointestinal microbiota of wild and inbred individuals of two house mouse subspecies assessed using high-throughput parallel pyrosequencing. Molecular Ecology, 2014, 23, 5048-5060.	2.0	66
938	Syntrophs Dominate Sequences Associated with the Mercury Methylation-Related Gene <i>hgcA</i> in the Water Conservation Areas of the Florida Everglades. Applied and Environmental Microbiology, 2014, 80, 6517-6526.	1.4	91
939	Comparative assessment of the bacterial communities associated with <i>Aedes aegypti</i> larvae and water from domestic water storage containers. Parasites and Vectors, 2014, 7, 391.	1.0	71
940	Characterization of the nasopharyngeal microbiota in health and during rhinovirus challenge. Microbiome, 2014, 2, 22.	4.9	107
941	Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. Microbiome, 2014, 2, 24.	4.9	81
942	Different pioneer plant species select specific rhizosphere bacterial communities in a high mountain environment. SpringerPlus, 2014, 3, 391.	1.2	34
943	Immunoglobulin A Coating Identifies Colitogenic Bacteria in Inflammatory Bowel Disease. Cell, 2014, 158, 1000-1010.	13.5	982
944	Data analysis for 16S microbial profiling from different benchtop sequencing platforms. Journal of Microbiological Methods, 2014, 107, 30-37.	0.7	221
945	A Hidden Pitfall in the Preparation of Agar Media Undermines Microorganism Cultivability. Applied and Environmental Microbiology, 2014, 80, 7659-7666.	1.4	192
946	Microbial Engineering of Floc Fe and Trace Element Geochemistry in a Circumneutral, Remote Lake. Environmental Science & Technology, 2014, 48, 6578-6587.	4.6	10
947	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. ISME Journal, 2014, 8, 2431-2444.	4.4	149
948	Minor Changes in Soil Bacterial and Fungal Community Composition Occur in Response to Monsoon Precipitation in a Semiarid Grassland. Microbial Ecology, 2014, 68, 370-378.	1.4	37

#	ARTICLE	IF	CITATIONS
949	New PCR primers based on <i>mcrA</i> gene for retrieving more anaerobic methanotrophic archaea from coastal reedbed sediments. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4663-4670.	1.7	8
950	Occurrence and diversity of nitrite-dependent anaerobic methane oxidation bacteria in the sediments of the South China Sea revealed by amplification of both 16S rRNA and <i>pmoA</i> genes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5685-5696.	1.7	80
951	Analyses of dryland biological soil crusts highlight lichens as an important regulator of microbial communities. <i>Biodiversity and Conservation</i> , 2014, 23, 1735-1755.	1.2	72
952	Strong functional stability of soil microbial communities under semiarid Mediterranean conditions and subjected to long-term shifts in baseline precipitation. <i>Soil Biology and Biochemistry</i> , 2014, 69, 223-233.	4.2	121
953	The soil carbon/nitrogen ratio and moisture affect microbial community structures in alkaline permafrost-affected soils with different vegetation types on the Tibetan plateau. <i>Research in Microbiology</i> , 2014, 165, 128-139.	1.0	112
954	Bacterial diversity associated with feeding dry forage at different dietary concentrations in the rumen contents of Mehshana buffalo (<i>Bubalus bubalis</i>) using 16S pyrotags. <i>Anaerobe</i> , 2014, 25, 31-41.	1.0	84
955	Recovering glycoside hydrolase genes from active tundra cellulolytic bacteria. <i>Canadian Journal of Microbiology</i> , 2014, 60, 469-476.	0.8	29
956	Airway Microbiome Dynamics in Exacerbations of Chronic Obstructive Pulmonary Disease. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2813-2823.	1.8	272
957	Effects of Season and Host Physiological State on the Diversity, Density, and Activity of the Arctic Ground Squirrel Cecal Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5611-5622.	1.4	87
958	Farming behaviour of reef fishes increases the prevalence of coral disease associated microbes and black band disease. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141032.	1.2	84
959	Impact of subacute ruminal acidosis on the diversity of liquid and solid-associated bacteria in the rumen of goats. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 669-680.	1.7	108
960	Molecular diversity of the ammonia-oxidizing bacteria community in disused tin-mining ponds located within Kampar, Perak, Malaysia. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 757-766.	1.7	5
961	Molecular diversity of the methanotrophic bacteria communities associated with disused tin-mining ponds in Kampar, Perak, Malaysia. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 2645-2653.	1.7	4
962	Merging metagenomics and geochemistry reveals environmental controls on biological diversity and evolution. <i>BMC Ecology</i> , 2014, 14, 16.	3.0	24
963	pH is a good predictor of the distribution of anoxygenic purple phototrophic bacteria in Arctic soils. <i>Soil Biology and Biochemistry</i> , 2014, 74, 193-200.	4.2	55
964	454 pyrosequencing reveals changes in the faecal microbiota of adults consuming <i>Lactobacillus casei</i> . <i>FEMS Microbiology Ecology</i> , 2014, 88, 612-622.	1.3	64
965	The nitrogen cycle in cryoconites: naturally occurring nitrification and denitrification granules on a glacier. <i>Environmental Microbiology</i> , 2014, 16, 3250-3262.	1.8	72
966	Spatial heterogeneity and co-occurrence patterns of human mucosal-associated intestinal microbiota. <i>ISME Journal</i> , 2014, 8, 881-893.	4.4	206

#	ARTICLE	IF	CITATIONS
967	Diversity and Community Structure of Primary Wood-Inhabiting Bacteria in Boreal Forest. <i>Geomicrobiology Journal</i> , 2014, 31, 315-324.	1.0	37
968	Analysis of Multiple Tsetse Fly Populations in Uganda Reveals Limited Diversity and Species-Specific Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4301-4312.	1.4	95
969	Communities of sediment ammonia-oxidizing bacteria along a coastal pollution gradient in the East China Sea. <i>Marine Pollution Bulletin</i> , 2014, 86, 147-153.	2.3	15
970	<i>Bifidobacterium longum</i> subsp. <i>infantis</i> in experimental necrotizing enterocolitis: alterations in inflammation, innate immune response, and the microbiota. <i>Pediatric Research</i> , 2014, 76, 326-333.	1.1	95
971	Pyrosequencing analysis of microbiota reveals that lactic acid bacteria are dominant in Korean flat fish fermented food, <i>gajami</i> - <i>sikhae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 1611-1618.	0.6	14
972	Neotropical Andes hot springs harbor diverse and distinct planktonic microbial communities. <i>FEMS Microbiology Ecology</i> , 2014, 89, 56-66.	1.3	21
973	Metatranscriptomics of the Human Oral Microbiome during Health and Disease. <i>MBio</i> , 2014, 5, e01012-14.	1.8	311
974	Patterns of phylogenetic beta diversity in China's grasslands in relation to geographical and environmental distance. <i>Basic and Applied Ecology</i> , 2014, 15, 416-425.	1.2	17
975	Bacterial community variations in an alfalfa-rice rotation system revealed by 16S rRNA gene 454-pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2014, 87, 650-663.	1.3	72
976	Wastewater Irrigation Increases the Abundance of Potentially Harmful Gammaproteobacteria in Soils in Mezquital Valley, Mexico. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5282-5291.	1.4	80
977	Pyrosequencing Analysis Yields Comprehensive Assessment of Microbial Communities in Pilot-Scale Two-Stage Membrane Biofilm Reactors. <i>Environmental Science & Technology</i> , 2014, 48, 7511-7518.	4.6	37
978	Differential distribution and abundance of diazotrophic bacterial communities across different soil niches using a gene-targeted clone library approach. <i>FEMS Microbiology Letters</i> , 2014, 360, 117-125.	0.7	40
979	Response of Soil-Associated Microbial Communities to Intrusion of Coal Mine-Derived Acid Mine Drainage. <i>Environmental Science & Technology</i> , 2014, 48, 8556-8563.	4.6	51
980	Effects of long-term differential fertilization on eukaryotic microbial communities in an arable soil: a multiple barcoding approach. <i>Molecular Ecology</i> , 2014, 23, 3341-3355.	2.0	163
981	Members of the human gut microbiota involved in recovery from <i>Vibrio cholerae</i> infection. <i>Nature</i> , 2014, 515, 423-426.	13.7	335
982	Arbuscular Mycorrhizal Fungal Communities Associated with <i>Vitis vinifera</i> Vines under Different Frequencies of Irrigation. <i>American Journal of Enology and Viticulture</i> , 2014, 65, 222-229.	0.9	13
983	Targeted 16S rRNA high-throughput sequencing to characterize microbial communities during composting of livestock mortalities. <i>Journal of Applied Microbiology</i> , 2014, 116, 1181-1194.	1.4	43
984	<i>Artemisia</i> supplementation differentially affects the mucosal and luminal ileal microbiota of diet-induced obese mice. <i>Nutrition</i> , 2014, 30, S26-S30.	1.1	9

#	ARTICLE	IF	CITATIONS
985	Impact of sampler selection on the characterization of the indoor microbiome via high-throughput sequencing. <i>Building and Environment</i> , 2014, 80, 274-282.	3.0	45
986	The source of inoculum plays a defining role in the development of MEC microbial consortia fed with acetic and propionic acid mixtures. <i>Journal of Biotechnology</i> , 2014, 182-183, 11-18.	1.9	52
987	Strong elevational trends in soil bacterial community composition on Mt. Halla, South Korea. <i>Soil Biology and Biochemistry</i> , 2014, 68, 140-149.	4.2	152
988	Mulching practices altered soil bacterial community structure and improved orchard productivity and apple quality after five growing seasons. <i>Scientia Horticulturae</i> , 2014, 172, 248-257.	1.7	92
989	Substrate type drives variation in reactor microbiomes of anaerobic digesters. <i>Bioresource Technology</i> , 2014, 151, 397-401.	4.8	68
990	Microbial diversities (16S and 18S rRNA gene pyrosequencing) and environmental pathogens within drinking water biofilms grown on the common premise plumbing materials unplasticized polyvinylchloride and copper. <i>FEMS Microbiology Ecology</i> , 2014, 88, 280-295.	1.3	67
991	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. <i>ISME Journal</i> , 2014, 8, 1989-2001.	4.4	221
992	Generation of colonic IgA-secreting cells in the caecal patch. <i>Nature Communications</i> , 2014, 5, 3704.	5.8	121
993	Is bacterial moisture niche a good predictor of shifts in community composition under long-term drought?. <i>Ecology</i> , 2014, 95, 110-122.	1.5	97
994	The Cockroach Origin of the Termite Gut Microbiota: Patterns in Bacterial Community Structure Reflect Major Evolutionary Events. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2261-2269.	1.4	229
995	rRNA-based monitoring of the microbiota involved in Fontina PDO cheese production in relation to different stages of cow lactation. <i>International Journal of Food Microbiology</i> , 2014, 185, 127-135.	2.1	46
996	Soil properties and tree species drive α -diversity of soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2014, 76, 201-209.	4.2	92
997	High-throughput sequencing shows inconsistent results with a microscope-based analysis of the soil prokaryotic community. <i>Soil Biology and Biochemistry</i> , 2014, 76, 53-56.	4.2	13
998	Microbial community composition is consistent across anaerobic digesters processing wheat-based fuel ethanol waste streams. <i>Bioresource Technology</i> , 2014, 157, 127-133.	4.8	19
999	Phylogenetic beta diversity, similarity, and differentiation measures based on Hill numbers. <i>Ecological Monographs</i> , 2014, 84, 21-44.	2.4	107
1000	Effects of Elevated Carbon Dioxide, Elevated Temperature, and Rice Growth Stage on the Community Structure of Rice Root-associated Bacteria. <i>Microbes and Environments</i> , 2014, 29, 184-190.	0.7	41
1001	Molecular Methods To Study Complex Microbial Communities. , 2014, , 323-345.		0
1002	Nitrogen cycling processes and microbial community composition in bed sediments in the Yukon River at Pilot Station. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2014, 119, 2328-2344.	1.3	42

#	ARTICLE	IF	CITATIONS
1003	High-Throughput Sequencing Characterizes Intertidal Meiofaunal Communities in Northern Gulf of Mexico (Dauphin Island and Mobile Bay, Alabama). <i>Biological Bulletin</i> , 2014, 227, 161-174.	0.7	32
1004	PATTERNS OF UNCULTURED BACTERIA PHYLA IN DIFFERENT WASTEWATER TREATMENT SLUDGES. <i>Journal of Japan Society of Civil Engineers Ser G (Environmental Research)</i> , 2014, 70, 42-52.	0.1	1
1005	The dynamics of biofilm bacterial communities is driven by flow wax and wane in a temporary stream. <i>Limnology and Oceanography</i> , 2014, 59, 2057-2067.	1.6	30
1006	Supervised method for periodontitis phenotypes prediction based on microbial composition using 16S rRNA sequences. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 214.	0.3	4
1007	Bacterial symbiont sharing in <i>Megalomyrmex</i> social parasites and their fungus-growing ant hosts. <i>Molecular Ecology</i> , 2015, 24, 3151-3169.	2.0	43
1008	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. <i>Springer Protocols</i> , 2015, , 89-113.	0.1	4
1009	Soy Protein Compared with Milk Protein in a Western Diet Increases Gut Microbial Diversity and Reduces Serum Lipids in Golden Syrian Hamsters. <i>Journal of Nutrition</i> , 2016, 146, 697-705.	1.3	80
1010	Characterization of Microbial Communities in Household Washing Machines. <i>Tenside, Surfactants, Detergents</i> , 2015, 52, 432-440.	0.5	34
1011	Dynamics of marine bacterial community diversity of the coastal waters of the reefs, inlets, and wastewater outfalls of southeast Florida. <i>MicrobiologyOpen</i> , 2015, 4, 390-408.	1.2	81
1012	Microbial eukaryotic diversity and distribution in a river plume and cyclonic eddy-influenced ecosystem in the South China Sea. <i>MicrobiologyOpen</i> , 2015, 4, 826-840.	1.2	12
1013	Community Analysis of Root- and Tuber-Associated Bacteria in Field-Grown Potato Plants Harboring Different Resistance Levels against Common Scab. <i>Microbes and Environments</i> , 2015, 30, 301-309.	0.7	34
1014	Characterization of Leaf Blade- and Leaf Sheath-Associated Bacterial Communities and Assessment of Their Responses to Environmental Changes in CO ₂ , Temperature, and Nitrogen Levels under Field Conditions. <i>Microbes and Environments</i> , 2015, 30, 51-62.	0.7	24
1015	Microbial ecology and geoelectric responses across a groundwater plume. <i>Interpretation</i> , 2015, 3, SAB9-SAB21.	0.5	3
1016	Fecal microbiota imbalance in Mexican children with type 1 diabetes. <i>Scientific Reports</i> , 2014, 4, 3814.	1.6	193
1017	The nasopharyngeal microbiota of feedlot cattle. <i>Scientific Reports</i> , 2015, 5, 15557.	1.6	64
1018	Variations of gastric corpus microbiota are associated with early esophageal squamous cell carcinoma and squamous dysplasia. <i>Scientific Reports</i> , 2015, 5, 8820.	1.6	85
1019	Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. <i>Scientific Reports</i> , 2015, 5, 14405.	1.6	499
1020	Annual periodicity in planktonic bacterial and archaeal community composition of eutrophic Lake Taihu. <i>Scientific Reports</i> , 2015, 5, 15488.	1.6	74

#	ARTICLE	IF	CITATIONS
1021	Increased diversity of egg-associated bacteria on brown trout (<i>Salmo trutta</i>) at elevated temperatures. <i>Scientific Reports</i> , 2015, 5, 17084.	1.6	29
1022	Investigation of Contamination Sources in a Small Urban Creek Using Microbial Source Tracking and Isotopic Analysis. , 2015, , .		0
1023	Potential applications of next generation DNA sequencing of 16S rRNA gene amplicons in microbial water quality monitoring. <i>Water Science and Technology</i> , 2015, 72, 1962-1972.	1.2	53
1024	Microbial Community Analysis Using High-Throughput Amplicon Sequencing. , 2015, , 2.4.2-1-2.4.2-26.		4
1025	Characterising the bacterial microbiota across the gastrointestinal tracts of dairy cattle: membership and potential function. <i>Scientific Reports</i> , 2015, 5, 16116.	1.6	495
1026	In situ environment rather than substrate type dictates microbial community structure of biofilms in a cold seep system. <i>Scientific Reports</i> , 2014, 4, 3587.	1.6	49
1027	Distinct composition of the oral indigenous microbiota in South Korean and Japanese adults. <i>Scientific Reports</i> , 2014, 4, 6990.	1.6	58
1028	In vitro characterisation of the fermentation profile and prebiotic capacity of gold-fleshed kiwifruit. <i>Beneficial Microbes</i> , 2015, 6, 829-839.	1.0	10
1029	Cecum microbial communities from steers differing in feed efficiency ^{1,2,3} . <i>Journal of Animal Science</i> , 2015, 93, 5327-5340.	0.2	58
1030	Spatial heterogeneity of gut microbiota reveals multiple bacterial communities with distinct characteristics. <i>Scientific Reports</i> , 2014, 4, 6185.	1.6	35
1031	Preen secretions encode information on MHC similarity in certain sex-dyads in a monogamous seabird. <i>Scientific Reports</i> , 2014, 4, 6920.	1.6	57
1032	Short Course in the Microbiome. <i>Journal of Circulating Biomarkers</i> , 2015, 4, 8.	0.8	9
1033	Pyridine-type alkaloid composition affects bacterial community composition of floral nectar. <i>Scientific Reports</i> , 2015, 5, 11536.	1.6	29
1034	Spatially extensive microbial biogeography of the Indian Ocean provides insights into the unique community structure of a pristine coral atoll. <i>Scientific Reports</i> , 2015, 5, 15383.	1.6	28
1035	Surveying the endomicrobiome and ectomicrobiome of bark beetles: The case of <i>Dendroctonus simplex</i> . <i>Scientific Reports</i> , 2015, 5, 17190.	1.6	51
1036	Inflammation-associated microbiota in pediatric eosinophilic esophagitis. <i>Microbiome</i> , 2015, 3, 23.	4.9	128
1037	Genetic associations and shared environmental effects on the skin microbiome of Korean twins. <i>BMC Genomics</i> , 2015, 16, 992.	1.2	61
1038	Protist diversity along a salinity gradient in a coastal lagoon. <i>Aquatic Microbial Ecology</i> , 2015, 74, 263-277.	0.9	82

#	ARTICLE	IF	CITATIONS
1039	Faecal microbiota characterisation of horses using 16 rdna barcoded pyrosequencing, and carriage rate of clostridium difficile at hospital admission. BMC Microbiology, 2015, 15, 181.	1.3	82
1040	An accurate and efficient experimental approach for characterization of the complex oral microbiota. Microbiome, 2015, 3, 48.	4.9	95
1041	Characterization of intestinal bacterial communities of western lowland gorillas (&i>Gorilla Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 forest elephant (&i>Loxodonta africana cyclotis&i>) living in Moukalaba-Doudou National Park in Gabon. Tropics, 2015, 23, 175-183.	0.2	11
1042	Resistivity and induced polarization monitoring of biogas combined with microbial ecology at a brownfield site. Interpretation, 2015, 3, SAB43-SAB56.	0.5	4
1043	Measuring similarity among plots including similarity among species: an extension of traditional approaches. Journal of Vegetation Science, 2015, 26, 1061-1067.	1.1	13
1044	Atmospheric N deposition alters connectance, but not functional potential among saprotrophic bacterial communities. Molecular Ecology, 2015, 24, 3170-3180.	2.0	41
1045	Alterations of the Subgingival Microbiota in Pediatric Crohn's Disease Studied Longitudinally in Discovery and Validation Cohorts. Inflammatory Bowel Diseases, 2015, 21, 2797-2805.	0.9	46
1046	Characterisation of the faecal metabolome and microbiome of Thoroughbred racehorses. Equine Veterinary Journal, 2015, 47, 580-586.	0.9	51
1047	<i>Lactobacillus rhamnosus</i> GG Dosage Affects the Adjuvanticity and Protection Against Rotavirus Diarrhea in Gnotobiotic Pigs. Journal of Pediatric Gastroenterology and Nutrition, 2015, 60, 834-843.	0.9	33
1048	The effect of antibiotics on the microbiome in acute exacerbations of chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2015, 5, 884-893.	1.5	38
1049	Fecal Microbiota Composition of Breast-Fed Infants Is Correlated With Human Milk Oligosaccharides Consumed. Journal of Pediatric Gastroenterology and Nutrition, 2015, 60, 825-833.	0.9	201
1050	Changes in soil nutrient content and bacterial community after 12%years of organic amendment application to a vineyard. European Journal of Soil Science, 2015, 66, 802-812.	1.8	49
1051	Relating belowground microbial composition to the taxonomic, phylogenetic, and functional trait distributions of trees in a tropical forest. Ecology Letters, 2015, 18, 1397-1405.	3.0	183
1052	Does Maternal Perinatal Probiotic Supplementation Alter the Intestinal Microbiota of Mother and Child?. Journal of Pediatric Gastroenterology and Nutrition, 2015, 61, 200-207.	0.9	88
1053	Potential Use of Bacterial Community Succession in Decaying Human Bone for Estimating Postmortem Interval[,][,]. Journal of Forensic Sciences, 2015, 60, 844-850.	0.9	104
1054	Diversity and antibiotic resistance profiles of Pseudomonads from a hospital wastewater treatment plant. Journal of Applied Microbiology, 2015, 119, 1527-1540.	1.4	31
1055	The Role of Curcumin in Modulating Colonic Microbiota During Colitis and Colon Cancer Prevention. Inflammatory Bowel Diseases, 2015, 21, 2483-2494.	0.9	166
1056	The Intestinal Microbiota in Acute Anorexia Nervosa and During Renourishment. Psychosomatic Medicine, 2015, 77, 969-981.	1.3	237

#	ARTICLE	IF	CITATIONS
1057	Enhanced salinities, as a proxy of seawater desalination discharges, impact coastal microbial communities of the eastern Mediterranean Sea. <i>Environmental Microbiology</i> , 2015, 17, 4105-4120.	1.8	33
1058	Composition Diversity and Abundance of Gut Microbiome in Prediabetes and Type 2 Diabetes. <i>Journal of Diabetes and Obesity</i> , 2015, 2, 108-114.	0.2	159
1059	Oral microbiome and history of smoking and colorectal cancer. <i>Journal of Epidemiological Research</i> , 2015, 2, 92-101.	0.6	58
1060	Determination of Algae and Macrophyte Species Distribution in Three Wastewater Stabilization Ponds Using Metagenomics Analysis. <i>Water (Switzerland)</i> , 2015, 7, 3225-3242.	1.2	11
1061	The Microbial Community of a Passive Biochemical Reactor Treating Arsenic, Zinc, and Sulfate-Rich Seepage. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 27.	2.0	88
1062	Milk- and solid-feeding practices and daycare attendance are associated with differences in bacterial diversity, predominant communities, and metabolic and immune function of the infant gut microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 3.	1.8	174
1063	Intestinal Microbial Dysbiosis and Colonic Epithelial Cell Hyperproliferation by Dietary β -Mangostin is Independent of Mouse Strain. <i>Nutrients</i> , 2015, 7, 764-784.	1.7	19
1064	The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. <i>Frontiers in Genetics</i> , 2015, 6, 348.	1.1	252
1065	Cropping systems modulate the rate and magnitude of soil microbial autotrophic CO ₂ fixation in soil. <i>Frontiers in Microbiology</i> , 2015, 6, 379.	1.5	47
1066	Standard filtration practices may significantly distort planktonic microbial diversity estimates. <i>Frontiers in Microbiology</i> , 2015, 6, 547.	1.5	65
1067	High resolution depth distribution of Bacteria, Archaea, methanotrophs, and methanogens in the bulk and rhizosphere soils of a flooded rice paddy. <i>Frontiers in Microbiology</i> , 2015, 6, 639.	1.5	116
1068	Primer and platform effects on 16S rRNA tag sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 771.	1.5	435
1069	Microbial mineral colonization across a subsurface redox transition zone. <i>Frontiers in Microbiology</i> , 2015, 6, 858.	1.5	20
1070	Response of bacterioplankton to iron fertilization of the Southern Ocean, Antarctica. <i>Frontiers in Microbiology</i> , 2015, 6, 863.	1.5	24
1071	Soil bacterial and fungal community responses to nitrogen addition across soil depth and microhabitat in an arid shrubland. <i>Frontiers in Microbiology</i> , 2015, 6, 891.	1.5	127
1072	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.	1.5	30
1073	Bacterial endophyte communities in the foliage of coast redwood and giant sequoia. <i>Frontiers in Microbiology</i> , 2015, 6, 1008.	1.5	49
1074	Evolutionary history influences the salinity preference of bacterial taxa in wetland soils. <i>Frontiers in Microbiology</i> , 2015, 6, 1013.	1.5	73

#	ARTICLE	IF	CITATIONS
1075	Patterns of benthic bacterial diversity in coastal areas contaminated by heavy metals, polycyclic aromatic hydrocarbons (PAHs) and polychlorinated biphenyls (PCBs). <i>Frontiers in Microbiology</i> , 2015, 6, 1053.	1.5	145
1076	Rumen microbial communities influence metabolic phenotypes in lambs. <i>Frontiers in Microbiology</i> , 2015, 6, 1060.	1.5	98
1077	Effects of sludge inoculum and organic feedstock on active microbial communities and methane yield during anaerobic digestion. <i>Frontiers in Microbiology</i> , 2015, 6, 1114.	1.5	40
1078	Responses of soil microeukaryotic communities to short-term fumigation-incubation revealed by MiSeq amplicon sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 1149.	1.5	23
1079	Resistance of Undisturbed Soil Microbiomes to Ceftriaxone Indicates Extended Spectrum β -Lactamase Activity. <i>Frontiers in Microbiology</i> , 2015, 6, 1233.	1.5	14
1080	Weak Coherence in Abundance Patterns Between Bacterial Classes and Their Constituent OTUs Along a Regulated River. <i>Frontiers in Microbiology</i> , 2015, 6, 1293.	1.5	14
1081	Comparative Gut Microbiota of 59 Neotropical Bird Species. <i>Frontiers in Microbiology</i> , 2015, 6, 1403.	1.5	216
1082	Deep Sequencing and Ecological Characterization of Gut Microbial Communities of Diverse Bumble Bee Species. <i>PLoS ONE</i> , 2015, 10, e0118566.	1.1	22
1083	The Unique Chemistry of Eastern Mediterranean Water Masses Selects for Distinct Microbial Communities by Depth. <i>PLoS ONE</i> , 2015, 10, e0120605.	1.1	65
1084	The Source of the River as a Nursery for Microbial Diversity. <i>PLoS ONE</i> , 2015, 10, e0120608.	1.1	44
1085	The Gut Microbiota Composition in Dichorionic Triplet Sets Suggests a Role for Host Genetic Factors. <i>PLoS ONE</i> , 2015, 10, e0122561.	1.1	35
1086	Patterns of Gut Bacterial Colonization in Three Primate Species. <i>PLoS ONE</i> , 2015, 10, e0124618.	1.1	50
1087	Microbial Diversity in a Permanently Cold and Alkaline Environment in Greenland. <i>PLoS ONE</i> , 2015, 10, e0124863.	1.1	45
1088	Exercise Is More Effective at Altering Gut Microbial Composition and Producing Stable Changes in Lean Mass in Juvenile versus Adult Male F344 Rats. <i>PLoS ONE</i> , 2015, 10, e0125889.	1.1	150
1089	The Effect of Sampling and Storage on the Fecal Microbiota Composition in Healthy and Diseased Subjects. <i>PLoS ONE</i> , 2015, 10, e0126685.	1.1	147
1090	Oral Administration of <i>P. gingivalis</i> Induces Dysbiosis of Gut Microbiota and Impaired Barrier Function Leading to Dissemination of Enterobacteria to the Liver. <i>PLoS ONE</i> , 2015, 10, e0134234.	1.1	252
1091	Rumen Microbiome from Steers Differing in Feed Efficiency. <i>PLoS ONE</i> , 2015, 10, e0129174.	1.1	307
1092	Litter Breakdown and Microbial Succession on Two Submerged Leaf Species in a Small Forested Stream. <i>PLoS ONE</i> , 2015, 10, e0130801.	1.1	21

#	ARTICLE	IF	CITATIONS
1093	Metabarcoding Analysis of Fungal Diversity in the Phyllosphere and Carposphere of Olive (<i>Olea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.1	123
1094	Genetic Variability of Bovine Viral Diarrhea Virus and Evidence for a Possible Genetic Bottleneck during Vertical Transmission in Persistently Infected Cattle. <i>PLoS ONE</i> , 2015, 10, e0131972.	1.1	23
1095	Assessment of Zooplankton Community Composition along a Depth Profile in the Central Red Sea. <i>PLoS ONE</i> , 2015, 10, e0133487.	1.1	30
1096	Temporal and Spatial Distribution of the Microbial Community of Winogradsky Columns. <i>PLoS ONE</i> , 2015, 10, e0134588.	1.1	32
1097	Rescue of Fructose-Induced Metabolic Syndrome by Antibiotics or Faecal Transplantation in a Rat Model of Obesity. <i>PLoS ONE</i> , 2015, 10, e0134893.	1.1	135
1098	Characterization of the Intestinal Lactobacilli Community following Galactooligosaccharides and Polydextrose Supplementation in the Neonatal Piglet. <i>PLoS ONE</i> , 2015, 10, e0135494.	1.1	21
1099	Characterization of Bacterial, Archaeal and Eukaryote Symbionts from Antarctic Sponges Reveals a High Diversity at a Three-Domain Level and a Particular Signature for This Ecosystem. <i>PLoS ONE</i> , 2015, 10, e0138837.	1.1	118
1100	Implementation of a Pan-Genomic Approach to Investigate Holobiont-Infesting Microbe Interaction: A Case Report of a Leukemic Patient with Invasive Mucormycosis. <i>PLoS ONE</i> , 2015, 10, e0139851.	1.1	47
1101	Flea-Associated Bacterial Communities across an Environmental Transect in a Plague-Endemic Region of Uganda. <i>PLoS ONE</i> , 2015, 10, e0141057.	1.1	16
1102	Impact of Water Chemistry, Pipe Material and Stagnation on the Building Plumbing Microbiome. <i>PLoS ONE</i> , 2015, 10, e0141087.	1.1	128
1103	Plant Invasions Associated with Change in Root-Zone Microbial Community Structure and Diversity. <i>PLoS ONE</i> , 2015, 10, e0141424.	1.1	64
1104	The Influence of Age and Gender on Skin-Associated Microbial Communities in Urban and Rural Human Populations. <i>PLoS ONE</i> , 2015, 10, e0141842.	1.1	181
1105	Antepartum Antibiotic Treatment Increases Offspring Susceptibility to Experimental Colitis: A Role of the Gut Microbiota. <i>PLoS ONE</i> , 2015, 10, e0142536.	1.1	137
1106	Design and Investigation of PolyFermS In Vitro Continuous Fermentation Models Inoculated with Immobilized Fecal Microbiota Mimicking the Elderly Colon. <i>PLoS ONE</i> , 2015, 10, e0142793.	1.1	59
1107	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. <i>PLoS ONE</i> , 2015, 10, e0142825.	1.1	84
1108	Oral Microbiota and Risk for Esophageal Squamous Cell Carcinoma in a High-Risk Area of China. <i>PLoS ONE</i> , 2015, 10, e0143603.	1.1	146
1109	Spatial Homogeneity of Bacterial Communities Associated with the Surface Mucus Layer of the Reef-Building Coral <i>Acropora palmata</i> . <i>PLoS ONE</i> , 2015, 10, e0143790.	1.1	20
1110	Fibrolytic Bacteria Isolated from the Rumen of North American Moose (<i>Alces alces</i>) and Their Use as a Probiotic in Neonatal Lambs. <i>PLoS ONE</i> , 2015, 10, e0144804.	1.1	22

#	ARTICLE	IF	CITATIONS
1111	Comparative Analysis of Prokaryotic Communities Associated with Organic and Conventional Farming Systems. <i>PLoS ONE</i> , 2015, 10, e0145072.	1.1	83
1112	Expression of the Blood-Group-Related Gene B4galnt2 Alters Susceptibility to Salmonella Infection. <i>PLoS Pathogens</i> , 2015, 11, e1005008.	2.1	50
1113	Non-Human Primates Harbor Diverse Mammalian and Avian Astroviruses Including Those Associated with Human Infections. <i>PLoS Pathogens</i> , 2015, 11, e1005225.	2.1	68
1114	Temporal Relationships Exist Between Cecum, Ileum, and Litter Bacterial Microbiomes in a Commercial Turkey Flock, and Subtherapeutic Penicillin Treatment Impacts Ileum Bacterial Community Establishment. <i>Frontiers in Veterinary Science</i> , 2015, 2, 56.	0.9	48
1115	<i>Salmonella enterica</i> Serovars Enteritidis Infection Alters the Indigenous Microbiota Diversity in Young Layer Chicks. <i>Frontiers in Veterinary Science</i> , 2015, 2, 61.	0.9	100
1116	Molecular Genetic Analysis of Wetland Soils. <i>Soil Science Society of America Book Series</i> , 0, , 349-372.	0.3	3
1117	Bacterial Communities in Neonatal Feces are Similar to Mothersâ€™ Placentae. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2015, 26, 90-94.	0.7	40
1118	The effect of copper sulfate addition on the performance of an anaerobic digester treating dairy manure. , 2015, , .		0
1119	The effect of polydextrose and probiotic lactobacilli in a <i>Clostridium difficile</i> infected human colonic model. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 27988.	3.8	16
1120	Bioinformation and TM Omic Approaches for Characterization of Environmental Microorganisms. , 2015, , 483-505.		4
1121	Gut bacteria in children with autism spectrum disorders: challenges and promise of studying how a complex community influences a complex disease. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 26914.	3.8	105
1122	Metagenomic Analysis of Chicken Gut Microbiota for Improving Metabolism and Health of Chickens â€™ A Review. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015, 28, 1217-1225.	2.4	90
1123	Microbial Forensic Analysis of Bacterial Fingerprint by Sequence Comparison of 16S rRNA Gene. <i>Journal of Forensics Research</i> , 2015, 06, .	0.1	2
1124	Effect of different heterotrophic plate count methods on the estimation of the composition of the culturable microbial community. <i>PeerJ</i> , 2015, 3, e862.	0.9	27
1125	Diversity in gut bacterial community of school-age children in Asia. <i>Scientific Reports</i> , 2015, 5, 8397.	1.6	221
1126	Monitoring the dynamics of syntrophic Î²-oxidizing bacteria during anaerobic degradation of oleic acid by quantitative PCR. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	41
1127	Temperature sensitivity of soil bacterial community along contrasting warming gradient. <i>Applied Soil Ecology</i> , 2015, 94, 40-48.	2.1	77
1128	Variation in koala microbiomes within and between individuals: effect of body region and captivity status. <i>Scientific Reports</i> , 2015, 5, 10189.	1.6	78

#	ARTICLE	IF	CITATIONS
1129	Microbial biogeography of the transnational fermented milk matsoni. <i>Food Microbiology</i> , 2015, 50, 12-19.	2.1	47
1130	Unexpected diversity of basidiomycetous endophytes in sapwood and leaves of <i>Hevea</i> . <i>Mycologia</i> , 2015, 107, 284-297.	0.8	73
1131	Soil pH and biome are both key determinants of soil archaeal community structure. <i>Soil Biology and Biochemistry</i> , 2015, 88, 1-8.	4.2	94
1132	Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBl.S12462.	1.0	317
1133	The Bamboo-Eating Giant Panda Harbors a Carnivore-Like Gut Microbiota, with Excessive Seasonal Variations. <i>MBio</i> , 2015, 6, e00022-15.	1.8	282
1134	Bio-electrochemical characterization of air-cathode microbial fuel cells with microporous polyethylene/silica membrane as separator. <i>Bioelectrochemistry</i> , 2015, 106, 115-124.	2.4	18
1135	Aerobic biodegradation of organic compounds in hydraulic fracturing fluids. <i>Biodegradation</i> , 2015, 26, 271-287.	1.5	83
1136	Targeted disruption of CD1d prevents NKT cell development in pigs. <i>Mammalian Genome</i> , 2015, 26, 264-270.	1.0	20
1137	Shifts in the phylogenetic structure of arbuscular mycorrhizal fungi in response to experimental nitrogen and carbon dioxide additions. <i>Oecologia</i> , 2015, 179, 175-185.	0.9	26
1138	Response of PAH-degrading genes to PAH bioavailability in the overlying water, suspended sediment, and deposited sediment of the Yangtze River. <i>Chemosphere</i> , 2015, 128, 236-244.	4.2	33
1139	A Modified R-Type Bacteriocin Specifically Targeting <i>Clostridium difficile</i> Prevents Colonization of Mice without Affecting Gut Microbiota Diversity. <i>MBio</i> , 2015, 6, .	1.8	115
1140	Gut Microbial Succession Follows Acute Secretory Diarrhea in Humans. <i>MBio</i> , 2015, 6, e00381-15.	1.8	150
1141	Soil microbial community structure is unaltered by plant invasion, vegetation clipping, and nitrogen fertilization in experimental semi-arid grasslands. <i>Frontiers in Microbiology</i> , 2015, 6, 466.	1.5	73
1142	Composition and variation of the skin microbiota in sympatric species of European newts (<i>Salamandridae</i>). <i>Amphibia - Reptilia</i> , 2015, 36, 5-12.	0.1	8
1143	The Microbiome, Intestinal Function, and Arginine Metabolism of Healthy Indian Women Are Different from Those of American and Jamaican Women. <i>Journal of Nutrition</i> , 2016, 146, 706-713.	1.3	40
1144	A novel dimensionality reduction algorithm based on Laplace matrix for microbiome data analysis. , 2015, , .		0
1145	Meta-barcoded evaluation of the <i>ISO</i> standard 11063 <i>DNA</i> extraction procedure to characterize soil bacterial and fungal community diversity and composition. <i>Microbial Biotechnology</i> , 2015, 8, 131-142.	2.0	50
1146	Characterization of microbial community structure during continuous anaerobic digestion of straw and cow manure. <i>Microbial Biotechnology</i> , 2015, 8, 815-827.	2.0	197

#	ARTICLE	IF	CITATIONS
1147	Rhythmicity of the intestinal microbiota is regulated by gender and the host circadian clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10479-10484.	3.3	410
1148	<i>Asteropeia mcphersonii</i> , a potential mycorrhizal facilitator for ecological restoration in Madagascar wet tropical rainforests. <i>Forest Ecology and Management</i> , 2015, 358, 202-211.	1.4	14
1149	Gravidas with class III obesity: evaluating the abdominal skin microbiota above and below the panniculus. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2016, 29, 1-5.	0.7	3
1150	Seasonal dynamics of the microbiome of chernozems of the long-term agrochemical experiment in Kamennaya Steppe. <i>Eurasian Soil Science</i> , 2015, 48, 1349-1353.	0.5	10
1151	Bipartite graphs for metagenomic data analysis and visualization. , 2015, , .		1
1152	Geographic patterns in the bacterial microbiome of the glassy-winged sharpshooter, <i>Homalodisca vitripennis</i> (Hemiptera: Cicadellidae). <i>Symbiosis</i> , 2015, 66, 1-12.	1.2	17
1153	Interactions between multiple helminths and the gut microbiota in wild rodents. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140295.	1.8	139
1154	Novel Mass Bio System (MBS) and its potential application in advanced treatment of coal gasification wastewater. <i>RSC Advances</i> , 2015, 5, 88692-88702.	1.7	25
1155	Long-term rice-rice-green manure rotation changing the microbial communities in typical red paddy soil in South China. <i>Journal of Integrative Agriculture</i> , 2015, 14, 2512-2520.	1.7	41
1156	Protocols for the Study of Microbeâ€“Mineral Interactions in Modern Microbialites. Springer Protocols, 2015, , 319-341.	0.1	0
1157	Origins and environmental mobility of antibiotic resistance genes, virulence factors and bacteria in a tidal creek's watershed. <i>Journal of Applied Microbiology</i> , 2015, 118, 764-776.	1.4	10
1158	Gut microbiome composition is associated with temperament during early childhood. <i>Brain, Behavior, and Immunity</i> , 2015, 45, 118-127.	2.0	148
1159	Diet strongly influences the gut microbiota of surgeonfishes. <i>Molecular Ecology</i> , 2015, 24, 656-672.	2.0	194
1160	GrammR: graphical representation and modeling of count data with application in metagenomics. <i>Bioinformatics</i> , 2015, 31, 1648-1654.	1.8	11
1161	A phylo-functional core of gut microbiota in healthy young Chinese cohorts across lifestyles, geography and ethnicities. <i>ISME Journal</i> , 2015, 9, 1979-1990.	4.4	339
1162	Seasonal Community Succession of the Phyllosphere Microbiome. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 274-285.	1.4	275
1163	Soil carbon content drives the biogeographical distribution of fungal communities in the black soil zone of northeast China. <i>Soil Biology and Biochemistry</i> , 2015, 83, 29-39.	4.2	272
1164	Distributed Computing and Internet Technology. <i>Lecture Notes in Computer Science</i> , 2015, , .	1.0	3

#	ARTICLE	IF	CITATIONS
1165	Bacterial Communities Associated with Surfaces of Leafy Greens: Shift in Composition and Decrease in Richness over Time. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1530-1539.	1.4	97
1166	Complex community of nitrite-dependent anaerobic methane oxidation bacteria in coastal sediments of the Mai Po wetland by PCR amplification of both 16S rRNA and pmoA genes. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1463-1473.	1.7	74
1167	Synchronous shifts in dissolved organic carbon bioavailability and bacterial community responses over the course of an upwelling-driven phytoplankton bloom. <i>Limnology and Oceanography</i> , 2015, 60, 657-677.	1.6	78
1168	Gut microbial and short-chain fatty acid profiles in adults with chronic constipation before and after treatment with lubiprostone. <i>Anaerobe</i> , 2015, 33, 33-41.	1.0	49
1169	Analysis of gene-environment interactions in postnatal development of the mammalian intestine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1929-1936.	3.3	77
1170	Dental plaque development on a hydroxyapatite disk in young adults observed by using a barcoded pyrosequencing approach. <i>Scientific Reports</i> , 2015, 5, 8136.	1.6	52
1171	Soil bacterial communities are shaped by temporal and environmental filtering: evidence from a long-term chronosequence. <i>Environmental Microbiology</i> , 2015, 17, 3208-3218.	1.8	85
1172	The contrasting responses of soil microorganisms in two rice cultivars to elevated ground-level ozone. <i>Environmental Pollution</i> , 2015, 197, 195-202.	3.7	43
1173	Infant gut microbiota and food sensitization: associations in the first year of life. <i>Clinical and Experimental Allergy</i> , 2015, 45, 632-643.	1.4	333
1174	Molecular analysis of the caecal and tracheal microbiome of heat-stressed broilers supplemented with prebiotic and probiotic. <i>Avian Pathology</i> , 2015, 44, 67-74.	0.8	66
1175	A classical measure of phylogenetic dissimilarity and its relationship with beta diversity. <i>Basic and Applied Ecology</i> , 2015, 16, 10-18.	1.2	15
1176	The composition of the gut microbiota shapes the colon mucus barrier. <i>EMBO Reports</i> , 2015, 16, 164-177.	2.0	519
1177	Ammonia-oxidizing archaea respond positively to inorganic nitrogen addition in desert soils. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	1.3	17
1178	Structural modulation of gut microbiota during alleviation of type 2 diabetes with a Chinese herbal formula. <i>ISME Journal</i> , 2015, 9, 552-562.	4.4	362
1179	Antibiotics in ingested human blood affect the mosquito microbiota and capacity to transmit malaria. <i>Nature Communications</i> , 2015, 6, 5921.	5.8	154
1180	Assessment of Bacterial and Archaeal Community Structure in Swine Wastewater Treatment Processes. <i>Microbial Ecology</i> , 2015, 70, 77-87.	1.4	39
1181	Wastewater Treatment Plant Effluents Change Abundance and Composition of Ammonia-Oxidizing Microorganisms in Mediterranean Urban Stream Biofilms. <i>Microbial Ecology</i> , 2015, 69, 66-74.	1.4	44
1182	Topographic Diversity of the Respiratory Tract Mycobiome and Alteration in HIV and Lung Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 191, 932-942.	2.5	113

#	ARTICLE	IF	CITATIONS
1183	Divergence across diet, time and populations rules out parallel evolution in the gut microbiomes of Trinidadian guppies. <i>ISME Journal</i> , 2015, 9, 1508-1522.	4.4	133
1184	Microbiota-Mediated Inflammation and Antimicrobial Defense in the Intestine. <i>Annual Review of Immunology</i> , 2015, 33, 227-256.	9.5	227
1185	Metagenomic Insights into the Effects of Fructo-oligosaccharides (FOS) on the Composition of Fecal Microbiota in Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 856-863.	2.4	90
1186	Selection of models for the analysis of risk-factor trees: leveraging biological knowledge to mine large sets of risk factors with application to microbiome data. <i>Bioinformatics</i> , 2015, 31, 1607-1613.	1.8	12
1187	The Role of Host Phylogeny Varies in Shaping Microbial Diversity in the Hindguts of Lower Termites. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1059-1070.	1.4	87
1188	Dietary emulsifiers impact the mouse gut microbiota promoting colitis and metabolic syndrome. <i>Nature</i> , 2015, 519, 92-96.	13.7	1,457
1189	Using carbon dioxide to maintain an elevated oleaginous microalga concentration in mixed-culture photo-bioreactors. <i>Bioresource Technology</i> , 2015, 185, 178-184.	4.8	11
1190	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. <i>Briefings in Bioinformatics</i> , 2015, 16, 745-758.	3.2	66
1191	Diversity, Abundance, and Distribution of nirS-Harboring Denitrifiers in Intertidal Sediments of the Yangtze Estuary. <i>Microbial Ecology</i> , 2015, 70, 30-40.	1.4	57
1192	Changes in plant community composition and reduced precipitation have limited effects on the structure of soil bacterial and fungal communities present in a semiarid grassland. <i>Plant and Soil</i> , 2015, 388, 175-186.	1.8	47
1193	Mimosa caesalpinifolia rhizobial isolates from different origins of the Brazilian Northeast. <i>Archives of Microbiology</i> , 2015, 197, 459-469.	1.0	13
1194	Prokaryotic community structure in deep bedrock aquifers of the Austrian Central Alps. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 687-701.	0.7	6
1195	Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. <i>Cell Host and Microbe</i> , 2015, 17, 385-391.	5.1	273
1196	A systematic evaluation of high-dimensional, ensemble-based regression for exploring large model spaces in microbiome analyses. <i>BMC Bioinformatics</i> , 2015, 16, 31.	1.2	16
1197	Homogeneity of the Vaginal Microbiome at the Cervix, Posterior Fornix, and Vaginal Canal in Pregnant Chinese Women. <i>Microbial Ecology</i> , 2015, 69, 407-414.	1.4	60
1198	Association between tobacco use and the upper gastrointestinal microbiome among Chinese men. <i>Cancer Causes and Control</i> , 2015, 26, 581-588.	0.8	39
1199	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. <i>Microbial Ecology</i> , 2015, 70, 411-424.	1.4	118
1200	Electron donors and co-contaminants affect microbial community composition and activity in perchlorate degradation. <i>Environmental Science and Pollution Research</i> , 2015, 22, 6057-6067.	2.7	20

#	ARTICLE	IF	CITATIONS
1201	Mapping axillary microbiota responsible for body odours using a culture-independent approach. <i>Microbiome</i> , 2015, 3, 3.	4.9	100
1202	Larval exposure to polychlorinated biphenyl 126 (PCB126) causes persistent alteration of the amphibian gut microbiota. <i>Environmental Toxicology and Chemistry</i> , 2015, 34, 1113-1118.	2.2	42
1203	Persistent shifts in Caribbean coral microbiota are linked to the 2010 warm thermal anomaly. <i>Environmental Microbiology Reports</i> , 2015, 7, 471-479.	1.0	33
1204	Distinct soil bacterial communities along a small-scale elevational gradient in alpine tundra. <i>Frontiers in Microbiology</i> , 2015, 6, 582.	1.5	137
1205	Evident bacterial community changes but only slight degradation when polluted with pyrene in a red soil. <i>Frontiers in Microbiology</i> , 2015, 6, 22.	1.5	85
1206	Plant genotype-specific archaeal and bacterial endophytes but similar <i>Bacillus</i> antagonists colonize Mediterranean olive trees. <i>Frontiers in Microbiology</i> , 2015, 6, 138.	1.5	154
1207	The Gut Microbiome of Wild Lemurs: A Comparison of Sympatric <i>Lemur catta</i> and <i>Propithecus verreauxi</i> . <i>Folia Primatologica</i> , 2015, 86, 85-95.	0.3	46
1208	Toolbox Approaches Using Molecular Markers and 16S rRNA Gene Amplicon Data Sets for Identification of Fecal Pollution in Surface Water. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7067-7077.	1.4	68
1209	Shifts in the microbial community structure explain the response of soil respiration to land-use change but not to climate warming. <i>Soil Biology and Biochemistry</i> , 2015, 89, 123-134.	4.2	63
1210	High-intensity sweetener consumption and gut microbiome content and predicted gene function in a cross-sectional study of adults in the United States. <i>Annals of Epidemiology</i> , 2015, 25, 736-742.e4.	0.9	87
1211	Assessment of the genetic and phenotypic diversity among rhizogenic <i>Agrobacterium</i> biovar 1 strains infecting solanaceous and cucurbit crops. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv081.	1.3	19
1212	Structure and diversity of ssDNA Microviridae viruses in two peri-alpine lakes (Annecy and Bourget). <i>Trends in Microbiology</i> , 2015, 23, 107-114.	1.0	35
1213	Effect of headspace carbon dioxide sequestration on microbial biohydrogen communities. <i>International Journal of Hydrogen Energy</i> , 2015, 40, 9966-9976.	3.8	18
1214	Cecal drop reflects the chickens' cecal microbiome, fecal drop does not. <i>Journal of Microbiological Methods</i> , 2015, 117, 164-170.	0.7	41
1215	Comparing the inhibitory thresholds of dairy manure co-digesters after prolonged acclimation periods: Part 2 – correlations between microbiomes and environment. <i>Water Research</i> , 2015, 87, 458-466.	5.3	33
1216	Microbial community composition and diversity in Caspian Sea sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	1.3	70
1217	Census of bacterial microbiota associated with the glacier ice worm <i>Mesenchytraeus solifugus</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	35
1218	Bacterial community structure in treated sewage sludge with mesophilic and thermophilic anaerobic digestion. <i>Folia Microbiologica</i> , 2015, 60, 531-539.	1.1	18

#	ARTICLE	IF	CITATIONS
1219	Coral transplantation triggers shift in microbiome and promotion of coral disease associated potential pathogens. <i>Scientific Reports</i> , 2015, 5, 11903.	1.6	85
1220	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.	1.0	30
1221	The evolution of the gut microbiota in the giant and the red pandas. <i>Scientific Reports</i> , 2015, 5, 10185.	1.6	71
1222	Sulfate Reducing Bacteria and Mycobacteria Dominate the Biofilm Communities in a Chloraminated Drinking Water Distribution System. <i>Environmental Science & Technology</i> , 2015, 49, 8432-8440.	4.6	86
1223	Effects of water stratification and mixing on microbial community structure in a subtropical deep reservoir. <i>Scientific Reports</i> , 2014, 4, 5821.	1.6	110
1224	Pyrosequencing revealed highly microbial phylogenetic diversity in ferromanganese nodules from farmland. <i>Environmental Sciences: Processes and Impacts</i> , 2015, 17, 213-224.	1.7	6
1225	Attenuation of Colitis by <i>Lactobacillus casei</i> BL23 Is Dependent on the Dairy Delivery Matrix. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6425-6435.	1.4	54
1226	Adaptively Evolving Bacterial Communities for Complete and Selective Reduction of Cr(VI), Cu(II), and Cd(II) in Biocathode Bioelectrochemical Systems. <i>Environmental Science & Technology</i> , 2015, 49, 9914-9924.	4.6	140
1227	Hologenome theory supported by cooccurrence networks of species-specific bacterial communities in siphonous algae (<i>Caulerpa</i>). <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv067.	1.3	55
1228	Using Amplicon Sequencing To Characterize and Monitor Bacterial Diversity in Drinking Water Distribution Systems. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6463-6473.	1.4	63
1229	Proton Pump Inhibitors Alter Specific Taxa in the Human Gastrointestinal Microbiome: A Crossover Trial. <i>Gastroenterology</i> , 2015, 149, 883-885.e9.	0.6	268
1230	Benthic ammonia oxidizers differ in community structure and biogeochemical potential across a riverine delta. <i>Frontiers in Microbiology</i> , 2014, 5, 743.	1.5	28
1231	Out of the dark: transitional subsurface-to-surface microbial diversity in a terrestrial serpentinizing seep (Manleluag, Pangasinan, the Philippines). <i>Frontiers in Microbiology</i> , 2015, 6, 44.	1.5	79
1232	High-grain feeding causes strong shifts in ruminal epithelial bacterial community and expression of Toll-like receptor genes in goats. <i>Frontiers in Microbiology</i> , 2015, 6, 167.	1.5	96
1233	Engineering the gut microbiota to treat hyperammonemia. <i>Journal of Clinical Investigation</i> , 2015, 125, 2841-2850.	3.9	154
1234	Structure, mineralogy, and microbial diversity of geothermal spring microbialites associated with a deep oil drilling in Romania. <i>Frontiers in Microbiology</i> , 2015, 6, 253.	1.5	24
1235	Enterolignan-Producing Phenotypes Are Associated with Increased Gut Microbial Diversity and Altered Composition in Premenopausal Women in the United States. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 546-554.	1.1	55
1236	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. <i>Nature Communications</i> , 2015, 6, 7486.	5.8	317

#	ARTICLE	IF	CITATIONS
1237	Explaining Diversity in Metagenomic Datasets by Phylogenetic-Based Feature Weighting. PLoS Computational Biology, 2015, 11, e1004186.	1.5	24
1238	Impacts of dimethyl phthalate on the bacterial community and functions in black soils. Frontiers in Microbiology, 2015, 6, 405.	1.5	27
1239	Differences in the faecal microbiome of non-diarrhoeic clinically healthy dogs and cats associated with Giardia duodenalis infection: impact of hookworms and coccidia. International Journal for Parasitology, 2015, 45, 585-594.	1.3	59
1240	phylogeo: an R package for geographic analysis and visualization of microbiome data. Bioinformatics, 2015, 31, 2909-2911.	1.8	20
1241	Dietary input of microbes and host genetic variation shape among-population differences in stickleback gut microbiota. ISME Journal, 2015, 9, 2515-2526.	4.4	291
1242	Plant nitrogen uptake drives rhizosphere bacterial community assembly during plant growth. Soil Biology and Biochemistry, 2015, 85, 170-182.	4.2	137
1243	Microbial community structure and functional diversity of nitrogen-fixing bacteria associated with Colophospermum mopane. FEMS Microbiology Ecology, 2015, 91, .	1.3	10
1244	Influence of plant communities and soil properties during natural vegetation restoration on arbuscular mycorrhizal fungal communities in a karst region. Ecological Engineering, 2015, 82, 57-65.	1.6	62
1245	Elevated atmospheric CO2 levels affect community structure of rice root-associated bacteria. Frontiers in Microbiology, 2015, 6, 136.	1.5	38
1246	Microbial 16S gene-based composition of a sorghum cropped rhizosphere soil under different fertilization managements. Biology and Fertility of Soils, 2015, 51, 661-672.	2.3	41
1247	Evaluating variation in human gut microbiota profiles due to DNA extraction method and inter-subject differences. Frontiers in Microbiology, 2015, 6, 130.	1.5	152
1248	Loss of Microbiota-Mediated Colonization Resistance to <i>Clostridium difficile</i> Infection With Oral Vancomycin Compared With Metronidazole. Journal of Infectious Diseases, 2015, 212, 1656-1665.	1.9	157
1249	The microbiome of uncontacted Amerindians. Science Advances, 2015, 1, .	4.7	721
1250	The Microbiome of Field-Caught and Laboratory-Adapted Australian Tephritid Fruit Fly Species with Different Host Plant Use and Specialisation. Microbial Ecology, 2015, 70, 498-508.	1.4	125
1251	Characterization of the microbial diversity in yacon spontaneous fermentation at 20°C. International Journal of Food Microbiology, 2015, 203, 35-40.	2.1	15
1252	Microbiome, Metagenomics, and High-Dimensional Compositional Data Analysis. Annual Review of Statistics and Its Application, 2015, 2, 73-94.	4.1	226
1253	Method Optimization for Fecal Sample Collection and Fecal DNA Extraction. Biopreservation and Biobanking, 2015, 13, 79-93.	0.5	48
1254	Marine Oxygen-Deficient Zones Harbor Depauperate Denitrifying Communities Compared to Novel Genetic Diversity in Coastal Sediments. Microbial Ecology, 2015, 70, 311-321.	1.4	10

#	ARTICLE	IF	CITATIONS
1255	Clostridium cluster I and their pathogenic members in a full-scale operating biogas plant. Applied Microbiology and Biotechnology, 2015, 99, 3585-3598.	1.7	9
1256	Cyanobacterial diversity in benthic mats of the McMurdo Dry Valley lakes, Antarctica. Polar Biology, 2015, 38, 1097-1110.	0.5	52
1257	Ethnic/Racial and Genetic Influences on Cerumen Odorant Profiles. Journal of Chemical Ecology, 2015, 41, 67-74.	0.9	17
1258	Bacterial community composition at anodes of microbial fuel cells for paddy soils: the effects of soil properties. Journal of Soils and Sediments, 2015, 15, 926-936.	1.5	51
1259	Application of Meta-EMesh on the analysis of microbial communities from human associated habitats. Quantitative Biology, 2015, 3, 4-18.	0.3	2
1260	Dynamics of extracellular DNA decomposition and bacterial community composition in soil. Soil Biology and Biochemistry, 2015, 86, 42-49.	4.2	69
1261	High-throughput sequencing for the detection of the bacterial and fungal diversity in Mongolian naturally fermented cow's milk in Russia. BMC Microbiology, 2015, 15, 45.	1.3	67
1262	A molecular survey of Australian and North American termite genera indicates that vertical inheritance is the primary force shaping termite gut microbiomes. Microbiome, 2015, 3, 5.	4.9	110
1263	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent Clostridium difficile infection. Microbiome, 2015, 3, 10.	4.9	218
1264	Bacterial diversity and Clostridia abundance decrease with increasing severity of necrotizing enterocolitis. Microbiome, 2015, 3, 11.	4.9	107
1265	Effects of Diurnal Variation of Gut Microbes and High-Fat Feeding on Host Circadian Clock Function and Metabolism. Cell Host and Microbe, 2015, 17, 681-689.	5.1	634
1266	Diversity of Miscellaneous Crenarchaeotic Group archaea in freshwater karstic lakes and their segregation between planktonic and sediment habitats. FEMS Microbiology Ecology, 2015, 91, .	1.3	44
1267	Kinship, inbreeding and fine-scale spatial structure influence gut microbiota in a hindgut-fermenting tortoise. Molecular Ecology, 2015, 24, 2521-2536.	2.0	96
1268	High throughput sequencing reveals distinct microbial populations within the mucosal and luminal niches in healthy individuals. Gut Microbes, 2015, 6, 173-181.	4.3	164
1269	Evaluation of water sampling methodologies for amplicon-based characterization of bacterial community structure. Journal of Microbiological Methods, 2015, 114, 43-50.	0.7	42
1270	Microbiota's implications for immunity and transplantation. Nature Reviews Nephrology, 2015, 11, 342-353.	4.1	47
1271	The integration of sequencing and bioinformatics in metagenomics. Reviews in Environmental Science and Biotechnology, 2015, 14, 357-383.	3.9	13
1272	Forensic analysis of the microbiome of phones and shoes. Microbiome, 2015, 3, 21.	4.9	140

#	ARTICLE	IF	CITATIONS
1273	Resistant starch diet induces change in the swine microbiome and a predominance of beneficial bacterial populations. <i>Microbiome</i> , 2015, 3, 16.	4.9	132
1274	Mongolians core gut microbiota and its correlation with seasonal dietary changes. <i>Scientific Reports</i> , 2014, 4, 5001.	1.6	126
1275	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015, 17, 690-703.	5.1	2,276
1276	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. <i>Microbial Ecology</i> , 2015, 69, 333-345.	1.4	20
1277	Monitoring of the microbiota of fermented sausages by culture independent rRNA-based approaches. <i>International Journal of Food Microbiology</i> , 2015, 212, 67-75.	2.1	96
1278	Impact of metagenomic DNA extraction procedures on the identifiable endophytic bacterial diversity in <i>Sorghum bicolor</i> (L. Moench). <i>Journal of Microbiological Methods</i> , 2015, 112, 104-117.	0.7	71
1279	Parent Material and Vegetation Influence Soil Microbial Community Structure Following 30-Years of Rock Weathering and Pedogenesis. <i>Microbial Ecology</i> , 2015, 69, 383-394.	1.4	36
1280	Contrasting spatial patterns and ecological attributes of soil bacterial and archaeal taxa across a landscape. <i>MicrobiologyOpen</i> , 2015, 4, 518-531.	1.2	40
1281	The bacterial community inhabiting temperate deciduous forests is vertically stratified and undergoes seasonal dynamics. <i>Soil Biology and Biochemistry</i> , 2015, 87, 43-50.	4.2	112
1282	Oligofructose protects against arsenic-induced liver injury in a model of environment/obesity interaction. <i>Toxicology and Applied Pharmacology</i> , 2015, 284, 304-314.	1.3	28
1283	Two decades of warming increases diversity of a potentially lignolytic bacterial community. <i>Frontiers in Microbiology</i> , 2015, 6, 480.	1.5	73
1284	Microbial Community Composition and Diversity via 16S rRNA Gene Amplicons: Evaluating the Illumina Platform. <i>PLoS ONE</i> , 2015, 10, e0116955.	1.1	284
1285	Testing in Microbiome-Profiling Studies with MiRKAT, the Microbiome Regression-Based Kernel Association Test. <i>American Journal of Human Genetics</i> , 2015, 96, 797-807.	2.6	248
1286	Microbiological functioning, diversity, and structure of bacterial communities in ultramafic soils from a tropical savanna. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 935-949.	0.7	32
1287	Power and sample-size estimation for microbiome studies using pairwise distances and PERMANOVA. <i>Bioinformatics</i> , 2015, 31, 2461-2468.	1.8	326
1288	Effect of preservation method on spider monkey (<i>Ateles geoffroyi</i>) fecal microbiota over 8 weeks. <i>Journal of Microbiological Methods</i> , 2015, 113, 16-26.	0.7	118
1289	Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. <i>Nature Communications</i> , 2015, 6, 6440.	5.8	107
1290	Declining diversity of egg-associated bacteria during development of naturally spawned whitefish embryos (<i>Coregonus</i> spp.). <i>Aquatic Sciences</i> , 2015, 77, 481-497.	0.6	17

#	ARTICLE	IF	CITATIONS
1291	Molecular cartography of the human skin surface in 3D. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2120-9.	3.3	288
1292	The human gut microbiome, a taxonomic conundrum. Systematic and Applied Microbiology, 2015, 38, 276-286.	1.2	113
1293	The bacterial communities associated with fecal types and body weight of rex rabbits. Scientific Reports, 2015, 5, 9342.	1.6	115
1294	Size-fraction partitioning of community gene transcription and nitrogen metabolism in a marine oxygen minimum zone. ISME Journal, 2015, 9, 2682-2696.	4.4	169
1295	Bacterial diversity of polluted surface sediments in the northern Adriatic Sea. Systematic and Applied Microbiology, 2015, 38, 189-197.	1.2	45
1296	Concordance of bacterial communities of two tick species and blood of their shared rodent host. Molecular Ecology, 2015, 24, 2566-2579.	2.0	100
1297	Influence of age, reproductive cycling status, and menstruation on the vaginal microbiome in baboons (<i>Papio anubis</i>). American Journal of Primatology, 2015, 77, 563-578.	0.8	44
1298	Regulators of Gut Motility Revealed by a Gnotobiotic Model of Diet-Microbiome Interactions Related to Travel. Cell, 2015, 163, 95-107.	13.5	190
1299	Microbial community profiles of the colon from steers differing in feed efficiency. SpringerPlus, 2015, 4, 454.	1.2	52
1300	Vineyard soil bacterial diversity and composition revealed by 16S rRNA genes: Differentiation by geographic features. Soil Biology and Biochemistry, 2015, 91, 232-247.	4.2	143
1301	Binary combination of epsilon-poly-L-lysine and isoeugenol affect progression of spoilage microbiota in fresh turkey meat, and delay onset of spoilage in <i>Pseudomonas putida</i> challenged meat. International Journal of Food Microbiology, 2015, 215, 131-142.	2.1	22
1302	Cilantro microbiome before and after nonselective pre-enrichment for <i>Salmonella</i> using 16S rRNA and metagenomic sequencing. BMC Microbiology, 2015, 15, 160.	1.3	53
1303	Rapid Change of Microbiota Diversity in the Gut but Not the Hepatopancreas During Gonadal Development of the New Shrimp Model <i>Neocaridina denticulata</i> . Marine Biotechnology, 2015, 17, 811-819.	1.1	61
1304	Statistical Tools for Data Analysis. Springer Protocols, 2015, , 41-57.	0.1	0
1305	Oral microbiota in patients with atherosclerosis. Atherosclerosis, 2015, 243, 573-578.	0.4	103
1306	The microbiome of <i>Folsomia candida</i> : an assessment of bacterial diversity in a <i>Wolbachia</i> -containing animal. FEMS Microbiology Ecology, 2015, 91, fiv128.	1.3	32
1307	Evaluation of bacterial contamination in raw milk, ultra-high temperature milk and infant formula using single molecule, real-time sequencing technology. Journal of Dairy Science, 2015, 98, 8464-8472.	1.4	73
1308	Arsenic induces structural and compositional colonic microbiome change and promotes host nitrogen and amino acid metabolism. Toxicology and Applied Pharmacology, 2015, 289, 397-408.	1.3	89

#	ARTICLE	IF	CITATIONS
1309	Commensal <i>Bifidobacterium</i> promotes antitumor immunity and facilitates anti-PD-L1 efficacy. <i>Science</i> , 2015, 350, 1084-1089.	6.0	2,782
1310	Athletic equipment microbiota are shaped by interactions with human skin. <i>Microbiome</i> , 2015, 3, 25.	4.9	36
1311	MHC variation sculpts individualized microbial communities that control susceptibility to enteric infection. <i>Nature Communications</i> , 2015, 6, 8642.	5.8	132
1312	Substrate sources regulate spatial variation of metabolically active methanogens from two contrasting freshwater wetlands. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10779-10791.	1.7	17
1313	Stool Bacteriomic Profiling in Patients with Metastatic Renal Cell Carcinoma Receiving Vascular Endothelial Growth Factor Tyrosine Kinase Inhibitors. <i>Clinical Cancer Research</i> , 2015, 21, 5286-5293.	3.2	52
1314	Dietary analysis on the shallow-water hydrothermal vent crab <i>Xenograpsus testudinatus</i> using Illumina sequencing. <i>Marine Biology</i> , 2015, 162, 1787-1798.	0.7	21
1315	Genetic diversity along the life cycle of the cyanobacterium <i>Microcystis</i> : highlight on the complexity of benthic and planktonic interactions. <i>Environmental Microbiology</i> , 2015, 17, 901-911.	1.8	10
1316	Determinism of bacterial metacommunity dynamics in the southern East China Sea varies depending on hydrography. <i>Ecography</i> , 2015, 38, 198-212.	2.1	61
1317	Changes in Microbial Biofilm Communities during Colonization of Sewer Systems. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7271-7280.	1.4	43
1318	The prebiotics Sialyllactose and Galactylactose diminish stressor-induced anxiety-like behavior and colonic microbiota alterations: Evidence for effects on the gut-brain axis. <i>Brain, Behavior, and Immunity</i> , 2015, 50, 166-177.	2.0	233
1319	Microhabitat heterogeneity across leaves and flower organs promotes bacterial diversity. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv097.	1.3	97
1320	Hand bacteria as an identifier: a biometric evaluation. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1.	1.2	2
1321	Feeding on microbiomes: effects of detritivory on the taxonomic and phylogenetic bacterial composition of animal manures. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv117.	1.3	53
1322	The unifrac significance test is sensitive to tree topology. <i>BMC Bioinformatics</i> , 2015, 16, 211.	1.2	22
1323	The airway microbiome in patients with severe asthma: Associations with disease features and severity. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 874-884.	1.5	395
1324	Freshwater Conservation and Biomonitoring of Structure and Function. , 2015, , 241-271.		3
1325	Microbial Malaise: How Can We Classify the Microbiome?. <i>Trends in Microbiology</i> , 2015, 23, 671-679.	3.5	36
1326	Phylogenetic approaches to microbial community classification. <i>Microbiome</i> , 2015, 3, 47.	4.9	39

#	ARTICLE	IF	CITATIONS
1327	Shifts in microbial diversity through land use intensity as drivers of carbon mineralization in soil. <i>Soil Biology and Biochemistry</i> , 2015, 90, 204-213.	4.2	159
1328	Microbial composition of purified waters and implications for regrowth control in municipal water systems. <i>Environmental Science: Water Research and Technology</i> , 2015, 1, 882-892.	1.2	11
1329	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6200-6209.	1.4	167
1330	Gut Microbial Dysbiosis Due to <i>Helicobacter</i> Drives an Increase in Marginal Zone B Cells in the Absence of IL-10 Signaling in Macrophages. <i>Journal of Immunology</i> , 2015, 195, 3071-3085.	0.4	21
1331	Illumina MiSeq investigations on the changes of microbial community in the <i>Fusarium oxysporum</i> f.sp. cubense infected soil during and after reductive soil disinfestation. <i>Microbiological Research</i> , 2015, 181, 33-42.	2.5	143
1332	Distribution, Activities, and Interactions of Methanogens and Sulfate-Reducing Prokaryotes in the Florida Everglades. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7431-7442.	1.4	25
1333	Response of the rumen archaeal and bacterial populations to anti-methanogenic organosulphur compounds in continuous-culture fermenters. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv079.	1.3	23
1334	Alteration of the rat cecal microbiome during colonization with the helminth <i>Hymenolepis diminuta</i> . <i>Gut Microbes</i> , 2015, 6, 182-193.	4.3	99
1335	Multi-Layer and Recursive Neural Networks for Metagenomic Classification. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 608-616.	2.2	78
1336	Rumen Metagenomics. , 2015, , 223-245.		5
1337	The Human Skin Microbiome Associates with the Outcome of and Is Influenced by Bacterial Infection. <i>MBio</i> , 2015, 6, e01315-15.	1.8	94
1338	Functional diversity: an overview of its history and applicability. <i>Natureza A Conservacao</i> , 2015, 13, 112-116.	2.5	153
1339	The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 309, E840-E851.	1.8	57
1340	454 Pyrosequencing-based assessment of bacterial diversity and community structure in termite guts, mounds and surrounding soils. <i>SpringerPlus</i> , 2015, 4, 471.	1.2	44
1341	Evaluation of the bacterial microbiome of two flea species using different DNA-isolation techniques provides insights into flea host ecology. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv134.	1.3	31
1342	Anaerobic Infections. , 2015, , 875-897.		2
1343	Comparative analysis of alkaline phosphatase-encoding genes (<i>phoX</i>) in two contrasting zones of Lake Taihu. <i>Canadian Journal of Microbiology</i> , 2015, 61, 227-236.	0.8	15
1344	Effects of nutrients and warming on <i>Plectonothrix</i> dynamics and diversity: a palaeolimnological view based on sedimentary DNA and RNA. <i>Freshwater Biology</i> , 2015, 60, 31-49.	1.2	34

#	ARTICLE	IF	CITATIONS
1345	Existence of Novel Phylotypes of Nitrite-Dependent Anaerobic Methane-Oxidizing Bacteria in Surface and Subsurface Sediments of the South China Sea. <i>Geomicrobiology Journal</i> , 2015, 32, 1-10.	1.0	38
1346	Assessment of the bacterial and fungal diversity in home-made yoghurts of Xinjiang, China by pyrosequencing. <i>Journal of the Science of Food and Agriculture</i> , 2015, 95, 2007-2015.	1.7	28
1347	Sulfur Dioxide Treatment Alters Wine Microbial Diversity and Fermentation Progression in a Dose-Dependent Fashion. <i>American Journal of Enology and Viticulture</i> , 2015, 66, 73-79.	0.9	56
1348	Characterization of bacterial community of raw milk from dairy cows during subacute ruminal acidosis challenge by high-throughput sequencing. <i>Journal of the Science of Food and Agriculture</i> , 2015, 95, 1072-1079.	1.7	59
1349	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.	1.8	292
1350	Mycorrhizal fungal diversity and community composition in a lithophytic and epiphytic orchid. <i>Mycorrhiza</i> , 2015, 25, 289-296.	1.3	41
1351	<i>Bacillus asahii</i> comes to the fore in organic manure fertilized alkaline soils. <i>Soil Biology and Biochemistry</i> , 2015, 81, 186-194.	4.2	84
1352	Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. <i>Water Research</i> , 2015, 69, 30-39.	5.3	49
1353	Ecological Succession and Viability of Human-Associated Microbiota on Restroom Surfaces. <i>Applied and Environmental Microbiology</i> , 2015, 81, 765-773.	1.4	89
1354	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015, 17, 622-636.	1.8	32
1355	Spatial structuring of arbuscular mycorrhizal communities in benchmark and modified temperate eucalypt woodlands. <i>Mycorrhiza</i> , 2015, 25, 41-54.	1.3	5
1356	Oceanographic structure drives the assembly processes of microbial eukaryotic communities. <i>ISME Journal</i> , 2015, 9, 990-1002.	4.4	115
1357	Bacterial community shifts associated with high abundance of <i>Rhizobium</i> spp. in potato roots under macronutrient-deficient conditions. <i>Soil Biology and Biochemistry</i> , 2015, 80, 232-236.	4.2	10
1358	In-depth diversity analysis of the bacterial community resident in the camel rumen. <i>Systematic and Applied Microbiology</i> , 2015, 38, 67-76.	1.2	92
1359	Bacterial biogeographical patterns in a cooking center for hospital foodservice. <i>International Journal of Food Microbiology</i> , 2015, 193, 99-108.	2.1	22
1360	Intestinal epithelial vitamin D receptor deletion leads to defective autophagy in colitis. <i>Gut</i> , 2015, 64, 1082-1094.	6.1	279
1361	Community Composition of Known and Uncultured Archaeal Lineages in Anaerobic or Anoxic Wastewater Treatment Sludge. <i>Microbial Ecology</i> , 2015, 69, 586-596.	1.4	59
1362	Species sorting and seasonal dynamics primarily shape bacterial communities in the Upper Mississippi River. <i>Science of the Total Environment</i> , 2015, 505, 435-445.	3.9	133

#	ARTICLE	IF	CITATIONS
1363	Precision microbiome reconstitution restores bile acid mediated resistance to <i>Clostridium difficile</i> . <i>Nature</i> , 2015, 517, 205-208.	13.7	1,506
1364	Pyrosequencing reveals the effect of mobilizing agents and lignocellulosic substrate amendment on microbial community composition in a real industrial PAH-polluted soil. <i>Journal of Hazardous Materials</i> , 2015, 283, 35-43.	6.5	62
1365	Considering external information to improve the phylogenetic comparison of microbial communities: a new approach based on constrained Double Principal Coordinates Analysis (<sc>cDPCoA</sc>). <i>Molecular Ecology Resources</i> , 2015, 15, 242-249.	2.2	19
1366	Host adaptive immunity alters gut microbiota. <i>ISME Journal</i> , 2015, 9, 770-781.	4.4	198
1367	Analysis of raw goat milk microbiota: Impact of stage of lactation and lysozyme on microbial diversity. <i>Food Microbiology</i> , 2015, 46, 121-131.	2.1	61
1368	Phylogenetics and the Human Microbiome. <i>Systematic Biology</i> , 2015, 64, e26-e41.	2.7	36
1369	Marine bacterioplankton community turnover within seasonally hypoxic waters of a subtropical sound: <sc>D</sc>'s <sc>H</sc>ole, <sc>B</sc>ermuda. <i>Environmental Microbiology</i> , 2015, 17, 3481-3499.	1.8	32
1370	Contrasting spatiotemporal patterns and environmental drivers of diversity and community structure of ammonia oxidizers, denitrifiers, and anammox bacteria in sediments of estuarine tidal flats. <i>Annals of Microbiology</i> , 2015, 65, 879-890.	1.1	16
1371	Interpreting 16S metagenomic data without clustering to achieve sub-OTU resolution. <i>ISME Journal</i> , 2015, 9, 68-80.	4.4	184
1372	Microbial mucosal colonic shifts associated with the development of colorectal cancer reveal the presence of different bacterial and archaeal biomarkers. <i>Journal of Gastroenterology</i> , 2015, 50, 167-179.	2.3	224
1373	Probing the diversity of healthy oral microbiome with bioinformatics approaches. <i>BMB Reports</i> , 2016, 49, 662-670.	1.1	39
1374	Decline in Performance of Biochemical Reactors for Sulphate Removal from Mine-Influenced Water is Accompanied by Changes in Organic Matter Characteristics and Microbial Population Composition. <i>Water (Switzerland)</i> , 2016, 8, 124.	1.2	12
1375	Distinctly altered gut microbiota in the progression of liver disease. <i>Oncotarget</i> , 2016, 7, 19355-19366.	0.8	180
1376	Microbial profiling of dental plaque from mechanically ventilated patients. <i>Journal of Medical Microbiology</i> , 2016, 65, 147-159.	0.7	33
1377	The Gut Microbiome Is Altered in a Letrozole-Induced Mouse Model of Polycystic Ovary Syndrome. <i>PLoS ONE</i> , 2016, 11, e0146509.	1.1	145
1378	The Bacteriomes of Ileal Mucosa and Cecal Content of Broiler Chickens and Turkeys as Revealed by Metagenomic Analysis. <i>International Journal of Microbiology</i> , 2016, 2016, 1-12.	0.9	14
1379	Microbiota-driven transcriptional changes in prefrontal cortex override genetic differences in social behavior. <i>ELife</i> , 2016, 5, .	2.8	226
1380	Microbial community profiles of the jejunum from steers differing in feed efficiency ^{1,2,3} . <i>Journal of Animal Science</i> , 2016, 94, 327-338.	0.2	62

#	ARTICLE	IF	CITATIONS
1381	Ileal mucosa and digesta associated microbiota of starter pigs and changes linked to time postweaning and dietary interventions ¹ . <i>Journal of Animal Science</i> , 2016, 94, 344-348.	0.2	4
1382	Co-occurrence patterns in aquatic bacterial communities across changing permafrost landscapes. <i>Biogeosciences</i> , 2016, 13, 175-190.	1.3	64
1383	Tissue-Associated Bacterial Alterations in Rectal Carcinoma Patients Revealed by 16S rRNA Community Profiling. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 179.	1.8	125
1384	Worldwide Analysis of Sedimentary DNA Reveals Major Gaps in Taxonomic Knowledge of Deep-Sea Benthos. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	138
1385	Bacterioplankton Dynamics within a Large Anthropogenically Impacted Urban Estuary. <i>Frontiers in Microbiology</i> , 2015, 6, 1438.	1.5	98
1386	A Lipid-Accumulating Alga Maintains Growth in Outdoor, Alkaliphilic Raceway Pond with Mixed Microbial Communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1480.	1.5	30
1387	Methane Emission in a Specific Riparian-Zone Sediment Decreased with Bioelectrochemical Manipulation and Corresponded to the Microbial Community Dynamics. <i>Frontiers in Microbiology</i> , 2015, 6, 1523.	1.5	12
1388	Sulfur Biogeochemistry of an Oil Sands Composite Tailings Deposit. <i>Frontiers in Microbiology</i> , 2015, 6, 1533.	1.5	27
1389	Human Microbiota of the Argentine Population- A Pilot Study. <i>Frontiers in Microbiology</i> , 2016, 7, 51.	1.5	14
1390	High Molecular Weight Barley β -Glucan Alters Gut Microbiota Toward Reduced Cardiovascular Disease Risk. <i>Frontiers in Microbiology</i> , 2016, 7, 129.	1.5	133
1391	Characterization of the Core and Caste-Specific Microbiota in the Termite, <i>Reticulitermes flavipes</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 171.	1.5	71
1392	Distinct Spatial Patterns of SAR11, SAR86, and Actinobacteria Diversity along a Transect in the Ultra-oligotrophic South Pacific Ocean. <i>Frontiers in Microbiology</i> , 2016, 7, 234.	1.5	45
1393	Fate of Viable but Non-culturable <i>Listeria monocytogenes</i> in Pig Manure Microcosms. <i>Frontiers in Microbiology</i> , 2016, 7, 245.	1.5	18
1394	Spatial-Temporal Changes of Bacterioplankton Community along an Exhorheic River. <i>Frontiers in Microbiology</i> , 2016, 7, 250.	1.5	32
1395	The Features of Fecal and Ileal Mucosa-Associated Microbiota in Dairy Calves during Early Infection with <i>Mycobacterium avium</i> Subspecies <i>paratuberculosis</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 426.	1.5	44
1396	<i>Mycobacterium avium</i> Subspecies <i>paratuberculosis</i> Infection Modifies Gut Microbiota under Different Dietary Conditions in a Rabbit Model. <i>Frontiers in Microbiology</i> , 2016, 7, 446.	1.5	56
1397	Temporal and Spatial Dynamics of Archaeal Communities in Two Freshwater Lakes at Different Trophic Status. <i>Frontiers in Microbiology</i> , 2016, 7, 451.	1.5	37
1398	Coral-Associated Bacterial Diversity Is Conserved across Two Deep-Sea Anthothela Species. <i>Frontiers in Microbiology</i> , 2016, 7, 458.	1.5	93

#	ARTICLE	IF	CITATIONS
1399	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 459.	1.5	659
1400	Municipal Solid Waste Landfills Harbor Distinct Microbiomes. <i>Frontiers in Microbiology</i> , 2016, 7, 534.	1.5	107
1401	Individuality, Stability, and Variability of the Plaque Microbiome. <i>Frontiers in Microbiology</i> , 2016, 7, 564.	1.5	75
1402	Development of Ruminal and Fecal Microbiomes Are Affected by Weaning But Not Weaning Strategy in Dairy Calves. <i>Frontiers in Microbiology</i> , 2016, 7, 582.	1.5	148
1403	Molecular Characterization and Meta-Analysis of Gut Microbial Communities Illustrate Enrichment of <i>Prevotella</i> and <i>Megasphaera</i> in Indian Subjects. <i>Frontiers in Microbiology</i> , 2016, 7, 660.	1.5	110
1404	Comparison of Microbial Communities Isolated from Feces of Asymptomatic Salmonella-Shedding and Non-Salmonella Shedding Dairy Cows. <i>Frontiers in Microbiology</i> , 2016, 7, 691.	1.5	7
1405	Unearthing the Ecology of Soil Microorganisms Using a High Resolution DNA-SIP Approach to Explore Cellulose and Xylose Metabolism in Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 703.	1.5	154
1406	Pika Population Density Is Associated with the Composition and Diversity of Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 758.	1.5	68
1407	Large Differences in Bacterial Community Composition among Three Nearby Extreme Waterbodies of the High Andean Plateau. <i>Frontiers in Microbiology</i> , 2016, 7, 976.	1.5	54
1408	Biogeographic Distribution Patterns of Bacteria in Typical Chinese Forest Soils. <i>Frontiers in Microbiology</i> , 2016, 7, 1106.	1.5	90
1409	Changes in the Structure of the Microbial Community Associated with <i>Nannochloropsis salina</i> following Treatments with Antibiotics and Bioactive Compounds. <i>Frontiers in Microbiology</i> , 2016, 7, 1155.	1.5	37
1410	Characterization of Chemosynthetic Microbial Mats Associated with Intertidal Hydrothermal Sulfur Vents in White Point, San Pedro, CA, USA. <i>Frontiers in Microbiology</i> , 2016, 7, 1163.	1.5	13
1411	Honey Bee Gut Microbiome Is Altered by In-Hive Pesticide Exposures. <i>Frontiers in Microbiology</i> , 2016, 7, 1255.	1.5	165
1412	Pika Gut May Select for Rare but Diverse Environmental Bacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 1269.	1.5	65
1413	The Salivary Microbiome in Polycystic Ovary Syndrome (PCOS) and Its Association with Disease-Related Parameters: A Pilot Study. <i>Frontiers in Microbiology</i> , 2016, 7, 1270.	1.5	34
1414	Geographical Distribution of Methanogenic Archaea in Nine Representative Paddy Soils in China. <i>Frontiers in Microbiology</i> , 2016, 7, 1447.	1.5	19
1415	Effects of Dietary Forage and Calf Starter Diet on Ruminal pH and Bacteria in Holstein Calves during Weaning Transition. <i>Frontiers in Microbiology</i> , 2016, 7, 1575.	1.5	80
1416	The Madeira Archipelago As a Significant Source of Marine-Derived Actinomycete Diversity with Anticancer and Antimicrobial Potential. <i>Frontiers in Microbiology</i> , 2016, 7, 1594.	1.5	32

#	ARTICLE	IF	CITATIONS
1417	Alteration of Fecal Microbiota Profiles in Juvenile Idiopathic Arthritis. Associations with HLA-B27 Allele and Disease Status. <i>Frontiers in Microbiology</i> , 2016, 7, 1703.	1.5	65
1418	Polycyclic Aromatic Hydrocarbon-Induced Changes in Bacterial Community Structure under Anoxic Nitrate Reducing Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 1775.	1.5	29
1419	The Microbiota of Recreational Freshwaters and the Implications for Environmental and Public Health. <i>Frontiers in Microbiology</i> , 2016, 7, 1826.	1.5	70
1420	Waste Conversion into n-Caprylate and n-Caproate: Resource Recovery from Wine Lees Using Anaerobic Reactor Microbiomes and In-line Extraction. <i>Frontiers in Microbiology</i> , 2016, 7, 1892.	1.5	108
1421	Primer Sets Developed for Functional Genes Reveal Shifts in Functionality of Fungal Community in Soils. <i>Frontiers in Microbiology</i> , 2016, 7, 1897.	1.5	9
1422	Application of Taxonomic Modeling to Microbiota Data Mining for Detection of Helminth Infection in Global Populations. <i>Data</i> , 2016, 1, 19.	1.2	6
1423	Household air pollution and the lung microbiome of healthy adults in Malawi: a cross-sectional study. <i>BMC Microbiology</i> , 2016, 16, 182.	1.3	49
1424	An adaptive association test for microbiome data. <i>Genome Medicine</i> , 2016, 8, 56.	3.6	69
1425	Bipartite Graphs for Visualization Analysis of Microbiome Data. <i>Evolutionary Bioinformatics</i> , 2016, 12s1, EBO.S38546.	0.6	9
1426	Vitamin A deficiency impacts the structural segregation of gut microbiota in children with persistent diarrhea. <i>Journal of Clinical Biochemistry and Nutrition</i> , 2016, 59, 113-121.	0.6	49
1427	The Potential of Class II Bacteriocins to Modify Gut Microbiota to Improve Host Health. <i>PLoS ONE</i> , 2016, 11, e0164036.	1.1	102
1428	Cervical Microbiome and Cytokine Profile at Various Stages of Cervical Cancer: A Pilot Study. <i>PLoS ONE</i> , 2016, 11, e0153274.	1.1	275
1429	Chronic Psychological Stress Disrupted the Composition of the Murine Colonic Microbiota and Accelerated a Murine Model of Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2016, 11, e0150559.	1.1	25
1430	<i>Helicobacter pylori</i> Eradication Causes Perturbation of the Human Gut Microbiome in Young Adults. <i>PLoS ONE</i> , 2016, 11, e0151893.	1.1	109
1431	Longitudinal Analysis of the Intestinal Microbiota in Persistently Stunted Young Children in South India. <i>PLoS ONE</i> , 2016, 11, e0155405.	1.1	94
1432	Effects of Diets Supplemented with Ensiled Mulberry Leaves and Sun-Dried Mulberry Fruit Pomace on the Ruminal Bacterial and Archaeal Community Composition of Finishing Steers. <i>PLoS ONE</i> , 2016, 11, e0156836.	1.1	18
1433	Effect of Co-Composting Cattle Manure with Construction and Demolition Waste on the Archaeal, Bacterial, and Fungal Microbiota, and on Antimicrobial Resistance Determinants. <i>PLoS ONE</i> , 2016, 11, e0157539.	1.1	54
1434	Mothers Secretor Status Affects Development of Childrens Microbiota Composition and Function: A Pilot Study. <i>PLoS ONE</i> , 2016, 11, e0161211.	1.1	63

#	ARTICLE	IF	CITATIONS
1435	Characterization of Intestinal Microbiomes of Hirschsprung's Disease Patients with or without Enterocolitis Using Illumina-MiSeq High-Throughput Sequencing. PLoS ONE, 2016, 11, e0162079.	1.1	58
1436	Key Microbiota Identification Using Functional Gene Analysis during Pepper (<i>Piper nigrum</i> L.) Peeling. PLoS ONE, 2016, 11, e0165206.	1.1	0
1437	Rhizospheric Bacterial Community of Endemic <i>Rhododendron arboreum</i> Sm. Ssp. <i>delavayi</i> along Eastern Himalayan Slope in Tawang. Frontiers in Plant Science, 2016, 07, 1345.	1.7	14
1438	Spatial and Temporal Changes in the Broiler Chicken Cecal and Fecal Microbiomes and Correlations of Bacterial Taxa with Cytokine Gene Expression. Frontiers in Veterinary Science, 2016, 3, 11.	0.9	169
1439	Estimating and comparing microbial diversity in the presence of sequencing errors. PeerJ, 2016, 4, e1634.	0.9	73
1440	Surface Biofilm Interactions in Epizootic Shell Disease of the American Lobster (<i>Homarus americanus</i>).		5
1441	Direct and indirect effects of native range expansion on soil microbial community structure and function. Journal of Ecology, 2016, 104, 1271-1283.	1.9	55
1442	Bacterial microbiomes from vertically transmitted fungal inocula of the leaf-cutting ant <i>Atta texana</i> . Environmental Microbiology Reports, 2016, 8, 630-640.	1.0	50
1443	Metabarcoding reveals environmental factors influencing spatio-temporal variation in pelagic microeukaryotes. Molecular Ecology, 2016, 25, 3593-3604.	2.0	37
1444	Growth of high-elevation <i>Cryptococcus</i> sp. during extreme freeze-thaw cycles. Extremophiles, 2016, 20, 579-588.	0.9	17
1445	Novel <i>acsF</i> Gene Primers Revealed a Diverse Phototrophic Bacterial Population, Including Gemmatimonadetes, in Lake Taihu (China). Applied and Environmental Microbiology, 2016, 82, 5587-5594.	1.4	18
1446	Phylogenetic test of speciation by host shift in leaf cone moths (<i>Caloptilia</i>) feeding on maples (<i>Acer</i>)	1.0784314	25
1447	Increases in mean annual temperature do not alter soil bacterial community structure in tropical montane wet forests. Ecosphere, 2016, 7, e01296.	1.0	23
1448	Spatial scale drives patterns in soil bacterial diversity. Environmental Microbiology, 2016, 18, 2039-2051.	1.8	194
1449	Multiple opportunistic pathogens can cause a bleaching disease in the red seaweed <i>Delisea pulchra</i> . Environmental Microbiology, 2016, 18, 3962-3975.	1.8	113
1450	Connectivity between surface and deep waters determines prokaryotic diversity in the North Atlantic Deep Water. Environmental Microbiology, 2016, 18, 2052-2063.	1.8	58
1451	Dissecting phylogenetic fuzzy weighting: theory and application in metacommunity phylogenetics. Methods in Ecology and Evolution, 2016, 7, 937-946.	2.2	42
1452	Application of multivariate statistical techniques in microbial ecology. Molecular Ecology, 2016, 25, 1032-1057.	2.0	298

#	ARTICLE	IF	CITATIONS
1453	Field degradation of aminopyralid and clopyralid and microbial community response to application in Alaskan soils. <i>Environmental Toxicology and Chemistry</i> , 2016, 35, 485-493.	2.2	13
1454	The gut microbiome of the sea urchin, <i>Lytechinus variegatus</i> , from its natural habitat demonstrates selective attributes of microbial taxa and predictive metabolic profiles. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw146.	1.3	113
1455	Ligature-induced periodontitis in mice induces elevated levels of circulating interleukin-6 but shows only weak effects on adipose and liver tissues. <i>Journal of Periodontal Research</i> , 2016, 51, 639-646.	1.4	47
1456	Development, diet and dynamism: longitudinal and cross-sectional predictors of gut microbial communities in wild baboons. <i>Environmental Microbiology</i> , 2016, 18, 1312-1325.	1.8	61
1457	Recent and emerging innovations in <i>Salmonella</i> detection: a food and environmental perspective. <i>Microbial Biotechnology</i> , 2016, 9, 279-292.	2.0	129
1458	Age polyethism drives community structure of the bacterial gut microbiota in the fungus-cultivating termite <i>Odontotermes formosanus</i> . <i>Environmental Microbiology</i> , 2016, 18, 1440-1451.	1.8	33
1459	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152
1460	Acute dextran sulfate sodium (DSS)-induced colitis promotes gut microbial dysbiosis in mice. <i>Journal of Basic Microbiology</i> , 2016, 56, 986-998.	1.8	208
1461	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016, 535, 94-103.	13.7	595
1462	Determinants of bacterial communities in Canadian agroforestry systems. <i>Environmental Microbiology</i> , 2016, 18, 1805-1816.	1.8	202
1463	Geological connectivity drives microbial community structure and connectivity in polar, terrestrial ecosystems. <i>Environmental Microbiology</i> , 2016, 18, 1834-1849.	1.8	51
1464	Variance and potential niche separation of microbial communities in subseafloor sediments off Shimokita Peninsula, Japan. <i>Environmental Microbiology</i> , 2016, 18, 1889-1906.	1.8	48
1465	Cultivating microbial dark matter in benzene-degrading methanogenic consortia. <i>Environmental Microbiology</i> , 2016, 18, 2923-2936.	1.8	54
1466	A multiplayer game: species of <i>Clostridium</i> , <i>Acinetobacter</i> , and <i>Pseudomonas</i> are responsible for the persistence of antibiotic resistance genes in manure-treated soils. <i>Environmental Microbiology</i> , 2016, 18, 3494-3508.	1.8	91
1467	Influence of tree shape and evolutionary time-scale on phylogenetic diversity metrics. <i>Ecography</i> , 2016, 39, 913-920.	2.1	118
1468	Diversity of ribosomal 16S DNA- and RNA-based bacterial community in an office building drinking water system. <i>Journal of Applied Microbiology</i> , 2016, 120, 1723-1738.	1.4	47
1469	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.	1.4	43
1470	Comparison of the oral microbiome of siblings using next-generation sequencing: a pilot study. <i>Oral Diseases</i> , 2016, 22, 549-556.	1.5	8

#	ARTICLE	IF	CITATIONS
1471	Coupling of soil prokaryotic diversity and plant diversity across latitudinal forest ecosystems. <i>Scientific Reports</i> , 2016, 6, 19561.	1.6	50
1472	Gut Microbiota Regulate Motor Deficits and Neuroinflammation in a Model of Parkinson's Disease. <i>Cell</i> , 2016, 167, 1469-1480.e12.	13.5	2,399
1473	What could the entire cornstover contribute to the enhancement of waste activated sludge acidification? Performance assessment and microbial community analysis. <i>Biotechnology for Biofuels</i> , 2016, 9, 241.	6.2	30
1474	Ecophysiological consequences of alcoholism on human gut microbiota: implications for ethanol-related pathogenesis of colon cancer. <i>Scientific Reports</i> , 2016, 6, 27923.	1.6	66
1475	Large-scale benchmarking reveals false discoveries and count transformation sensitivity in 16S rRNA gene amplicon data analysis methods used in microbiome studies. <i>Microbiome</i> , 2016, 4, 62.	4.9	138
1476	Disturbance Regimes Predictably Alter Diversity in an Ecologically Complex Bacterial System. <i>MBio</i> , 2016, 7, .	1.8	47
1477	The microbiomes and metagenomes of forest biochars. <i>Scientific Reports</i> , 2016, 6, 26425.	1.6	43
1478	Comparison and Interpretation of Taxonomical Structure of Bacterial Communities in Two Types of Lakes on Yun-Gui plateau of China. <i>Scientific Reports</i> , 2016, 6, 30616.	1.6	45
1479	Anode potential influences the structure and function of anodic electrode and electrolyte-associated microbiomes. <i>Scientific Reports</i> , 2016, 6, 39114.	1.6	57
1480	Effects of early feeding on the host rumen transcriptome and bacterial diversity in lambs. <i>Scientific Reports</i> , 2016, 6, 32479.	1.6	148
1481	Stability of peatland carbon to rising temperatures. <i>Nature Communications</i> , 2016, 7, 13723.	5.8	162
1482	Bacterial communities of the cotton aphid <i>Aphis gossypii</i> associated with Bt cotton in northern China. <i>Scientific Reports</i> , 2016, 6, 22958.	1.6	46
1483	Chemical composition of preen wax reflects major histocompatibility complex similarity in songbirds. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161966.	1.2	45
1484	Deep sequencing of the 16S ribosomal RNA of the neonatal oral microbiome: a comparison of breast-fed and formula-fed infants. <i>Scientific Reports</i> , 2016, 6, 38309.	1.6	51
1485	Integrated Role of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Supplementation in Gut Microbiota, Immunity, and Metabolism of Infant Rhesus Monkeys. <i>MSystems</i> , 2016, 1, .	1.7	21
1486	Effects of grain feeding on microbiota in the digestive tract of cattle. <i>Animal Frontiers</i> , 2016, 6, 13-19.	0.8	97
1487	Skład mikrobiomu jelit we wczesnym okresie życia a ustępowanie alergii na białka mleka. <i>Alergologia Polska - Polish Journal of Allergology</i> , 2016, 3, T69-T81.	0.0	0
1488	Influence of maternal breast milk ingestion on acquisition of the intestinal microbiome in preterm infants. <i>Microbiome</i> , 2016, 4, 68.	4.9	155

#	ARTICLE	IF	CITATIONS
1489	Identifying Host Genetic Variants Associated with Microbiome Composition by Testing Multiple Beta Diversity Matrices. <i>Human Heredity</i> , 2016, 81, 117-126.	0.4	7
1491	Transition from freshwater to seawater reshapes the skin-associated microbiota of Atlantic salmon. <i>Scientific Reports</i> , 2016, 6, 19707.	1.6	173
1492	Bacterial and protist community changes during a phytoplankton bloom. <i>Limnology and Oceanography</i> , 2016, 61, 198-213.	1.6	22
1494	Metagenomic Profiling, Interaction of Genomics with Meta-genomics. <i>Translational Bioinformatics</i> , 2016, , 241-267.	0.0	0
1495	It's all relative: analyzing microbiome data as compositions. <i>Annals of Epidemiology</i> , 2016, 26, 322-329.	0.9	216
1496	Host genetics is associated with the gut microbial community membership rather than the structure. <i>Molecular BioSystems</i> , 2016, 12, 1676-1686.	2.9	11
1497	Comparative studies of the composition of bacterial microbiota associated with the ruminal content, ruminal epithelium and in the faeces of lactating dairy cows. <i>Microbial Biotechnology</i> , 2016, 9, 257-268.	2.0	150
1498	Randomized Control Trial of Human Recombinant Lactoferrin: A Substudy Reveals Effects on the Fecal Microbiome of Very Low Birth Weight Infants. <i>Journal of Pediatrics</i> , 2016, 173, S37-S42.	0.9	42
1499	Depth-dependent and seasonal variability in archaeal community structure in the subarctic and subtropical western North Pacific. <i>Journal of Oceanography</i> , 2016, 72, 427-438.	0.7	8
1500	Immunization with a heat-killed preparation of the environmental bacterium <i>Mycobacterium vaccae</i> promotes stress resilience in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3130-9.	3.3	186
1501	Subaerial biofilms on granitic historic buildings: microbial diversity and development of phototrophic multi-species cultures. <i>Biofouling</i> , 2016, 32, 657-669.	0.8	49
1502	Prevalent high-risk HPV infection and vaginal microbiota in Nigerian women. <i>Epidemiology and Infection</i> , 2016, 144, 123-137.	1.0	104
1503	A compositional shift in the soil microbiome induced by tetracycline, sulfamonomethoxine and ciprofloxacin entering a plant-soil system. <i>Environmental Pollution</i> , 2016, 212, 440-448.	3.7	71
1504	Composition and function of the pediatric colonic mucosal microbiome in untreated patients with ulcerative colitis. <i>Gut Microbes</i> , 2016, 7, 384-396.	4.3	84
1505	Comparison of Diet versus Exercise on Metabolic Function and Gut Microbiota in Obese Rats. <i>Medicine and Science in Sports and Exercise</i> , 2016, 48, 1688-1698.	0.2	97
1506	Insight into how organic amendments can shape the soil microbiome in long-term field experiments as revealed by network analysis. <i>Soil Biology and Biochemistry</i> , 2016, 99, 137-149.	4.2	282
1507	Metagenomic analysis shows diverse, distinct bacterial communities in biofilters among different marine recirculating aquaculture systems. <i>Aquaculture International</i> , 2016, 24, 1393-1408.	1.1	29
1508	The importance of the microbiome in epidemiologic research. <i>Annals of Epidemiology</i> , 2016, 26, 301-305.	0.9	35

#	ARTICLE	IF	CITATIONS
1509	The distribution characteristics of the major capsid gene (g23) of T4-type phages in paddy floodwater in Northeast China. <i>Soil Science and Plant Nutrition</i> , 2016, 62, 133-139.	0.8	4
1510	Multiple paths of electron flow to current in microbial electrolysis cells fed with low and high concentrations of propionate. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 5999-6011.	1.7	56
1511	Gut microbiota analysis reveals a marked shift to bifidobacteria by a starter infant formula containing a synbiotic of bovine milk-derived oligosaccharides and <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> ...CNCM I-3446. <i>Environmental Microbiology</i> , 2016, 18, 2185-2195.	1.8	68
1512	Gut microbiome remodeling induces depressive-like behaviors through a pathway mediated by the host's metabolism. <i>Molecular Psychiatry</i> , 2016, 21, 786-796.	4.1	1,397
1513	Compositional analysis: a valid approach to analyze microbiome high-throughput sequencing data. <i>Canadian Journal of Microbiology</i> , 2016, 62, 692-703.	0.8	294
1514	Unique microbial-derived volatile organic compounds in portal venous circulation in murine non-alcoholic fatty liver disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1337-1344.	1.8	20
1515	Differential Effects of Azithromycin, Doxycycline, and Cotrimoxazole in Ingested Blood on the Vectorial Capacity of Malaria Mosquitoes. <i>Open Forum Infectious Diseases</i> , 2016, 3, ofw074.	0.4	26
1516	Assessment of Bacterial Communities and Predictive Functional Profiling in Soils Subjected to Short-Term Fumigation-Incubation. <i>Microbial Ecology</i> , 2016, 72, 240-251.	1.4	22
1517	Microbiome response to controlled shifts in ammonium and LCFA levels in co-digestion systems. <i>Journal of Biotechnology</i> , 2016, 220, 35-44.	1.9	32
1518	Structural and functional differentiation of the root-associated bacterial microbiomes of perennial ryegrass. <i>Soil Biology and Biochemistry</i> , 2016, 98, 1-10.	4.2	99
1519	Mx1 reveals innate pathways to antiviral resistance and lethal influenza disease. <i>Science</i> , 2016, 352, 463-466.	6.0	210
1520	pH affects bacterial community composition in soils across the Huashan Watershed, China. <i>Canadian Journal of Microbiology</i> , 2016, 62, 726-734.	0.8	6
1521	Respiratory syncytial virus and rhinovirus severe bronchiolitis are associated with distinct nasopharyngeal microbiota. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1909-1913.e4.	1.5	82
1522	Maternal IgG and IgA Antibodies Dampen Mucosal T Helper Cell Responses in Early Life. <i>Cell</i> , 2016, 165, 827-841.	13.5	231
1523	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in <i>Opisthorchis viverrini</i> Associated Cholangiocarcinoma. <i>EBioMedicine</i> , 2016, 8, 195-202.	2.7	94
1524	An Efficient Algorithm for Microbiome Sample Visualization Based on UniFrac Distance and Laplace Matrix. <i>IEEE Transactions on Nanobioscience</i> , 2016, 15, 390-396.	2.2	0
1525	Incorporating microbiota data into epidemiologic models: examples from vaginal microbiota research. <i>Annals of Epidemiology</i> , 2016, 26, 360-365.	0.9	17
1526	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. <i>MSystems</i> , 2016, 1, .	1.7	367

#	ARTICLE	IF	CITATIONS
1527	Evidence for a distinct gut microbiome in kidney stone formers compared to non-stone formers. <i>Urolithiasis</i> , 2016, 44, 399-407.	1.2	122
1528	From Sample to Multi-Omics Conclusions in under 48 Hours. <i>MSystems</i> , 2016, 1, .	1.7	53
1529	Multidrug resistance phenotypes are widespread over different bacterial taxonomic groups thriving in surface water. <i>Science of the Total Environment</i> , 2016, 563-564, 1-9.	3.9	56
1530	Longitudinal Analysis of Microbiota in Microalga <i>Nannochloropsis salina</i> Cultures. <i>Microbial Ecology</i> , 2016, 72, 14-24.	1.4	13
1531	Mineralogy and Microbial Diversity of the Microbialites in the Hypersaline Storr's Lake, the Bahamas. <i>Astrobiology</i> , 2016, 16, 282-300.	1.5	23
1532	Genetic assessment of meiobenthic community composition and spatial distribution in coastal sediments along northern Gulf of Mexico. <i>Marine Environmental Research</i> , 2016, 119, 166-175.	1.1	15
1533	Effects of soil substrate quality, microbial diversity and community composition on the plant community during primary succession. <i>Soil Biology and Biochemistry</i> , 2016, 99, 75-84.	4.2	53
1534	Evaluating communityâ€environment relationships along fine to broad taxonomic resolutions reveals evolutionary forces underlying community assembly. <i>ISME Journal</i> , 2016, 10, 2867-2878.	4.4	31
1535	Resistant starch alters gut microbiome and metabolomic profiles concurrent with amelioration of chronic kidney disease in rats. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 310, F857-F871.	1.3	208
1536	Early-life gut microbiome composition and milk allergy resolution. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 1122-1130.	1.5	307
1537	Deterministic assembly processes govern bacterial community structure in the Fynbos, South Africa. <i>Microbial Ecology</i> , 2016, 72, 313-323.	1.4	22
1538	Microbiome changes through ontogeny of a tick pathogen vector. <i>Molecular Ecology</i> , 2016, 25, 4963-4977.	2.0	140
1539	Latitudinal distribution of microbial communities in anaerobic biological stabilization ponds: effect of the mean annual temperature. <i>Microbial Biotechnology</i> , 2016, 9, 834-845.	2.0	5
1540	Disease Progression and Resolution in Rodent Models of <i>Clostridium difficile</i> Infection and Impact of Antitoxin Antibodies and Vancomycin. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6471-6482.	1.4	28
1541	Distinctive gut microbial community structure in both the wild and farmed Swan goose (<i>Anser</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.8	36
1542	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw191.	1.3	102
1543	Bacterial microbiota associated with flower pollen is influenced by pollination type, and shows a high degree of diversity and speciesâ€specificity. <i>Environmental Microbiology</i> , 2016, 18, 5161-5174.	1.8	132
1544	Vineyard soil bacterial diversity and composition revealed by 16S rRNA genes: Differentiation by vineyard management. <i>Soil Biology and Biochemistry</i> , 2016, 103, 337-348.	4.2	95

#	ARTICLE	IF	CITATIONS
1545	Effects of field conditions on fecal microbiota. <i>Journal of Microbiological Methods</i> , 2016, 130, 180-188.	0.7	28
1546	Effect of dietary interventions on the intestinal microbiota of Mongolian hosts. <i>Science Bulletin</i> , 2016, 61, 1605-1614.	4.3	16
1547	Structure and temporal dynamics of the bacterial communities associated to microhabitats of the coral <i>Oculina patagonica</i> . <i>Environmental Microbiology</i> , 2016, 18, 4564-4578.	1.8	37
1548	Detailed methods of two home-based vegetable gardening intervention trials to improve diet, physical activity, and quality of life in two different populations of cancer survivors. <i>Contemporary Clinical Trials</i> , 2016, 50, 201-212.	0.8	22
1549	Characterization and comparison of the temporal dynamics of ruminal bacterial microbiota colonizing rice straw and alfalfa hay within ruminants. <i>Journal of Dairy Science</i> , 2016, 99, 9668-9681.	1.4	100
1551	Rapid change of fecal microbiome and disappearance of <i>Clostridium difficile</i> in a colonized infant after transition from breast milk to cow milk. <i>Microbiome</i> , 2016, 4, 53.	4.9	59
1552	High-throughput metabarcoding of eukaryotic diversity for environmental monitoring of offshore oil-drilling activities. <i>Molecular Ecology</i> , 2016, 25, 4392-4406.	2.0	77
1553	Oral microbiome diversity among Cheyenne and Arapaho individuals from Oklahoma. <i>American Journal of Physical Anthropology</i> , 2016, 161, 321-327.	2.1	25
1554	A modified weighted mixture model for the interpretation of spatial and temporal changes in the microbial communities in drinking water reservoirs using compositional phospholipid fatty acid data. <i>Talanta</i> , 2016, 160, 148-156.	2.9	0
1555	Bacterial microbiota compositions of naturally fermented milk are shaped by both geographic origin and sample type. <i>Journal of Dairy Science</i> , 2016, 99, 7832-7841.	1.4	69
1556	The Oral and Skin Microbiomes of Captive Komodo Dragons Are Significantly Shared with Their Habitat. <i>MSystems</i> , 2016, 1, .	1.7	61
1557	Purified rutin and rutin-rich asparagus attenuates disease severity and tissue damage following dextran sodium sulfate-induced colitis. <i>Molecular Nutrition and Food Research</i> , 2016, 60, 2396-2412.	1.5	27
1559	Preparation of a standardised faecal slurry for ex-vivo microbiota studies which reduces inter-individual donor bias. <i>Journal of Microbiological Methods</i> , 2016, 129, 109-116.	0.7	29
1560	Long-term antibiotic exposure in soil is associated with changes in microbial community structure and prevalence of class 1 integrons. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw159.	1.3	46
1561	Does adaptive radiation of a host lineage promote ecological diversity of its bacterial communities? A test using gut microbiota of <i>Anolis</i> lizards. <i>Molecular Ecology</i> , 2016, 25, 4793-4804.	2.0	63
1562	Using PacBio Long-Read High-Throughput Microbial Gene Amplicon Sequencing To Evaluate Infant Formula Safety. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 6993-7001.	2.4	24
1563	Patterns of bacterial biodiversity in the glacial meltwater streams of the McMurdo Dry Valleys, Antarctica. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw148.	1.3	41
1564	Effects of host genetics and environment on egg-associated microbiotas in brown trout (<i>Salmo</i>)	2.0	28

#	ARTICLE	IF	CITATIONS
1565	Lactulose Differently Modulates the Composition of Luminal and Mucosal Microbiota in C57BL/6J Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 6240-6247.	2.4	98
1566	Activation of CO ₂ -reducing methanogens in oil reservoir after addition of nutrient. <i>Journal of Bioscience and Bioengineering</i> , 2016, 122, 740-747.	1.1	12
1567	Bacterial Ecology of Fermented Cucumber Rising pH Spoilage as Determined by Nonculture-Based Methods. <i>Journal of Food Science</i> , 2016, 81, M121-9.	1.5	41
1568	PhyloMeasures: a package for computing phylogenetic biodiversity measures and their statistical moments. <i>Ecography</i> , 2016, 39, 709-714.	2.1	159
1569	PhyloCore: A phylogenetic approach to identifying core taxa in microbial communities. <i>Gene</i> , 2016, 593, 330-333.	1.0	11
1570	Response of diatom-associated bacteria to host growth state, nutrient concentrations, and viral host infection in a model system. <i>Environmental Microbiology Reports</i> , 2016, 8, 917-927.	1.0	15
1571	Captivity humanizes the primate microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10376-10381.	3.3	369
1572	Proteobacteria become predominant during regrowth after water disinfection. <i>Science of the Total Environment</i> , 2016, 573, 313-323.	3.9	77
1573	Molecular Microbiological Profile of Chronic Suppurative Otitis Media. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2538-2546.	1.8	48
1574	Effect of Wild and Cultivated Rice Genotypes on Rhizosphere Bacterial Community Composition. <i>Rice</i> , 2016, 9, 42.	1.7	75
1575	<i>Solanum lycopersicum</i> (tomato) hosts robust phyllosphere and rhizosphere bacterial communities when grown in soil amended with various organic and synthetic fertilizers. <i>Science of the Total Environment</i> , 2016, 573, 555-563.	3.9	51
1576	Extreme Dysbiosis of the Microbiome in Critical Illness. <i>MSphere</i> , 2016, 1, .	1.3	283
1577	Dissecting host-associated communities with DNA barcodes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150328.	1.8	23
1578	Gene Sequencing-Based Analysis of Microbial-Mat Morphotypes, Caicos Platform, British West Indies. <i>Journal of Sedimentary Research</i> , 2016, 86, 629-636.	0.8	38
1579	Local Environmental Factors Drive Divergent Grassland Soil Bacterial Communities in the Western Swiss Alps. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6303-6316.	1.4	63
1580	Pyrene dissipation potential varies with soil type and associated bacterial community changes. <i>Soil Biology and Biochemistry</i> , 2016, 103, 71-85.	4.2	43
1582	Macroevolution of Specificity in Cyanolichens of the Genus <i>Peltigera</i> Section <i>Polydactylon</i> (Lecanoromycetes, Ascomycota). <i>Systematic Biology</i> , 2017, 66, syw065.	2.7	56
1583	Experimental sulfate amendment alters peatland bacterial community structure. <i>Science of the Total Environment</i> , 2016, 566-567, 1289-1296.	3.9	22

#	ARTICLE	IF	CITATIONS
1584	Fat and vitamin intakes during pregnancy have stronger relations with a pro-inflammatory maternal microbiota than does carbohydrate intake. <i>Microbiome</i> , 2016, 4, 55.	4.9	101
1585	Sulfur Fertilization Changes the Community Structure of Rice Root-, and Soil- Associated Bacteria. <i>Microbes and Environments</i> , 2016, 31, 70-75.	0.7	20
1586	H ₂ -Producing Bacterial Community during Rice Straw Decomposition in Paddy Field Soil: Estimation by an Analysis of [FeFe]-Hydrogenase Gene Transcripts. <i>Microbes and Environments</i> , 2016, 31, 226-233.	0.7	11
1587	Chronic Repression of mTOR Complex 2 Induces Changes in the Gut Microbiota of Diet-induced Obese Mice. <i>Scientific Reports</i> , 2016, 6, 30887.	1.6	142
1588	ABO antigen and secretor statuses are not associated with gut microbiota composition in 1,500 twins. <i>BMC Genomics</i> , 2016, 17, 941.	1.2	61
1589	Nutrient enrichment induces dormancy and decreases diversity of active bacteria in salt marsh sediments. <i>Nature Communications</i> , 2016, 7, 12881.	5.8	119
1590	Cecal bacterial communities in wild Japanese rock ptarmigans and captive Svalbard rock ptarmigans. <i>Journal of Veterinary Medical Science</i> , 2016, 78, 251-257.	0.3	25
1591	Shifting the balance of fermentation products between hydrogen and volatile fatty acids: microbial community structure and function. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw195.	1.3	14
1592	Gut microbiota are linked to increased susceptibility to hepatic steatosis in low-aerobic-capacity rats fed an acute high-fat diet. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, G166-G179.	1.6	32
1593	Water management impacts rice methylmercury and the soil microbiome. <i>Science of the Total Environment</i> , 2016, 572, 608-617.	3.9	62
1594	High-fat diet modifies the PPAR- β pathway leading to disruption of microbial and physiological ecosystem in murine small intestine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5934-E5943.	3.3	180
1595	Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. <i>Journal of Insect Science</i> , 2016, 16, 97.	0.6	49
1596	Neonatal gut microbiota associates with childhood multisensitized atopy and T cell differentiation. <i>Nature Medicine</i> , 2016, 22, 1187-1191.	15.2	844
1597	A Community of Clones: Snow Algae Are Diverse Communities of Spatially Structured Clones. <i>International Journal of Plant Sciences</i> , 2016, 177, 432-439.	0.6	52
1598	Bacterial community dynamics in a rumen fluid bioreactor during in-vitro cultivation. <i>Journal of Biotechnology</i> , 2016, 234, 43-49.	1.9	10
1599	Recurrent <i>Clostridium difficile</i> infection associates with distinct bile acid and microbiome profiles. <i>Alimentary Pharmacology and Therapeutics</i> , 2016, 43, 1142-1153.	1.9	151
1600	Antibiotics, birth mode, and diet shape microbiome maturation during early life. <i>Science Translational Medicine</i> , 2016, 8, 343ra82.	5.8	1,012
1601	Introductions do not compensate for functional and phylogenetic losses following extinctions in insular bird assemblages. <i>Ecology Letters</i> , 2016, 19, 1091-1100.	3.0	61

#	ARTICLE	IF	CITATIONS
1602	Exploring the potential of anaerobic sulfate reduction process in treating sulfonated diazo dye: Microbial community analysis using bar-coded pyrosequencing. <i>Journal of Hazardous Materials</i> , 2016, 318, 641-649.	6.5	31
1603	Soil microbial communities of three major Chinese truffles in southwest China. <i>Canadian Journal of Microbiology</i> , 2016, 62, 970-979.	0.8	22
1604	Chronic nitrogen additions fundamentally restructure the soil fungal community in a temperate forest. <i>Fungal Ecology</i> , 2016, 23, 48-57.	0.7	172
1605	Grazers structure the bacterial and algal diversity of aquatic metacommunities. <i>Ecology</i> , 2016, 97, 3472-3484.	1.5	13
1606	Bacterial communities involved in sulfur transformations in wastewater treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 10125-10135.	1.7	34
1607	Forensic analysis using microbial community between skin bacteria and fabrics. <i>Toxicology and Environmental Health Sciences</i> , 2016, 8, 263-270.	1.1	23
1608	Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. <i>Nature Microbiology</i> , 2016, 1, 16177.	5.9	194
1609	A high-resolution map of the gut microbiota in Atlantic salmon (<i>Salmo salar</i>): A basis for comparative gut microbial research. <i>Scientific Reports</i> , 2016, 6, 30893.	1.6	246
1610	Weight gain in anorexia nervosa does not ameliorate the faecal microbiota, branched chain fatty acid profiles and gastrointestinal complaints. <i>Scientific Reports</i> , 2016, 6, 26752.	1.6	233
1611	Bacterial abundance and diversity in pond water supplied with different feeds. <i>Scientific Reports</i> , 2016, 6, 35232.	1.6	88
1612	<i>Microbiome.</i> , 2016, , 14-18.		0
1613	Spatial Patterns of bphA Gene Diversity Reveal Local Adaptation of Microbial Communities to PCB and PAH Contaminants. <i>Microbial Ecology</i> , 2016, 72, 559-570.	1.4	12
1614	Effects of acute intra-abdominal hypertension on multiple intestinal barrier functions in rats. <i>Scientific Reports</i> , 2016, 6, 22814.	1.6	39
1615	Environmental selection of planktonic methanogens in permafrost thaw ponds. <i>Scientific Reports</i> , 2016, 6, 31312.	1.6	25
1616	Local adaptation of a bacterium is as important as its presence in structuring a natural microbial community. <i>Nature Communications</i> , 2016, 7, 12453.	5.8	79
1617	Dairy and plant based food intakes are associated with altered faecal microbiota in 2 to 3 year old Australian children. <i>Scientific Reports</i> , 2016, 6, 32385.	1.6	58
1618	Gut microbiota of dung beetles correspond to dietary specializations of adults and larvae. <i>Molecular Ecology</i> , 2016, 25, 6092-6106.	2.0	79
1619	Stygofauna enhance prokaryotic transport in groundwater ecosystems. <i>Scientific Reports</i> , 2016, 6, 32738.	1.6	23

#	ARTICLE	IF	CITATIONS
1620	Translational Biomedical Informatics. <i>Advances in Experimental Medicine and Biology</i> , 2016, , .	0.8	1
1621	Metagenomics and Single-Cell Omics Data Analysis for Human Microbiome Research. <i>Advances in Experimental Medicine and Biology</i> , 2016, 939, 117-137.	0.8	3
1622	The Impact of Dietary Energy Intake Early in Life on the Colonic Microbiota of Adult Mice. <i>Scientific Reports</i> , 2016, 6, 19083.	1.6	18
1623	Illumina Miseq platform analysis caecum bacterial communities of rex rabbits fed with different antibiotics. <i>AMB Express</i> , 2016, 6, 100.	1.4	30
1624	Tongue Coating and the Salivary Microbial Communities Vary in Children with Halitosis. <i>Scientific Reports</i> , 2016, 6, 24481.	1.6	51
1625	N-fixing trees in wetland restoration plantings: effects on nitrogensupply and soil microbial communities. <i>Environmental Science and Pollution Research</i> , 2016, 23, 24749-24757.	2.7	11
1626	Alterations of the human gut microbiome in multiple sclerosis. <i>Nature Communications</i> , 2016, 7, 12015.	5.8	957
1627	Assessing quality of <i>Medicago sativa</i> silage by monitoring bacterial composition with single molecule, real-time sequencing technology and various physiological parameters. <i>Scientific Reports</i> , 2016, 6, 28358.	1.6	75
1628	Metagenomic approach reveals microbial diversity and predictive microbial metabolic pathways in Yucha, a traditional Li fermented food. <i>Scientific Reports</i> , 2016, 6, 32524.	1.6	74
1629	Genome and metagenome analyses reveal adaptive evolution of the host and interaction with the gut microbiota in the goose. <i>Scientific Reports</i> , 2016, 6, 32961.	1.6	36
1630	The microenvironment of injured murine gut elicits a local pro-restitutive microbiota. <i>Nature Microbiology</i> , 2016, 1, 15021.	5.9	182
1631	Testing the Neutral Theory of Biodiversity with Human Microbiome Datasets. <i>Scientific Reports</i> , 2016, 6, 31448.	1.6	83
1632	Fecal metabolomics in pediatric spondyloarthritis implicate decreased metabolic diversity and altered tryptophan metabolism as pathogenic factors. <i>Genes and Immunity</i> , 2016, 17, 400-405.	2.2	57
1633	Responses of soil nitrogen fixation to <i>Spartina alterniflora</i> invasion and nitrogen addition in a Chinese salt marsh. <i>Scientific Reports</i> , 2016, 6, 20384.	1.6	48
1634	Role of <i>Fusobacteria</i> in the serrated pathway of colorectal carcinogenesis. <i>Scientific Reports</i> , 2016, 6, 25271.	1.6	55
1635	Antibiotic-induced perturbations in gut microbial diversity influences neuro-inflammation and amyloidosis in a murine model of Alzheimer's disease. <i>Scientific Reports</i> , 2016, 6, 30028.	1.6	469
1636	Structural modulation of the gut microbiota and the relationship with body weight: compared evaluation of liraglutide and saxagliptin treatment. <i>Scientific Reports</i> , 2016, 6, 33251.	1.6	117
1637	High-throughput sequencing-based analysis of endogenetic fungal communities inhabiting the Chinese <i>Cordyceps</i> reveals unexpectedly high fungal diversity. <i>Scientific Reports</i> , 2016, 6, 33437.	1.6	45

#	ARTICLE	IF	CITATIONS
1638	Association of nasopharyngeal microbiota profiles with bronchiolitis severity in infants hospitalised for bronchiolitis. <i>European Respiratory Journal</i> , 2016, 48, 1329-1339.	3.1	144
1639	Potential use of bacterial community succession for estimating post-mortem interval as revealed by high-throughput sequencing. <i>Scientific Reports</i> , 2016, 6, 24197.	1.6	77
1640	Oral microbial community typing of caries and pigment in primary dentition. <i>BMC Genomics</i> , 2016, 17, 558.	1.2	35
1641	Diversity and Biogeography of Picoeukaryotes: New Insights into the Rare Biosphere. , 2016, , 315-328.		1
1642	Comparison of placenta samples with contamination controls does not provide evidence for a distinct placenta microbiota. <i>Microbiome</i> , 2016, 4, 29.	4.9	447
1643	Habitat heterogeneity and connectivity shape microbial communities in South American peatlands. <i>Scientific Reports</i> , 2016, 6, 25712.	1.6	31
1644	Biogeochemical Stoichiometry Reveals P and N Limitation Across the Post-glacial Landscape of Denali National Park, Alaska. <i>Ecosystems</i> , 2016, 19, 1164-1177.	1.6	45
1645	Antibiotic Treatment Induces Long-lasting Changes in the Fecal Microbiota that Protect Against Colitis. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 2328-2340.	0.9	20
1646	Linkages between mineralogy, fluid chemistry, and microbial communities within hydrothermal chimneys from the Endeavour Segment, Juan de Fuca Ridge. <i>Geochemistry, Geophysics, Geosystems</i> , 2016, 17, 300-323.	1.0	25
1647	Effect of Formula Containing <i>Lactobacillus reuteri</i> DSM 17938 on Fecal Microbiota of Infants Born by Cesarean Section. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 63, 681-687.	0.9	49
1648	Dead or Alive: Deoxyribonuclease I Sensitive Bacteria and Implications for the Sinus Microbiome. <i>American Journal of Rhinology and Allergy</i> , 2016, 30, 94-98.	1.0	25
1649	Species-specific diversity of novel bacterial lineages and differential abundance of predicted pathways for toxic compound degradation in scorpion gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 1364-1378.	1.8	20
1650	A guide through a family of phylogenetic dissimilarity measures among sites. <i>Oikos</i> , 2016, 125, 1719-1732.	1.2	31
1651	Geography and Location Are the Primary Drivers of Office Microbiome Composition. <i>MSystems</i> , 2016, 1, .	1.7	110
1652	Correlation of the lung microbiota with metabolic profiles in bronchoalveolar lavage fluid in HIV infection. <i>Microbiome</i> , 2016, 4, 3.	4.9	83
1653	Presence of pathogenic <i>Escherichia coli</i> is correlated with bacterial community diversity and composition on pre-harvest cattle hides. <i>Microbiome</i> , 2016, 4, 9.	4.9	25
1654	Dynamics of size-fractionated bacterial communities during the coastal dispersal of treated municipal effluents. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 5839-5848.	1.7	12
1655	Short-term waterlogging increases arbuscular mycorrhizal fungal species richness and shifts community composition. <i>Plant and Soil</i> , 2016, 404, 373-384.	1.8	28

#	ARTICLE	IF	CITATIONS
1656	Evaluation of 16S rRNA amplicon sequencing using two next-generation sequencing technologies for phylogenetic analysis of the rumen bacterial community in steers. <i>Journal of Microbiological Methods</i> , 2016, 127, 132-140.	0.7	79
1657	The pediatric intestinal mucosal microbiome remains altered after clinical resolution of inflammatory and ischemic disease. <i>Surgery</i> , 2016, 160, 350-358.	1.0	8
1658	Gut microbiota translocation to the pancreatic lymph nodes triggers NOD2 activation and contributes to T1D onset. <i>Journal of Experimental Medicine</i> , 2016, 213, 1223-1239.	4.2	163
1659	Site-specific environmental factors control bacterial and viral diversity in stormwater retention ponds. <i>Aquatic Microbial Ecology</i> , 2016, 77, 23-36.	0.9	16
1660	<i>Caenorhabditis elegans</i> responses to bacteria from its natural habitats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3941-9.	3.3	317
1661	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. <i>MBio</i> , 2016, 7, .	1.8	325
1662	The Microbiota of Breast Tissue and Its Association with Breast Cancer. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5039-5048.	1.4	397
1663	Prebiotics and Bioactive Milk Fractions Affect Gut Development, Microbiota, and Neurotransmitter Expression in Piglets. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 63, 688-697.	0.9	60
1664	A watering manipulation in a semiarid grassland induced changes in fungal but not bacterial community composition. <i>Pedobiologia</i> , 2016, 59, 121-127.	0.5	24
1665	Responses of ammonia-oxidizing bacterial communities to land-use and seasonal changes in Mollisols of Northeast China. <i>European Journal of Soil Biology</i> , 2016, 74, 121-127.	1.4	6
1666	Design Defines the Effects of Nanoceria at a Low Dose on Soil Microbiota and the Potentiation of Impacts by the Canola Plant. <i>Environmental Science & Technology</i> , 2016, 50, 6892-6901.	4.6	30
1667	Enhanced electrical power generation using flame-oxidized stainless steel anode in microbial fuel cells and the anodic community structure. <i>Biotechnology for Biofuels</i> , 2016, 9, 62.	6.2	42
1668	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. <i>Microbiome</i> , 2016, 4, 11.	4.9	51
1669	Bacterial communities in penile skin, male urethra, and vaginas of heterosexual couples with and without bacterial vaginosis. <i>Microbiome</i> , 2016, 4, 16.	4.9	124
1670	Bioinformatics for agriculture in the Next-Generation sequencing era. <i>Chemical and Biological Technologies in Agriculture</i> , 2016, 3, .	1.9	31
1671	Physiological and microbial adjustments to diet quality permit facultative herbivory in an omnivorous lizard. <i>Journal of Experimental Biology</i> , 2016, 219, 1903-1912.	0.8	38
1672	Relationship of Bacterial Richness to Organic Degradation Rate and Sediment Age in Subseafloor Sediment. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4994-4999.	1.4	47
1673	A Brief Review on the Ecological Network Analysis with Applications in the Emerging Medical Ecology. <i>Springer Protocols</i> , 2016, , 7-39.	0.1	7

#	ARTICLE	IF	CITATIONS
1674	PERMANOVA-S: association test for microbial community composition that accommodates confounders and multiple distances. <i>Bioinformatics</i> , 2016, 32, 2618-2625.	1.8	120
1675	Composition of the Cutaneous Bacterial Community in Japanese Amphibians: Effects of Captivity, Host Species, and Body Region. <i>Microbial Ecology</i> , 2016, 72, 460-469.	1.4	70
1676	Analysis of bacterial diversity of Chinese Luzhou-flavor liquor brewed in different seasons by Illumina Miseq sequencing. <i>Annals of Microbiology</i> , 2016, 66, 1293-1301.	1.1	56
1677	A hollow bacterial diversity pattern with elevation in Wolong Nature Reserve, Western Sichuan Plateau. <i>Journal of Soils and Sediments</i> , 2016, 16, 2365-2374.	1.5	20
1678	An extended single-index multiplexed 16S rRNA sequencing for microbial community analysis on MiSeq illumina platforms. <i>Journal of Basic Microbiology</i> , 2016, 56, 321-326.	1.8	93
1679	Deterministic processes dominate nematode community structure in the Fynbos Mediterranean heathland of South Africa. <i>Evolutionary Ecology</i> , 2016, 30, 685-701.	0.5	24
1680	Predominance of <i>Lactobacillus</i> spp. Among Patients Who Do Not Acquire Multidrug-Resistant Organisms. <i>Clinical Infectious Diseases</i> , 2016, 63, 937-943.	2.9	28
1681	Piglet nasal microbiota at weaning may influence the development of <i>Claserr</i> 's disease during the rearing period. <i>BMC Genomics</i> , 2016, 17, 404.	1.2	56
1682	Maternal group B <i>Streptococcus</i> and the infant gut microbiota. <i>Journal of Developmental Origins of Health and Disease</i> , 2016, 7, 45-53.	0.7	31
1683	Millions of reads, thousands of taxa: microbial community structure and associations analyzed via marker genes. <i>FEMS Microbiology Reviews</i> , 2016, 40, 686-700.	3.9	159
1684	Indoor air bacterial communities in <i>Hong Kong</i> households assemble independently of occupant skin microbiomes. <i>Environmental Microbiology</i> , 2016, 18, 1754-1763.	1.8	47
1685	Microbiome change by symbiotic invasion in lichens. <i>Environmental Microbiology</i> , 2016, 18, 1428-1439.	1.8	41
1686	Microbiome metabolome analysis reveals unhealthy alterations in the composition and metabolism of ruminal microbiota with increasing dietary grain in a goat model. <i>Environmental Microbiology</i> , 2016, 18, 525-541.	1.8	217
1687	Examining the diversity of microbes in a deep-sea coral community impacted by the Deepwater Horizon oil spill. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 129, 157-166.	0.6	32
1688	Arbuscular mycorrhizal fungal communities and <i>Rhizophagus irregularis</i> populations shift in response to short-term ploughing and fertilisation in a buffer strip. <i>Mycorrhiza</i> , 2016, 26, 33-46.	1.3	34
1689	The microbiome and functions of black soils are altered by dibutyl phthalate contamination. <i>Applied Soil Ecology</i> , 2016, 99, 51-61.	2.1	62
1690	Assembly of the <i>Caenorhabditis elegans</i> gut microbiota from diverse soil microbial environments. <i>ISME Journal</i> , 2016, 10, 1998-2009.	4.4	296
1691	Impact of Nisin-Activated Packaging on Microbiota of Beef Burgers during Storage. <i>Applied and Environmental Microbiology</i> , 2016, 82, 549-559.	1.4	47

#	ARTICLE	IF	CITATIONS
1692	Bacterial Diversity and Community Structure in Two Bornean <i>Nepenthes</i> Species with Differences in Nitrogen Acquisition Strategies. <i>Microbial Ecology</i> , 2016, 71, 938-953.	1.4	11
1693	Impact of combined β -glucanase and xylanase enzymes on growth performance, nutrients utilization and gut microbiota in broiler chickens fed corn or wheat-based diets. <i>Poultry Science</i> , 2016, 95, 528-540.	1.5	105
1694	Microbial community structure and predicted bacterial metabolic functions in biochar pellets aged in soil after 34 months. <i>Applied Soil Ecology</i> , 2016, 100, 135-143.	2.1	43
1695	Diet-induced extinctions in the gut microbiota compound over generations. <i>Nature</i> , 2016, 529, 212-215.	13.7	1,287
1696	Intestinal Epithelial Toll-Like Receptor 4 Signaling Affects Epithelial Function and Colonic Microbiota and Promotes a Risk for Transmissible Colitis. <i>Infection and Immunity</i> , 2016, 84, 798-810.	1.0	114
1697	Biodiversity patterns of plankton assemblages at the extremes of the Red Sea. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw002.	1.3	31
1698	Conversion of orange peel waste biomass to bioelectricity using a mediator-less microbial fuel cell. <i>Science of the Total Environment</i> , 2016, 547, 197-205.	3.9	104
1699	Human milk microbiota profiles in relation to birthing method, gestation and infant gender. <i>Microbiome</i> , 2016, 4, 1.	4.9	315
1700	The dual oxidase gene <i>BdDuoX</i> regulates the intestinal bacterial community homeostasis of <i>Bactrocera dorsalis</i> . <i>ISME Journal</i> , 2016, 10, 1037-1050.	4.4	118
1701	Aquatic nitrogen-fixing cyanobacteria associated with blooms of <i>Didymosphenia geminata</i> : insights from a field study. <i>Hydrobiologia</i> , 2016, 770, 37-52.	1.0	3
1702	The role of gut microbiota in fetal methylmercury exposure: Insights from a pilot study. <i>Toxicology Letters</i> , 2016, 242, 60-67.	0.4	56
1703	Mucosal Barrier Depletion and Loss of Bacterial Diversity are Primary Abnormalities in Paediatric Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 462-471.	0.6	178
1704	Two Healthy Diets Modulate Gut Microbial Community Improving Insulin Sensitivity in a Human Obese Population. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 233-242.	1.8	223
1705	Effects of organic-inorganic compound fertilizer with reduced chemical fertilizer application on crop yields, soil biological activity and bacterial community structure in a rice-wheat cropping system. <i>Applied Soil Ecology</i> , 2016, 99, 1-12.	2.1	286
1706	Inhibitory effects of laminaran and alginate on production of putrefactive compounds from soy protein by intestinal microbiota in vitro and in rats. <i>Carbohydrate Polymers</i> , 2016, 143, 61-69.	5.1	51
1707	Is there a convergence of deciduous leaf litter stoichiometry, biochemistry and microbial population during decay?. <i>Geoderma</i> , 2016, 272, 93-100.	2.3	33
1708	The human milk oligosaccharide β -fucosyllactose augments the adaptive response to extensive intestinal. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 310, G427-G438.	1.6	35
1709	Analysis of factors contributing to variation in the C57BL/6J fecal microbiota across German animal facilities. <i>International Journal of Medical Microbiology</i> , 2016, 306, 343-355.	1.5	196

#	ARTICLE	IF	CITATIONS
1710	Diversity and dynamics of algal Megaviridae members during a harmful brown tide caused by the pelagophyte, <i>Aureococcus anophagefferens</i> . FEMS Microbiology Ecology, 2016, 92, fiw058.	1.3	41
1711	Effect of Dust Storms on the Atmospheric Microbiome in the Eastern Mediterranean. Environmental Science & Technology, 2016, 50, 4194-4202.	4.6	90
1712	Host origin and tissue microhabitat shaping the microbiota of the terrestrial isopod <i>Armadillidium vulgare</i> . FEMS Microbiology Ecology, 2016, 92, fiw063.	1.3	41
1713	Bacterioplankton community resilience to ocean acidification: evidence from microbial network analysis. ICES Journal of Marine Science, 2016, 73, 865-875.	1.2	67
1714	Measuring Cluster Stability in a Large Scale Phylogenetic Analysis of Functional Genes in Metagenomes Using pplacer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 341-349.	1.9	1
1715	The microbiota-derived metabolite indole decreases mucosal inflammation and injury in a murine model of NSAID enteropathy. Gut Microbes, 2016, 7, 246-261.	4.3	103
1716	High-throughput sequencing reveals the core gut microbiome of Bar-headed goose (<i>Anser t. t.</i>)	1.2	38
1717	The Effects of Bowel Preparation on Microbiota-Related Metrics Differ in Health and in Inflammatory Bowel Disease and for the Mucosal and Luminal Microbiota Compartments. Clinical and Translational Gastroenterology, 2016, 7, e143.	1.3	76
1718	Sediments and Soils Act as Reservoirs for Taxonomic and Functional Bacterial Diversity in the Upper Mississippi River. Microbial Ecology, 2016, 71, 814-824.	1.4	29
1719	Using in situ bacterial communities to monitor contaminants in river sediments. Environmental Pollution, 2016, 212, 348-357.	3.7	89
1720	Walls talk: Microbial biogeography of homes spanning urbanization. Science Advances, 2016, 2, e1501061.	4.7	72
1721	Indoor microbial communities: Influence on asthma severity in atopic and nonatopic children. Journal of Allergy and Clinical Immunology, 2016, 138, 76-83.e1.	1.5	117
1722	Intestinal microbiome disruption in patients in a long-term acute care hospital: A case for development of microbiome disruption indices to improve infection prevention. American Journal of Infection Control, 2016, 44, 830-836.	1.1	43
1723	Salinity drives archaeal distribution patterns in high altitude lake sediments on the Tibetan Plateau. FEMS Microbiology Ecology, 2016, 92, .	1.3	73
1724	Divergent responses of methanogenic archaeal communities in two rice cultivars to elevated ground-level O ₃ . Environmental Pollution, 2016, 213, 127-134.	3.7	25
1725	Changes of soil prokaryotic communities after clear-cutting in a karst forest: evidences for cutting-based disturbance promoting deterministic processes. FEMS Microbiology Ecology, 2016, 92, fiw026.	1.3	28
1726	Effect of Advanced HIV Infection on the Respiratory Microbiome. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 226-235.	2.5	83
1727	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. Cell Reports, 2016, 14, 945-955.	2.9	49

#	ARTICLE	IF	CITATIONS
1728	Antarctic eukaryotic soil diversity of the Prince Charles Mountains revealed by high-throughput sequencing. <i>Soil Biology and Biochemistry</i> , 2016, 95, 112-121.	4.2	66
1729	Bacterial community dynamics in an anoxic-aerobic membrane bioreactor – Impact on nutrient and trace organic contaminant removal. <i>International Biodeterioration and Biodegradation</i> , 2016, 109, 61-72.	1.9	63
1730	Nutrient limitation of microbial phototrophs on a debris-covered glacier. <i>Soil Biology and Biochemistry</i> , 2016, 95, 156-163.	4.2	53
1731	Increased water contamination and grow-out Pekin duck mortality when raised with water troughs compared to pin-metered water lines using a United States management system. <i>Poultry Science</i> , 2016, 95, 736-748.	1.5	15
1732	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016, 22, 250-253.	15.2	736
1733	Biodiversity Conservation and Phylogenetic Systematics. <i>Topics in Biodiversity and Conservation</i> , 2016, , .	0.3	37
1734	Control of sulfide and methane production in anaerobic sewer systems by means of Downstream Nitrite Dosage. <i>Science of the Total Environment</i> , 2016, 550, 1116-1125.	3.9	32
1735	Regional Similarities and Consistent Patterns of Local Variation in Beach Sand Bacterial Communities throughout the Northern Hemisphere. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2751-2762.	1.4	42
1736	MiSeq HV4 16S rRNA gene analysis of bacterial community composition among the cave sediments of Indo-Burma biodiversity hotspot. <i>Environmental Science and Pollution Research</i> , 2016, 23, 12216-12226.	2.7	23
1737	Aflatoxin B ₁ -Induced Compositional Changes in Gut Microbial Communities of Male F344 Rats. <i>Toxicological Sciences</i> , 2016, 150, 54-63.	1.4	78
1738	Phylogenetics and Conservation Biology: Drawing a Path into the Diversity of Life. <i>Topics in Biodiversity and Conservation</i> , 2016, , 1-15.	0.3	8
1739	The Rarefaction of Phylogenetic Diversity: Formulation, Extension and Application. <i>Topics in Biodiversity and Conservation</i> , 2016, , 197-217.	0.3	7
1740	The Future of Phylogenetic Systematics in Conservation Biology: Linking Biodiversity and Society. <i>Topics in Biodiversity and Conservation</i> , 2016, , 375-383.	0.3	6
1741	The PD Phylogenetic Diversity Framework: Linking Evolutionary History to Feature Diversity for Biodiversity Conservation. <i>Topics in Biodiversity and Conservation</i> , 2016, , 39-56.	0.3	31
1742	Using Phylogenetic Dissimilarities Among Sites for Biodiversity Assessments and Conservation. <i>Topics in Biodiversity and Conservation</i> , 2016, , 119-139.	0.3	1
1743	Phylogenetic Diversity Measures and Their Decomposition: A Framework Based on Hill Numbers. <i>Topics in Biodiversity and Conservation</i> , 2016, , 141-172.	0.3	36
1744	Gut bacterial communities across tadpole ecomorphs in two diverse tropical anuran faunas. <i>Die Naturwissenschaften</i> , 2016, 103, 25.	0.6	85
1745	Does the intestinal microbial community of Korean Crohn's disease patients differ from that of western patients?. <i>BMC Gastroenterology</i> , 2016, 16, 28.	0.8	36

#	ARTICLE	IF	CITATIONS
1746	Elucidating the role of the host genome in shaping microbiome composition. <i>Gut Microbes</i> , 2016, 7, 178-184.	4.3	76
1747	Wind and sunlight shape microbial diversity in surface waters of the North Pacific Subtropical Gyre. <i>ISME Journal</i> , 2016, 10, 1308-1322.	4.4	73
1748	SIV Infection-Mediated Changes in Gastrointestinal Bacterial Microbiome and Virome Are Associated with Immunodeficiency and Prevented by Vaccination. <i>Cell Host and Microbe</i> , 2016, 19, 323-335.	5.1	78
1749	Altered Virome and Bacterial Microbiome in Human Immunodeficiency Virus-Associated Acquired Immunodeficiency Syndrome. <i>Cell Host and Microbe</i> , 2016, 19, 311-322.	5.1	330
1750	Changes in the soil microbial community after reductive soil disinfestation and cucumber seedling cultivation. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 5581-5593.	1.7	90
1751	Impact of the [<i>GAR</i> ⁺] Prion on Fermentation and Bacterial Community Composition with <i>Saccharomyces cerevisiae</i> UCD932. <i>American Journal of Enology and Viticulture</i> , 2016, 67, 296-307.	0.9	22
1752	Bacterial communities in different locations, seasons and segments of a dairy wastewater treatment system consisting of six segments. <i>Journal of Environmental Sciences</i> , 2016, 46, 109-115.	3.2	1
1753	Perinatal Lead Exposure Alters Gut Microbiota Composition and Results in Sex-specific Bodyweight Increases in Adult Mice. <i>Toxicological Sciences</i> , 2016, 151, 324-333.	1.4	113
1754	Bacterial diversity of Grenache and Carignan grape surface from different vineyards at Priorat wine region (Catalonia, Spain). <i>International Journal of Food Microbiology</i> , 2016, 219, 56-63.	2.1	108
1755	Novel Rhizosphere Soil Alleles for the Enzyme 1-Aminocyclopropane-1-Carboxylate Deaminase Queried for Function with an <i>In Vivo</i> Competition Assay. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1050-1059.	1.4	13
1756	Dietary flaxseed modulates the colonic microenvironment in healthy C57Bl/6 male mice which may alter susceptibility to gut-associated diseases. <i>Journal of Nutritional Biochemistry</i> , 2016, 28, 61-69.	1.9	58
1757	Legacy effects of soil moisture on microbial community structure and N ₂ O emissions. <i>Soil Biology and Biochemistry</i> , 2016, 95, 40-50.	4.2	175
1758	Effect of different biochars on antibiotic resistance genes and bacterial community during chicken manure composting. <i>Bioresource Technology</i> , 2016, 203, 11-17.	4.8	286
1759	Contribution of neutral processes to the assembly of gut microbial communities in the zebrafish over host development. <i>ISME Journal</i> , 2016, 10, 655-664.	4.4	627
1760	Impact of different ratios of feedstock to liquid anaerobic digestion effluent on the performance and microbiome of solid-state anaerobic digesters digesting corn stover. <i>Bioresource Technology</i> , 2016, 200, 744-752.	4.8	47
1761	Glyphosate effects on soil rhizosphere-associated bacterial communities. <i>Science of the Total Environment</i> , 2016, 543, 155-160.	3.9	171
1762	Fine-scale monitoring of shifts in microbial community composition after high organic loading in a pilot-scale membrane bioreactor. <i>Journal of Bioscience and Bioengineering</i> , 2016, 121, 550-556.	1.1	35
1763	Bacterial Diversity in the Soda Saline Crater Lake from Isabel Island, Mexico. <i>Microbial Ecology</i> , 2016, 71, 68-77.	1.4	18

#	ARTICLE	IF	CITATIONS
1764	Diets enriched with cranberry beans alter the microbiota and mitigate colitis severity and associated inflammation. <i>Journal of Nutritional Biochemistry</i> , 2016, 28, 129-139.	1.9	90
1765	An omics™ approach towards the characterisation of laboratory scale anaerobic digesters treating municipal sewage sludge. <i>Water Research</i> , 2016, 88, 346-357.	5.3	63
1766	Comparative analysis of the gastrointestinal microbial communities of bar-headed goose (<i>Anser</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 2016, 182, 59-67.	2.5	65
1767	Seasonal variation in parasite infection patterns of marine fish species from the Northern Wadden Sea in relation to interannual temperature fluctuations. <i>Journal of Sea Research</i> , 2016, 113, 73-84.	0.6	18
1768	Assembly of Active Bacterial and Fungal Communities Along a Natural Environmental Gradient. <i>Microbial Ecology</i> , 2016, 71, 57-67.	1.4	37
1769	Diversity of phototrophic phytoplankton in Northern South China Sea indicated by rbcL analysis. <i>Journal of Applied Phycology</i> , 2016, 28, 773-781.	1.5	13
1770	Metadata-mining of 18S rDNA sequences reveals that "everything is not everywhere" for glomeromycotan fungi. <i>Annals of Microbiology</i> , 2016, 66, 361-371.	1.1	5
1771	Shifts in bacterial community composition associated with increased carbon cycling in a mosaic of phytoplankton blooms. <i>ISME Journal</i> , 2016, 10, 39-50.	4.4	136
1772	Carcass mass has little influence on the structure of gravesoil microbial communities. <i>International Journal of Legal Medicine</i> , 2016, 130, 253-263.	1.2	49
1773	One-Time Addition of Nano-TiO ₂ Triggers Short-Term Responses in Benthic Bacterial Communities in Artificial Streams. <i>Microbial Ecology</i> , 2016, 71, 266-275.	1.4	14
1774	Molecular characterization of microbial communities and quantification of <i>Mycobacterium</i> immunogenum in metal removal fluids and their associated biofilms. <i>Environmental Science and Pollution Research</i> , 2016, 23, 4086-4094.	2.7	4
1775	Influence of housing characteristics on bacterial and fungal communities in homes of asthmatic children. <i>Indoor Air</i> , 2016, 26, 179-192.	2.0	147
1776	Inoculation of tannin-degrading bacteria into novel hosts increases performance on tannin-rich diets. <i>Environmental Microbiology</i> , 2016, 18, 1720-1729.	1.8	67
1777	Using environmental (e)DNA sequencing for aquatic biodiversity surveys: a beginner's guide. <i>Marine and Freshwater Research</i> , 2017, 68, 20.	0.7	36
1778	Effectiveness of ecological rescue for altered soil microbial communities and functions. <i>ISME Journal</i> , 2017, 11, 272-283.	4.4	135
1779	Bacterial community structure in intertidal sediments of Fildes Peninsula, maritime Antarctica. <i>Polar Biology</i> , 2017, 40, 339-349.	0.5	28
1780	Biochar alters the soil microbiome and soil function: results of next-generation amplicon sequencing across Europe. <i>GCB Bioenergy</i> , 2017, 9, 591-612.	2.5	126
1781	Fungal and bacterial growth in floor dust at elevated relative humidity levels. <i>Indoor Air</i> , 2017, 27, 354-363.	2.0	108

#	ARTICLE	IF	CITATIONS
1782	<i>In vitro</i> effects of sodium bicarbonate buffer on rumen fermentation, levels of lipopolysaccharide and biogenic amine, and composition of rumen microbiota. <i>Journal of the Science of Food and Agriculture</i> , 2017, 97, 1276-1285.	1.7	21
1783	Effects of low-level dietary microalgae supplementation on the distal intestinal microbiome of farmed rainbow trout <i>Oncorhynchus mykiss</i> (Walbaum). <i>Aquaculture Research</i> , 2017, 48, 2438-2452.	0.9	78
1784	Periapical and periodontal microbiome diversity in aggressive periodontitis patients: a pilot study. <i>Clinical Oral Implants Research</i> , 2017, 28, 558-570.	1.9	34
1785	Geographical patterns of phylogenetic beta-diversity components in terrestrial mammals. <i>Global Ecology and Biogeography</i> , 2017, 26, 573-583.	2.7	39
1786	Antimicrobial Probiotics Reduce <i>Salmonella enterica</i> in Turkey Gastrointestinal Tracts. <i>Scientific Reports</i> , 2017, 7, 40695.	1.6	84
1787	Phylogenetic analysis of the human antibody repertoire reveals quantitative signatures of immune senescence and aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1105-1110.	3.3	120
1788	Constructing Predictive Microbial Signatures at Multiple Taxonomic Levels. <i>Journal of the American Statistical Association</i> , 2017, 112, 1022-1031.	1.8	25
1789	Subclinical alteration of the cervical-vaginal microbiome in women with idiopathic infertility. <i>Journal of Cellular Physiology</i> , 2017, 232, 1681-1688.	2.0	70
1790	Influence of attapulgitite addition on the biological performance and microbial communities of submerged dynamic membrane bioreactor. <i>Journal of Water Reuse and Desalination</i> , 2017, 7, 488-501.	1.2	3
1791	Gut microbiota composition associated with alterations in cardiorespiratory fitness and psychosocial outcomes among breast cancer survivors. <i>Supportive Care in Cancer</i> , 2017, 25, 1563-1570.	1.0	59
1792	Distinct bacterial communities across a gradient of vegetation from a preserved Brazilian Cerrado. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 457-469.	0.7	30
1793	Inside Out: HIV, the Gut Microbiome, and the Mucosal Immune System. <i>Journal of Immunology</i> , 2017, 198, 605-614.	0.4	59
1794	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017, 21, 7-10.	5.1	95
1795	Archaea and bacteria mediate the effects of native species root loss on fungi during plant invasion. <i>ISME Journal</i> , 2017, 11, 1261-1275.	4.4	50
1796	Colonization with <i>Helicobacter</i> is concomitant with modified gut microbiota and drastic failure of the immune control of <i>Mycobacterium tuberculosis</i> . <i>Mucosal Immunology</i> , 2017, 10, 1178-1189.	2.7	46
1797	Variation of the microbiota and metabolome along the canine gastrointestinal tract. <i>Metabolomics</i> , 2017, 13, 1.	1.4	51
1798	Evaluating the core microbiota in complex communities: A systematic investigation. <i>Environmental Microbiology</i> , 2017, 19, 1450-1462.	1.8	187
1799	Polymetallic nodules, sediments, and deep waters in the equatorial North Pacific exhibit highly diverse and distinct bacterial, archaeal, and microeukaryotic communities. <i>MicrobiologyOpen</i> , 2017, 6, e00428.	1.2	93

#	ARTICLE	IF	CITATIONS
1800	Inhibitory effects of soybean oligosaccharides and water-soluble soybean fibre on formation of putrefactive compounds from soy protein by gut microbiota. <i>International Journal of Biological Macromolecules</i> , 2017, 97, 173-180.	3.6	43
1801	Odour-based discrimination of similarity at the major histocompatibility complex in birds. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162466.	1.2	56
1802	A comparative evaluation of community structure in full-scale digesters indicates that two-phase digesters exhibit greater microbial diversity than single-phase digesters. <i>Environmental Science: Water Research and Technology</i> , 2017, 3, 304-311.	1.2	9
1803	Laboratory silo type and inoculation effects on nutritional composition, fermentation, and bacterial and fungal communities of oat silage. <i>Journal of Dairy Science</i> , 2017, 100, 1812-1828.	1.4	73
1804	The differentiation of soil bacterial communities along a precipitation and temperature gradient in the eastern Inner Mongolia steppe. <i>Catena</i> , 2017, 152, 47-56.	2.2	87
1805	Symbiotic bacterial communities in ants are modified by invasion pathway bottlenecks and alter host behavior. <i>Ecology</i> , 2017, 98, 861-874.	1.5	16
1806	A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 2327-2339.	1.9	46
1807	Effects of Exogenous Yeast and Bacteria on the Microbial Population Dynamics and Outcomes of Olive Fermentations. <i>MSphere</i> , 2017, 2, .	1.3	9
1808	The gut microbiome in human neurological disease: A review. <i>Annals of Neurology</i> , 2017, 81, 369-382.	2.8	388
1809	The fecal microbiome of dogs with exocrine pancreatic insufficiency. <i>Anaerobe</i> , 2017, 45, 50-58.	1.0	55
1810	A family of interaction-adjusted indices of community similarity. <i>ISME Journal</i> , 2017, 11, 791-807.	4.4	39
1811	Differential sharing and distinct co-occurrence networks among spatially close bacterial microbiota of bark, mosses and lichens. <i>Molecular Ecology</i> , 2017, 26, 2826-2838.	2.0	79
1812	MiRKAT-S: a community-level test of association between the microbiota and survival times. <i>Microbiome</i> , 2017, 5, 17.	4.9	50
1813	Characterization of bacterial communities from Masseiras, a unique Portuguese greenhouse agricultural system. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 665-676.	0.7	3
1814	The Potential Effect of Oral Microbiota in the Prediction of Mucositis During Radiotherapy for Nasopharyngeal Carcinoma. <i>EBioMedicine</i> , 2017, 18, 23-31.	2.7	109
1815	Structural modulation of gut microbiota during alleviation of antibiotic-associated diarrhea with herbal formula. <i>International Journal of Biological Macromolecules</i> , 2017, 105, 1622-1629.	3.6	73
1816	Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. <i>Nature Communications</i> , 2017, 8, 14319.	5.8	357
1817	Assessment of complementary feeding of Canadian infants: effects on microbiome & oxidative stress, a randomized controlled trial. <i>BMC Pediatrics</i> , 2017, 17, 54.	0.7	57

#	ARTICLE	IF	CITATIONS
1818	The choice of the DNA extraction method may influence the outcome of the soil microbial community structure analysis. <i>MicrobiologyOpen</i> , 2017, 6, e00453.	1.2	50
1819	Microbiota composition of simultaneously colonized mice housed under either a gnotobiotic isolator or individually ventilated cage regime. <i>Scientific Reports</i> , 2017, 7, 42245.	1.6	37
1820	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	1.7	1,339
1821	Divergent extremes but convergent recovery of bacterial and archaeal soil communities to an ongoing subterranean coal mine fire. <i>ISME Journal</i> , 2017, 11, 1447-1459.	4.4	108
1822	Plant traits, stoichiometry and microbes as drivers of decomposition in the rhizosphere in a temperate grassland. <i>Journal of Ecology</i> , 2017, 105, 1750-1765.	1.9	60
1823	Corexit 9500 Enhances Oil Biodegradation and Changes Active Bacterial Community Structure of Oil-Enriched Microcosms. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	94
1824	Multi-Omics Reveals that Lead Exposure Disturbs Gut Microbiome Development, Key Metabolites, and Metabolic Pathways. <i>Chemical Research in Toxicology</i> , 2017, 30, 996-1005.	1.7	141
1825	Understanding the mechanisms of zinc bacitracin and avilamycin on animal production: linking gut microbiota and growth performance in chickens. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4547-4559.	1.7	85
1826	Fungal diversity in soils across a gradient of preserved Brazilian Cerrado. <i>Journal of Microbiology</i> , 2017, 55, 273-279.	1.3	21
1827	Transplantation of fecal microbiota from patients with irritable bowel syndrome alters gut function and behavior in recipient mice. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	366
1828	Retrospective analysis of phytoplankton assemblages on the Iwate coast before and after the 2011 tsunami using cryopreserved <scp>DNA</scp> samples. <i>Fisheries Oceanography</i> , 2017, 26, 234-250.	0.9	5
1829	Predominance and Metabolic Potential of Halanaerobium spp. in Produced Water from Hydraulically Fractured Marcellus Shale Wells. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	64
1830	A comprehensive profiling of supragingival bacterial composition in Chinese twin children and their mothers. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 615-627.	0.7	10
1831	Tumour-associated and non-tumour-associated microbiota in colorectal cancer. <i>Gut</i> , 2017, 66, 633-643.	6.1	623
1832	Examining the potential use and long-term stability of guaiac faecal occult blood test cards for microbial DNA 16S rRNA sequencing. <i>Journal of Clinical Pathology</i> , 2017, 70, 600-606.	1.0	16
1833	Bacterial community diversity associated with different levels of dietary nutrition in the rumen of sheep. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3717-3728.	1.7	55
1834	Human and rat gut microbiome composition is maintained following sleep restriction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1564-E1571.	3.3	106
1835	Microbiomic differences in tumor and paired-normal tissue in head and neck squamous cell carcinomas. <i>Genome Medicine</i> , 2017, 9, 14.	3.6	97

#	ARTICLE	IF	CITATIONS
1836	Process assessment associated to microbial community response provides insight on possible mechanism of waste activated sludge digestion under typical chemical pretreatments. <i>Energy</i> , 2017, 137, 457-467.	4.5	26
1837	Diet affects arctic ground squirrel gut microbial metatranscriptome independent of community structure. <i>Environmental Microbiology</i> , 2017, 19, 1518-1535.	1.8	17
1838	Biological Uptake, Distribution, and Depuration of Radio-Labeled Graphene in Adult Zebrafish: Effects of Graphene Size and Natural Organic Matter. <i>ACS Nano</i> , 2017, 11, 2872-2885.	7.3	98
1839	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
1840	The microbiome of the ant's built home: the microbial communities of a tropical arboreal ant and its nest. <i>Ecosphere</i> , 2017, 8, e01639.	1.0	31
1841	Uncovering the Horseshoe Effect in Microbial Analyses. <i>MSystems</i> , 2017, 2, .	1.7	67
1842	Fecal Bacterial Communities in treated HIV infected individuals on two antiretroviral regimens. <i>Scientific Reports</i> , 2017, 7, 43741.	1.6	67
1843	Microbiota fingerprints lose individually identifying features over time. <i>Microbiome</i> , 2017, 5, 1.	4.9	300
1844	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	5.9	830
1846	Coupled Effects of Electrical Stimulation and Antibiotics on Microbial Community in Three-Dimensional Biofilm-Electrode Reactors. <i>Water, Air, and Soil Pollution</i> , 2017, 228, 1.	1.1	27
1847	Assessment of bacterial profiles in aged, home-made Sichuan paocai brine with varying titratable acidity by PacBio SMRT sequencing technology. <i>Food Control</i> , 2017, 78, 14-23.	2.8	143
1848	Ecogenomics of Zooplankton Community Reveals Ecological Threshold of Ammonia Nitrogen. <i>Environmental Science & Technology</i> , 2017, 51, 3057-3064.	4.6	83
1849	Differences in Gut Metabolites and Microbial Composition and Functions between Egyptian and U.S. Children Are Consistent with Their Diets. <i>MSystems</i> , 2017, 2, .	1.7	111
1850	Ovarian cycling and reproductive state shape the vaginal microbiota in wild baboons. <i>Microbiome</i> , 2017, 5, 8.	4.9	41
1851	Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. <i>Movement Disorders</i> , 2017, 32, 739-749.	2.2	649
1852	Fumigation with dazomet modifies soil microbiota in apple orchards affected by replant disease. <i>Applied Soil Ecology</i> , 2017, 113, 71-79.	2.1	62
1853	Host Genotype and Gut Microbiome Modulate Insulin Secretion and Diet-Induced Metabolic Phenotypes. <i>Cell Reports</i> , 2017, 18, 1739-1750.	2.9	143
1854	Chickpea-supplemented diet alters the gut microbiome and enhances gut barrier integrity in C57Bl/6 male mice. <i>Journal of Functional Foods</i> , 2017, 38, 663-674.	1.6	46

#	ARTICLE	IF	CITATIONS
1855	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science & Technology</i> , 2017, 51, 2879-2889.	4.6	15
1857	Determination of Spoilage Microbiota of Pacific White Shrimp During Ambient and Cold Storage Using Next-Generation Sequencing and Culture-Dependent Method. <i>Journal of Food Science</i> , 2017, 82, 1178-1183.	1.5	32
1858	The influence of diet on the grass carp intestinal microbiota and bile acids. <i>Aquaculture Research</i> , 2017, 48, 4934-4944.	0.9	26
1859	Whole-Genome Sequencing of Drug-Resistant <i>Salmonella enterica</i> Isolates from Dairy Cattle and Humans in New York and Washington States Reveals Source and Geographic Associations. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	89
1860	Sediment anoxia limits microbial-driven seagrass carbon remineralization under warming conditions. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	82
1861	Functional diversity in a fragmented landscape " Habitat alterations affect functional trait composition of frog assemblages in Madagascar. <i>Global Ecology and Conservation</i> , 2017, 10, 173-183.	1.0	39
1862	Analysis of the Duodenal Microbiome in Autistic Individuals. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2017, 64, e110-e116.	0.9	71
1863	Mixing of water masses caused by a drifting iceberg affects bacterial activity, community composition and substrate utilization capability in the Southern Ocean. <i>Environmental Microbiology</i> , 2017, 19, 2453-2467.	1.8	21
1864	Short Term High Fat Diet Induces Obesity-Enhancing Changes in Mouse Gut Microbiota That are Partially Reversed by Cessation of the High Fat Diet. <i>Lipids</i> , 2017, 52, 499-511.	0.7	66
1865	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	4.4	136
1867	The effects of probiotics administration on the milk production, milk components and fecal bacteria microbiota of dairy cows. <i>Science Bulletin</i> , 2017, 62, 767-774.	4.3	96
1868	Codiversification of gastrointestinal microbiota and phylogeny in passerines is not explained by ecological divergence. <i>Molecular Ecology</i> , 2017, 26, 5292-5304.	2.0	63
1869	Global-Scale Structure of the Eelgrass Microbiome. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	147
1870	Microbial succession dynamics along glacier forefield chronosequences in Tierra del Fuego (Chile). <i>Polar Biology</i> , 2017, 40, 1939-1957.	0.5	73
1871	Liver microbiome of <i>Peromyscus leucopus</i> , a key reservoir host species for emerging infectious diseases in North America. <i>Infection, Genetics and Evolution</i> , 2017, 52, 10-18.	1.0	14
1872	Intestinal alkaline phosphatase deficiency leads to dysbiosis and bacterial translocation in the newborn intestine. <i>Journal of Surgical Research</i> , 2017, 218, 35-42.	0.8	20
1873	Bayesian Nonparametric Ordination for the Analysis of Microbial Communities. <i>Journal of the American Statistical Association</i> , 2017, 112, 1430-1442.	1.8	30
1874	Interaction Between Familial Transmission and a Constitutively Active Immune System Shapes Gut Microbiota in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2017, 206, 889-904.	1.2	30

#	ARTICLE	IF	CITATIONS
1875	Effect of fumigation with chloropicrin on soil bacterial communities and genes encoding key enzymes involved in nitrogen cycling. <i>Environmental Pollution</i> , 2017, 227, 534-542.	3.7	84
1876	Microbial community compositional analysis for membrane bioreactor treating antibiotics containing wastewater. <i>Chemical Engineering Journal</i> , 2017, 325, 300-309.	6.6	131
1877	Community composition and assembly processes of the free-living and particle-attached bacteria in Taihu Lake. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	52
1878	Compositional Changes in the Gut Mucus Microbiota Precede the Onset of Colitis-Induced Inflammation. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 912-922.	0.9	47
1879	A powerful microbiome-based association test and a microbial taxa discovery framework for comprehensive association mapping. <i>Microbiome</i> , 2017, 5, 45.	4.9	63
1880	Endothelial TLR4 and the microbiome drive cerebral cavernous malformations. <i>Nature</i> , 2017, 545, 305-310.	13.7	247
1881	Arginine Improves pH Homeostasis via Metabolism and Microbiome Modulation. <i>Journal of Dental Research</i> , 2017, 96, 924-930.	2.5	54
1882	The digestive and defensive basis of carcass utilization by the burying beetle and its microbiota. <i>Nature Communications</i> , 2017, 8, 15186.	5.8	112
1883	Single Delivery of High-Diversity Fecal Microbiota Preparation by Colonoscopy Is Safe and Effective in Increasing Microbial Diversity in Active Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 903-911.	0.9	91
1884	Characterization of biocarbon-source recovery and microbial community shifts from waste activated sludge by conditioning with cornstover: Assessment of cellulosic compositions. <i>Scientific Reports</i> , 2017, 7, 42887.	1.6	9
1885	Differences in gut microbial composition correlate with regional brain volumes in irritable bowel syndrome. <i>Microbiome</i> , 2017, 5, 49.	4.9	228
1886	Effect of abattoir and cut on variations in microbial communities of vacuum-packaged beef. <i>Meat Science</i> , 2017, 131, 34-39.	2.7	29
1887	Responses of denitrifying bacterial communities to short-term waterlogging of soils. <i>Scientific Reports</i> , 2017, 7, 803.	1.6	38
1888	Oral treponeme major surface protein: Sequence diversity and distributions within periodontal niches. <i>Molecular Oral Microbiology</i> , 2017, 32, 455-474.	1.3	9
1889	<i>Saccharomyces boulardii</i> Administration Changes Gut Microbiota and Attenuates D-Galactosamine-Induced Liver Injury. <i>Scientific Reports</i> , 2017, 7, 1359.	1.6	62
1890	CO ₂ assimilation strategies in stratified lakes: Diversity and distribution patterns of chemolithoautotrophs. <i>Environmental Microbiology</i> , 2017, 19, 2754-2768.	1.8	37
1891	Resilience of the prokaryotic microbial community of <i>Acropora digitifera</i> to elevated temperature. <i>MicrobiologyOpen</i> , 2017, 6, e00478.	1.2	35
1892	Effects of fumigation with metam-sodium on soil microbial biomass, respiration, nitrogen transformation, bacterial community diversity and genes encoding key enzymes involved in nitrogen cycling. <i>Science of the Total Environment</i> , 2017, 598, 1027-1036.	3.9	63

#	ARTICLE	IF	CITATIONS
1893	Distinct roles for dietary lipids and <i>Porphyromonas gingivalis</i> infection on atherosclerosis progression and the gut microbiota. <i>Anaerobe</i> , 2017, 45, 19-30.	1.0	28
1894	Next-generation sequencing and culture-based techniques offer complementary insights into fungi and prokaryotes in beach sands. <i>Marine Pollution Bulletin</i> , 2017, 119, 351-358.	2.3	18
1895	Perinatal Bacterial Exposure Contributes to IL-13 Aeroallergen Response. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 419-427.	1.4	13
1896	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. <i>Microbiome</i> , 2017, 5, 22.	4.9	33
1897	Biological Aging and the Human Gut Microbiota. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017, 72, 1474-1482.	1.7	159
1898	Hydrocarbon and Lipid Microbiology Protocols. <i>Springer Protocols</i> , 2017, , .	0.1	0
1899	Omic-style statistical clustering reveals old and new patterns in the Gulf of Maine ecosystem. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 973-979.	0.7	8
1900	Spatiotemporal dynamics of bacterial community composition in large shallow eutrophic Lake Taihu: High overlap between free-living and particle-attached assemblages. <i>Limnology and Oceanography</i> , 2017, 62, 1366-1382.	1.6	101
1901	A Study of the Microbial Spatial Heterogeneity of Bahamian Thrombolites Using Molecular, Biochemical, and Stable Isotope Analyses. <i>Astrobiology</i> , 2017, 17, 413-430.	1.5	37
1902	Is the rate of mineralization of soil organic carbon under microbiological control?. <i>Soil Biology and Biochemistry</i> , 2017, 112, 127-139.	4.2	51
1903	Diabetes-associated microbiota in fa/fa rats is modified by Roux-en-Y gastric bypass. <i>ISME Journal</i> , 2017, 11, 2035-2046.	4.4	52
1904	The heterogeneity of composition and assembly processes of the microbial community between different nutrient loading lake zones in Taihu Lake. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5913-5923.	1.7	49
1905	Influence of chronic azithromycin treatment on the composition of the oropharyngeal microbial community in patients with severe asthma. <i>BMC Microbiology</i> , 2017, 17, 109.	1.3	26
1906	16S rRNA genes Illumina sequencing revealed differential cecal microbiome in specific pathogen free chickens infected with different subgroup of avian leukosis viruses. <i>Veterinary Microbiology</i> , 2017, 207, 195-204.	0.8	24
1907	Epidemic and endemic pathogen dynamics correspond to distinct host population microbiomes at a landscape scale. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170944.	1.2	71
1908	The Diet and Gut Microbial Communities of Two Closely Related Combtooth Blennies, <i>Chasmodes saburrae</i> and <i>Scartella cristata</i> . <i>Copeia</i> , 2017, 105, 249-256.	1.4	5
1909	Soil prokaryotic communities in Chernobyl waste disposal trench T22 are modulated by organic matter and radionuclide contamination. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	20
1910	Daily Changes in Composition and Diversity of the Intestinal Microbiota in Patients with Anorexia Nervosa: A Series of Three Cases. <i>European Eating Disorders Review</i> , 2017, 25, 423-427.	2.3	43

#	ARTICLE	IF	CITATIONS
1911	Effect of urea-supplemented diets on the ruminal bacterial and archaeal community composition of finishing bulls. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6205-6216.	1.7	22
1912	Design features of offshore oil production platforms influence their susceptibility to biocorrosion. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6517-6529.	1.7	15
1913	Chronosequencing methanogenic archaea in ancient Longji rice Terraces in China. <i>Science Bulletin</i> , 2017, 62, 879-887.	4.3	5
1914	Fecal microbiota variation across the lifespan of the healthy laboratory rat. <i>Gut Microbes</i> , 2017, 8, 428-439.	4.3	93
1915	Probiotic <i>Bifidobacterium bifidum</i> attenuates 5-fluorouracil-induced intestinal mucositis in mice via suppression of dysbiosis-related secondary inflammatory responses. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2017, 44, 1017-1025.	0.9	52
1916	Optimizing methods and dodging pitfalls in microbiome research. <i>Microbiome</i> , 2017, 5, 52.	4.9	420
1917	Changes in microbial ecology after fecal microbiota transplantation for recurrent <i>C. difficile</i> infection affected by underlying inflammatory bowel disease. <i>Microbiome</i> , 2017, 5, 55.	4.9	118
1918	Wheat straw-derived biochar amendment stimulated N ₂ O emissions from rice paddy soils by regulating the amoA genes of ammonia-oxidizing bacteria. <i>Soil Biology and Biochemistry</i> , 2017, 113, 89-98.	4.2	157
1919	Health benefit of vegetable/fruit juice-based diet: Role of microbiome. <i>Scientific Reports</i> , 2017, 7, 2167.	1.6	94
1920	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	248
1921	Selective Induction of Homeostatic Th17 Cells in the Murine Intestine by Cholera Toxin Interacting with the Microbiota. <i>Journal of Immunology</i> , 2017, 199, 312-322.	0.4	18
1922	Effects of replacing <i>Leymus chinensis</i> with whole-crop wheat hay on Holstein bull apparent digestibility, plasma parameters, rumen fermentation, and microbiota. <i>Scientific Reports</i> , 2017, 7, 2114.	1.6	19
1923	Organic compounds stimulate horizontal transfer of antibiotic resistance genes in mixed wastewater treatment systems. <i>Chemosphere</i> , 2017, 184, 53-61.	4.2	91
1924	Kisameet Glacial Clay: an Unexpected Source of Bacterial Diversity. <i>MBio</i> , 2017, 8, .	1.8	18
1925	Relative roles of competition, environmental selection and spatial processes in structuring soil bacterial communities in the Qinghai-Tibetan Plateau. <i>Applied Soil Ecology</i> , 2017, 117-118, 223-232.	2.1	24
1926	Centralized Drinking Water Treatment Operations Shape Bacterial and Fungal Community Structure. <i>Environmental Science & Technology</i> , 2017, 51, 7648-7657.	4.6	35
1927	Meta-analysis To Define a Core Microbiota in the Swine Gut. <i>MSystems</i> , 2017, 2, .	1.7	240
1928	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <i>MSystems</i> , 2017, 2, .	1.7	141

#	ARTICLE	IF	CITATIONS
1929	Temporal dynamics of relative abundances and bacterial succession in chronic wound communities. <i>Wound Repair and Regeneration</i> , 2017, 25, 673-679.	1.5	26
1930	Soy compared with milk protein in a Western diet changes fecal microbiota and decreases hepatic steatosis in obese OLETF rats. <i>Journal of Nutritional Biochemistry</i> , 2017, 46, 125-136.	1.9	32
1931	A phylogenetic framework for the kingdom Fungi based on 18S rRNA gene sequences. <i>Marine Genomics</i> , 2017, 36, 33-39.	0.4	47
1932	Sedimentary and egg-bank DNA from 3 European lakes reveal concurrent changes in the composition and diversity of cyanobacterial and <i>Daphnia</i> communities. <i>Hydrobiologia</i> , 2017, 800, 155-172.	1.0	17
1933	Characterization of the Gastric Microbiota in a Pediatric Population According to <i>Helicobacter pylori</i> Status. <i>Pediatric Infectious Disease Journal</i> , 2017, 36, 173-178.	1.1	71
1934	Methanotrophic bacterial diversity in two diverse soils under varying land-use practices as determined by high-throughput sequencing of the <i>pmoA</i> gene. <i>Applied Soil Ecology</i> , 2017, 119, 35-45.	2.1	45
1935	Characterization of suspended bacteria from processing units in an advanced drinking water treatment plant of China. <i>Environmental Science and Pollution Research</i> , 2017, 24, 12176-12184.	2.7	7
1936	Metagenomic analysis in Lake Onego (Russia) <i>Synechococcus cyanobacteria</i> . <i>Journal of Great Lakes Research</i> , 2017, 43, 43-54.	0.8	2
1937	Sequential bioavailability of sedimentary organic matter to heterotrophic bacteria. <i>Environmental Microbiology</i> , 2017, 19, 2629-2644.	1.8	39
1938	Identification of Microbial Profile of <i>Koji</i> Using Single Molecule, Real-time Sequencing Technology. <i>Journal of Food Science</i> , 2017, 82, 1193-1199.	1.5	25
1939	Symbiosis and microbiome flexibility in calcifying benthic foraminifera of the Great Barrier Reef. <i>Microbiome</i> , 2017, 5, 38.	4.9	38
1940	MicroSIA: A Gut-Microbes Information-Extraction Method with Semantic Inverse Analysis for Discovering Unique Bacteria-Combinations in Nationality. , 2017, , .		0
1941	Methods for Microbiome Analysis. <i>Translational Medicine Research</i> , 2017, , 269-298.	0.0	1
1942	The Dynamic Microbiota Profile During Pepper (<i>Piper nigrum</i> L.) Peeling by Solid-State Fermentation. <i>Current Microbiology</i> , 2017, 74, 739-746.	1.0	10
1943	Dynamic profile of the microbiota during coconut water pre-fermentation for nata de coco production. <i>LWT - Food Science and Technology</i> , 2017, 81, 87-93.	2.5	19
1944	The Microbiome and Human Biology. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 65-86.	2.5	266
1945	Weaning age influences the severity of gastrointestinal microbiome shifts in dairy calves. <i>Scientific Reports</i> , 2017, 7, 198.	1.6	87
1946	Profile analysis of microbiomes in soils of solonetz complex in the Caspian Lowland. <i>Eurasian Soil Science</i> , 2017, 50, 64-69.	0.5	11

#	ARTICLE	IF	CITATIONS
1947	Low-dose penicillin in early life induces long-term changes in murine gut microbiota, brain cytokines and behavior. <i>Nature Communications</i> , 2017, 8, 15062.	5.8	329
1948	Associations of the vaginal microbiota with HIV infection, bacterial vaginosis, and demographic factors. <i>Aids</i> , 2017, 31, 895-904.	1.0	44
1949	Bacterial diversity in traditional Jiaozi and sourdough revealed by high-throughput sequencing of 16S rRNA amplicons. <i>LWT - Food Science and Technology</i> , 2017, 81, 319-325.	2.5	51
1950	Restoration of cefixime-induced gut microbiota changes by <i>Lactobacillus</i> cocktails and fructooligosaccharides in a mouse model. <i>Microbiological Research</i> , 2017, 200, 14-24.	2.5	54
1951	The nasopharyngeal microbiota of beef cattle before and after transport to a feedlot. <i>BMC Microbiology</i> , 2017, 17, 70.	1.3	69
1952	Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. <i>Engineering</i> , 2017, 3, 66-70.	3.2	30
1953	Anaerobic Bacterial Fermentation Products Increase Tuberculosis Risk in Antiretroviral-Drug-Treated HIV Patients. <i>Cell Host and Microbe</i> , 2017, 21, 530-537.e4.	5.1	95
1955	Impact of water heater temperature setting and water use frequency on the building plumbing microbiome. <i>ISME Journal</i> , 2017, 11, 1318-1330.	4.4	102
1956	Exploring the microbial community (microflora) associated with ovine <i>Haemonchus contortus</i> (macroflora) field strains. <i>Scientific Reports</i> , 2017, 7, 70.	1.6	42
1957	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. <i>MSystems</i> , 2017, 2, .	1.7	91
1958	Pyrosequencing based assessment of bacterial diversity in Turkish <i>Rhipicephalus annulatus</i> and <i>Dermacentor marginatus</i> ticks (Acari: Ixodidae). <i>Parasitology Research</i> , 2017, 116, 1055-1061.	0.6	16
1959	Sensitivity to oxazolone induced dermatitis is transferable with gut microbiota in mice. <i>Scientific Reports</i> , 2017, 7, 44385.	1.6	52
1960	The fate of soybean residue-carbon links to changes of bacterial community composition in Mollisols differing in soil organic carbon. <i>Soil Biology and Biochemistry</i> , 2017, 109, 50-58.	4.2	41
1961	The role of adaptive immunity as an ecological filter on the gut microbiota in zebrafish. <i>ISME Journal</i> , 2017, 11, 1630-1639.	4.4	93
1962	A Fast Small-Sample Kernel Independence Test for Microbiome Community-Level Association Analysis. <i>Biometrics</i> , 2017, 73, 1453-1463.	0.8	36
1963	Delayed utilization of some fast-fermenting soluble dietary fibers by human gut microbiota when presented in a mixture. <i>Journal of Functional Foods</i> , 2017, 32, 347-357.	1.6	91
1964	Microbial communities of aquatic environments on Heard Island characterized by pyrotag sequencing and environmental data. <i>Scientific Reports</i> , 2017, 7, 44480.	1.6	12
1965	High-cholesterol diet does not alter gut microbiota composition in mice. <i>Nutrition and Metabolism</i> , 2017, 14, 15.	1.3	36

#	ARTICLE	IF	CITATIONS
1966	Alternative Protein Sources in the Diet Modulate Microbiota and Functionality in the Distal Intestine of Atlantic Salmon (<i>Salmo salar</i>). <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	142
1967	Intestinal adaptation in proximal and distal segments: Two epithelial responses diverge after intestinal separation. <i>Surgery</i> , 2017, 161, 1016-1027.	1.0	6
1968	A small-sample multivariate kernel machine test for microbiome association studies. <i>Genetic Epidemiology</i> , 2017, 41, 210-220.	0.6	37
1969	Exploration of bacterial species associated with the salivary microbiome of individuals with a low susceptibility to dental caries. <i>Clinical Oral Investigations</i> , 2017, 21, 2399-2406.	1.4	17
1970	Microbial diversity and autotrophic activity in Kamchatka hot springs. <i>Extremophiles</i> , 2017, 21, 307-317.	0.9	76
1971	Ecogenomic responses of benthic communities under multiple stressors along the marine and adjacent riverine areas of northern Bohai Sea, China. <i>Chemosphere</i> , 2017, 172, 166-174.	4.2	31
1972	How the performance of a biological pre-oxidation step can affect a downstream photo-Fenton process on the remediation of mature landfill leachates: Assessment of kinetic parameters and characterization of the bacterial communities. <i>Separation and Purification Technology</i> , 2017, 175, 274-286.	3.9	21
1973	Temporal dynamics of bacterioplankton communities in response to excessive nitrate loading in oligotrophic coastal water. <i>Marine Pollution Bulletin</i> , 2017, 114, 656-663.	2.3	8
1974	Influences of pH and Iron Concentration on the Salivary Microbiome in Individual Humans with and without Caries. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	38
1975	Regional synchrony in full-scale activated sludge bioreactors due to deterministic microbial community assembly. <i>ISME Journal</i> , 2017, 11, 500-511.	4.4	124
1976	Behavior of tetracycline and sulfamethoxazole and their corresponding resistance genes in three-dimensional biofilm-electrode reactors with low current. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2017, 52, 333-340.	0.9	8
1977	Rhizosphere microbiomes of potato cultivated in the High Andes show stable and dynamic core microbiomes with different responses to plant development. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw242.	1.3	114
1978	Comparative analysis of the microbial community in the sediments of two constructed wetlands differentially influenced by the concentrated poultry feeding operations. <i>Journal of Soils and Sediments</i> , 2017, 17, 557-566.	1.5	9
1979	The effect of coagulants and antiscalants discharged with seawater desalination brines on coastal microbial communities: A laboratory and in situ study from the southeastern Mediterranean. <i>Water Research</i> , 2017, 110, 321-331.	5.3	61
1980	Tideless estuaries in brackish seas as possible freshwater-marine transition zones for bacteria: the case study of the Vistula river estuary. <i>Environmental Microbiology Reports</i> , 2017, 9, 129-143.	1.0	28
1981	A first insight into the intestinal microbiota of snow trout (<i>Schizothorax zarudnyi</i>). <i>Symbiosis</i> , 2017, 72, 183-193.	1.2	16
1982	Molecular scatology and high-throughput sequencing reveal predominately herbivorous insects in the diets of adult and nestling Western Bluebirds (<i>Sialia mexicana</i>) in California vineyards. <i>Auk</i> , 2017, 134, 116-127.	0.7	57
1983	The influence of e-waste recycling on the molecular ecological network of soil microbial communities in Pakistan and China. <i>Environmental Pollution</i> , 2017, 231, 173-181.	3.7	50

#	ARTICLE	IF	CITATIONS
1984	Agricultural land use determines functional genetic diversity of soil microbial communities. <i>Soil Biology and Biochemistry</i> , 2017, 115, 423-432.	4.2	48
1985	Dynamics of the human antibody repertoire after B cell depletion in systemic sclerosis. <i>Science Immunology</i> , 2017, 2, .	5.6	41
1986	Whole-Grain Starch and Fiber Composition Modifies Ileal Flow of Nutrients and Nutrient Availability in the Hindgut, Shifting Fecal Microbial Profiles in Pigs. <i>Journal of Nutrition</i> , 2017, 147, jn255851.	1.3	13
1987	Associations between acute gastrointestinal GvHD and the baseline gut microbiota of allogeneic hematopoietic stem cell transplant recipients and donors. <i>Bone Marrow Transplantation</i> , 2017, 52, 1643-1650.	1.3	63
1988	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
1989	Oral microbial dysbiosis precedes development of pancreatic cancer. <i>Journal of Oral Microbiology</i> , 2017, 9, 1374148.	1.2	2
1990	Photochemical alteration of organic carbon draining permafrost soils shifts microbial metabolic pathways and stimulates respiration. <i>Nature Communications</i> , 2017, 8, 772.	5.8	112
1991	Community structure of gut bacteria of <i>Dendroctonus armandi</i> (Coleoptera: Curculionidae): Tj ETQq1 1 0.784314 μ gBT /Overlock 10 μ g BT	1.6	10
1992	Microbial community and ovine host response varies with early and late stages of <i>Haemonchus contortus</i> infection. <i>Veterinary Research Communications</i> , 2017, 41, 263-277.	0.6	33
1993	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.	1.7	1
1994	Processing and Analyzing Human Microbiome Data. <i>Methods in Molecular Biology</i> , 2017, 1666, 649-677.	0.4	4
1996	Evaluation of the efficacy and safety of <i>Ganoderma lucidum</i> mycelium-fermented liquid on gut microbiota and its impact on cardiovascular risk factors in human. <i>RSC Advances</i> , 2017, 7, 45093-45100.	1.7	14
1997	Bioinformatics for Microbiome Research: Concepts, Strategies, and Advances. , 2017, , 111-123.		3
1998	Shifts in microbial communities with increasing soil fertility across a chronosequence of paddy cultivation in subtropical China. <i>Applied Soil Ecology</i> , 2017, 120, 153-159.	2.1	27
1999	The microbiome beyond the horizon of ecological and evolutionary theory. <i>Nature Ecology and Evolution</i> , 2017, 1, 1606-1615.	3.4	216
2000	Perinatal Bisphenol A Exposure Induces Chronic Inflammation in Rabbit Offspring via Modulation of Gut Bacteria and Their Metabolites. <i>MSystems</i> , 2017, 2, .	1.7	75
2001	How to boost marine fungal research: A first step towards a multidisciplinary approach by combining molecular fungal ecology and natural products chemistry. <i>Marine Genomics</i> , 2017, 36, 57-75.	0.4	41
2002	Gut bacterial communities of diarrheic patients with indications of <i>Clostridioides difficile</i> infection. <i>Scientific Data</i> , 2017, 4, 170152.	2.4	15

#	ARTICLE	IF	CITATIONS
2003	Altered Gut Microbiota in a Mouse Model of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017, 60, 1241-1257.	1.2	319
2004	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017, 8, .	1.8	219
2005	High reactivity of deep biota under anthropogenic CO2 injection into basalt. <i>Nature Communications</i> , 2017, 8, 1063.	5.8	55
2006	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	1,228
2007	The Female Genital Tract Microbiome Is Associated With Vaginal Antiretroviral Drug Concentrations in Human Immunodeficiency Virus-Infected Women on Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2017, 216, 990-999.	1.9	23
2008	Prokaryotic Community Distribution along an Ecological Gradient of Salinity in Surface and Subsurface Saline Soils. <i>Scientific Reports</i> , 2017, 7, 13332.	1.6	33
2009	Group Living and Male Dispersal Predict the Core Gut Microbiome in Wild Baboons. <i>Integrative and Comparative Biology</i> , 2017, 57, 770-785.	0.9	69
2010	Host-microbiota interaction induces bi-phasic inflammation and glucose intolerance in mice. <i>Molecular Metabolism</i> , 2017, 6, 1371-1380.	3.0	30
2011	Seawater transfer alters the intestinal microbiota profiles of Atlantic salmon (<i>Salmo salar</i> L.). <i>Scientific Reports</i> , 2017, 7, 13877.	1.6	121
2012	Core fecal microbiota of domesticated herbivorous ruminant, hindgut fermenters, and monogastric animals. <i>MicrobiologyOpen</i> , 2017, 6, e00509.	1.2	83
2013	Elevated precipitation modifies the relationship between plant diversity and soil bacterial diversity under nitrogen deposition in <i>Stipa baicalensis</i> steppe. <i>Applied Soil Ecology</i> , 2017, 119, 345-353.	2.1	24
2014	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. <i>Science</i> , 2017, 357, 802-806.	6.0	694
2015	Differences in Temperature and Water Chemistry Shape Distinct Diversity Patterns in Thermophilic Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	20
2016	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	1.9	84
2017	The sponge microbiome project. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	193
2018	Recurrent Reverse Evolution Maintains Polymorphism after Strong Bottlenecks in Commensal Gut Bacteria. <i>Molecular Biology and Evolution</i> , 2017, 34, 2879-2892.	3.5	38
2019	Leaf endophytic fungus interacts with precipitation to alter belowground microbial communities in primary successional dunes. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	35
2020	Intestinal microbiota is altered in patients with colon cancer and modified by probiotic intervention. <i>BMJ Open Gastroenterology</i> , 2017, 4, e000145.	1.1	266

#	ARTICLE	IF	CITATIONS
2021	Biogeography of cryoconite forming cyanobacteria on polar and Asian glaciers. <i>Journal of Biogeography</i> , 2017, 44, 2849-2861.	1.4	46
2022	Microbial Disruption Indices to Detect Colonization With Multidrug-Resistant Organisms. <i>Infection Control and Hospital Epidemiology</i> , 2017, 38, 1312-1318.	1.0	11
2023	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	1.6	123
2024	Gut microbiota from multiple sclerosis patients enables spontaneous autoimmune encephalomyelitis in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10719-10724.	3.3	666
2025	Low <i>Lactobacilli</i> abundance and polymicrobial diversity in the lower reproductive tract of female rhesus monkeys do not compromise their reproductive success. <i>American Journal of Primatology</i> , 2017, 79, e22691.	0.8	4
2026	Dietary pomegranate extract and inulin affect gut microbiome differentially in mice fed an obesogenic diet. <i>Anaerobe</i> , 2017, 48, 184-193.	1.0	39
2027	Biodiversity and species competition regulate the resilience of microbial biofilm community. <i>Molecular Ecology</i> , 2017, 26, 6170-6182.	2.0	299
2028	Metagenomics for Monitoring Environmental Biodiversity: Challenges, Progress, and Opportunities. <i>Health Information Science</i> , 2017, , 73-87.	0.3	2
2029	Protected sampling is preferable in bronchoscopic studies of the airway microbiome. <i>ERJ Open Research</i> , 2017, 3, 00019-2017.	1.1	34
2030	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.	1.7	21
2031	Consumption of Two Healthy Dietary Patterns Restored Microbiota Dysbiosis in Obese Patients with Metabolic Dysfunction. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1700300.	1.5	107
2033	Changes in the intestinal microbiota following the administration of azithromycin in a randomised placebo-controlled trial among infants in south India. <i>Scientific Reports</i> , 2017, 7, 9168.	1.6	55
2034	Microbiota in the coelomic fluid of two common coastal starfish species and characterization of an abundant <i>Helicobacter</i> -related taxon. <i>Scientific Reports</i> , 2017, 7, 8764.	1.6	34
2035	Bacterial diversity among four healthcare-associated institutes in Taiwan. <i>Scientific Reports</i> , 2017, 7, 8230.	1.6	18
2036	Deciphering the enigma of undetected species, phylogenetic, and functional diversity based on Goodäturing theory. <i>Ecology</i> , 2017, 98, 2914-2929.	1.5	17
2037	Antibiotic-induced perturbations in microbial diversity during post-natal development alters amyloid pathology in an aged APPSWE/PS1 ^{E9} murine model of Alzheimer's disease. <i>Scientific Reports</i> , 2017, 7, 10411.	1.6	206
2038	Soy Improves Cardiometabolic Health and Cecal Microbiota in Female Low-Fit Rats. <i>Scientific Reports</i> , 2017, 7, 9261.	1.6	43
2039	Purple spot damage dynamics investigated by an integrated approach on a 1244 A.D. parchment roll from the Secret Vatican Archive. <i>Scientific Reports</i> , 2017, 7, 9521.	1.6	32

#	ARTICLE	IF	CITATIONS
2040	Microbiome Alterations Are Correlated with Occurrence of Postharvest Stem-End Rot in Mango Fruit. <i>Phytobiomes Journal</i> , 2017, 1, 117-127.	1.4	72
2041	An <i>In Vitro</i> Chicken Gut Model Demonstrates Transfer of a Multidrug Resistance Plasmid from <i>Salmonella</i> to Commensal <i>Escherichia coli</i> . <i>MBio</i> , 2017, 8, .	1.8	60
2042	The microbial colonization of activated carbon block point-of-use (PoU) filters with and without chlorinated phenol disinfection by-products. <i>Environmental Science: Water Research and Technology</i> , 2017, 3, 830-843.	1.2	23
2043	Drought Stress Results in a Compartment-Specific Restructuring of the Rice Root-Associated Microbiomes. <i>MBio</i> , 2017, 8, .	1.8	336
2044	Gut microbiota may predict host divergence time during Glires evolution. <i>FEMS Microbiology Ecology</i> , 2017, 93, fix009.	1.3	30
2045	The dynamics of the bacterial communities developed in maize silage. <i>Microbial Biotechnology</i> , 2017, 10, 1663-1676.	2.0	77
2046	Assessing impacts of DNA extraction methods on next generation sequencing of water and wastewater samples. <i>Journal of Microbiological Methods</i> , 2017, 141, 10-16.	0.7	46
2047	Spatial autocorrelation of microbial communities atop a debris-covered glacier is evidence of a supraglacial chronosequence. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	19
2048	A Method to Assess Bacteriocin Effects on the Gut Microbiota of Mice. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	3
2049	Heart failure is associated with depletion of core intestinal microbiota. <i>ESC Heart Failure</i> , 2017, 4, 282-290.	1.4	202
2050	Microbiome Associated with Severe Caries in Canadian First Nations Children. <i>Journal of Dental Research</i> , 2017, 96, 1378-1385.	2.5	78
2051	Successful collection of stool samples for microbiome analyses from a large community-based population of elderly men. <i>Contemporary Clinical Trials Communications</i> , 2017, 7, 158-162.	0.5	38
2052	Insect frass in stored cereal products as a potential source of <i>Lactobacillus sanfranciscensis</i> for sourdough ecosystem. <i>Journal of Applied Microbiology</i> , 2017, 123, 944-955.	1.4	24
2053	Major phylum-level differences between porefluid and host rock bacterial communities in the terrestrial deep subsurface. <i>Environmental Microbiology Reports</i> , 2017, 9, 501-511.	1.0	46
2054	Effect of low COD/N ratios on stability of single-stage partial nitrification/anammox (SPN/A) process in a long-term operation. <i>Bioresource Technology</i> , 2017, 244, 192-197.	4.8	66
2055	Stressor exposure has prolonged effects on colonic microbial community structure in <i>Citrobacter rodentium</i> -challenged mice. <i>Scientific Reports</i> , 2017, 7, 45012.	1.6	38
2056	Effects of dietary threonine supplementation on intestinal barrier function and gut microbiota of laying hens. <i>Poultry Science</i> , 2017, 96, 3654-3663.	1.5	59
2057	Modulation of the tick gut milieu by a secreted tick protein favors <i>Borrelia burgdorferi</i> colonization. <i>Nature Communications</i> , 2017, 8, 184.	5.8	85

#	ARTICLE	IF	CITATIONS
2058	Zooplankton Community Profiling in a Eutrophic Freshwater Ecosystem-Lake Tai Basin by DNA Metabarcoding. <i>Scientific Reports</i> , 2017, 7, 1773.	1.6	52
2059	Comparison of DNA-, PMA-, and RNA-based 16S rRNA Illumina sequencing for detection of live bacteria in water. <i>Scientific Reports</i> , 2017, 7, 5752.	1.6	116
2060	Alterations of microbiota structure in the larynx relevant to laryngeal carcinoma. <i>Scientific Reports</i> , 2017, 7, 5507.	1.6	39
2061	Advantages of phylogenetic distance based constrained ordination analyses for the examination of microbial communities. <i>Scientific Reports</i> , 2017, 7, 6481.	1.6	40
2062	Microbial planktonic communities in the Red Sea: high levels of spatial and temporal variability shaped by nutrient availability and turbulence. <i>Scientific Reports</i> , 2017, 7, 6611.	1.6	54
2063	Soil nutritional status and biogeography influence rhizosphere microbial communities associated with the invasive tree <i>Acacia dealbata</i> . <i>Scientific Reports</i> , 2017, 7, 6472.	1.6	54
2064	Occurrence and expression of novel methyl-coenzyme M reductase gene (<i>mcrA</i>) variants in hot spring sediments. <i>Scientific Reports</i> , 2017, 7, 7252.	1.6	37
2065	Dramatic Differences in Gut Bacterial Densities Correlate with Diet and Habitat in Rainforest Ants. <i>Integrative and Comparative Biology</i> , 2017, 57, 705-722.	0.9	77
2066	The oral microbiota in patients with pancreatic cancer, patients with IPMNs, and controls: a pilot study. <i>Cancer Causes and Control</i> , 2017, 28, 959-969.	0.8	69
2067	Bacterial diversity of the Colombian fermented milk "Suero Costeño" assessed by culturing and high-throughput sequencing and DGGE analysis of 16S rRNA gene amplicons. <i>Food Microbiology</i> , 2017, 68, 129-136.	2.1	54
2068	High-grain diets altered rumen fermentation and epithelial bacterial community and resulted in rumen epithelial injuries of goats. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6981-6992.	1.7	46
2069	Bacterial communities incorporating plant-derived carbon in the soybean rhizosphere in Mollisols that differ in soil organic carbon content. <i>Applied Soil Ecology</i> , 2017, 119, 375-383.	2.1	18
2070	The role of microbial diversity and composition in minimizing sludge production in the oxic-settling-anoxic process. <i>Science of the Total Environment</i> , 2017, 607-608, 558-567.	3.9	28
2071	Predator trait evolution alters prey community composition. <i>Ecosphere</i> , 2017, 8, e01803.	1.0	1
2072	Effects of Disodium Fumarate on In Vitro Rumen Fermentation, The Production of Lipopolysaccharide and Biogenic Amines, and The Rumen Bacterial Community. <i>Current Microbiology</i> , 2017, 74, 1337-1342.	1.0	10
2073	The use of nemabiome metabarcoding to explore gastro-intestinal nematode species diversity and anthelmintic treatment effectiveness in beef calves. <i>International Journal for Parasitology</i> , 2017, 47, 893-902.	1.3	91
2074	Navy and black bean supplementation primes the colonic mucosal microenvironment to improve gut health. <i>Journal of Nutritional Biochemistry</i> , 2017, 49, 89-100.	1.9	59
2075	Mesocosm Studies on the Efficacy of Bioamended Activated Carbon for Treating PCB-Impacted Sediment. <i>Environmental Science & Technology</i> , 2017, 51, 10691-10699.	4.6	29

#	ARTICLE	IF	CITATIONS
2076	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. <i>Pedosphere</i> , 2017, 27, 832-845.	2.1	8
2077	A wellness study of 108 individuals using personal, dense, dynamic data clouds. <i>Nature Biotechnology</i> , 2017, 35, 747-756.	9.4	340
2078	Dietary perturbations alter the ecological significance of ingested <i>Lactobacillus plantarum</i> in the digestive tract. <i>Scientific Reports</i> , 2017, 7, 7267.	1.6	9
2079	Changes in fibre-adherent and fluid-associated microbial communities and fermentation profiles in the rumen of cattle fed diets differing in hay quality and concentrate amount. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	44
2080	Gut microbiomes of free-ranging and captive Namibian cheetahs: Diversity, putative functions and occurrence of potential pathogens. <i>Molecular Ecology</i> , 2017, 26, 5515-5527.	2.0	84
2081	Copolymers enhance selective bacterial community colonization for potential root zone applications. <i>Scientific Reports</i> , 2017, 7, 15902.	1.6	8
2082	Cecal microbiome divergence of broiler chickens by sex and body weight. <i>Journal of Microbiology</i> , 2017, 55, 939-945.	1.3	69
2083	Carbonate-rich dendrolitic cones: insights into a modern analog for incipient microbialite formation, Little Hot Creek, Long Valley Caldera, California. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 32.	2.9	30
2084	Contemporary Applications of Fecal Microbiota Transplantation to Treat Intestinal Diseases in Humans. <i>Archives of Medical Research</i> , 2017, 48, 766-773.	1.5	37
2085	Effect of Sulfur Content on Microbial Composition and Biodegradation of a Brazilian Diesel and Biodiesel Blend (B10). <i>Energy & Fuels</i> , 2017, 31, 12305-12316.	2.5	7
2086	Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017, 7, 15497.	1.6	112
2087	Brown rice and retrograded brown rice alleviate inflammatory response in dextran sulfate sodium (DSS)-induced colitis mice. <i>Food and Function</i> , 2017, 8, 4630-4643.	2.1	30
2088	Host-genotype dependent gut microbiota drives zooplankton tolerance to toxic cyanobacteria. <i>Nature Communications</i> , 2017, 8, 1608.	5.8	113
2089	Wild bonobos host geographically restricted malaria parasites including a putative new <i>Laverania</i> species. <i>Nature Communications</i> , 2017, 8, 1635.	5.8	45
2090	Fermentation Cover Brine Reformulation for Cucumber Processing with Low Salt to Reduce BLOATER Defect. <i>Journal of Food Science</i> , 2017, 82, 2987-2996.	1.5	4
2091	Captive bottlenose dolphins and killer whales harbor a species-specific skin microbiota that varies among individuals. <i>Scientific Reports</i> , 2017, 7, 15269.	1.6	31
2092	Salt-responsive gut commensal modulates TH17 axis and disease. <i>Nature</i> , 2017, 551, 585-589.	13.7	896
2093	An intact gut microbiota may be required for lactoferrin-driven immunomodulation in rats. <i>Journal of Functional Foods</i> , 2017, 39, 268-278.	1.6	13

#	ARTICLE	IF	CITATIONS
2094	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. <i>Nature</i> , 2017, 551, 340-345.	13.7	396
2095	Shifts in microbial communities in soil, rhizosphere and roots of two major crop systems under elevated CO ₂ and O ₃ . <i>Scientific Reports</i> , 2017, 7, 15019.	1.6	75
2096	Vertical and horizontal assemblage patterns of bacterial communities in a eutrophic river receiving domestic wastewater in southeast China. <i>Environmental Pollution</i> , 2017, 230, 469-478.	3.7	65
2097	High Temporal and Spatial Variability of Atmospheric-Methane Oxidation in Alpine Glacier Forefield Soils. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	21
2098	Application of the entomogenous fungus, <i>Metarhizium anisopliae</i> , for leafroller (<i>Cnaphalocrocis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 Biotechnology, 2017, 101, 6793-6807.	1.7	26
2099	Polydextrose changes the gut microbiome and attenuates fasting triglyceride and cholesterol levels in Western diet fed mice. <i>Scientific Reports</i> , 2017, 7, 5294.	1.6	71
2100	Hypothesis testing and statistical analysis of microbiome. <i>Genes and Diseases</i> , 2017, 4, 138-148.	1.5	142
2101	Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. <i>Veterinary Microbiology</i> , 2017, 207, 267-279.	0.8	17
2102	Fecal microbial characterization of hospitalized patients with suspected infectious diarrhea shows significant dysbiosis. <i>Scientific Reports</i> , 2017, 7, 1088.	1.6	30
2103	Bacterial profile in human atherosclerotic plaques. <i>Atherosclerosis</i> , 2017, 263, 177-183.	0.4	49
2104	Characterisation and comparison of bacterial communities on reverse osmosis membranes of a full-scale desalination plant by bacterial 16S rRNA gene metabarcoding. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 13.	2.9	47
2105	Temporal variation of the microbiome is dependent on body region in a wild mammal (<i>Tamiasciurus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 13	1.3	13
2106	Diversity and Persistence of the Gut Microbiome of the Giant Neotropical Bullet Ant. <i>Integrative and Comparative Biology</i> , 2017, 57, 682-689.	0.9	21
2107	Community analysis of biofilms on flame-oxidized stainless steel anodes in microbial fuel cells fed with different substrates. <i>BMC Microbiology</i> , 2017, 17, 145.	1.3	22
2108	Microbiome Structural and Functional Interactions across Host Dietary Niche Space. <i>Integrative and Comparative Biology</i> , 2017, 57, 743-755.	0.9	30
2109	Social Influences on <i>Prevotella</i> and the Gut Microbiome of Young Monkeys. <i>Psychosomatic Medicine</i> , 2017, 79, 888-897.	1.3	47
2110	Microbial composition of spiny ants (Hymenoptera: Formicidae: <i>Polyrhachis</i>) across their geographic range. <i>BMC Evolutionary Biology</i> , 2017, 17, 96.	3.2	42
2111	Do biofilm communities respond to the chemical signatures of fracking? A test involving streams in North-central Arkansas. <i>BMC Microbiology</i> , 2017, 17, 29.	1.3	19

#	ARTICLE	IF	CITATIONS
2112	Dominant bacterial phyla in caves and their predicted functional roles in C and N cycle. BMC Microbiology, 2017, 17, 90.	1.3	70
2113	Relationship between nasopharyngeal and bronchoalveolar microbial communities in clinically healthy feedlot cattle. BMC Microbiology, 2017, 17, 138.	1.3	55
2114	treeman: an R package for efficient and intuitive manipulation of phylogenetic trees. BMC Research Notes, 2017, 10, 30.	0.6	17
2115	The community structure of Methanomassiliicoccales in the rumen of Chinese goats and its response to a high-grain diet. Journal of Animal Science and Biotechnology, 2017, 8, 47.	2.1	19
2116	The development of lower respiratory tract microbiome in mice. Microbiome, 2017, 5, 61.	4.9	49
2117	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. Microbiome, 2017, 5, 65.	4.9	62
2118	Profound perturbation induced by triclosan exposure in mouse gut microbiome: a less resilient microbial community with elevated antibiotic and metal resistomes. BMC Pharmacology & Toxicology, 2017, 18, 46.	1.0	37
2119	Effect of Nitrooxy Compounds with Different Molecular Structures on the Rumen Methanogenesis, Metabolic Profile, and Methanogenic Community. Current Microbiology, 2017, 74, 891-898.	1.0	16
2120	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. MSphere, 2017, 2, .	1.3	84
2121	Distribution, Community Composition, and Potential Metabolic Activity of Bacterioplankton in an Urbanized Mediterranean Sea Coastal Zone. Applied and Environmental Microbiology, 2017, 83, .	1.4	30
2122	Ancient Heavy Metal Contamination in Soils as a Driver of Tolerant Anthyllis vulneraria Rhizobial Communities. Applied and Environmental Microbiology, 2017, 83, .	1.4	20
2123	Trade-offs between microbiome diversity and productivity in a stratified microbial mat. ISME Journal, 2017, 11, 405-414.	4.4	26
2124	Nutritional Correlates of Human Oral Microbiome. Journal of the American College of Nutrition, 2017, 36, 88-98.	1.1	87
2125	Changes in the bacterial community in the fermentation process of kÅ'so, a Japanese sugar-vegetable fermented beverage. Bioscience, Biotechnology and Biochemistry, 2017, 81, 403-410.	0.6	11
2126	White Syndrome-Affected Corals Have a Distinct Microbiome at Disease Lesion Fronts. Applied and Environmental Microbiology, 2017, 83, .	1.4	52
2127	Effects of the dose and viability of Saccharomyces cerevisiae. 1. Diversity of ruminal microbes as analyzed by Illumina MiSeq sequencing and quantitative PCR. Journal of Dairy Science, 2017, 100, 325-342.	1.4	59
2128	Combined effects of reduced irrigation and water quality on the soil microbial community of a citrus orchard under semi-arid conditions. Soil Biology and Biochemistry, 2017, 104, 226-237.	4.2	94
2129	Phylogenetic and functional characterization of the distal intestinal microbiome of rainbow trout (Oncorhynchus mykiss) from both farm and aquarium settings. Journal of Applied Microbiology, 2017, 122, 347-363.	1.4	107

#	ARTICLE	IF	CITATIONS
2130	Exploring lot-to-lot variation in spoilage bacterial communities on commercial modified atmosphere packaged beef. <i>Food Microbiology</i> , 2017, 62, 147-152.	2.1	49
2131	Exploring the diversity of the root-associated microbiome of <i>Ilex paraguariensis</i> St. Hil. (Yerba Mate). <i>Applied Soil Ecology</i> , 2017, 109, 23-31.	2.1	21
2132	Serum cathelicidin, nasopharyngeal microbiota, and disease severity among infants hospitalized with bronchiolitis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1383-1386.e6.	1.5	25
2133	The rectal mucosa and condomless receptive anal intercourse in HIV-negative MSM: implications for HIV transmission and prevention. <i>Mucosal Immunology</i> , 2017, 10, 996-1007.	2.7	135
2134	Gut microbial ecology of lizards: insights into diversity in the wild, effects of captivity, variation across gut regions and transmission. <i>Molecular Ecology</i> , 2017, 26, 1175-1189.	2.0	144
2135	Phyllosphere Metaproteomes of Trees from the Brazilian Atlantic Forest Show High Levels of Functional Redundancy. <i>Microbial Ecology</i> , 2017, 73, 123-134.	1.4	49
2136	Spatial Microbial Composition Along the Gastrointestinal Tract of Captive Attwater's Prairie Chicken. <i>Microbial Ecology</i> , 2017, 73, 966-977.	1.4	21
2137	Analysis of the Fungal Diversity in Citrus Leaves with Greasy Spot Disease Symptoms. <i>Microbial Ecology</i> , 2017, 73, 739-749.	1.4	28
2138	Dynamic change of surface microbiota with different environmental cleaning methods between two wards in a hospital. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 771-781.	1.7	13
2139	Impacts of detrital nano- and micro-scale particles (dNP) on contaminant dynamics in a coal mine AMD treatment system. <i>Science of the Total Environment</i> , 2017, 575, 941-955.	3.9	12
2140	Biochar-stimulated plant performance is strongly linked to microbial diversity and metabolic potential in the rhizosphere. <i>New Phytologist</i> , 2017, 213, 1393-1404.	3.5	201
2141	Identification of the Bacterial Reservoirs for the Middle Ear Using Phylogenetic Analysis. <i>JAMA Otolaryngology - Head and Neck Surgery</i> , 2017, 143, 155.	1.2	24
2142	Microbiome in the pathogenesis of cystic fibrosis and lung transplant-related disease. <i>Translational Research</i> , 2017, 179, 84-96.	2.2	29
2143	Root microbiota dynamics of perennial <i>Arabis alpina</i> are dependent on soil residence time but independent of flowering time. <i>ISME Journal</i> , 2017, 11, 43-55.	4.4	133
2144	A guide to phylogenetic metrics for conservation, community ecology and macroecology. <i>Biological Reviews</i> , 2017, 92, 698-715.	4.7	570
2145	Comprehensive Molecular Characterization of Bacterial Communities in Feces of Pet Birds Using 16S Marker Sequencing. <i>Microbial Ecology</i> , 2017, 73, 224-235.	1.4	28
2146	The microbiome of a striped dolphin (<i>Stenella coeruleoalba</i>) stranded in Portugal. <i>Research in Microbiology</i> , 2017, 168, 85-93.	1.0	38
2147	Manifold influences of phylogenetic structure on a plant-herbivore network. <i>Oikos</i> , 2017, 126, 703-712.	1.2	11

#	ARTICLE	IF	CITATIONS
2148	Seasonal variation in an acid mine drainage microbial community. <i>Canadian Journal of Microbiology</i> , 2017, 63, 137-152.	0.8	16
2149	D-tryptophan from probiotic bacteria influences the gut microbiome and allergic airway disease. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1525-1535.	1.5	119
2150	Iron oxide magnetic nanoparticles deteriorate the mutual interaction between arbuscular mycorrhizal fungi and plant. <i>Journal of Soils and Sediments</i> , 2017, 17, 841-851.	1.5	44
2151	The influence of the autochthonous wastewater microbiota and gene host on the fate of invasive antibiotic resistance genes. <i>Science of the Total Environment</i> , 2017, 575, 932-940.	3.9	11
2152	Mineral Type Structures Soil Microbial Communities. <i>Geomicrobiology Journal</i> , 2017, 34, 538-545.	1.0	16
2153	Dynamic genetic features of eukaryotic plankton diversity in the Nakdong River estuary of Korea. <i>Chinese Journal of Oceanology and Limnology</i> , 2017, 35, 844-857.	0.7	4
2154	Oral colostrum priming shortens hospitalization without changing the immunomicrobial milieu. <i>Journal of Perinatology</i> , 2017, 37, 36-41.	0.9	37
2155	Impact of Cropping Systems, Soil Inoculum, and Plant Species Identity on Soil Bacterial Community Structure. <i>Microbial Ecology</i> , 2017, 73, 417-434.	1.4	46
2156	Culture-independent study of bacterial communities in tropical river sediment. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 200-209.	0.6	8
2157	Environmental and physiological factors shape the gut microbiota of Atlantic salmon parr (<i>Salmo</i>) Tj ETQq1 1 0.784314 rgBT /Overload 1.7 354	1.7	354
2158	Molecular analysis of the gut microbiome of diabetic rats supplemented with prebiotic, probiotic, and synbiotic foods. <i>International Journal of Diabetes in Developing Countries</i> , 2017, 37, 419-425.	0.3	9
2159	Immune Response and Mortality Risk Relate to Distinct Lung Microbiomes in Patients with HIV and Pneumonia. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 104-114.	2.5	60
2160	Abundant and rare picoeukaryotic subcommunities present contrasting patterns in the epipelagic waters of marginal seas in the northwestern Pacific Ocean. <i>Environmental Microbiology</i> , 2017, 19, 287-300.	1.8	183
2161	Dual-specificity phosphatase 6 deficiency regulates gut microbiome and transcriptome response against diet-induced obesity in mice. <i>Nature Microbiology</i> , 2017, 2, 16220.	5.9	47
2162	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. <i>Nature Microbiology</i> , 2017, 2, 16221.	5.9	138
2163	Influence of plantation on microbial community in porous concrete treating polluted surface water. <i>International Biodeterioration and Biodegradation</i> , 2017, 117, 8-13.	1.9	22
2164	Microbial, metabolomic, and immunologic dynamics in a relapsing genetic mouse model of colitis induced by T-synthase deficiency. <i>Gut Microbes</i> , 2017, 8, 1-16.	4.3	43
2165	Compositional shifts in bacterial communities associated with the coral <i>Palythoa caribaeorum</i> due to anthropogenic effects. <i>Marine Pollution Bulletin</i> , 2017, 114, 1024-1030.	2.3	10

#	ARTICLE	IF	CITATIONS
2166	Honey bee gut microbial communities are robust to the fungicide Pristine® consumed in pollen. <i>Apidologie</i> , 2017, 48, 340-352.	0.9	21
2167	Experimental metagenomics and ribosomal profiling of the human skin microbiome. <i>Experimental Dermatology</i> , 2017, 26, 211-219.	1.4	34
2168	Changes in the bacterial microbiome of patients with chronic rhinosinusitis after endoscopic sinus surgery. <i>International Forum of Allergy and Rhinology</i> , 2017, 7, 7-15.	1.5	39
2169	Harnessing the microbiomes of Brassica vegetables for health issues. <i>Scientific Reports</i> , 2017, 7, 17649.	1.6	47
2170	Intraruminal infusion of oligofructose alters ruminal microbiota and induces acute laminitis in sheep ^{1,2} . <i>Journal of Animal Science</i> , 2017, 95, 5407-5419.	0.2	5
2171	Phylogeny-Based Kernels with Application to Microbiome Association Studies. <i>ICSA Book Series in Statistics</i> , 2017, , 217-237.	0.0	3
2172	Food-grade cationic antimicrobial $\hat{\mu}$ -polylysine transiently alters the gut microbial community and predicted metagenome function in CD-1 mice. <i>Npj Science of Food</i> , 2017, 1, 8.	2.5	31
2173	Disordered oropharyngeal microbial communities in H7N9 patients with or without secondary bacterial lung infection. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-11.	3.0	59
2174	Long-term nitrogen addition affects the phylogenetic turnover of soil microbial community responding to moisture pulse. <i>Scientific Reports</i> , 2017, 7, 17492.	1.6	79
2175	Ground <i>Juniperus pinchotii</i> and urea in supplements fed to Rambouillet ewe lambs Part 2: Ewe lamb rumen microbial communities ¹ . <i>Journal of Animal Science</i> , 2017, 95, 4587-4599.	0.2	15
2176	Bioinformatics in Microbiome Analysis. <i>Methods in Microbiology</i> , 2017, 44, 1-18.	0.4	4
2177	Environmental influences on the skin microbiome of humans and cattle in rural Madagascar. <i>Evolution, Medicine and Public Health</i> , 2017, 2017, 144-153.	1.1	17
2178	Analysis of the gut bacterial communities in beef cattle and their association with feed intake, growth, and efficiency ^{1,2,3} . <i>Journal of Animal Science</i> , 2017, 95, 3215-3224.	0.2	48
2179	Genetic influences on the human oral microbiome. <i>BMC Genomics</i> , 2017, 18, 659.	1.2	66
2180	Moderate Exercise Has Limited but Distinguishable Effects on the Mouse Microbiome. <i>MSystems</i> , 2017, 2, .	1.7	65
2181	Circadian oscillations of microbial and functional composition in the human salivary microbiome. <i>DNA Research</i> , 2017, 24, 261-270.	1.5	85
2182	A comparison of sequencing platforms and bioinformatics pipelines for compositional analysis of the gut microbiome. <i>BMC Microbiology</i> , 2017, 17, 194.	1.3	196
2183	Enrichment of beneficial bacteria in the skin microbiota of bats persisting with white-nose syndrome. <i>Microbiome</i> , 2017, 5, 115.	4.9	174

#	ARTICLE	IF	CITATIONS
2184	A phylogeny-free microbiome dysbiosis detection pipeline for non-invasive disease diagnosis. , 2017, , .		0
2185	Impact of hypoxia on gene expression patterns by the human pathogen, <i>Vibrio vulnificus</i> , and bacterial community composition in a North Carolina estuary. <i>GeoHealth</i> , 2017, 1, 37-50.	1.9	7
2186	Comparative analysis of the intestinal flora in type 2 diabetes and nondiabetic mice. <i>Experimental Animals</i> , 2017, 66, 405-416.	0.7	94
2187	Reconstructing a herbivore's diet using a novel rbcL DNA mini-barcode for plants. <i>AoB PLANTS</i> , 2017, 9, plx015.	1.2	61
2188	The microbial community shifts of subgingival plaque in patients with generalized aggressive periodontitis following non-surgical periodontal therapy: a pilot study. <i>Oncotarget</i> , 2017, 8, 10609-10619.	0.8	26
2189	Root Hair Mutations Displace the Barley Rhizosphere Microbiota. <i>Frontiers in Plant Science</i> , 2017, 8, 1094.	1.7	85
2190	Pearl Millet Genetic Traits Shape Rhizobacterial Diversity and Modulate Rhizosphere Aggregation. <i>Frontiers in Plant Science</i> , 2017, 8, 1288.	1.7	23
2191	Template Preparation Affects 16S rRNA High-Throughput Sequencing Analysis of Phyllosphere Microbial Communities. <i>Frontiers in Plant Science</i> , 2017, 8, 1623.	1.7	14
2192	Individual Signatures Define Canine Skin Microbiota Composition and Variability. <i>Frontiers in Veterinary Science</i> , 2017, 4, 6.	0.9	26
2193	Starter feeding altered ruminal epithelial bacterial communities and some key immune-related genes' expression before weaning in lambs. <i>Journal of Animal Science</i> , 2017, 95, 910-921.	0.2	21
2194	Distinct gut microbiota profiles in patients with primary sclerosing cholangitis and ulcerative colitis. <i>World Journal of Gastroenterology</i> , 2017, 23, 4548.	1.4	274
2195	Dynamics of the Bacterial Community Associated with <i>Phaeodactylum tricornutum</i> Cultures. <i>Processes</i> , 2017, 5, 77.	1.3	25
2196	Sampling Terrestrial Environments for Bacterial Polyketides. <i>Molecules</i> , 2017, 22, 707.	1.7	10
2197	Qualitative Analysis of Microbial Dynamics during Anaerobic Digestion of Microalgal Biomass in a UASB Reactor. <i>International Journal of Microbiology</i> , 2017, 2017, 1-12.	0.9	23
2198	16S rRNA Gene-Based Metagenomic Analysis of Ozark Cave Bacteria. <i>Diversity</i> , 2017, 9, 31.	0.7	30
2199	Diversity of Cervical Microbiota in Asymptomatic <i>Chlamydia trachomatis</i> Genital Infection: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 321.	1.8	38
2200	Oral Microbiota: Microbial Biomarkers of Metabolic Syndrome Independent of Host Genetic Factors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 516.	1.8	53
2201	Reactivation of Intestinal Inflammation Is Suppressed by Catestatin in a Murine Model of Colitis via M1 Macrophages and Not the Gut Microbiota. <i>Frontiers in Immunology</i> , 2017, 8, 985.	2.2	38

#	ARTICLE	IF	CITATIONS
2202	Microbial Community Structure and Interannual Change in the Last Epishelf Lake Ecosystem in the North Polar Region. <i>Frontiers in Marine Science</i> , 2017, 3, .	1.2	21
2203	Seasonal and Interannual Changes in Ciliate and Dinoflagellate Species Assemblages in the Arctic Ocean (Amundsen Gulf, Beaufort Sea, Canada). <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	35
2204	Characterization of Gut Microbiome Dynamics in Developing Pekin Ducks and Impact of Management System. <i>Frontiers in Microbiology</i> , 2016, 7, 2125.	1.5	46
2205	Linking Peripartal Dynamics of Ruminant Microbiota to Dietary Changes and Production Parameters. <i>Frontiers in Microbiology</i> , 2017, 7, 2143.	1.5	58
2206	Human Catestatin Alters Gut Microbiota Composition in Mice. <i>Frontiers in Microbiology</i> , 2016, 7, 2151.	1.5	37
2207	Temporal Stability and the Effect of Transgenerational Transfer on Fecal Microbiota Structure in a Long Distance Migratory Bird. <i>Frontiers in Microbiology</i> , 2017, 8, 50.	1.5	70
2208	Home-Made Cost Effective Preservation Buffer Is a Better Alternative to Commercial Preservation Methods for Microbiome Research. <i>Frontiers in Microbiology</i> , 2017, 8, 102.	1.5	73
2209	Assessment of Ruminant Bacterial and Archaeal Community Structure in Yak (<i>Bos grunniens</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 179.	1.5	68
2210	Bacterial Community Structure after Long-term Organic and Inorganic Fertilization Reveals Important Associations between Soil Nutrients and Specific Taxa Involved in Nutrient Transformations. <i>Frontiers in Microbiology</i> , 2017, 8, 187.	1.5	212
2211	Compositional Stability of the Bacterial Community in a Climate-Sensitive Sub-Arctic Peatland. <i>Frontiers in Microbiology</i> , 2017, 8, 317.	1.5	20
2212	Dysbiosis of Gut Microbiota Associated with Clinical Parameters in Polycystic Ovary Syndrome. <i>Frontiers in Microbiology</i> , 2017, 8, 324.	1.5	224
2213	Starter Feeding Supplementation Alters Colonic Mucosal Bacterial Communities and Modulates Mucosal Immune Homeostasis in Newborn Lambs. <i>Frontiers in Microbiology</i> , 2017, 8, 429.	1.5	60
2214	<i>Caenorhabditis elegans</i> as a Model for Microbiome Research. <i>Frontiers in Microbiology</i> , 2017, 8, 485.	1.5	177
2215	Mineral Ecology: Surface Specific Colonization and Geochemical Drivers of Biofilm Accumulation, Composition, and Phylogeny. <i>Frontiers in Microbiology</i> , 2017, 8, 491.	1.5	37
2216	The Type of Forage Substrate Preparation Included as Substrate in a RUSITEC System Affects the Ruminant Microbiota and Fermentation Characteristics. <i>Frontiers in Microbiology</i> , 2017, 8, 704.	1.5	44
2217	Evolutionary Biology Needs Wild Microbiomes. <i>Frontiers in Microbiology</i> , 2017, 8, 725.	1.5	179
2218	Biogeographic Comparison of <i>Lophelia</i> -Associated Bacterial Communities in the Western Atlantic Reveals Conserved Core Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 796.	1.5	50
2219	BSocial: Deciphering Social Behaviors within Mixed Microbial Populations. <i>Frontiers in Microbiology</i> , 2017, 8, 919.	1.5	6

#	ARTICLE	IF	CITATIONS
2220	The Shift of the Intestinal Microbiome in the Innate Immunity-Deficient Mutant rde-1 Strain of <i>C. elegans</i> upon Orsay Virus Infection. <i>Frontiers in Microbiology</i> , 2017, 8, 933.	1.5	4
2221	Bacterial Composition and Diversity in Breast Milk Samples from Mothers Living in Taiwan and Mainland China. <i>Frontiers in Microbiology</i> , 2017, 8, 965.	1.5	114
2222	Different Types of Dietary Fibers Trigger Specific Alterations in Composition and Predicted Functions of Colonic Bacterial Communities in BALB/c Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 966.	1.5	47
2223	Multigenerational Influences of the <i>Fut2</i> Gene on the Dynamics of the Gut Microbiota in Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 991.	1.5	20
2224	Vaginal and Uterine Bacterial Communities in Postpartum Lactating Cows. <i>Frontiers in Microbiology</i> , 2017, 8, 1047.	1.5	52
2225	Incubation Temperature, But Not Pequi Oil Supplementation, Affects Methane Production, and the Ruminal Microbiota in a Ruminal Simulation Technique (Rusitec) System. <i>Frontiers in Microbiology</i> , 2017, 8, 1076.	1.5	24
2226	Microbial Eukaryote Diversity and Activity in the Water Column of the South China Sea Based on DNA and RNA High Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 1121.	1.5	63
2227	Tufts-in-Phosphorylcholine Maintains Normal Gut Microbiota in Collagen Induced Arthritic Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 1222.	1.5	25
2228	Burn Injury Leads to Increase in Relative Abundance of Opportunistic Pathogens in the Rat Gastrointestinal Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1237.	1.5	36
2229	Gut Microbiota Co-microevolution with Selection for Host Humoral Immunity. <i>Frontiers in Microbiology</i> , 2017, 8, 1243.	1.5	39
2230	Effects of Physiochemical Factors on Prokaryotic Biodiversity in Malaysian Circumneutral Hot Springs. <i>Frontiers in Microbiology</i> , 2017, 8, 1252.	1.5	49
2231	Cutaneous Microbial Community Variation across Populations of Eastern Hellbenders (<i>Cryptobranchus alleganiensis alleganiensis</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 1379.	1.5	39
2232	Unraveling the Fecal Microbiota and Metagenomic Functional Capacity Associated with Feed Efficiency in Pigs. <i>Frontiers in Microbiology</i> , 2017, 8, 1555.	1.5	171
2233	Seasonality Affects the Diversity and Composition of Bacterioplankton Communities in Dongjiang River, a Drinking Water Source of Hong Kong. <i>Frontiers in Microbiology</i> , 2017, 8, 1644.	1.5	38
2234	Prophylactic Supplementation of <i>Bifidobacterium longum</i> 51A Protects Mice from Ovariectomy-Induced Exacerbated Allergic Airway Inflammation and Airway Hyperresponsiveness. <i>Frontiers in Microbiology</i> , 2017, 8, 1732.	1.5	27
2235	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. <i>Frontiers in Microbiology</i> , 2017, 8, 1749.	1.5	86
2236	Bacterial, Archaeal, and Eukaryotic Diversity across Distinct Microhabitats in an Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2017, 8, 1756.	1.5	88
2237	A Novel Lactobacilli-Based Teat Disinfectant for Improving Bacterial Communities in the Milks of Cow Teats with Subclinical Mastitis. <i>Frontiers in Microbiology</i> , 2017, 8, 1782.	1.5	27

#	ARTICLE	IF	CITATIONS
2238	Dietary Heme Induces Gut Dysbiosis, Aggravates Colitis, and Potentiates the Development of Adenomas in Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 1809.	1.5	117
2239	An Investigation into Rumen Fungal and Protozoal Diversity in Three Rumen Fractions, during High-Fiber or Grain-Induced Sub-Acute Ruminal Acidosis Conditions, with or without Active Dry Yeast Supplementation. <i>Frontiers in Microbiology</i> , 2017, 8, 1943.	1.5	40
2240	Antibiotic-Induced Alterations in Gut Microbiota Are Associated with Changes in Glucose Metabolism in Healthy Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 2306.	1.5	103
2241	Differential Ecological Specificity of Protist and Bacterial Microbiomes across a Set of Termite Species. <i>Frontiers in Microbiology</i> , 2017, 8, 2518.	1.5	32
2242	<i>Bacillus amyloliquefaciens</i> L-S60 Reforms the Rhizosphere Bacterial Community and Improves Growth Conditions in Cucumber Plug Seedling. <i>Frontiers in Microbiology</i> , 2017, 8, 2620.	1.5	39
2243	16S rRNA Next Generation Sequencing Analysis Shows Bacteria in Alzheimer's Post-Mortem Brain. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 195.	1.7	234
2244	Dietary Prebiotics and Bioactive Milk Fractions Improve NREM Sleep, Enhance REM Sleep Rebound and Attenuate the Stress-Induced Decrease in Diurnal Temperature and Gut Microbial Alpha Diversity. <i>Frontiers in Behavioral Neuroscience</i> , 2016, 10, 240.	1.0	67
2245	Emerging Statistical Methodologies in the Field of Microbiome Studies. <i>Handbook of Statistics</i> , 2017, , 37-52.	0.4	0
2246	A phylogenetic transform enhances analysis of compositional microbiota data. <i>ELife</i> , 2017, 6, .	2.8	247
2247	RNA-Based Stable Isotope Probing Suggests <i>Allobaculum</i> spp. as Particularly Active Glucose Assimilators in a Complex Murine Microbiota Cultured In Vitro. <i>BioMed Research International</i> , 2017, 1-13.	0.9	56
2248	Rett Syndrome: A Focus on Gut Microbiota. <i>International Journal of Molecular Sciences</i> , 2017, 18, 344.	1.8	63
2249	Restoring the Duality between Principal Components of a Distance Matrix and Linear Combinations of Predictors, with Application to Studies of the Microbiome. <i>PLoS ONE</i> , 2017, 12, e0168131.	1.1	12
2250	Microbiome sharing between children, livestock and household surfaces in western Kenya. <i>PLoS ONE</i> , 2017, 12, e0171017.	1.1	49
2251	Differences in gut microbiota profile between women with active lifestyle and sedentary women. <i>PLoS ONE</i> , 2017, 12, e0171352.	1.1	336
2252	Urinary catheter-associated microbiota change in accordance with treatment and infection status. <i>PLoS ONE</i> , 2017, 12, e0177633.	1.1	37
2253	Variation between the oral and faecal microbiota in a free-living passerine bird, the great tit (<i>Parus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	1.1	24
2254	Bacterial communities found in placental tissues are associated with severe chorioamnionitis and adverse birth outcomes. <i>PLoS ONE</i> , 2017, 12, e0180167.	1.1	97
2255	Bacterial and diazotrophic diversities of endophytes in <i>Dendrobium catenatum</i> determined through barcoded pyrosequencing. <i>PLoS ONE</i> , 2017, 12, e0184717.	1.1	36

#	ARTICLE	IF	CITATIONS
2256	Vildagliptin increases butyrate-producing bacteria in the gut of diabetic rats. PLoS ONE, 2017, 12, e0184735.	1.1	80
2257	Comparative characterization of bacterial communities in geese fed all-grass or high-grain diets. PLoS ONE, 2017, 12, e0185590.	1.1	29
2258	Species-specific signatures of the microbiome from Camponotus and Colobopsis ants across developmental stages. PLoS ONE, 2017, 12, e0187461.	1.1	36
2259	The Gut-Brain Axis in Healthy Females: Lack of Significant Association between Microbial Composition and Diversity with Psychiatric Measures. PLoS ONE, 2017, 12, e0170208.	1.1	41
2260	Gut microbiome of mothers delivering prematurely shows reduced diversity and lower relative abundance of Bifidobacterium and Streptococcus. PLoS ONE, 2017, 12, e0184336.	1.1	53
2261	Comparative analysis of fecal microbial communities in cattle and Bactrian camels. PLoS ONE, 2017, 12, e0173062.	1.1	16
2262	The oral bacterial microbiome of occlusal surfaces in children and its association with diet and caries. PLoS ONE, 2017, 12, e0180621.	1.1	55
2263	Variable habitat conditions drive species covariation in the human microbiota. PLoS Computational Biology, 2017, 13, e1005435.	1.5	9
2264	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. PLoS Computational Biology, 2017, 13, e1005706.	1.5	64
2265	Impact of supplementation with a food-derived microbial community on obesity-associated inflammation and gut microbiota composition. Genes and Nutrition, 2017, 12, 25.	1.2	26
2266	Comparison of rumen bacterial communities in dairy herds of different production. BMC Microbiology, 2017, 17, 190.	1.3	62
2267	The human microbiome in evolution. BMC Biology, 2017, 15, 127.	1.7	243
2268	Bile acid is a significant host factor shaping the gut microbiome of diet-induced obese mice. BMC Biology, 2017, 15, 120.	1.7	208
2269	Microbial community composition along the digestive tract in forage- and grain-fed bison. BMC Veterinary Research, 2017, 13, 253.	0.7	41
2270	Longitudinal profiling reveals a persistent intestinal dysbiosis triggered by conventional anti-tuberculosis therapy. Microbiome, 2017, 5, 71.	4.9	117
2271	Normal milk microbiome is reestablished following experimental infection with Escherichia coli independent of intramammary antibiotic treatment with a third-generation cephalosporin in bovines. Microbiome, 2017, 5, 74.	4.9	54
2272	The structure of the Brassica napus seed microbiome is cultivar-dependent and affects the interactions of symbionts and pathogens. Microbiome, 2017, 5, 104.	4.9	144
2273	Oxalobacter formigenes-associated host features and microbial community structures examined using the American Gut Project. Microbiome, 2017, 5, 108.	4.9	59

#	ARTICLE	IF	CITATIONS
2274	Individual signatures and environmental factors shape skin microbiota in healthy dogs. <i>Microbiome</i> , 2017, 5, 139.	4.9	38
2275	Indoor microbiota in severely moisture damaged homes and the impact of interventions. <i>Microbiome</i> , 2017, 5, 138.	4.9	40
2276	Morphological and genetic factors shape the microbiome of a seabird species (<i>Oceanodroma</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	4.9	72
2277	Multi-level comparisons of cloacal, skin, feather and nest-associated microbiota suggest considerable influence of horizontal acquisition on the microbiota assembly of sympatric woodlarks and skylarks. <i>Microbiome</i> , 2017, 5, 156.	4.9	73
2278	Seasonal, spatial, and maternal effects on gut microbiome in wild red squirrels. <i>Microbiome</i> , 2017, 5, 163.	4.9	148
2279	The gut microbiota in larvae of the housefly <i>Musca domestica</i> and their horizontal transfer through feeding. <i>AMB Express</i> , 2017, 7, 147.	1.4	49
2280	Evaluating the accuracy of amplicon-based microbiome computational pipelines on simulated human gut microbial communities. <i>BMC Bioinformatics</i> , 2017, 18, 283.	1.2	51
2281	Visibiome: an efficient microbiome search engine based on a scalable, distributed architecture. <i>BMC Bioinformatics</i> , 2017, 18, 353.	1.2	0
2282	Development of bacterial communities in biological soil crusts along a revegetation chronosequence in the Tengger Desert, northwest China. <i>Biogeosciences</i> , 2017, 14, 3801-3814.	1.3	51
2284	Fungal diversity and community structure in gut, mound and surrounding soil of fungus-cultivating termites. <i>African Journal of Microbiology Research</i> , 2017, 11, 504-515.	0.4	3
2285	The Effect of Probiotics, Antibiotics, and Antipyretic Analgesics on Gut Microbiota Modification. <i>Journal of Bacteriology and Virology</i> , 2017, 47, 64.	0.0	3
2286	Multi-targeting therapeutic mechanisms of the Chinese herbal medicine QHD in the treatment of non-alcoholic fatty liver disease. <i>Oncotarget</i> , 2017, 8, 27820-27838.	0.8	55
2287	Removal of 17 β -Estradiol in a Biological Active Carbon Reactor with Acetic Acid and Humic Acid. <i>Water Environment Research</i> , 2017, 89, 871-879.	1.3	3
2288	Sex-Specific Effects of Organophosphate Diazinon on the Gut Microbiome and Its Metabolic Functions. <i>Environmental Health Perspectives</i> , 2017, 125, 198-206.	2.8	96
2289	A comparison of sampling methods for examining the laryngeal microbiome. <i>PLoS ONE</i> , 2017, 12, e0174765.	1.1	7
2290	Subsurface DNA Sequencing. , 2017, , 131-150.		0
2291	Alteration of gut microbial community after N,N-Dimethylformamide exposure. <i>Journal of Toxicological Sciences</i> , 2017, 42, 241-250.	0.7	10
2292	Diverse bacterial communities exist on canine skin and are impacted by cohabitation and time. <i>PeerJ</i> , 2017, 5, e3075.	0.9	30

#	ARTICLE	IF	CITATIONS
2293	Metaproteomics of Colonic Microbiota Unveils Discrete Protein Functions among Colitic Mice and Control Groups. <i>Proteomics</i> , 2018, 18, 1700391.	1.3	10
2294	Biofilm formation and potential for iron cycling in serpentinization-influenced groundwater of the Zambales and Coast Range ophiolites. <i>Extremophiles</i> , 2018, 22, 407-431.	0.9	9
2295	Cyanobacteria inhabiting biological soil crusts of a polar desert: SÅr Rondane Mountains, Antarctica. <i>Systematic and Applied Microbiology</i> , 2018, 41, 363-373.	1.2	34
2296	Decaying <i>Picea abies</i> log bark hosts diverse fungal communities. <i>Fungal Ecology</i> , 2018, 33, 1-12.	0.7	23
2297	Barrett's esophagus is associated with a distinct oral microbiome. <i>Clinical and Translational Gastroenterology</i> , 2018, 9, e135.	1.3	49
2298	Market Integration Predicts Human Gut Microbiome Attributes across a Gradient of Economic Development. <i>MSystems</i> , 2018, 3, .	1.7	31
2299	A global analysis on the distribution pattern of the bacteria coupling simultaneous methane oxidation to nitrite reduction. <i>International Biodeterioration and Biodegradation</i> , 2018, 129, 123-132.	1.9	9
2300	Neuroprotective effects of fecal microbiota transplantation on MPTP-induced Parkinsonâ€™s disease mice: Gut microbiota, glial reaction and TLR4/TNF-Î± signaling pathway. <i>Brain, Behavior, and Immunity</i> , 2018, 70, 48-60.	2.0	448
2301	Acute and repeated exposure to social stress reduces gut microbiota diversity in Syrian hamsters. <i>Behavioural Brain Research</i> , 2018, 345, 39-48.	1.2	57
2302	Depth matters: effects of precipitation regime on soil microbial activity upon rewetting of a plant-soil system. <i>ISME Journal</i> , 2018, 12, 1061-1071.	4.4	94
2303	Dog introduction alters the home dust microbiota. <i>Indoor Air</i> , 2018, 28, 539-547.	2.0	46
2304	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.	1.0	7
2305	Effects of repeated subacute ruminal acidosis challenges on the adaptation of the rumen bacterial community in Holstein bulls. <i>Journal of Dairy Science</i> , 2018, 101, 4424-4436.	1.4	39
2306	Effect of dry-rewetting stress on response pattern of soil prokaryotic communities in alpine meadow soil. <i>Applied Soil Ecology</i> , 2018, 126, 98-106.	2.1	12
2307	Probing promise versus performance in longer read fungal metabarcoding. <i>New Phytologist</i> , 2018, 217, 973-976.	3.5	24
2308	Featured article: Structure moderation of gut microbiota in liraglutide-treated diabetic male rats. <i>Experimental Biology and Medicine</i> , 2018, 243, 34-44.	1.1	56
2309	Primer selection impacts specific population abundances but not community dynamics in a monthly timeâ€series 16S rRNA gene amplicon analysis of coastal marine bacterioplankton. <i>Environmental Microbiology</i> , 2018, 20, 2709-2726.	1.8	98
2310	Temporal Variability of Oral Microbiota over 10 Months and the Implications for Future Epidemiologic Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 594-600.	1.1	24

#	ARTICLE	IF	CITATIONS
2311	Arginine Metabolism Is Altered in Adults with A ¹ + ² Ketosis-Prone Diabetes. <i>Journal of Nutrition</i> , 2018, 148, 185-193.	1.3	16
2312	Evaluation of magnetic cellulose bead-based DNA extraction from faecal materials for high-throughput bacterial community analyses. <i>Applied Entomology and Zoology</i> , 2018, 53, 281-286.	0.6	5
2313	Bacterial Diversity and Phylogenetic Analysis of Type II Polyketide Synthase Gene from Manao-Pee Cave, Thailand. <i>Geomicrobiology Journal</i> , 2018, 35, 518-527.	1.0	8
2314	Biodegradation of Poly(3-hydroxybutyrate- <i>co</i> -3-hydroxyhexanoate) Plastic under Anaerobic Sludge and Aerobic Seawater Conditions: Gas Evolution and Microbial Diversity. <i>Environmental Science & Technology</i> , 2018, 52, 5700-5709.	4.6	72
2315	Effects of Baicalein on Cortical Proinflammatory Cytokines and the Intestinal Microbiome in Senescence Accelerated Mouse Prone 8. <i>ACS Chemical Neuroscience</i> , 2018, 9, 1714-1724.	1.7	47
2316	Bacterial-derived exopolysaccharides enhance antifungal drug tolerance in a cross-kingdom oral biofilm. <i>ISME Journal</i> , 2018, 12, 1427-1442.	4.4	111
2317	Meta-scale mountain grassland observatories uncover commonalities as well as specific interactions among plant and non-rhizosphere soil bacterial communities. <i>Scientific Reports</i> , 2018, 8, 5758.	1.6	15
2318	Imidacloprid Decreases Honey Bee Survival Rates but Does Not Affect the Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
2319	Preterm infants have distinct microbiomes not explained by mode of delivery, breastfeeding duration or antibiotic exposure. <i>International Journal of Epidemiology</i> , 2018, 47, 1658-1669.	0.9	61
2320	Microbial communities in Bakken region produced water. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	27
2321	In situ microbiota distinguished primary anthropogenic stressor in freshwater sediments. <i>Environmental Pollution</i> , 2018, 239, 189-197.	3.7	19
2322	River Flow Impacts Bacterial and Archaeal Community Structure in Surface Sediments in the Northern Gulf of Mexico. <i>Microbial Ecology</i> , 2018, 76, 941-953.	1.4	4
2323	Effects of triclosan in breast milk on the infant fecal microbiome. <i>Chemosphere</i> , 2018, 203, 467-473.	4.2	64
2324	Guided Protocol for Fecal Microbial Characterization by 16S rRNA-Amplicon Sequencing. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	14
2325	Antibiotic distribution, risk assessment, and microbial diversity in river water and sediment in Hong Kong. <i>Environmental Geochemistry and Health</i> , 2018, 40, 2191-2203.	1.8	41
2326	Microbial diversity changes with rhizosphere and hydrocarbons in contrasting soils. <i>Ecotoxicology and Environmental Safety</i> , 2018, 156, 434-442.	2.9	37
2327	Soil pH and plant diversity shape soil bacterial community structure in the active layer across the latitudinal gradients in continuous permafrost region of Northeastern China. <i>Scientific Reports</i> , 2018, 8, 5619.	1.6	96
2328	Invited Commentary: The Microbiome and Population Health—Considerations for Enhancing Study Design and Data Analysis in Observational and Interventional Epidemiology. <i>American Journal of Epidemiology</i> , 2018, 187, 1291-1294.	1.6	3

#	ARTICLE	IF	CITATIONS
2329	Yeast culture dietary supplementation modulates gut microbiota, growth and biochemical parameters of grass carp. <i>Microbial Biotechnology</i> , 2018, 11, 551-565.	2.0	36
2330	Citric acid as a functional supplement in diets for juvenile turbot, <i>Scophthalmus maximus</i> L.: Effects on phosphorus discharge, growth performance, and intestinal health. <i>Aquaculture</i> , 2018, 495, 643-653.	1.7	25
2331	eDNA-based bioassessment of coastal sediments impacted by an oil spill. <i>Environmental Pollution</i> , 2018, 238, 739-748.	3.7	47
2332	A Consistent and Predictable Commercial Broiler Chicken Bacterial Microbiota in Antibiotic-Free Production Displays Strong Correlations with Performance. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	122
2333	Microbial diversity of thermophiles with biomass deconstruction potential in a foliage-rich hot spring. <i>MicrobiologyOpen</i> , 2018, 7, e00615.	1.2	27
2334	Composition and functional diversity of microbial community across a mangrove-inhabited mudflat as revealed by 16S rDNA gene sequences. <i>Science of the Total Environment</i> , 2018, 633, 518-528.	3.9	120
2335	High-throughput sequencing reveals microbial communities in drinking water treatment sludge from six geographically distributed plants, including potentially toxic cyanobacteria and pathogens. <i>Science of the Total Environment</i> , 2018, 634, 769-779.	3.9	40
2336	Using standard microbiome reference groups to simplify beta-diversity analyses and facilitate independent validation. <i>Bioinformatics</i> , 2018, 34, 3249-3257.	1.8	10
2337	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. <i>MBio</i> , 2018, 9, .	1.8	34
2338	A large-scale survey of the postmortem human microbiome, and its potential to provide insight into the living health condition. <i>Scientific Reports</i> , 2018, 8, 5724.	1.6	102
2339	Dietary supplementation with flaxseed meal and oat hulls modulates intestinal histomorphometric characteristics, digesta- and mucosa-associated microbiota in pigs. <i>Scientific Reports</i> , 2018, 8, 5880.	1.6	30
2340	Microbiome profiling of commercial pigs from farrow to finish. <i>Journal of Animal Science</i> , 2018, 96, 1778-1794.	0.2	87
2341	Fecal Microbiota Composition Drives Immune Activation in HIV-infected Individuals. <i>EBioMedicine</i> , 2018, 30, 192-202.	2.7	78
2342	No Significant Association Between the Fecal Microbiome and the Presence of Irritable Bowel Syndrome-type Symptoms in Patients with Quiescent Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 1597-1605.	0.9	20
2343	Diversity and metabolic potential of the microbiota associated with a soil arthropod. <i>Scientific Reports</i> , 2018, 8, 2491.	1.6	39
2344	Delayed gut microbiota development in high-risk for asthma infants is temporarily modifiable by <i>Lactobacillus</i> supplementation. <i>Nature Communications</i> , 2018, 9, 707.	5.8	158
2345	Biogeographical Differences in the Influence of Maternal Microbial Sources on the Early Successional Development of the Bovine Neonatal Gastrointestinal tract. <i>Scientific Reports</i> , 2018, 8, 3197.	1.6	133
2346	Lasting effect of repeated application of organic waste products on microbial communities in arable soils. <i>Applied Soil Ecology</i> , 2018, 125, 278-287.	2.1	16

#	ARTICLE	IF	CITATIONS
2347	Lactobacillus gasseri SF1183 protects the intestinal epithelium and prevents colitis symptoms in vivo. <i>Journal of Functional Foods</i> , 2018, 42, 195-202.	1.6	28
2348	Transient influence of blood meal and natural environment on blacklegged tick bacterial communities. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 563-572.	1.1	41
2349	Longitudinal Effects of Supplemental Forage on the Honey Bee (<i>Apis mellifera</i>) Microbiota and Inter- and Intra-Colony Variability. <i>Microbial Ecology</i> , 2018, 76, 814-824.	1.4	36
2350	Solar treatment (H ₂ O ₂ , TiO ₂ -P25 and GO-TiO ₂ photocatalysis, photo-Fenton) of organic micropollutants, human pathogen indicators, antibiotic resistant bacteria and related genes in urban wastewater. <i>Water Research</i> , 2018, 135, 195-206.	5.3	197
2351	Effects of land use on arbuscular mycorrhizal fungal communities in Estonia. <i>Mycorrhiza</i> , 2018, 28, 259-268.	1.3	24
2352	In vivo microbiome and associated immune markers: New insights into the pathogenesis of vaginal dysbiosis. <i>Scientific Reports</i> , 2018, 8, 2307.	1.6	45
2353	The restoration age of <i>Robinia pseudoacacia</i> plantation impacts soil microbial biomass and microbial community structure in the Loess Plateau. <i>Catena</i> , 2018, 165, 192-200.	2.2	56
2354	Microbial communities and their potential for degradation of dissolved organic carbon in cryoconite hole environments of Himalaya and Antarctica. <i>Microbiological Research</i> , 2018, 208, 32-42.	2.5	48
2355	Association of gut microbial communities with plasma lipopolysaccharide-binding protein (LBP) in premenopausal women. <i>ISME Journal</i> , 2018, 12, 1631-1641.	4.4	49
2356	Bacterial density rather than diversity correlates with hatching success across different avian species. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	21
2357	Bacterial and fungal communities, fermentation, and aerobic stability of conventional hybrids and brown midrib hybrids ensiled at low moisture with or without a homo- and heterofermentative inoculant. <i>Journal of Dairy Science</i> , 2018, 101, 3057-3076.	1.4	36
2358	Bioaugmentation of sidestream nitrifying-denitrifying phosphorus-accumulating granules in a low-SRT activated sludge system at low temperature. <i>Water Research</i> , 2018, 135, 241-250.	5.3	46
2359	Time-course responses of ileal and fecal microbiota and metabolite profiles to antibiotics in cannulated pigs. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2289-2299.	1.7	52
2360	Differential Susceptibility to T Cell-Induced Colitis in Mice: Role of the Intestinal Microbiota. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 361-379.	0.9	54
2361	Gut Microbial Diversity in Women With Polycystic Ovary Syndrome Correlates With Hyperandrogenism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 1502-1511.	1.8	224
2362	Mosquito vector-associated microbiota: Metabarcoding bacteria and eukaryotic symbionts across habitat types in Thailand endemic for dengue and other arthropod-borne diseases. <i>Ecology and Evolution</i> , 2018, 8, 1352-1368.	0.8	99
2363	Temperature and nutrients as drivers of microbially mediated arsenic oxidation and removal from acid mine drainage. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2413-2424.	1.7	17
2364	A distance-based approach for testing the mediation effect of the human microbiome. <i>Bioinformatics</i> , 2018, 34, 1875-1883.	1.8	43

#	ARTICLE	IF	CITATIONS
2365	Establishment and convergence of photosynthetic microbial biomats in shallow unit process open-water wetlands. <i>Water Research</i> , 2018, 133, 132-141.	5.3	12
2366	Bacterial diversity is positively correlated with soil heterogeneity. <i>Ecosphere</i> , 2018, 9, e02079.	1.0	68
2367	Restoration of real sewage partial nitrification-anammox process from nitrate accumulation using free nitrous acid treatment. <i>Bioresource Technology</i> , 2018, 251, 341-349.	4.8	50
2368	Drylands soil bacterial community is affected by land use change and different irrigation practices in the Mezquital Valley, Mexico. <i>Scientific Reports</i> , 2018, 8, 1413.	1.6	58
2369	Bolus Weekly Vitamin D3 Supplementation Impacts Gut and Airway Microbiota in Adults With Cystic Fibrosis: A Double-Blind, Randomized, Placebo-Controlled Clinical Trial. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 564-574.	1.8	82
2370	An additive effect of elevated atmospheric CO ₂ and rising temperature on methane emissions related to methanogenic community in rice paddies. <i>Agriculture, Ecosystems and Environment</i> , 2018, 257, 165-174.	2.5	45
2371	Assembly and ecological function of the root microbiome across angiosperm plant species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1157-E1165.	3.3	739
2372	Metabolic Fate of ¹³ C-Labeled Polydextrose and Impact on the Gut Microbiome: A Triple-Phase Study in a Colon Simulator. <i>Journal of Proteome Research</i> , 2018, 17, 1041-1053.	1.8	17
2373	Intestinal epithelial Toll-like receptor 4 prevents metabolic syndrome by regulating interactions between microbes and intestinal epithelial cells in mice. <i>Mucosal Immunology</i> , 2018, 11, 727-740.	2.7	34
2374	Differences in fecal microbial metabolites and microbiota of children with autism spectrum disorders. <i>Anaerobe</i> , 2018, 49, 121-131.	1.0	249
2375	Key microbial taxa in the rhizosphere of sorghum and sunflower grown in crop rotation. <i>Science of the Total Environment</i> , 2018, 624, 530-539.	3.9	69
2376	An Attenuated <i>Salmonella enterica</i> Serovar Typhimurium Strain and Galacto-Oligosaccharides Accelerate Clearance of <i>Salmonella</i> Infections in Poultry through Modifications to the Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	59
2377	Spatiotemporal dynamics of marine bacterial and archaeal communities in surface waters off the northern Antarctic Peninsula. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 149, 150-160.	0.6	23
2378	Comparative Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1704, 243-260.	0.4	2
2379	Early-life gut microbiome and cow's milk allergy- a prospective case - control 6-month follow-up study. <i>Saudi Journal of Biological Sciences</i> , 2018, 25, 875-880.	1.8	45
2380	High growth potential and nitrogen removal performance of marine anammox bacteria in shrimp-aquaculture sediment. <i>Chemosphere</i> , 2018, 196, 69-77.	4.2	35
2381	A biosynthetically informed distance measure to compare secondary metabolite profiles. <i>Chemoecology</i> , 2018, 28, 29-37.	0.6	42
2382	Bacterial community structure and functional potential of rhizosphere soils as influenced by nitrogen addition and bacterial wilt disease under continuous sesame cropping. <i>Applied Soil Ecology</i> , 2018, 125, 117-127.	2.1	59

#	ARTICLE	IF	CITATIONS
2383	High-throughput analysis of anammox bacteria in wetland and dryland soils along the altitudinal gradient in Qinghai-Tibet Plateau. <i>MicrobiologyOpen</i> , 2018, 7, e00556.	1.2	21
2384	Diversity of intestinal bacterial lactase gene in antibiotics-induced diarrhea mice treated with Chinese herbs compound Qi Wei Bai Zhu San. <i>3 Biotech</i> , 2018, 8, 4.	1.1	21
2385	Condensed Tannins Affect Bacterial and Fungal Microbiomes and Mycotoxin Production during Ensiling and upon Aerobic Exposure. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	46
2386	Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. <i>Environmental Microbiology</i> , 2018, 20, 402-419.	1.8	120
2387	Gut microbiome populations are associated with structure-specific changes in white matter architecture. <i>Translational Psychiatry</i> , 2018, 8, 6.	2.4	63
2388	Early-life gut microbiome and egg allergy. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2018, 73, 1515-1524.	2.7	151
2390	Low amounts of dietary fibre increase in vitro production of short-chain fatty acids without changing human colonic microbiota structure. <i>Scientific Reports</i> , 2018, 8, 435.	1.6	75
2391	Effects of humic acid on pentachlorophenol biodegrading microorganisms elucidated by stable isotope probing and high-throughput sequencing approaches. <i>European Journal of Soil Science</i> , 2018, 69, 380-391.	1.8	17
2392	Characterizing the bacterial microbiota in different gastrointestinal tract segments of the Bactrian camel. <i>Scientific Reports</i> , 2018, 8, 654.	1.6	69
2393	Profiling of metabolome and bacterial community dynamics in ensiled <i>Medicago sativa</i> inoculated without or with <i>Lactobacillus plantarum</i> or <i>Lactobacillus buchneri</i> . <i>Scientific Reports</i> , 2018, 8, 357.	1.6	118
2394	The rhizosphere microbial community response to a bio-organic fertilizer: finding the mechanisms behind the suppression of watermelon <i>Fusarium</i> wilt disease. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	14
2395	Evaluation of the effects of different diets on microbiome diversity and fatty acid composition of rumen liquor in dairy goat. <i>Animal</i> , 2018, 12, 1856-1866.	1.3	41
2396	Impact of land use, fertilization and seasonal variation on the abundance and diversity of nirS-type denitrifying bacterial communities in a Mollisol in Northeast China. <i>European Journal of Soil Biology</i> , 2018, 85, 4-11.	1.4	37
2397	The role of ozone pretreatment on optimization of membrane bioreactor for treatment of oil sands process-affected water. <i>Journal of Hazardous Materials</i> , 2018, 347, 470-477.	6.5	22
2398	Immunosuppressive effect of the gut microbiome altered by high-dose tacrolimus in mice. <i>American Journal of Transplantation</i> , 2018, 18, 1646-1656.	2.6	71
2399	A mixture of <i>Lactobacillus</i> species isolated from traditional fermented foods promote recovery from antibiotic-induced intestinal disruption in mice. <i>Journal of Applied Microbiology</i> , 2018, 124, 842-854.	1.4	45
2400	High-grain diets supplemented with phytogetic compounds or autolyzed yeast modulate ruminal bacterial community and fermentation in dry cows. <i>Journal of Dairy Science</i> , 2018, 101, 2335-2349.	1.4	46
2401	Diversity patterns of microbial eukaryotes mirror those of bacteria in Antarctic cryoconite holes. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	65

#	ARTICLE	IF	CITATIONS
2402	Microbial Communities of High-Elevation Fumaroles, Penitentes, and Dry Tephra "Soils" of the Puna de Atacama Volcanic Zone. <i>Microbial Ecology</i> , 2018, 76, 340-351.	1.4	27
2403	The reestablishment of microbial communities after surface cleaning in schools. <i>Journal of Applied Microbiology</i> , 2018, 125, 897-906.	1.4	19
2404	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	6.0	447
2405	Studying microbial functionality within the gut ecosystem by systems biology. <i>Genes and Nutrition</i> , 2018, 13, 5.	1.2	31
2406	A highly adaptive microbiome-based association test for survival traits. <i>BMC Genomics</i> , 2018, 19, 210.	1.2	34
2407	Molybdenum anode: a novel electrode for enhanced power generation in microbial fuel cells, identified via extensive screening of metal electrodes. <i>Biotechnology for Biofuels</i> , 2018, 11, 39.	6.2	45
2408	Microbial community and diversity in the feces of Sichuan takin (<i>Budorcas taxicolor tibetana</i>) as revealed by Illumina Miseq sequencing and quantitative real-time PCR. <i>AMB Express</i> , 2018, 8, 68.	1.4	5
2409	Tributyltin exposure induces gut microbiome dysbiosis with increased body weight gain and dyslipidemia in mice. <i>Environmental Toxicology and Pharmacology</i> , 2018, 60, 202-208.	2.0	29
2410	Distinct shifts in the oral microbiota are associated with the progression and aggravation of mucositis during radiotherapy. <i>Radiotherapy and Oncology</i> , 2018, 129, 44-51.	0.3	72
2411	A microbiome case-control study of recurrent acute otitis media identified potentially protective bacterial genera. <i>BMC Microbiology</i> , 2018, 18, 13.	1.3	126
2412	Woody forages effect the intestinal bacteria diversity of golden pompano <i>Trachinotus ovatus</i> . <i>AMB Express</i> , 2018, 8, 29.	1.4	22
2413	Kernel-penalized regression for analysis of microbiome data. <i>Annals of Applied Statistics</i> , 2018, 12, 540-566.	0.5	31
2414	Sediment bacterial community structures and their predicted functions implied the impacts from natural processes and anthropogenic activities in coastal area. <i>Marine Pollution Bulletin</i> , 2018, 131, 481-495.	2.3	92
2415	EMDUniFrac: exact linear time computation of the UniFrac metric and identification of differentially abundant organisms. <i>Journal of Mathematical Biology</i> , 2018, 77, 935-949.	0.8	26
2416	Comparison of rhizosphere and endophytic microbial communities of Chinese leek through high-throughput 16S rRNA gene Illumina sequencing. <i>Journal of Integrative Agriculture</i> , 2018, 17, 359-367.	1.7	23
2417	Diversity, structure and sources of bacterial communities in earthworm cocoons. <i>Scientific Reports</i> , 2018, 8, 6632.	1.6	20
2418	Guano exposed: Impact of aerobic conditions on bat fecal microbiota. <i>Ecology and Evolution</i> , 2018, 8, 5563-5574.	0.8	11
2419	Effect of live yeast <i>Saccharomyces cerevisiae</i> (Actisaf Sc 47) supplementation on the performance and hindgut microbiota composition of weanling pigs. <i>Scientific Reports</i> , 2018, 8, 5315.	1.6	44

#	ARTICLE	IF	CITATIONS
2420	Stable Isotope Probing for Microbial Iron Reduction in Chocolate Pots Hot Spring, Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	46
2421	Kenaf addition has mixed effects on process performance of sequencing batch reactors treating municipal wastewater. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 711-720.	1.2	1
2422	Temporal response of soil prokaryotic communities to acidification and alkalization under laboratory conditions. <i>European Journal of Soil Biology</i> , 2018, 86, 63-71.	1.4	3
2423	Allometry and Ecology of the Bilaterian Gut Microbiome. <i>MBio</i> , 2018, 9, .	1.8	29
2424	Structure and dynamics of microbiomes associated with the marine sponge <i>Tedania</i> sp. during its life cycle. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
2425	The nasal microbiome in asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 834-843.e2.	1.5	111
2426	Spatio-temporal dynamics of soil bacterial communities as a function of Amazon forest phenology. <i>Scientific Reports</i> , 2018, 8, 4382.	1.6	40
2427	A Lachnospiraceae-dominated bacterial signature in the fecal microbiota of HIV-infected individuals from Colombia, South America. <i>Scientific Reports</i> , 2018, 8, 4479.	1.6	34
2428	Incubation with macroalgae induces large shifts in water column microbiota, but minor changes to the epibiota of co-occurring macroalgae. <i>Molecular Ecology</i> , 2018, 27, 1966-1979.	2.0	50
2429	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
2430	Earthworm-induced shifts in microbial diversity in soils with rare versus established invasive earthworm populations. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	19
2431	Convergent shifts in host-associated microbial communities across environmentally elicited phenotypes. <i>Nature Communications</i> , 2018, 9, 952.	5.8	61
2432	Species Level Description of the Human Ileal Bacterial Microbiota. <i>Scientific Reports</i> , 2018, 8, 4736.	1.6	80
2433	Degradation shaped bacterial and archaeal communities with predictable taxa and their association patterns in Zoige wetland at Tibet plateau. <i>Scientific Reports</i> , 2018, 8, 3884.	1.6	42
2434	Dietary butyrate glycerides modulate intestinal microbiota composition and serum metabolites in broilers. <i>Scientific Reports</i> , 2018, 8, 4940.	1.6	32
2435	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. <i>MSystems</i> , 2018, 3, .	1.7	204
2436	Biogeographic patterns of aerobic anoxygenic phototrophic bacteria reveal an ecological consistency of phylogenetic clades in different oceanic biomes. <i>Scientific Reports</i> , 2018, 8, 4105.	1.6	19
2437	A global comparison of the microbiome compositions of three gut locations in commercial pigs with extreme feed conversion ratios. <i>Scientific Reports</i> , 2018, 8, 4536.	1.6	121

#	ARTICLE	IF	CITATIONS
2438	LysMD3 is a type II membrane protein without a role in the response to a range of pathogens. <i>Journal of Biological Chemistry</i> , 2018, 293, 6022-6038.	1.6	11
2439	Phylogenetic diversity of bacteria in the Arctic Ocean sediments neighboring the Bering Strait. <i>Acta Ecologica Sinica</i> , 2018, 38, 356-362.	0.9	1
2440	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018, 3, .	1.7	123
2441	Destabilization of the gut microbiome marks the end-stage of simian immunodeficiency virus infection in wild chimpanzees. <i>American Journal of Primatology</i> , 2018, 80, e22515.	0.8	27
2442	Comparative analyses of the bacterial community of hydrothermal deposits and seafloor sediments across Okinawa Trough. <i>Journal of Marine Systems</i> , 2018, 180, 162-172.	0.9	18
2443	Dietary Changes Impact the Gut Microbe Composition in Overweight and Obese Men with Prostate Cancer Undergoing Radical Prostatectomy. <i>Journal of the Academy of Nutrition and Dietetics</i> , 2018, 118, 714-723.e1.	0.4	25
2444	Radiation induces proinflammatory dysbiosis: transmission of inflammatory susceptibility by host cytokine induction. <i>Gut</i> , 2018, 67, 97-107.	6.1	229
2445	A comparative study of gut microbiota profiles of earthworms fed in three different substrates. <i>Symbiosis</i> , 2018, 74, 21-29.	1.2	51
2446	Vertical and Horizontal Distribution of Bacterial Communities in Alluvial Groundwater of the Nakdong River Bank. <i>Geomicrobiology Journal</i> , 2018, 35, 74-80.	1.0	9
2447	Human oral microbiome and prospective risk for pancreatic cancer: a population-based nested case-control study. <i>Gut</i> , 2018, 67, 120-127.	6.1	536
2448	Community structure and diversity of endophytic bacteria in seeds of three consecutive generations of <i>Crotalaria pumila</i> growing on metal mine residues. <i>Plant and Soil</i> , 2018, 422, 51-66.	1.8	70
2449	Power and sample size calculations for high-throughput sequencing-based experiments. <i>Briefings in Bioinformatics</i> , 2018, 19, 1247-1255.	3.2	32
2450	Infant Gut Microbiome Associated With Cognitive Development. <i>Biological Psychiatry</i> , 2018, 83, 148-159.	0.7	362
2451	Diet Versus Phylogeny: a Comparison of Gut Microbiota in Captive Colobine Monkey Species. <i>Microbial Ecology</i> , 2018, 75, 515-527.	1.4	106
2452	Population-Specific Responses to Interspecific Competition in the Gut Microbiota of Two Atlantic Salmon (<i>Salmo salar</i>) Populations. <i>Microbial Ecology</i> , 2018, 75, 140-151.	1.4	21
2453	Lung Microbiota Is Related to Smoking Status and to Development of Acute Respiratory Distress Syndrome in Critically Ill Trauma Patients. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 621-631.	2.5	114
2454	Male-specific Association Between Fat-Free Mass Index and Fecal Microbiota in 2- to 3-Year-Old Australian Children. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2018, 66, 147-151.	0.9	11
2455	Effects of reclamation years on composition and diversity of soil bacterial communities in Northwest China. <i>Canadian Journal of Microbiology</i> , 2018, 64, 28-40.	0.8	21

#	ARTICLE	IF	CITATIONS
2456	Impact of Age-Related Mitochondrial Dysfunction and Exercise on Intestinal Microbiota Composition. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 571-578.	1.7	28
2457	Effects of plant species on stream bacterial communities via leachate from leaf litter. <i>Hydrobiologia</i> , 2018, 807, 131-144.	1.0	9
2458	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018, 67, 1743-1745.	6.1	32
2459	Ophiopogonin D alleviates high-fat diet-induced metabolic syndrome and changes the structure of gut microbiota in mice. <i>FASEB Journal</i> , 2018, 32, 1139-1153.	0.2	35
2460	The organophosphate malathion disturbs gut microbiome development and the quorum-Sensing system. <i>Toxicology Letters</i> , 2018, 283, 52-57.	0.4	28
2461	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018, 359, 97-103.	6.0	3,126
2462	A comparison of bioinformatic approaches for 16S rRNA gene profiling of food bacterial microbiota. <i>International Journal of Food Microbiology</i> , 2018, 265, 9-17.	2.1	35
2463	Simultaneous measurement of bacterial abundance and composition in response to biochar in soybean field soil using 16S rRNA gene sequencing. <i>Land Degradation and Development</i> , 2018, 29, 2172-2182.	1.8	29
2464	Gut Microbiota Perturbations in Reactive Arthritis and Postinfectious Spondyloarthritis. <i>Arthritis and Rheumatology</i> , 2018, 70, 242-254.	2.9	88
2465	Supplementation of pancreatic digestive enzymes alters the composition of intestinal microbiota in mice. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 273-279.	1.0	43
2466	Bacteriocin biosynthesis contributes to the anti-inflammatory capacities of probiotic <i>Lactobacillus plantarum</i> . <i>Beneficial Microbes</i> , 2018, 9, 333-344.	1.0	35
2467	Decaffeinated green and black tea polyphenols decrease weight gain and alter microbiome populations and function in diet-induced obese mice. <i>European Journal of Nutrition</i> , 2018, 57, 2759-2769.	1.8	169
2468	Impacts of the Human Gut Microbiome on Therapeutics. <i>Annual Review of Pharmacology and Toxicology</i> , 2018, 58, 253-270.	4.2	74
2469	Aliphatic Hydrocarbon Enhances Phenanthrene Degradation by Autochthonous Prokaryotic Communities from a Pristine Seawater. <i>Microbial Ecology</i> , 2018, 75, 688-700.	1.4	10
2470	Polymorphism of antibiotic-inactivating enzyme driven by ecology expands the environmental resistome. <i>ISME Journal</i> , 2018, 12, 267-276.	4.4	19
2471	Aquatic urban ecology at the scale of a capital: community structure and interactions in street gutters. <i>ISME Journal</i> , 2018, 12, 253-266.	4.4	11
2472	Dietary copper-fructose interactions alter gut microbial activity in male rats. <i>American Journal of Physiology - Renal Physiology</i> , 2018, 314, G119-G130.	1.6	37
2473	Of mammals and bacteria in a rainforest: Temporal dynamics of soil bacteria in response to simulated N pulse from mammalian urine. <i>Functional Ecology</i> , 2018, 32, 773-784.	1.7	15

#	ARTICLE	IF	CITATIONS
2474	Microbiota Diversity Within and Between the Tissues of Two Wild Interbreeding Species. <i>Microbial Ecology</i> , 2018, 75, 799-810.	1.4	11
2475	Comparative analysis of microbial communities associated with bacteriomes, reproductive organs and eggs of the cicada <i>Subsalsaltria yangi</i> . <i>Archives of Microbiology</i> , 2018, 200, 227-235.	1.0	15
2476	A comparative study of composting the solid fraction of dairy manure with or without bulking material: Performance and microbial community dynamics. <i>Bioresource Technology</i> , 2018, 247, 443-452.	4.8	135
2477	Effect of hydraulic retention time on microbial community in biochemical passive reactors during treatment of acid mine drainage. <i>Bioresource Technology</i> , 2018, 247, 624-632.	4.8	46
2478	Intestinal microbiota in infants at high risk for allergy: Effects of prebiotics and role in eczema development. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1334-1342.e5.	1.5	128
2479	The bacterial composition of ventilation filter dust in Norwegian pre-school nurseries. <i>Indoor and Built Environment</i> , 2018, 27, 1392-1404.	1.5	9
2480	Fecal microbiota of lambs fed purple prairie clover (<i>Dalea purpurea</i> Vent.) and alfalfa (<i>Medicago</i>) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 5	1.0	26
2481	Toward the Drug Factory Microbiome: Microbial Community Variations in Antibiotic-Producing Clean Rooms. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 133-144.	1.0	13
2482	16S rRNA gene sequencing reveals site-specific signatures of the upper and lower airways of cystic fibrosis patients. <i>Journal of Cystic Fibrosis</i> , 2018, 17, 204-212.	0.3	31
2483	Effect of barley supplementation on the fecal microbiota, caecal biochemistry, and key biomarkers of obesity and inflammation in obese db/db mice. <i>European Journal of Nutrition</i> , 2018, 57, 2513-2528.	1.8	28
2484	Bacterial community structures in air conditioners installed in Japanese residential buildings. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 45-53.	0.7	6
2485	Distribution of apple and blackcurrant microbiota in Lithuania and the Czech Republic. <i>Microbiological Research</i> , 2018, 206, 1-8.	2.5	44
2486	Food restriction followed by refeeding with a casein- or whey-based diet differentially affects the gut microbiota of pre-pubertal male rats. <i>Journal of Nutritional Biochemistry</i> , 2018, 51, 27-39.	1.9	13
2487	Different <i>Lactobacillus</i> populations dominate in "Chorizo de Le ³ "-manufacturing performed in different production plants. <i>Food Microbiology</i> , 2018, 70, 94-102.	2.1	41
2488	Aerobic composting reduces antibiotic resistance genes in cattle manure and the resistome dissemination in agricultural soils. <i>Science of the Total Environment</i> , 2018, 612, 1300-1310.	3.9	190
2489	Soil Microbiomes Associated with Verticillium Wilt-Suppressive Broccoli and Chitin Amendments are Enriched with Potential Biocontrol Agents. <i>Phytopathology</i> , 2018, 108, 31-43.	1.1	71
2490	Sensitive community responses of microbiota to copper in sediment toxicity test. <i>Environmental Toxicology and Chemistry</i> , 2018, 37, 599-608.	2.2	23
2491	Microbiota of field-collected <i>Ixodes scapularis</i> and <i>Dermacentor variabilis</i> from eastern and southern Ontario, Canada. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 235-244.	1.1	43

#	ARTICLE	IF	CITATIONS
2492	Alterations in ruminal bacterial populations at induction and recovery from diet-induced milk fat depression in dairy cows. <i>Journal of Dairy Science</i> , 2018, 101, 295-309.	1.4	45
2493	VMG II transport medium stabilises oral microbiome samples for Next-Generation Sequencing. <i>Journal of Microbiological Methods</i> , 2018, 144, 91-98.	0.7	5
2494	Gut microbes limit growth in house sparrow nestlings (<i>Passer domesticus</i>) but not through limitations in digestive capacity. <i>Integrative Zoology</i> , 2018, 13, 139-151.	1.3	42
2495	Microbial Reduction of Fe(III) and SO ₄ ²⁻ and Associated Microbial Communities in the Alluvial Aquifer Groundwater and Sediments. <i>Microbial Ecology</i> , 2018, 76, 182-191.	1.4	5
2496	Gastrointestinal microbial diversity and short-chain fatty acid production in pigs fed different fibrous diets with or without cell wall-degrading enzyme supplementation. <i>Livestock Science</i> , 2018, 207, 105-116.	0.6	21
2497	Distribution and Diversity of Ocular Microbial Communities in Diabetic Patients Compared with Healthy Subjects. <i>Current Eye Research</i> , 2018, 43, 314-324.	0.7	49
2498	Diversity and Cyclical Seasonal Transitions in the Bacterial Community in a Large and Deep Perialpine Lake. <i>Microbial Ecology</i> , 2018, 76, 125-143.	1.4	81
2499	Homogenization of lake cyanobacterial communities over a century of climate change and eutrophication. <i>Nature Ecology and Evolution</i> , 2018, 2, 317-324.	3.4	133
2500	Comparison of bacterial diversity profiles and microbial safety assessment of salami, Chinese dry-cured sausage and Chinese smoked-cured sausage by high-throughput sequencing. <i>LWT - Food Science and Technology</i> , 2018, 90, 108-115.	2.5	94
2501	Removal of the cecum affects intestinal fermentation, enteric bacterial community structure, and acute colitis in mice. <i>Gut Microbes</i> , 2018, 9, 218-235.	4.3	63
2502	Temperature-Phased Conversion of Acid Whey Waste Into Medium-Chain Carboxylic Acids via Lactic Acid: No External e-Donor. <i>Joule</i> , 2018, 2, 280-295.	11.7	132
2503	Functional and phylogenetic response of soil prokaryotic community under an artificial moisture gradient. <i>Applied Soil Ecology</i> , 2018, 124, 372-378.	2.1	16
2504	Gancao-Gansui combination impacts gut microbiota diversity and related metabolic functions. <i>Journal of Ethnopharmacology</i> , 2018, 214, 71-82.	2.0	48
2505	Microbial life on a sand grain: from bulk sediment to single grains. <i>ISME Journal</i> , 2018, 12, 623-633.	4.4	99
2506	Gut Microbiota in Human Systemic Lupus Erythematosus and a Mouse Model of Lupus. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	223
2507	Gut microbiota composition is associated with environmental landscape in honey bees. <i>Ecology and Evolution</i> , 2018, 8, 441-451.	0.8	106
2508	Have you tried spermine? A rapid and cost-effective method to eliminate dextran sodium sulfate inhibition of PCR and RT-PCR. <i>Journal of Microbiological Methods</i> , 2018, 144, 1-7.	0.7	81
2509	Chronic chlorpyrifos exposure elicits diet-specific effects on metabolism and the gut microbiome in rats. <i>Food and Chemical Toxicology</i> , 2018, 111, 144-152.	1.8	85

#	ARTICLE	IF	CITATIONS
2510	Analysis of Bacterial and Fungal Nucleic Acid in Canine Sterile Granulomatous and Pyogranulomatous Dermatitis and Panniculitis. <i>Veterinary Pathology</i> , 2018, 55, 124-132.	0.8	7
2511	The Intestinal Microbiota of Tadpoles Differs from Those of Syntopic Aquatic Invertebrates. <i>Microbial Ecology</i> , 2018, 76, 121-124.	1.4	18
2512	Effect of vacuum and modified atmosphere packaging on the microbiological, chemical and sensory properties of tropical red drum (<i>Sciaenops ocellatus</i>) fillets stored at 4 A°C. <i>International Journal of Food Microbiology</i> , 2018, 266, 31-41.	2.1	45
2513	Sympatric kelp species share a large portion of their surface bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 658-670.	1.8	65
2514	Combination Immunotherapy Development in Melanoma. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2018, 38, 197-207.	1.8	39
2515	Quantitative Genetics of the Maize Leaf Microbiome. <i>Phytobiomes Journal</i> , 2018, 2, 208-224.	1.4	110
2516	Characterization of the Microbiota in Air- or Vacuum-Packed Crisp Grass Carp (<i>Ctenopharyngodon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Sequencing. <i>Journal of Food Protection</i> , 2018, 81, 1022-1029.	0.8	6
2517	Effects of tobacco smoke and electronic cigarette vapor exposure on the oral and gut microbiota in humans: a pilot study. <i>PeerJ</i> , 2018, 6, e4693.	0.9	84
2518	Filtration artefacts in bacterial community composition can affect the outcome of dissolved organic matter biolability assays. <i>Biogeosciences</i> , 2018, 15, 7141-7154.	1.3	9
2519	Bacterial microbiota composition of fermented fruit and vegetable juices (<i>jiaosu</i>) analyzed by single-molecule, real-time (SMRT) sequencing. <i>CYTA - Journal of Food</i> , 2018, 16, 950-956.	0.9	7
2520	Bacterial Epibiotic Communities of Ubiquitous and Abundant Marine Diatoms Are Distinct in Short- and Long-Term Associations. <i>Frontiers in Microbiology</i> , 2018, 9, 2879.	1.5	33
2521	Host species, pathogens and disease associated with divergent nasal microbial communities in tortoises. <i>Royal Society Open Science</i> , 2018, 5, 181068.	1.1	9
2522	Effects of acute exposures of 2,4,6-trinitrotoluene and inorganic lead on the fecal microbiome of the green anole (<i>Anolis carolinensis</i>). <i>PLoS ONE</i> , 2018, 13, e0208281.	1.1	8
2523	Impact of <i>Bactrocera oleae</i> on the fungal microbiota of ripe olive drupes. <i>PLoS ONE</i> , 2018, 13, e0199403.	1.1	9
2524	The bacterial community significantly promotes cast iron corrosion in reclaimed wastewater distribution systems. <i>Microbiome</i> , 2018, 6, 222.	4.9	32
2525	Comparison of differences in microbial compositions between negative controls and subject samples with varying analysis configurations. <i>Allergy Asthma & Respiratory Disease</i> , 2018, 6, 255.	0.3	0
2527	Increasing prevalence of epizootic shell disease in American lobster from the nearshore Gulf of Maine. <i>Bulletin of Marine Science</i> , 2018, 94, 903-921.	0.4	16
2528	<i>Burkholderia pseudomallei</i> -absent soil bacterial community results in secondary metabolites that kill this pathogen. <i>AMB Express</i> , 2018, 8, 136.	1.4	2

#	ARTICLE	IF	CITATIONS
2529	Microbiome shifts with onset and progression of Sea Star Wasting Disease revealed through time course sampling. <i>Scientific Reports</i> , 2018, 8, 16476.	1.6	34
2530	An exploration of Prevotella-rich microbiomes in HIV and men who have sex with men. <i>Microbiome</i> , 2018, 6, 198.	4.9	111
2531	Environmental DNA Metabarcoding Supporting Community Assessment of Environmental Stressors in a Field-Based Sediment Microcosm Study. <i>Environmental Science & Technology</i> , 2018, 52, 14469-14479.	4.6	30
2532	Influence of dietary supplementation with <i>Bacillus licheniformis</i> and <i>Saccharomyces cerevisiae</i> as alternatives to monensin on growth performance, antioxidant, immunity, ruminal fermentation and microbial diversity of fattening lambs. <i>Scientific Reports</i> , 2018, 8, 16712.	1.6	54
2533	Taxonomic classification for microbiome analysis, which correlates well with the metabolite milieu of the gut. <i>BMC Microbiology</i> , 2018, 18, 188.	1.3	38
2534	High Microbial Diversity Despite Extremely Low Biomass in a Deep Karst Aquifer. <i>Frontiers in Microbiology</i> , 2018, 9, 2823.	1.5	34
2535	Human milk oligosaccharides, milk microbiome and infant gut microbiome modulate neonatal rotavirus infection. <i>Nature Communications</i> , 2018, 9, 5010.	5.8	130
2536	Fermented <i>Astragalus</i> in diet altered the composition of fecal microbiota in broiler chickens. <i>AMB Express</i> , 2018, 8, 151.	1.4	20
2537	Comparison of Mothur and QIIME for the Analysis of Rumen Microbiota Composition Based on 16S rRNA Amplicon Sequences. <i>Frontiers in Microbiology</i> , 2018, 9, 3010.	1.5	67
2538	Island Biogeography of Cryoconite Hole Bacteria in Antarctica's Taylor Valley and Around the World. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	29
2539	Rutin and Its Combination With Inulin Attenuate Gut Dysbiosis, the Inflammatory Status and Endoplasmic Reticulum Stress in Paneth Cells of Obese Mice Induced by High-Fat Diet. <i>Frontiers in Microbiology</i> , 2018, 9, 2651.	1.5	60
2540	Decreased microbial co-occurrence network stability and SCFA receptor level correlates with obesity in African-origin women. <i>Scientific Reports</i> , 2018, 8, 17135.	1.6	42
2541	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. <i>MSystems</i> , 2018, 3, .	1.7	56
2542	Characterization of the Microbiome at the World's Largest Potable Water Reuse Facility. <i>Frontiers in Microbiology</i> , 2018, 9, 2435.	1.5	43
2543	The Effect of Dietary Mushroom <i>Agaricus bisporus</i> on Intestinal Microbiota Composition and Host Immunological Function. <i>Nutrients</i> , 2018, 10, 1721.	1.7	28
2544	Fecal microbiota associated with phytohaemagglutinin-induced immune response in nestlings of a passerine bird. <i>Ecology and Evolution</i> , 2018, 8, 9793-9802.	0.8	10
2545	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018, 3, .	1.7	58
2546	First Insights into the Gut Microbiota of Mexican Patients with Celiac Disease and Non-Celiac Gluten Sensitivity. <i>Nutrients</i> , 2018, 10, 1641.	1.7	39

#	ARTICLE	IF	CITATIONS
2547	Gut microbiota profiling in Norwegian weaner pigs reveals potentially beneficial effects of a high-fiber rapeseed diet. <i>PLoS ONE</i> , 2018, 13, e0209439.	1.1	26
2548	Vaginal microbiome variances in sample groups categorized by clinical criteria of bacterial vaginosis. <i>BMC Genomics</i> , 2018, 19, 876.	1.2	21
2549	Microbiome analysis of Pacific white shrimp gut and rearing water from Malaysia and Vietnam: implications for aquaculture research and management. <i>PeerJ</i> , 2018, 6, e5826.	0.9	71
2550	Commensals Suppress Intestinal Epithelial Cell Retinoic Acid Synthesis to Regulate Interleukin-22 Activity and Prevent Microbial Dysbiosis. <i>Immunity</i> , 2018, 49, 1103-1115.e6.	6.6	139
2551	Phosphorus-mineralizing Communities Reflect Nutrient-Rich Characteristics in Japanese Arable Andisols. <i>Microbes and Environments</i> , 2018, 33, 282-289.	0.7	17
2552	Effect of Tillage Treatment on the Diversity of Soil Arbuscular Mycorrhizal Fungal and Soil Aggregate-Associated Carbon Content. <i>Frontiers in Microbiology</i> , 2018, 9, 2986.	1.5	37
2553	The Dietary Intervention of Transgenic Low-Gliadin Wheat Bread in Patients with Non-Celiac Gluten Sensitivity (NCGS) Showed No Differences with Gluten Free Diet (GFD) but Provides Better Gut Microbiota Profile. <i>Nutrients</i> , 2018, 10, 1964.	1.7	28
2554	Iron Biofortified Carioca Bean (<i>Phaseolus vulgaris</i> L.)-Based Brazilian Diet Delivers More Absorbable Iron and Affects the Gut Microbiota In Vivo (<i>Gallus gallus</i>). <i>Nutrients</i> , 2018, 10, 1970.	1.7	36
2555	Impact of Individual Traits, Saturated Fat, and Protein Source on the Gut Microbiome. <i>MBio</i> , 2018, 9, .	1.8	70
2556	Sewer Sediment Bacterial Communities Suggest Potential to Transform Persistent Organic Pollutants. <i>Water Environment Research</i> , 2018, 90, 2022-2029.	1.3	6
2557	Effects of short-term endurance exercise on gut microbiota in elderly men. <i>Physiological Reports</i> , 2018, 6, e13935.	0.7	89
2558	Diet, physical activity and screen time but not body mass index are associated with the gut microbiome of a diverse cohort of college students living in university housing: a cross-sectional study. <i>BMC Microbiology</i> , 2018, 18, 210.	1.3	51
2559	Therapeutic faecal microbiota transplantation controls intestinal inflammation through IL10 secretion by immune cells. <i>Nature Communications</i> , 2018, 9, 5184.	5.8	190
2560	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. <i>MSystems</i> , 2018, 3, .	1.7	210
2561	Effect of inorganic nutrients on bacterial community composition in oil-bearing sandstones from the subsurface strata of an onshore oil reservoir and its potential use in Microbial Enhanced Oil Recovery. <i>PLoS ONE</i> , 2018, 13, e0198050.	1.1	8
2562	Bacterial microbiome of the chigger mite <i>Leptotrombidium imphalum</i> varies by life stage and infection with the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS ONE</i> , 2018, 13, e0208327.	1.1	16
2563	A practical introduction to microbial molecular ecology through the use of isolation chips. <i>Ecology and Evolution</i> , 2018, 8, 12286-12298.	0.8	5
2564	Potential of iturins as functional agents: safe, probiotic, and cytotoxic to cancer cells. <i>Food and Function</i> , 2018, 9, 5580-5587.	2.1	28

#	ARTICLE	IF	CITATIONS
2565	Microbiota-Induced TNF-like Ligand 1A Drives Group 3 Innate Lymphoid Cell-Mediated Barrier Protection and Intestinal T Cell Activation during Colitis. <i>Immunity</i> , 2018, 49, 1077-1089.e5.	6.6	108
2566	Practical considerations for sampling and data analysis in contemporary metagenomics-based environmental studies. <i>Journal of Microbiological Methods</i> , 2018, 154, 14-18.	0.7	12
2567	Use of sugarcane soybean intercropping in acid soil impacts the structure of the soil fungal community. <i>Scientific Reports</i> , 2018, 8, 14488.	1.6	29
2568	A Method for Collecting Atmospheric Microbial Samples From Set Altitudes for Use With Next-Generation Sequencing Techniques to Characterize Communities. <i>Air, Soil and Water Research</i> , 2018, 11, 117862211878887.	1.2	8
2569	Loss of murine Paneth cell function alters the immature intestinal microbiome and mimics changes seen in neonatal necrotizing enterocolitis. <i>PLoS ONE</i> , 2018, 13, e0204967.	1.1	53
2570	Accounting for Bacterial Overlap Between Raw Water Communities and Contaminating Sources Improves the Accuracy of Signature-Based Microbial Source Tracking. <i>Frontiers in Microbiology</i> , 2018, 9, 2364.	1.5	16
2571	Blow Your Nose, Shrimp! Unexpectedly Dense Bacterial Communities Occur on the Antennae and Antennules of Hydrothermal Vent Shrimp. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	18
2572	Divergence of Fecal Microbiota and Their Associations With Host Phylogeny in Cervinae. <i>Frontiers in Microbiology</i> , 2018, 9, 1823.	1.5	9
2573	Titanium as a modifier of the peri-implant microbiome structure. <i>Clinical Implant Dentistry and Related Research</i> , 2018, 20, 945-953.	1.6	58
2574	Novel association of <i>Psychrobacter</i> and <i>Pseudomonas</i> with malodour in bloodhound dogs, and the effects of a topical product composed of essential oils and plant-derived essential fatty acids in a randomized, blinded, placebo-controlled study. <i>Veterinary Dermatology</i> , 2018, 29, 465.	0.4	19
2575	Clinician Guide to Microbiome Testing. <i>Digestive Diseases and Sciences</i> , 2018, 63, 3167-3177.	1.1	22
2576	The impact of epidermal growth factor supernatant on pig performance and ileal microbiota1. <i>Translational Animal Science</i> , 2018, 2, 184-194.	0.4	7
2577	Monosodium glutamate induces limited modulation in gut microbiota. <i>Journal of Functional Foods</i> , 2018, 49, 493-500.	1.6	18
2578	Foliar application of Fe resonates to the belowground rhizosphere microbiome in Andean landrace potatoes. <i>Applied Soil Ecology</i> , 2018, 131, 89-98.	2.1	8
2579	Intestinal microbiota profiling and predicted metabolic dysregulation in psoriasis patients. <i>Experimental Dermatology</i> , 2018, 27, 1336-1343.	1.4	79
2580	Reduced colonic mucin degradation in breastfed infants colonized by <i>Bifidobacterium longum</i> subsp. <i>infantis</i> EVC001. <i>FEBS Open Bio</i> , 2018, 8, 1649-1657.	1.0	38
2581	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
2582	Diet induced changes in the microbiota and cell composition of rabbit gut associated lymphoid tissue (GALT). <i>Scientific Reports</i> , 2018, 8, 14103.	1.6	18

#	ARTICLE	IF	CITATIONS
2583	First insight into microbiome profile of fungivorous thrips <i>Hoplothrips carpathicus</i> (Insecta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 T Scientific Reports, 2018, 8, 14376.	1.6	24
2584	Drug pharmacomicrobiomics and toxicomicrobiomics: from scattered reports to systematic studies of drug-microbiome interactions. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2018, 14, 1043-1055.	1.5	36
2585	Integrating coalescent species delimitation with analysis of host specificity reveals extensive cryptic diversity despite minimal mitochondrial divergence in the malaria parasite genus <i>Leucocytozoon</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 128.	3.2	49
2586	A Metabolomic-Based Evaluation of the Role of Commensal Microbiota throughout the Gastrointestinal Tract in Mice. <i>Microorganisms</i> , 2018, 6, 101.	1.6	24
2587	Rabbit Microbiota Changes Throughout the Intestinal Tract. <i>Frontiers in Microbiology</i> , 2018, 9, 2144.	1.5	50
2588	The impacts of deglaciation and human activity on the taxonomic structure of prokaryotic communities in Antarctic soils on King George Island. <i>Antarctic Science</i> , 2018, 30, 278-288.	0.5	7
2589	Air and waterborne microbiome of a pharmaceutical plant provide insights on spatiotemporal variations and community resilience after disturbance. <i>BMC Microbiology</i> , 2018, 18, 124.	1.3	5
2590	Glyphosate perturbs the gut microbiota of honey bees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10305-10310.	3.3	469
2591	An assessment of the microbial community in an urban fringing tidal marsh with an emphasis on petroleum hydrocarbon degradative genes. <i>Marine Pollution Bulletin</i> , 2018, 136, 351-364.	2.3	4
2592	Highly cited papers in Microbiology: identification and conceptual analysis. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	16
2593	Unlocking preservation bias in the amber insect fossil record through experimental decay. <i>PLoS ONE</i> , 2018, 13, e0195482.	1.1	12
2594	Short-term microbial effects of a large-scale mine-tailing storage facility collapse on the local natural environment. <i>PLoS ONE</i> , 2018, 13, e0196032.	1.1	12
2595	Biases in Prokaryotic Community Amplicon Sequencing Affected by DNA Extraction Methods in Both Saline and Non-saline Soil. <i>Frontiers in Microbiology</i> , 2018, 9, 1796.	1.5	12
2596	Diversity-Function Relationships in Natural, Applied, and Engineered Microbial Ecosystems. <i>Advances in Applied Microbiology</i> , 2018, 105, 131-189.	1.3	13
2597	16S rRNA Gene Analysis with QIIME2. <i>Methods in Molecular Biology</i> , 2018, 1849, 113-129.	0.4	283
2598	Processing a 16S rRNA Sequencing Dataset with the Microbiome Helper Workflow. <i>Methods in Molecular Biology</i> , 2018, 1849, 131-141.	0.4	5
2599	Introductory Overview of Statistical Analysis of Microbiome Data. <i>ICSA Book Series in Statistics</i> , 2018, , 43-75.	0.0	7
2600	Microbial Changes and Host Response in F344 Rat Colon Depending on Sex and Age Following a High-Fat Diet. <i>Frontiers in Microbiology</i> , 2018, 9, 2236.	1.5	38

#	ARTICLE	IF	CITATIONS
2601	Multivariate Community Analysis. ICSA Book Series in Statistics, 2018, , 285-330.	0.0	2
2602	Stratification of microbial communities throughout a biological sulphate reducing up-flow anaerobic packed bed reactor, revealed through 16S metagenomics. Research in Microbiology, 2018, 169, 543-551.	1.0	13
2603	Increasing Dietary Fiber Intake Is Associated with a Distinct Esophageal Microbiome. Clinical and Translational Gastroenterology, 2018, 9, e199.	1.3	42
2604	Effects of antibiotic on microflora in ileum and cecum for broilers by 16S rRNA sequence analysis. Animal Science Journal, 2018, 89, 1680-1691.	0.6	16
2605	Gut microbiota and plasma metabolites associated with diabetes in women with, or at high risk for, HIV infection. EBioMedicine, 2018, 37, 392-400.	2.7	61
2606	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. Genome Medicine, 2018, 10, 78.	3.6	107
2607	Variations of the lung microbiome and immune response in mechanically ventilated surgical patients. PLoS ONE, 2018, 13, e0205788.	1.1	7
2608	Reduced diversity of gut microbiota in two Aedes mosquitoes species in areas of recent invasion. Scientific Reports, 2018, 8, 16091.	1.6	41
2609	Orally administered gold nanoparticles protect against colitis by attenuating Toll-like receptor 4- and reactive oxygen/nitrogen species-mediated inflammatory responses but could induce gut dysbiosis in mice. Journal of Nanobiotechnology, 2018, 16, 86.	4.2	48
2610	The Biogeographical Distribution of Soil Bacterial Communities in the Loess Plateau as Revealed by High-Throughput Sequencing. Frontiers in Microbiology, 2018, 9, 2456.	1.5	35
2611	Changes in the Fungal Microbiome of Maize During Hermetic Storage in the United States and Kenya. Frontiers in Microbiology, 2018, 9, 2336.	1.5	19
2612	Temporal development of the gut microbiome in early childhood from the TEDDY study. Nature, 2018, 562, 583-588.	13.7	1,220
2613	Changes in ruminal and reticular pH and bacterial communities in Holstein cattle fed a high-grain diet. BMC Veterinary Research, 2018, 14, 310.	0.7	46
2614	Biodiversityâ€“function relationships in methanogenic communities. Molecular Ecology, 2018, 27, 4641-4651.	2.0	30
2615	Community profiling of the urinary microbiota: considerations for low-biomass samples. Nature Reviews Urology, 2018, 15, 735-749.	1.9	87
2616	Changes in bacterial communities during two agricultural solid wastesâ€™ co-composting processes. Annals of Microbiology, 2018, 68, 743-754.	1.1	9
2617	Differential Activation of Hepatic Invariant NKT Cell Subsets Plays a Key Role in Progression of Nonalcoholic Steatohepatitis. Journal of Immunology, 2018, 201, 3017-3035.	0.4	69
2618	Microbiomes Associated With Foods From Plant and Animal Sources. Frontiers in Microbiology, 2018, 9, 2540.	1.5	35

#	ARTICLE	IF	CITATIONS
2619	Gut Microbiota of Great Spotted Cuckoo Nestlings is a Mixture of Those of Their Foster Magpie Siblings and of Cuckoo Adults. <i>Genes</i> , 2018, 9, 381.	1.0	18
2620	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018, 15, 847-848.	9.0	71
2621	The Cloacal Microbiome of Five Wild Duck Species Varies by Species and Influenza A Virus Infection Status. <i>MSphere</i> , 2018, 3, .	1.3	28
2622	A <i>Dehalogenimonas</i> Population Respires 1,2,4-Trichlorobenzene and Dichlorobenzenes. <i>Environmental Science & Technology</i> , 2018, 52, 13391-13398.	4.6	23
2623	Diversified gut microbiota in newborns of mothers with gestational diabetes mellitus. <i>PLoS ONE</i> , 2018, 13, e0205695.	1.1	62
2624	The severity of human peri-implantitis lesions correlates with the level of submucosal microbial dysbiosis. <i>Journal of Clinical Periodontology</i> , 2018, 45, 1498-1509.	2.3	60
2625	Tracing Antibody Repertoire Evolution by Systems Phylogeny. <i>Frontiers in Immunology</i> , 2018, 9, 2149.	2.2	26
2626	Increased transferrin saturation is associated with subgingival microbiota dysbiosis and severe periodontitis in genetic haemochromatosis. <i>Scientific Reports</i> , 2018, 8, 15532.	1.6	19
2627	Biogeographic and anthropogenic correlates of Aleutian Islands plant diversity: A machine learning approach. <i>Journal of Systematics and Evolution</i> , 2018, 56, 476-497.	1.6	9
2628	G3 PhyloChip Analysis Confirms the Promise of Plant-Based Culture Media for Unlocking the Composition and Diversity of the Maize Root Microbiome and for Recovering Unculturable Candidate Divisions/Phyla. <i>Microbes and Environments</i> , 2018, 33, 317-325.	0.7	21
2629	Diet-induced shifts in the crown-of-thorns (<i>Acanthaster</i> sp.) larval microbiome. <i>Marine Biology</i> , 2018, 165, 1.	0.7	28
2630	Influence of Physicochemical Factors on Bacterial Communities Along the Lower Mekong River Assessed by Illumina Next-Generation Sequencing. <i>Water, Air, and Soil Pollution</i> , 2018, 229, 1.	1.1	7
2631	Fecal microbiota and bile acid interactions with systemic and adipose tissue metabolism in diet-induced weight loss of obese postmenopausal women. <i>Journal of Translational Medicine</i> , 2018, 16, 244.	1.8	78
2632	Phylogenetic Diversity and Conservation Evaluation: Perspectives on Multiple Values, Indices, and Scales of Application. , 2018, , 1-26.		32
2633	Microbes in Marcellus Shale: Extremophiles living more than two kilometers inside the Earth?. <i>Fuel</i> , 2018, 234, 1205-1211.	3.4	3
2634	Alteration of the cutaneous microbiome in psoriasis and potential role in Th17 polarization. <i>Microbiome</i> , 2018, 6, 154.	4.9	190
2635	Do Ruminant Ciliates Select Their Preys and Prokaryotic Symbionts?. <i>Frontiers in Microbiology</i> , 2018, 9, 1710.	1.5	47
2636	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (<i>Oreochromis shiranus</i>) and North African catfish (<i>Clarias gariepinus</i>). <i>MicrobiologyOpen</i> , 2018, 7, e00716.	1.2	23

#	ARTICLE	IF	CITATIONS
2637	Bacterial community composition and diversity uncovered in experimental sludge treatment reed bed systems with different swine slurry hydraulic loadings. <i>Ecological Engineering</i> , 2018, 123, 175-184.	1.6	6
2638	Analysis of gut microbiota profiles and microbe-disease associations in children with autism spectrum disorders in China. <i>Scientific Reports</i> , 2018, 8, 13981.	1.6	128
2639	Aerobic cultivation of anaerobic rumen protozoa, <i>Entodinium caudatum</i> and <i>Epidinium caudatum</i> . <i>Journal of Microbiological Methods</i> , 2018, 152, 186-193.	0.7	15
2640	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 13974.	1.6	148
2641	Ceftriaxone Administration Disrupts Intestinal Homeostasis, Mediating Noninflammatory Proliferation and Dissemination of Commensal Enterococci. <i>Infection and Immunity</i> , 2018, 86, .	1.0	31
2642	Exposures Related to House Dust Microbiota in a U.S. Farming Population. <i>Environmental Health Perspectives</i> , 2018, 126, 067001.	2.8	23
2643	Direct-fed microbial supplementation influences the bacteria community composition of the gastrointestinal tract of pre- and post-weaned calves. <i>Scientific Reports</i> , 2018, 8, 14147.	1.6	50
2644	Bacterial community response to a preindustrialâ€”future CO ₂ gradient is limited and soil specific in Texas Prairie grassland. <i>Global Change Biology</i> , 2018, 24, 5815-5827.	4.2	8
2645	OBSOLETE: Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , .		1
2646	Bacterial communities and potential waterborne pathogens within the typical urban surface waters. <i>Scientific Reports</i> , 2018, 8, 13368.	1.6	54
2647	Effects of exogenous microbial inoculum on the structure and dynamics of bacterial communities in swine carcass composting. <i>Canadian Journal of Microbiology</i> , 2018, 64, 1042-1053.	0.8	9
2648	Characterization of the Functional Changes in Mouse Gut Microbiome Associated with Increased <i>Akkermansia muciniphila</i> Population Modulated by Dietary Black Raspberries. <i>ACS Omega</i> , 2018, 3, 10927-10937.	1.6	49
2649	Microbial Transplantation With Human Gut Commensals Containing CutC Is Sufficient to Transmit Enhanced Platelet Reactivity and Thrombosis Potential. <i>Circulation Research</i> , 2018, 123, 1164-1176.	2.0	122
2650	Temperature Driven Changes in Benthic Bacterial Diversity Influences Biogeochemical Cycling in Coastal Sediments. <i>Frontiers in Microbiology</i> , 2018, 9, 1730.	1.5	40
2651	Dysbiosis and early mortality in zebrafish larvae exposed to subclinical concentrations of streptomycin. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	48
2652	Preservation of microbial DNA in marine sediments: insights from extracellular DNA pools. <i>Environmental Microbiology</i> , 2018, 20, 4526-4542.	1.8	48
2653	Exposure to Yeast Shapes the Intestinal Bacterial Community Assembly in Zebrafish Larvae. <i>Frontiers in Microbiology</i> , 2018, 9, 1868.	1.5	35
2654	Design of Primers for Evaluation of Lactic Acid Bacteria Populations in Complex Biological Samples. <i>Frontiers in Microbiology</i> , 2018, 9, 2045.	1.5	42

#	ARTICLE	IF	CITATIONS
2655	Effects of dietary supplementation with combinations of organic and medium chain fatty acids as replacements for chlortetracycline on growth performance, serum immunity, and fecal microbiota of weaned piglets. <i>Livestock Science</i> , 2018, 216, 210-218.	0.6	22
2656	Impact of xylanases on gut microbiota of growing pigs fed corn- or wheat-based diets. <i>Animal Nutrition</i> , 2018, 4, 339-350.	2.1	41
2657	Oral Microbiome Shifts From Caries-Free to Caries-Affected Status in 3-Year-Old Chinese Children: A Longitudinal Study. <i>Frontiers in Microbiology</i> , 2018, 9, 2009.	1.5	42
2658	Pigmented microbial eukaryotes fuel the deep sea carbon pool in the tropical Western Pacific Ocean. <i>Environmental Microbiology</i> , 2018, 20, 3811-3824.	1.8	15
2659	Environmental temperature alters the digestive performance and gut microbiota of a terrestrial amphibian. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	98
2660	The microbiota of traumatic, open fracture wounds is associated with mechanism of injury. <i>Wound Repair and Regeneration</i> , 2018, 26, 127-135.	1.5	19
2661	High content analysis of sea buckthorn, black chokeberry, red and white currants microbiota – A pilot study. <i>Food Research International</i> , 2018, 111, 597-606.	2.9	14
2662	Differential metabolic effects of oral butyrate treatment in lean versus metabolic syndrome subjects. <i>Clinical and Translational Gastroenterology</i> , 2018, 9, e155.	1.3	123
2663	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	9.4	482
2664	Dynamic bacterial and fungal microbiomes during sweet sorghum ensiling impact bioethanol production. <i>Bioresource Technology</i> , 2018, 264, 163-173.	4.8	37
2665	Resilience to fire of phylogenetic diversity across biological domains. <i>Molecular Ecology</i> , 2018, 27, 2896-2908.	2.0	49
2666	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
2667	Inhalational exposure to particulate matter air pollution alters the composition of the gut microbiome. <i>Environmental Pollution</i> , 2018, 240, 817-830.	3.7	181
2668	Food Starch Structure Impacts Gut Microbiome Composition. <i>MSphere</i> , 2018, 3, .	1.3	106
2669	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	5.9	68
2670	Bacterial community of industrial raw sausage packaged in modified atmosphere throughout the shelf life. <i>International Journal of Food Microbiology</i> , 2018, 280, 78-86.	2.1	24
2671	Enrichment of Clinically Relevant Organisms in Spontaneous Preterm-Delivered Placentas and Reagent Contamination across All Clinical Groups in a Large Pregnancy Cohort in the United Kingdom. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
2672	The gut microbiome is associated with behavioural task in honey bees. <i>Insectes Sociaux</i> , 2018, 65, 419-429.	0.7	90

#	ARTICLE	IF	CITATIONS
2673	Fecal and Mucosa-Associated Intestinal Microbiota in Patients with Diarrhea-Predominant Irritable Bowel Syndrome. <i>Digestive Diseases and Sciences</i> , 2018, 63, 1890-1899.	1.1	72
2674	Response of microbial populations regulating nutrient biogeochemical cycles to oiling of coastal saltmarshes from the Deepwater Horizon oil spill. <i>Environmental Pollution</i> , 2018, 241, 136-147.	3.7	21
2675	Probiotic supplementation and associated infant gut microbiome and health: a cautionary retrospective clinical comparison. <i>Scientific Reports</i> , 2018, 8, 8283.	1.6	78
2676	Microbial community analyses of produced waters from high-temperature oil reservoirs reveal unexpected similarity between geographically distant oil reservoirs. <i>Microbial Biotechnology</i> , 2018, 11, 788-796.	2.0	31
2677	Application of PacBio Single Molecule Real-Time (SMRT) sequencing in bacterial source tracking analysis during milk powder production. <i>Food Control</i> , 2018, 93, 226-234.	2.8	12
2678	Impact of Iron-Enriched <i>Aspergillus oryzae</i> on Iron Bioavailability, Safety, and Gut Microbiota in Rats. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 6213-6218.	2.4	14
2679	Consistent patterns of high alpha and low beta diversity in tropical parasitic and free-living protists. <i>Molecular Ecology</i> , 2018, 27, 2846-2857.	2.0	43
2680	Microbiome dynamics during spontaneous fermentations of sound grapes in comparison with sour rot and <i>Botrytis</i> infected grapes. <i>International Journal of Food Microbiology</i> , 2018, 281, 36-46.	2.1	34
2681	Limited influence of hospital wastewater on the microbiome and resistome of wastewater in a community sewerage system. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	72
2682	Bacterial endophyte communities in <i>Pinus flexilis</i> are structured by host age, tissue type, and environmental factors. <i>Plant and Soil</i> , 2018, 428, 335-352.	1.8	32
2683	Disruption of microbial community composition and identification of plant growth promoting microorganisms after exposure of soil to rapeseed-derived glucosinolates. <i>PLoS ONE</i> , 2018, 13, e0200160.	1.1	54
2684	Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , 273-292.		3
2685	Meta-genomics study among four contact lens wearers from India. <i>Gene Reports</i> , 2018, 12, 208-217.	0.4	1
2686	A High-Throughput Organoid Microinjection Platform to Study Gastrointestinal Microbiota and Luminal Physiology. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 6, 301-319.	2.3	168
2687	Antimicrobial peptide expression in a wild tobacco plant reveals the limits of host-microbe-manipulations in the field. <i>ELife</i> , 2018, 7, .	2.8	19
2688	Analysis Methods for Shotgun Metagenomics. <i>Computational Biology</i> , 2018, , 71-112.	0.1	1
2689	Alterations to the Intestinal Microbiome and Metabolome of <i>Pimephales promelas</i> and <i>Mus musculus</i> Following Exposure to Dietary Methylmercury. <i>Environmental Science & Technology</i> , 2018, 52, 8774-8784.	4.6	77
2690	Illumina MiSeq Sequencing for Preliminary Analysis of Microbiome Causing Primary Endodontic Infections in Egypt. <i>International Journal of Microbiology</i> , 2018, 2018, 1-15.	0.9	18

#	ARTICLE	IF	CITATIONS
2691	Evaluation of the impact of dental prophylaxis on the oral microbiota of dogs. <i>PLoS ONE</i> , 2018, 13, e0199676.	1.1	24
2692	Improving the standards for gut microbiome analysis of fecal samples: insights from the field biology of Japanese macaques on Yakushima Island. <i>Primates</i> , 2018, 59, 423-436.	0.7	18
2693	Analytic Methods in Microbiome Studies. , 2018, , 29-42.		0
2694	Theoretical and Applied Aspects of Systems Biology. <i>Computational Biology</i> , 2018, , .	0.1	3
2695	Viral community predicts the geographical origin of fermented vegetable foods more precisely than bacterial community. <i>Food Microbiology</i> , 2018, 76, 319-327.	2.1	28
2696	A zero-inflated beta-binomial model for microbiome data analysis. <i>Stat</i> , 2018, 7, e185.	0.3	27
2697	Need for focus on microbial species following ice melt and changing freshwater regimes in a Janus Arctic Gateway. <i>Scientific Reports</i> , 2018, 8, 9405.	1.6	26
2698	Analysis of Bacterial Diversity in Different Heavy Oil Wells of a Reservoir in South Oman with Alkaline pH. <i>Scientifica</i> , 2018, 2018, 1-10.	0.6	4
2699	Early-life antibiotics attenuate regulatory T cell generation and increase the severity of murine house dust mite-induced asthma. <i>Pediatric Research</i> , 2018, 84, 426-434.	1.1	23
2700	Pea-protein alginate encapsulation adversely affects development of clinical signs of <i>Citrobacter rodentium</i> -induced colitis in mice treated with probiotics. <i>Canadian Journal of Microbiology</i> , 2018, 64, 744-760.	0.8	5
2701	<i>Spiroplasma</i> dominates the microbiome of khapra beetle: comparison with a congener, effects of life stage and temperature. <i>Symbiosis</i> , 2018, 76, 277-291.	1.2	6
2702	Overlapping Community Compositions of Gut and Fecal Microbiomes in Lab-Reared and Field-Collected German Cockroaches. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	67
2703	Influence of gender and menopausal status on gut microbiota. <i>Maturitas</i> , 2018, 116, 43-53.	1.0	153
2704	Bulk soil bacterial community structure and function respond to long-term organic and conventional agricultural management. <i>Canadian Journal of Microbiology</i> , 2018, 64, 901-914.	0.8	11
2705	β -Klotho deficiency shifts the gut-liver bile acid axis and induces hepatic alterations in mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 315, E833-E847.	1.8	13
2706	Shifts in intestinal microbiota after duodenal exclusion favor glycemic control and weight loss: a randomized controlled trial. <i>Surgery for Obesity and Related Diseases</i> , 2018, 14, 1748-1754.	1.0	27
2707	Topical ferumoxytol nanoparticles disrupt biofilms and prevent tooth decay in vivo via intrinsic catalytic activity. <i>Nature Communications</i> , 2018, 9, 2920.	5.8	129
2708	Alternate life history phases of a common seaweed have distinct microbial surface communities. <i>Molecular Ecology</i> , 2018, 27, 3555-3568.	2.0	41

#	ARTICLE	IF	CITATIONS
2709	Efficacy of Jia Wei Yang He formula as an adjunctive therapy for asthma: study protocol for a randomized, double blinded, controlled trial. <i>Trials</i> , 2018, 19, 355.	0.7	2
2710	Arbuscular mycorrhizal fungal community in the topsoil of a subtropical landfill restored after 18 years. <i>Journal of Environmental Management</i> , 2018, 225, 17-24.	3.8	9
2711	The effect of biogenic and chemically manufactured silver nanoparticles on the benthic bacterial communities in river sediments. <i>Science of the Total Environment</i> , 2018, 644, 1380-1390.	3.9	20
2712	Nasal microbiota clusters associate with inflammatory response, viral load, and symptom severity in experimental rhinovirus challenge. <i>Scientific Reports</i> , 2018, 8, 11411.	1.6	51
2713	Antibiotic-Induced Dysbiosis Predicts Mortality in an Animal Model of <i>Clostridium difficile</i> Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	18
2714	Sex differences in gut microbiota in patients with major depressive disorder. <i>Neuropsychiatric Disease and Treatment</i> , 2018, Volume 14, 647-655.	1.0	193
2715	Effects of prebiotic inulin-type fructans on blood metabolite and hormone concentrations and faecal microbiota and metabolites in overweight dogs. <i>British Journal of Nutrition</i> , 2018, 120, 711-720.	1.2	46
2716	Characterization of the fecal microbiota of healthy horses. <i>American Journal of Veterinary Research</i> , 2018, 79, 811-819.	0.3	37
2717	Microbial connectivity and sorting in a High Arctic watershed. <i>ISME Journal</i> , 2018, 12, 2988-3000.	4.4	33
2718	Selection of Appropriate Metagenome Taxonomic Classifiers for Ancient Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	35
2719	Gut Microbiota Composition and Fecal Metabolic Phenotype in Patients With Acute Anterior Uveitis. , 2018, 59, 1523.		77
2720	High species diversity of trichostrongyle parasite communities within and between Western Canadian commercial and conservation bison herds revealed by nemabiome metabarcoding. <i>Parasites and Vectors</i> , 2018, 11, 299.	1.0	31
2721	Responses of Intestinal Mucosal Barrier Functions of Rats to Simulated Weightlessness. <i>Frontiers in Physiology</i> , 2018, 9, 729.	1.3	27
2722	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. <i>Frontiers in Plant Science</i> , 2017, 8, 2241.	1.7	24
2723	When the Nose Doesnâ€™t Know: Canine Olfactory Function Associated With Health, Management, and Potential Links to Microbiota. <i>Frontiers in Veterinary Science</i> , 2018, 5, 56.	0.9	70
2724	Omeprazole Minimally Alters the Fecal Microbial Community in Six Cats: A Pilot Study. <i>Frontiers in Veterinary Science</i> , 2018, 5, 79.	0.9	15
2725	Beneficial Impact and Molecular Mechanism of <i>Bacillus coagulans</i> on Pigletsâ€™ Intestine. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2084.	1.8	29
2726	Diarrhea-Associated Intestinal Microbiota in Captive Sichuan Golden Snub-Nosed Monkeys (<i>Rhinopithecus roxellana</i>). <i>Microbes and Environments</i> , 2018, 33, 249-256.	0.7	14

#	ARTICLE	IF	CITATIONS
2727	Tree species mixture inhibits soil organic carbon mineralization accompanied by decreased r-selected bacteria. <i>Plant and Soil</i> , 2018, 431, 203-216.	1.8	24
2728	Gut microbiota components are associated with fixed airway obstruction in asthmatic patients living in the tropics. <i>Scientific Reports</i> , 2018, 8, 9582.	1.6	16
2729	Analyzing differences between microbiome communities using mixture distributions. <i>Statistics in Medicine</i> , 2018, 37, 4036-4053.	0.8	7
2730	Updating <i>Plakobranthus cf. ianthobapsus</i> (Gastropoda, Sacoglossa) host use: Diverse algal-animal interactions revealed by NGS with implications for invasive species management. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 172-181.	1.2	16
2731	Oropharyngeal microbiome evaluation highlights <i>Neisseria</i> abundance in active celiac patients. <i>Scientific Reports</i> , 2018, 8, 11047.	1.6	33
2732	Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. <i>Scientific Reports</i> , 2018, 8, 11159.	1.6	60
2733	Rapid gastrointestinal loss of Clostridial Clusters IV and XIVa in the ICU associates with an expansion of gut pathogens. <i>PLoS ONE</i> , 2018, 13, e0200322.	1.1	39
2734	The Microbial Landscape of Sea Stars and the Anatomical and Interspecies Variability of Their Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1829.	1.5	35
2735	Leaf-associated bacterial microbiota of coffee and its correlation with manganese and calcium levels on leaves. <i>Genetics and Molecular Biology</i> , 2018, 41, 455-465.	0.6	4
2736	Microbial community changes during a toxic cyanobacterial bloom in an alkaline Hungarian lake. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2425-2440.	0.7	12
2737	The impact of <i>Clostridium butyricum</i> MIYAIRI 588 on the murine gut microbiome and colonic tissue. <i>Anaerobe</i> , 2018, 54, 8-18.	1.0	45
2738	Chronic Rhinosinusitis: Potential Role of Microbial Dysbiosis and Recommendations for Sampling Sites. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 57.	1.8	75
2739	Computational Strategies for Dissecting the High-Dimensional Complexity of Adaptive Immune Repertoires. <i>Frontiers in Immunology</i> , 2018, 9, 224.	2.2	164
2740	Analyzing Immunoglobulin Repertoires. <i>Frontiers in Immunology</i> , 2018, 9, 462.	2.2	89
2741	Biogeographic Differences in the Microbiome and Pathobiome of the Coral <i>Cladocora caespitosa</i> in the Western Mediterranean Sea. <i>Frontiers in Microbiology</i> , 2018, 9, 22.	1.5	58
2742	Spatial Heterogeneity and Co-occurrence of Mucosal and Luminal Microbiome across Swine Intestinal Tract. <i>Frontiers in Microbiology</i> , 2018, 9, 48.	1.5	172
2743	Diversity of Rare and Abundant Prokaryotic Phylotypes in the Prony Hydrothermal Field and Comparison with Other Serpentinite-Hosted Ecosystems. <i>Frontiers in Microbiology</i> , 2018, 9, 102.	1.5	23
2744	Competitive Traits Are More Important than Stress-Tolerance Traits in a Cadmium-Contaminated Rhizosphere: A Role for Trait Theory in Microbial Ecology. <i>Frontiers in Microbiology</i> , 2018, 9, 121.	1.5	60

#	ARTICLE	IF	CITATIONS
2745	Soil Bacterial Community Was Changed after Brassicaceous Seed Meal Application for Suppression of Fusarium Wilt on Pepper. <i>Frontiers in Microbiology</i> , 2018, 9, 185.	1.5	22
2746	Environmental and Host Effects on Skin Bacterial Community Composition in Panamanian Frogs. <i>Frontiers in Microbiology</i> , 2018, 9, 298.	1.5	49
2747	Assessing the Influence of Vegan, Vegetarian and Omnivore Oriented Westernized Dietary Styles on Human Gut Microbiota: A Cross Sectional Study. <i>Frontiers in Microbiology</i> , 2018, 9, 317.	1.5	78
2748	Unique Microbial Diversity and Metabolic Pathway Features of Fermented Vegetables From Hainan, China. <i>Frontiers in Microbiology</i> , 2018, 9, 399.	1.5	53
2749	Skin Microbiomes of California Terrestrial Salamanders Are Influenced by Habitat More Than Host Phylogeny. <i>Frontiers in Microbiology</i> , 2018, 9, 442.	1.5	58
2750	Host and Aquatic Environment Shape the Amphibian Skin Microbiome but Effects on Downstream Resistance to the Pathogen <i>Batrachochytrium dendrobatidis</i> Are Variable. <i>Frontiers in Microbiology</i> , 2018, 9, 487.	1.5	63
2751	Variance Component Selection With Applications to Microbiome Taxonomic Data. <i>Frontiers in Microbiology</i> , 2018, 9, 509.	1.5	10
2752	Rumen Biohydrogenation and Microbial Community Changes Upon Early Life Supplementation of 22:6n-3 Enriched Microalgae to Goats. <i>Frontiers in Microbiology</i> , 2018, 9, 573.	1.5	35
2753	Comparative Analysis of the Microbiota Between Sheep Rumen and Rabbit Cecum Provides New Insight Into Their Differential Methane Production. <i>Frontiers in Microbiology</i> , 2018, 9, 575.	1.5	42
2754	Typical Soil Redox Processes in Pentachlorophenol Polluted Soil Following Biochar Addition. <i>Frontiers in Microbiology</i> , 2018, 9, 579.	1.5	28
2755	Lactobacilli Are Prominent Members of the Microbiota Involved in the Ruminal Digestion of Barley and Corn. <i>Frontiers in Microbiology</i> , 2018, 9, 718.	1.5	32
2756	Microbiome of Total Versus Live Bacteria in the Gut of Rex Rabbits. <i>Frontiers in Microbiology</i> , 2018, 9, 733.	1.5	30
2757	High Diversity of Myocyanophage in Various Aquatic Environments Revealed by High-Throughput Sequencing of Major Capsid Protein Gene With a New Set of Primers. <i>Frontiers in Microbiology</i> , 2018, 9, 887.	1.5	5
2758	Geographical and Cultivar Features Differentiate Grape Microbiota in Northern Italy and Spain Vineyards. <i>Frontiers in Microbiology</i> , 2018, 9, 946.	1.5	109
2759	Microscale Biosignatures and Abiotic Mineral Authigenesis in Little Hot Creek, California. <i>Frontiers in Microbiology</i> , 2018, 9, 997.	1.5	35
2760	In Vitro Modeling of Bile Acid Processing by the Human Fecal Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 1153.	1.5	36
2761	Exposure to Arsenic Alters the Microbiome of Larval Zebrafish. <i>Frontiers in Microbiology</i> , 2018, 9, 1323.	1.5	42
2762	Predictive Modeling of Microbiome Data Using a Phylogeny-Regularized Generalized Linear Mixed Model. <i>Frontiers in Microbiology</i> , 2018, 9, 1391.	1.5	35

#	ARTICLE	IF	CITATIONS
2763	Impaired Autophagy in Intestinal Epithelial Cells Alters Gut Microbiota and Host Immune Responses. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	72
2764	Consistent and reproducible long-term in vitro growth of health and disease-associated oral subgingival biofilms. <i>BMC Microbiology</i> , 2018, 18, 70.	1.3	20
2765	Core Sulphate-Reducing Microorganisms in Metal-Removing Semi-Passive Biochemical Reactors and the Co-Occurrence of Methanogens. <i>Microorganisms</i> , 2018, 6, 16.	1.6	31
2766	16S rDNA Profiling to Reveal the Influence of Seed-Applied Biostimulants on the Rhizosphere of Young Maize Plants. <i>Molecules</i> , 2018, 23, 1461.	1.7	49
2767	Effect of a Protein Supplement on the Gut Microbiota of Endurance Athletes: A Randomized, Controlled, Double-Blind Pilot Study. <i>Nutrients</i> , 2018, 10, 337.	1.7	84
2768	Digestive microbiota is different in pigs receiving antimicrobials or a feed additive during the nursery period. <i>PLoS ONE</i> , 2018, 13, e0197353.	1.1	32
2769	Effects of biochar on the ecological performance of a subtropical landfill. <i>Science of the Total Environment</i> , 2018, 644, 963-975.	3.9	29
2770	Establishing a mucosal gut microbial community in vitro using an artificial simulator. <i>PLoS ONE</i> , 2018, 13, e0197692.	1.1	44
2771	Effect of Dietary Fructooligosaccharide (FOS) Supplementation on Ileal Microbiota in Broiler Chickens. <i>Poultry Science</i> , 2018, 97, 3622-3634.	1.5	48
2772	The cecal microbiome of commercial broiler chickens varies significantly by season. <i>Poultry Science</i> , 2018, 97, 3635-3644.	1.5	26
2773	Aerodigestive dysbiosis in children with chronic cough. <i>Pediatric Pulmonology</i> , 2018, 53, 1288-1298.	1.0	6
2774	16S rRNA sequencing reveals likely beneficial core microbes within faecal samples of the EU protected slug <i>Geomalacus maculosus</i> . <i>Scientific Reports</i> , 2018, 8, 10402.	1.6	10
2775	Bio-cord plays a similar role as submerged macrophytes in harboring bacterial assemblages in an eco-ditch. <i>Environmental Science and Pollution Research</i> , 2018, 25, 26550-26561.	2.7	10
2776	Characterisation of the nasal microbiota in granulomatosis with polyangiitis. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1448-1453.	0.5	37
2777	Antibiotic-induced microbiome depletion alters metabolic homeostasis by affecting gut signaling and colonic metabolism. <i>Nature Communications</i> , 2018, 9, 2872.	5.8	343
2778	Western diet feeding influences gut microbiota profiles in apoE knockout mice. <i>Lipids in Health and Disease</i> , 2018, 17, 159.	1.2	61
2779	Body Mass Index and Sex Affect Diverse Microbial Niches within the Gut. <i>Frontiers in Microbiology</i> , 2018, 9, 213.	1.5	87
2780	The Ramazzini Institute 13-week pilot study on glyphosate and Roundup administered at human-equivalent dose to Sprague Dawley rats: effects on the microbiome. <i>Environmental Health</i> , 2018, 17, 50.	1.7	87

#	ARTICLE	IF	CITATIONS
2781	Ammonia-oxidizing bacteria and archaea within biofilters of a commercial recirculating marine aquaculture system. <i>AMB Express</i> , 2018, 8, 17.	1.4	16
2782	Holobionts and ecological speciation: the intestinal microbiota of lake whitefish species pairs. <i>Microbiome</i> , 2018, 6, 47.	4.9	67
2783	Similarity of the dog and human gut microbiomes in gene content and response to diet. <i>Microbiome</i> , 2018, 6, 72.	4.9	211
2784	Physicochemical differences between malanga (<i>Xanthosoma sagittifolium</i>) and potato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overlook Functional Foods, 2018, 45, 268-276.	1.6	11
2785	Microbial and metabolic multi-omic correlations in systemic sclerosis patients. <i>Annals of the New York Academy of Sciences</i> , 2018, 1421, 97-109.	1.8	50
2786	Predator size divergence depends on community context. <i>Ecology Letters</i> , 2018, 21, 1097-1107.	3.0	9
2787	Recent insights into the tick microbiome gained through next-generation sequencing. <i>Parasites and Vectors</i> , 2018, 11, 12.	1.0	146
2788	The association between anterior nares and nasopharyngeal microbiota in infants hospitalized for bronchiolitis. <i>Microbiome</i> , 2018, 6, 2.	4.9	56
2789	Influenza A virus infection impacts systemic microbiota dynamics and causes quantitative enteric dysbiosis. <i>Microbiome</i> , 2018, 6, 9.	4.9	194
2790	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. <i>Microbiome</i> , 2018, 6, 16.	4.9	208
2791	Crawling-induced floor dust resuspension affects the microbiota of the infant breathing zone. <i>Microbiome</i> , 2018, 6, 25.	4.9	40
2792	Filter forensics: microbiota recovery from residential HVAC filters. <i>Microbiome</i> , 2018, 6, 22.	4.9	35
2793	Microbiota inoculum composition affects holobiont assembly and host growth in <i>Daphnia</i> . <i>Microbiome</i> , 2018, 6, 56.	4.9	74
2794	Effect of heat shock on hot water plumbing microbiota and <i>Legionella pneumophila</i> control. <i>Microbiome</i> , 2018, 6, 30.	4.9	20
2795	Non-Ischemic Heart Failure With Reduced Ejection Fraction Is Associated With Altered Intestinal Microbiota. <i>Circulation Journal</i> , 2018, 82, 1640-1650.	0.7	41
2796	Exposure to toxic metals triggers unique responses from the rat gut microbiota. <i>Scientific Reports</i> , 2018, 8, 6578.	1.6	95
2797	Combined effects of phosphate-solubilizing bacterium XMT-5 (<i>Rhizobium</i> sp.) and submerged macrophyte <i>Ceratophyllum demersum</i> on phosphorus release in eutrophic lake sediments. <i>Environmental Science and Pollution Research</i> , 2018, 25, 18990-19000.	2.7	6
2798	A thin ice layer segregates two distinct fungal communities in Antarctic brines from Tarn Flat (Northern Victoria Land). <i>Scientific Reports</i> , 2018, 8, 6582.	1.6	21

#	ARTICLE	IF	CITATIONS
2799	Contrasting prevalence of selection and drift in the community structuring of bacteria and microbial eukaryotes. <i>Environmental Microbiology</i> , 2018, 20, 2231-2240.	1.8	153
2800	Tongue Microbiota and Oral Health Status in Community-Dwelling Elderly Adults. <i>MSphere</i> , 2018, 3, .	1.3	73
2801	Characteristics of the rhizosphere bacterial community across different cultivation years in saline-alkaline paddy soils of Songnen Plain of China. <i>Canadian Journal of Microbiology</i> , 2018, 64, 925-936.	0.8	28
2802	Effect of probiotic <i>Bifidobacterium bifidum</i> G9-1 on the relationship between gut microbiota profile and stress sensitivity in maternally separated rats. <i>Scientific Reports</i> , 2018, 8, 12384.	1.6	74
2803	Oral consumption of cinnamon enhances the expression of immunity and lipid absorption genes in the small intestinal epithelium and alters the gut microbiota in normal mice. <i>Journal of Functional Foods</i> , 2018, 49, 96-104.	1.6	3
2804	Effects of Different Doses of Fructooligosaccharides (FOS) on the Composition of Mice Fecal Microbiota, Especially the <i>Bifidobacterium</i> Composition. <i>Nutrients</i> , 2018, 10, 1105.	1.7	69
2805	Broad Phylogenetic Diversity Associated with Nitrogen Loss through Sulfur Oxidation in a Large Public Marine Aquarium. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	7
2806	Effect of Aging and Glucagon-like Peptide 2 on Intestinal Microbiota in SD Rats. , 2018, 9, 566.		12
2807	Microbial diversity in the rumen, reticulum, omasum, and abomasum of yak on a rapid fattening regime in an agro-pastoral transition zone. <i>Journal of Microbiology</i> , 2018, 56, 734-743.	1.3	44
2808	Microbial Community Composition Reveals Spatial Variation and Distinctive Core Microbiome of the Weaver Ant <i>Oecophylla smaragdina</i> in Malaysia. <i>Scientific Reports</i> , 2018, 8, 10777.	1.6	22
2809	A Comparative Study of Serum Biochemistry, Metabolome and Microbiome Parameters of Clinically Healthy, Normal Weight, Overweight, and Obese Companion Dogs. <i>Topics in Companion Animal Medicine</i> , 2018, 33, 126-135.	0.4	58
2810	Differential effects of selective and non-selective cyclooxygenase inhibitors on fecal microbiota in adult horses. <i>PLoS ONE</i> , 2018, 13, e0202527.	1.1	20
2811	Comparative evaluation of a new magnetic bead-based DNA extraction method from fecal samples for downstream next-generation 16S rRNA gene sequencing. <i>PLoS ONE</i> , 2018, 13, e0202858.	1.1	15
2812	Effects on survival and bacterial community composition of the aquaculture water and gastrointestinal tract of shrimp (<i>Litopenaeus vannamei</i>) exposed to probiotic treatments after an induced infection of acute hepatopancreatic necrosis disease. <i>Aquaculture Research</i> , 2018, 49, 3270-3288.	0.9	28
2813	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. <i>Scientific Reports</i> , 2018, 8, 12699.	1.6	37
2814	Insect exclusion limits variation in bacterial microbiomes of tomato flowers and fruit. <i>Journal of Applied Microbiology</i> , 2018, 125, 1749-1760.	1.4	23
2815	Feeding frequency influences process performance and microbial community composition in anaerobic digesters treating steam exploded food waste. <i>Bioresource Technology</i> , 2018, 269, 276-284.	4.8	35
2816	Intestinal fluke <i>Metagonimus yokogawai</i> infection increases probiotic <i>Lactobacillus</i> in mouse cecum. <i>Experimental Parasitology</i> , 2018, 193, 45-50.	0.5	13

#	ARTICLE	IF	CITATIONS
2817	The Microbiome and Metabolome of Preterm Infant Stool Are Personalized and Not Driven by Health Outcomes, Including Necrotizing Enterocolitis and Late-Onset Sepsis. <i>MSphere</i> , 2018, 3, .	1.3	107
2818	Cecal microbiome profile altered by <i>Salmonella enterica</i> , serovar Enteritidis inoculation in chicken. <i>Gut Pathogens</i> , 2018, 10, 34.	1.6	56
2819	Gut Microbiome in BALB/c and C57BL/6J Mice Undergoing Experimental Thyroid Autoimmunity Associate with Differences in Immunological Responses and Thyroid Function. <i>Hormone and Metabolic Research</i> , 2018, 50, 932-941.	0.7	39
2820	Southern South Australian groundwater microbe diversity. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	9
2821	Rhizosphere Bacterial Communities Differ According to Fertilizer Regimes and Cabbage (Brassica) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1620.	1.5	38
2822	Microbiome Composition in Both Wild-Type and Disease Model Mice Is Heavily Influenced by Mouse Facility. <i>Frontiers in Microbiology</i> , 2018, 9, 1598.	1.5	60
2823	Monitoring and evaluation of the interaction between deoxynivalenol and gut microbiota in Wistar rats by mass spectrometry-based metabolomics and next-generation sequencing. <i>Food and Chemical Toxicology</i> , 2018, 121, 124-130.	1.8	15
2824	CLOUD: a non-parametric detection test for microbiome outliers. <i>Microbiome</i> , 2018, 6, 137.	4.9	16
2825	Petroleum hydrocarbon and microbial community structure successions in marine oil-related aggregates associated with diatoms relevant for Arctic conditions. <i>Marine Pollution Bulletin</i> , 2018, 135, 759-768.	2.3	13
2826	Diet and other environmental factors shape the bacterial communities of fish gut in an eutrophic lake. <i>Journal of Applied Microbiology</i> , 2018, 125, 1626-1641.	1.4	47
2827	An anaerobic hybrid bioreactor for biologically enhanced primary treatment of domestic wastewater under low temperatures. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 1851-1866.	1.2	14
2828	Metagenomic analysis of rhizosphere microflora of oil-contaminated soil planted with barley and alfalfa. <i>PLoS ONE</i> , 2018, 13, e0202127.	1.1	45
2829	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.	1.1	13
2830	Metabolic Capability and Phylogenetic Diversity of Mono Lake during a Bloom of the Eukaryotic Phototroph <i>Picocystis</i> sp. Strain ML. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	18
2831	Unraveling the Composition of the Root-Associated Bacterial Microbiota of <i>Phragmites australis</i> and <i>Typha latifolia</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1650.	1.5	46
2832	Association of Exposure to Formula in the Hospital and Subsequent Infant Feeding Practices With Gut Microbiota and Risk of Overweight in the First Year of Life. <i>JAMA Pediatrics</i> , 2018, 172, e181161.	3.3	218
2833	Composition and richness of the serum microbiome differ by age and link to systemic inflammation. <i>GeroScience</i> , 2018, 40, 257-268.	2.1	63
2834	Methane and nitrous oxide cycling microbial communities in soils above septic leach fields: Abundances with depth and correlations with net surface emissions. <i>Science of the Total Environment</i> , 2018, 640-641, 429-441.	3.9	20

#	ARTICLE	IF	CITATIONS
2835	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. <i>MSystems</i> , 2018, 3, .	1.7	96
2836	Assessing Cat Flea Microbiomes in Northern and Southern California by 16S rRNA Next-Generation Sequencing. <i>Vector-Borne and Zoonotic Diseases</i> , 2018, 18, 491-499.	0.6	19
2837	Apparent total-tract macronutrient digestibility, serum chemistry, urinalysis, and fecal characteristics, metabolites and microbiota of adult dogs fed extruded, mildly cooked, and raw diets ¹ . <i>Journal of Animal Science</i> , 2018, 96, 3670-3683.	0.2	37
2838	Magnetite accelerates syntrophic acetate oxidation in methanogenic systems with high ammonia concentrations. <i>Microbial Biotechnology</i> , 2018, 11, 710-720.	2.0	56
2839	Next generation sequencing for gut microbiome characterization in rainbow trout (<i>Oncorhynchus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 e0193652.	1.1	108
2840	Analysis of the Gut Microbial Diversity of Dairy Cows During Peak Lactation by PacBio Single-Molecule Real-Time (SMRT) Sequencing. <i>Current Microbiology</i> , 2018, 75, 1316-1323.	1.0	13
2841	Small differences in ombrotrophy control regional-scale variation in methane cycling among Sphagnum-dominated peatlands. <i>Biogeochemistry</i> , 2018, 139, 155-177.	1.7	41
2842	Efficient biorefinery of waste activated sludge and vinegar residue into volatile fatty acids: effect of feedstock conditioning on performance and microbiology. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 1819-1828.	1.2	11
2843	Impact of Gut Microbiota and Diet on the Development of Atherosclerosis in <i>ApoE</i> Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 2318-2326.	1.1	123
2844	A seasonal study of a passive abandoned coalmine drainage remediation system reveals three distinct zones of contaminant levels and microbial communities. <i>MicrobiologyOpen</i> , 2018, 7, e00585.	1.2	3
2845	Decolorization of Reactive Black 5 and Reactive Blue 4 Dyes in Microbial Fuel Cells. <i>Applied Biochemistry and Biotechnology</i> , 2018, 186, 1017-1033.	1.4	13
2846	Contrasting patterns of taxonomic, phylogenetic and functional variation along a Costa Rican altitudinal gradient in the plant family Melastomataceae. <i>Journal of Tropical Ecology</i> , 2018, 34, 204-208.	0.5	4
2847	A dietary isothiocyanate-enriched moringa (<i>Moringa oleifera</i>) seed extract improves glucose tolerance in a high-fat-diet mouse model and modulates the gut microbiome. <i>Journal of Functional Foods</i> , 2018, 47, 376-385.	1.6	62
2848	Effect of antibiotic withdrawal in feed on chicken gut microbial dynamics, immunity, growth performance and prevalence of foodborne pathogens. <i>PLoS ONE</i> , 2018, 13, e0192450.	1.1	112
2849	Measuring Microbiome Diversity and Similarity with Hill Numbers. , 2018, , 157-178.		13
2850	<i>Helicobacter pylori</i> eradication with bismuth quadruple therapy leads to dysbiosis of gut microbiota with an increased relative abundance of Proteobacteria and decreased relative abundances of Bacteroidetes and Actinobacteria. <i>Helicobacter</i> , 2018, 23, e12498.	1.6	66
2851	Applying predictive models to decipher rhizobacterial modifications in common reed die-back affected populations. <i>Science of the Total Environment</i> , 2018, 642, 708-722.	3.9	14
2852	The benign helminth <i>Hymenolepis diminuta</i> ameliorates chemically induced colitis in a rat model system. <i>Parasitology</i> , 2018, 145, 1324-1335.	0.7	13

#	ARTICLE	IF	CITATIONS
2853	Microbiome niche modification drives diurnal rumen community assembly, overpowering individual variability and diet effects. <i>ISME Journal</i> , 2018, 12, 2446-2457.	4.4	66
2854	Age-related changes in the gut microbiota of wild House Sparrow nestlings. <i>Ibis</i> , 2019, 161, 184-191.	1.0	39
2855	Defective IgA response to atypical intestinal commensals in IL-21 receptor deficiency reshapes immune cell homeostasis and mucosal immunity. <i>Mucosal Immunology</i> , 2019, 12, 85-96.	2.7	30
2856	Response of treatment performance and microbial community structure to the temporary suspension of an industrial anaerobic bioreactor. <i>Science of the Total Environment</i> , 2019, 646, 229-237.	3.9	22
2857	Marked Succession of Cyanobacterial Communities Following Glacier Retreat in the High Arctic. <i>Microbial Ecology</i> , 2019, 77, 136-147.	1.4	34
2858	Rapid Microbial Community Changes During Initial Stages of Pine Litter Decomposition. <i>Microbial Ecology</i> , 2019, 77, 56-75.	1.4	40
2859	Evaluating the contribution of dispersal to community structure in Neotropical passerine birds. <i>Ecography</i> , 2019, 42, 390-399.	2.1	31
2860	Severe Obstructive Sleep Apnea Is Associated with Alterations in the Nasal Microbiome and an Increase in Inflammation. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 99-109.	2.5	51
2861	Initial description of the core ocular surface microbiome in dogs: Bacterial community diversity and composition in a defined canine population. <i>Veterinary Ophthalmology</i> , 2019, 22, 337-344.	0.6	29
2862	Microbial Translocation Does Not Drive Immune Activation in Ugandan Children Infected With HIV. <i>Journal of Infectious Diseases</i> , 2019, 219, 89-100.	1.9	11
2863	Insights into microbial community structure and function from a shallow, simulated CO ₂ leakage aquifer demonstrate microbial selection and adaptation. <i>Environmental Microbiology Reports</i> , 2019, 11, 338-351.	1.0	14
2864	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019, 13, 576-587.	4.4	236
2865	Effects of moderate, voluntary ethanol consumption on the rat and human gut microbiome. <i>Addiction Biology</i> , 2019, 24, 617-630.	1.4	46
2866	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy". <i>MBio</i> , 2019, 10, .	1.8	0
2867	Impacts of the rhizosphere effect and plant species on organic carbon mineralization rates and pathways, and bacterial community composition in a tidal marsh. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	16
2868	Quantitative evaluation of bioaerosols in different particle size fractions in dust collected on the International Space Station (ISS). <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7767-7782.	1.7	10
2869	Benchmarking Metagenomics Tools for Taxonomic Classification. <i>Cell</i> , 2019, 178, 779-794.	13.5	364
2870	Application of organic fertilizer improves microbial community diversity and alters microbial network structure in tea (<i>Camellia sinensis</i>) plantation soils. <i>Soil and Tillage Research</i> , 2019, 195, 104356.	2.6	117

#	ARTICLE	IF	CITATIONS
2871	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	29
2872	Insights into the Variations of Hao-Dependent Nitrifying and Nir-Dependent Denitrifying Microbial Communities in Ammonium-Graduated Lake Environments. <i>Applied Sciences (Switzerland)</i> , 2019, 9, 3229.	1.3	2
2873	The association between gut microbiota composition and BMI in Chinese male college students, as analysed by next-generation sequencing. <i>British Journal of Nutrition</i> , 2019, 122, 986-995.	1.2	46
2874	Modification of the equine gastrointestinal microbiota by Jerusalem artichoke meal supplementation. <i>PLoS ONE</i> , 2019, 14, e0220553.	1.1	11
2875	Experimental old nest material predicts hoopoe <i>Upupa epops</i> eggshell and uropygial gland microbiota. <i>Journal of Avian Biology</i> , 2019, 50, .	0.6	12
2876	A Commentary on Diversity Measures UniFrac in Very Small Sample Size. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431984351.	0.6	2
2877	Oral vancomycin treatment does not alter markers of postprandial inflammation in lean and obese subjects. <i>Physiological Reports</i> , 2019, 7, e14199.	0.7	10
2878	Diversity and structure of the bacterial microbiome of the American dog tick, <i>Dermacentor variabilis</i> , is dominated by the endosymbiont <i>Francisella</i> . <i>Symbiosis</i> , 2019, 79, 239-250.	1.2	20
2879	Cooked Red Lentils Dose-Dependently Modulate the Colonic Microenvironment in Healthy C57Bl/6 Male Mice. <i>Nutrients</i> , 2019, 11, 1853.	1.7	12
2880	Microbial Transformations of Organically Fermented Foods. <i>Metabolites</i> , 2019, 9, 165.	1.3	20
2881	The gastrointestinal fate of limonin and its effect on gut microbiota in mice. <i>Food and Function</i> , 2019, 10, 5521-5530.	2.1	12
2882	Comparative analysis of the gut microbial communities between two dominant amphipods from the Challenger Deep, Mariana Trench. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 151, 103081.	0.6	16
2883	Long-read amplicon denoising. <i>Nucleic Acids Research</i> , 2019, 47, e104-e104.	6.5	31
2884	Upper Respiratory Dysbiosis with a Facultative-dominated Ecotype in Advanced Lung Disease and Dynamic Change after Lung Transplant. <i>Annals of the American Thoracic Society</i> , 2019, 16, 1383-1391.	1.5	16
2885	The Effects of Sample Storage Conditions on the Microbial Community Composition in Hydraulic Fracturing Produced Water. <i>Geomicrobiology Journal</i> , 2019, 36, 630-638.	1.0	10
2886	Geochemical and microbial characterizations of flowback and produced water in three shale oil and gas plays in the central and western United States. <i>Water Research</i> , 2019, 164, 114942.	5.3	64
2887	Detection and isolation of bacteria affected by dietary cumin, coriander, turmeric, and red chili pepper in the caecum of ICR mice. <i>Journal of Functional Foods</i> , 2019, 61, 103467.	1.6	10
2888	Influence of Environment and Host Plant Genotype on the Structure and Diversity of the <i>Brassica napus</i> Seed Microbiota. <i>Phytobiomes Journal</i> , 2019, 3, 326-336.	1.4	34

#	ARTICLE	IF	CITATIONS
2889	Baseline microbiota composition modulates antibiotic-mediated effects on the gut microbiota and host. <i>Microbiome</i> , 2019, 7, 111.	4.9	50
2890	Hospital Microbiome Variations As Analyzed by High-Throughput Sequencing. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 426-438.	1.0	15
2891	Nitrogen Fertilizers Shape the Composition and Predicted Functions of the Microbiota of Field-Grown Tomato Plants. <i>Phytobiomes Journal</i> , 2019, 3, 315-325.	1.4	26
2892	Characteristics of the Salivary Microbiota in Patients With Various Digestive Tract Cancers. <i>Frontiers in Microbiology</i> , 2019, 10, 1780.	1.5	57
2893	A Metagenomics Study on Hirschsprung's Disease Associated Enterocolitis: Biodiversity and Gut Microbial Homeostasis Depend on Resection Length and Patient's Clinical History. <i>Frontiers in Pediatrics</i> , 2019, 7, 326.	0.9	19
2894	Colonization Characteristics of Bacterial Communities on Plastic Debris Influenced by Environmental Factors and Polymer Types in the Haihe Estuary of Bohai Bay, China. <i>Environmental Science & Technology</i> , 2019, 53, 10763-10773.	4.6	148
2895	Oral Administration of Clinically Relevant Antimalarial Drugs Does Not Modify the Murine Gut Microbiota. <i>Scientific Reports</i> , 2019, 9, 11952.	1.6	6
2896	Seasonal Changes of Airborne Bacterial Communities Over Tokyo and Influence of Local Meteorology. <i>Frontiers in Microbiology</i> , 2019, 10, 1572.	1.5	67
2897	Crypt- and Mucosa-Associated Core Microbiotas in Humans and Their Alteration in Colon Cancer Patients. <i>MBio</i> , 2019, 10, .	1.8	94
2898	Heart failure developed after myocardial infarction does not affect gut microbiota composition in the rat. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 317, G342-G348.	1.6	7
2899	TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. <i>Bioinformatics</i> , 2019, 35, i31-i40.	1.8	9
2900	Bovine digital dermatitis in Victoria, Australia. <i>Australian Veterinary Journal</i> , 2019, 97, 404-413.	0.5	12
2901	Spatial Variations of Bacterial Communities of an Anaerobic Lagoon-Type Biodigester Fed with Dairy Manure. <i>Processes</i> , 2019, 7, 408.	1.3	11
2902	Promotion of Metabolite Synthesis in <i>Isaria cicadae</i> , a Dominant Species in the Cicada Flower Microbiota, by Cicada Pupae. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8476-8484.	2.4	6
2903	Effects of starter feeding on caecal mucosal bacterial composition and expression of genes involved in immune and tight junctions in pre-weaned twin lambs. <i>Anaerobe</i> , 2019, 59, 167-175.	1.0	5
2904	Biodegradation of metformin and its transformation product, guanylurea, by natural and exposed microbial communities. <i>Ecotoxicology and Environmental Safety</i> , 2019, 182, 109414.	2.9	46
2905	Dynamics of bacterial communities in alfalfa and mung bean sprouts during refrigerated conditions. <i>Food Microbiology</i> , 2019, 84, 103261.	2.1	27
2906	Changes in the composition and function of bacterial communities during vermicomposting may explain beneficial properties of vermicompost. <i>Scientific Reports</i> , 2019, 9, 9657.	1.6	69

#	ARTICLE	IF	CITATIONS
2907	Characterization of bacterial community changes and antibiotic resistance genes in lamb manure of different incidence. <i>Scientific Reports</i> , 2019, 9, 10101.	1.6	5
2908	Effects of land-use change on community diversity and composition are highly variable among functional groups. <i>Ecological Applications</i> , 2019, 29, e01973.	1.8	23
2909	Revealing Cues for Fungal Interplay in the Plant-Air Interface in Vineyards. <i>Frontiers in Plant Science</i> , 2019, 10, 922.	1.7	36
2910	Multiple Data Analyses and Statistical Approaches for Analyzing Data from Metagenomic Studies and Clinical Trials. <i>Methods in Molecular Biology</i> , 2019, 1910, 605-634.	0.4	8
2911	Nieves penitentes are a new habitat for snow algae in one of the most extreme high-elevation environments on Earth. <i>Arctic, Antarctic, and Alpine Research</i> , 2019, 51, 190-200.	0.4	16
2912	Antiretroviral Therapy Administration in Healthy Rhesus Macaques Is Associated with Transient Shifts in Intestinal Bacterial Diversity and Modest Immunological Perturbations. <i>Journal of Virology</i> , 2019, 93, .	1.5	13
2913	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. <i>Microbiome</i> , 2019, 7, 100.	4.9	101
2914	Geographic location and food availability offer differing levels of influence on the bacterial communities associated with larval sea urchins. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	10
2915	Soil Microbiome Dynamics During Pyritic Mine Tailing Phytostabilization: Understanding Microbial Bioindicators of Soil Acidification. <i>Frontiers in Microbiology</i> , 2019, 10, 1211.	1.5	36
2916	Increasing phylogenetic stochasticity at high elevations on summits across a remote North American wilderness. <i>American Journal of Botany</i> , 2019, 106, 958-970.	0.8	4
2917	Taxonomic features and comparisons of the gut microbiome from two edible fungus-farming termites (<i>Macrotermes falciger</i> ; <i>M. natalensis</i>) harvested in the Vhembe district of Limpopo, South Africa. <i>BMC Microbiology</i> , 2019, 19, 164.	1.3	17
2918	Gut Microbiota Differs Between Parkinson's Disease Patients and Healthy Controls in Northeast China. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 171.	1.4	100
2919	A hydrocarbon-contaminated aquifer reveals a Piggyback-the-Persistent viral strategy. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	11
2920	Treatment-Specific Composition of the Gut Microbiota Is Associated With Disease Remission in a Pediatric Crohn's Disease Cohort. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 1927-1938.	0.9	20
2921	The human microbiota is associated with cardiometabolic risk across the epidemiologic transition. <i>PLoS ONE</i> , 2019, 14, e0215262.	1.1	29
2922	Interaction between high-fat diet and ethanol intake leads to changes on the fecal microbiome. <i>Journal of Nutritional Biochemistry</i> , 2019, 72, 108215.	1.9	16
2923	<i>Lactobacillus plantarum</i> PS128 ameliorates 2,5-Dimethoxy-4-iodoamphetamine-induced tic-like behaviors via its influences on the microbiota-gut-brain-axis. <i>Brain Research Bulletin</i> , 2019, 153, 59-73.	1.4	36
2924	Changes in cecum microbial community in response to total sulfur amino acid (TSAA: DL-methionine) in antibiotic-free and supplemented poultry birds. <i>Poultry Science</i> , 2019, 98, 5809-5819.	1.5	16

#	ARTICLE	IF	CITATIONS
2925	The Seasonal Dynamics and the Influence of Human Activities on Campus Outdoor Microbial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1579.	1.5	7
2926	Plant Diversity and Fertilizer Management Shape the Belowground Microbiome of Native Grass Bioenergy Feedstocks. <i>Frontiers in Plant Science</i> , 2019, 10, 1018.	1.7	19
2927	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. <i>PLoS ONE</i> , 2019, 14, e0217050.	1.1	65
2928	The feline cutaneous and oral microbiota are influenced by breed and environment. <i>PLoS ONE</i> , 2019, 14, e0220463.	1.1	33
2929	Longitudinal microbiome profiling reveals impermanence of probiotic bacteria in domestic pigeons. <i>PLoS ONE</i> , 2019, 14, e0217804.	1.1	12
2930	Changes in Gut Microbiome after Bariatric Surgery Versus Medical Weight Loss in a Pilot Randomized Trial. <i>Obesity Surgery</i> , 2019, 29, 3239-3245.	1.1	46
2931	Whole Body Vibration-Induced Omental Macrophage Polarization and Fecal Microbiome Modification in a Murine Model. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3125.	1.8	10
2932	The potential of sedimentary ancient DNA for reconstructing past sea ice evolution. <i>ISME Journal</i> , 2019, 13, 2566-2577.	4.4	32
2933	Emphasis on the deep or shallow parts of the tree provides a new characterization of phylogenetic distances. <i>Genome Biology</i> , 2019, 20, 131.	3.8	20
2934	Gut microbiome analysis by post: Evaluation of the optimal method to collect stool samples from infants within a national cohort study. <i>PLoS ONE</i> , 2019, 14, e0216557.	1.1	11
2935	The Composition and Assembly of Bacterial Communities across the Rhizosphere and Phyllosphere Compartments of <i>Phragmites Australis</i> . <i>Diversity</i> , 2019, 11, 98.	0.7	21
2936	Composting swine carcasses with nitrogen transformation microbial strains: Succession of microbial community and nitrogen functional genes. <i>Science of the Total Environment</i> , 2019, 688, 555-566.	3.9	50
2937	DNA extraction and amplicon production strategies deeply influence the outcome of gut microbiome studies. <i>Scientific Reports</i> , 2019, 9, 9328.	1.6	51
2938	Associations of the Fecal Microbial Proteome Composition and Proneness to Diet-induced Obesity. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1864-1879.	2.5	19
2939	Host mitochondria influence gut microbiome diversity: A role for ROS. <i>Science Signaling</i> , 2019, 12, .	1.6	106
2940	Purple Sweet Potato Polyphenols Differentially Influence the Microbial Composition Depending on the Fermentability of Dietary Fiber in a Mixed Culture of Swine Fecal Bacteria. <i>Nutrients</i> , 2019, 11, 1495.	1.7	18
2941	Effects of chitin and temperature on sub-Arctic soil microbial and fungal communities and biodegradation of hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) and 2,4-dinitrotoluene (DNT). <i>Biodegradation</i> , 2019, 30, 415-431.	1.5	11
2942	Pathogenic Autoreactive T and B Cells Cross-React with Mimotopes Expressed by a Common Human Gut Commensal to Trigger Autoimmunity. <i>Cell Host and Microbe</i> , 2019, 26, 100-113.e8.	5.1	109

#	ARTICLE	IF	CITATIONS
2943	The Diversity of Gut Microbiome is Associated With Favorable Responses to Anti-Programmed Death 1 Immunotherapy in Chinese Patients With NSCLC. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1378-1389.	0.5	310
2944	Adaptive gPCA: A method for structured dimensionality reduction with applications to microbiome data. <i>Annals of Applied Statistics</i> , 2019, 13, .	0.5	5
2945	Mucosa-associated microbiota drives pathogenic functions in IBD-derived intestinal iNKT cells. <i>Life Science Alliance</i> , 2019, 2, e201800229.	1.3	27
2946	Microbial communities in top- and subsoil of repacked soil columns respond differently to amendments but their diversity is negatively correlated with plant productivity. <i>Scientific Reports</i> , 2019, 9, 8890.	1.6	27
2947	Interannual comparison of core taxa and community composition of the blow microbiota from East Australian humpback whales. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	10
2948	Diversification of the gut fungi <i>Smittium</i> and allies (Harpellales) co-occurred with the origin of complete metamorphosis of their symbiotic insect hosts (lower Diptera). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106550.	1.2	8
2949	Phylogenetic Techniques in Geomicrobiology. , 2019, , 360-404.		0
2950	Uterine and vaginal bacterial community diversity prior to artificial insemination between pregnant and nonpregnant postpartum cows ¹ . <i>Journal of Animal Science</i> , 2019, 97, 4298-4304.	0.2	46
2951	Chemical Cross-Linking Controls in Vitro Fecal Fermentation Rate of High-Amylose Maize Starches and Regulates Gut Microbiota Composition. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 13728-13736.	2.4	42
2952	Dysbiosis signatures of the microbial profile in tissue from bladder cancer. <i>Cancer Medicine</i> , 2019, 8, 6904-6914.	1.3	74
2953	A single faecal microbiota transplantation modulates the microbiome and improves clinical manifestations in a rat model of colitis. <i>EBioMedicine</i> , 2019, 48, 630-641.	2.7	53
2954	Changes in the Bacterioplankton Community Structure from Southern Gulf of Mexico During a Simulated Crude Oil Spill at Mesocosm Scale. <i>Microorganisms</i> , 2019, 7, 441.	1.6	18
2955	Rhizobia population was favoured during in situ phytoremediation of vanadium-titanium magnetite mine tailings dam using <i>Pongamia pinnata</i> . <i>Environmental Pollution</i> , 2019, 255, 113167.	3.7	38
2956	Comprehensive relationships between gut microbiome and faecal metabolome in individuals with type 2 diabetes and its complications. <i>Endocrine</i> , 2019, 66, 526-537.	1.1	135
2957	Peptidoglycan Recognition Protein 4 Limits Bacterial Clearance and Inflammation in Lungs by Control of the Gut Microbiota. <i>Frontiers in Immunology</i> , 2019, 10, 2106.	2.2	17
2958	Positive effect of an electrolyzed reduced water on gut permeability, fecal microbiota and liver in an animal model of Parkinson's disease. <i>PLoS ONE</i> , 2019, 14, e0223238.	1.1	24
2959	Influence of Dietary Supplementation of Probiotic <i>Pediococcus acidilactici</i> MA18/5M During the Transition From Freshwater to Seawater on Intestinal Health and Microbiota of Atlantic Salmon (<i>Salmo salar</i> L.). <i>Frontiers in Microbiology</i> , 2019, 10, 2243.	1.5	45
2960	Similar Shift Patterns in Gut Bacterial and Fungal Communities Across the Life Stages of <i>Bactrocera minax</i> Larvae From Two Field Populations. <i>Frontiers in Microbiology</i> , 2019, 10, 2262.	1.5	28

#	ARTICLE	IF	CITATIONS
2961	Modulatory Effect of Protein and Carotene Dietary Levels on Pig gut Microbiota. <i>Scientific Reports</i> , 2019, 9, 14582.	1.6	18
2962	Pomegranate Juice and Extract Consumption Increases the Resistance to UVB-induced Erythema and Changes the Skin Microbiome in Healthy Women: a Randomized Controlled Trial. <i>Scientific Reports</i> , 2019, 9, 14528.	1.6	32
2963	Characterization of Microbial Communities Populating the Inflorescences of <i>Humulus lupulus</i> L.. <i>Journal of the American Society of Brewing Chemists</i> , 2019, 77, 243-250.	0.8	7
2964	Efficacy of Fecal Sampling as a Gut Proxy in the Study of Chicken Gut Microbiota. <i>Frontiers in Microbiology</i> , 2019, 10, 2126.	1.5	81
2965	Floral organs act as environmental filters and interact with pollinators to structure the yellow monkeyflower (<i>Mimulus guttatus</i>) floral microbiome. <i>Molecular Ecology</i> , 2019, 28, 5155-5171.	2.0	32
2966	Diel patterning in the bacterial community associated with the sea anemone <i>Nematostella vectensis</i> . <i>Ecology and Evolution</i> , 2019, 9, 9935-9947.	0.8	16
2967	Large-scale distribution of bacterial communities in the Qaidam Basin of the Qinghai-Tibet Plateau. <i>MicrobiologyOpen</i> , 2019, 8, e909.	1.2	21
2968	Community structure and distribution of benthic Bacteria and Archaea in a stratified coastal lagoon in the Southern Gulf of Mexico. <i>Estuarine, Coastal and Shelf Science</i> , 2019, 230, 106433.	0.9	7
2969	Enhanced quinoline removal by zero-valent iron-coupled novel anaerobic processes: performance and underlying function analysis. <i>RSC Advances</i> , 2019, 9, 1176-1186.	1.7	9
2970	Feeding Mode, but Not Prebiotics, Affects Colonic Microbiota Composition and Volatile Fatty Acid Concentrations in Sow-Reared, Formula-Fed, and Combination-Fed Piglets. <i>Journal of Nutrition</i> , 2019, 149, 2156-2163.	1.3	7
2971	Contrasting Biogeographic Patterns of Bacterial and Archaeal Diversity in the Top- and Subsoils of Temperate Grasslands. <i>MSystems</i> , 2019, 4, .	1.7	24
2972	Comprehensive Understanding of the Bacterial Populations and Metabolites Profile of Fermented Feed by 16S rRNA Gene Sequencing and Liquid Chromatography-Mass Spectrometry. <i>Metabolites</i> , 2019, 9, 239.	1.3	13
2973	Rapid Bacterial Community Changes during Vermicomposting of Grape Marc Derived from Red Winemaking. <i>Microorganisms</i> , 2019, 7, 473.	1.6	19
2974	Antibiotics and Host-Tailored Probiotics Similarly Modulate Effects on the Developing Avian Microbiome, Mycobiome, and Host Gene Expression. <i>MBio</i> , 2019, 10, .	1.8	33
2975	Deciphering Underlying Drivers of Disease Suppressiveness Against Pathogenic <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2535.	1.5	38
2976	Bacterial communities in the rhizosphere, phyllosphere and endosphere of tomato plants. <i>PLoS ONE</i> , 2019, 14, e0223847.	1.1	143
2977	Comparison of the fecal, cecal, and mucus microbiome in male and female mice after TNBS-induced colitis. <i>PLoS ONE</i> , 2019, 14, e0225079.	1.1	62
2978	Tissue-Specific Microbiomes of the Red Sea Giant Clam <i>Tridacna maxima</i> Highlight Differential Abundance of Endozoicomonadaceae. <i>Frontiers in Microbiology</i> , 2019, 10, 2661.	1.5	13

#	ARTICLE	IF	CITATIONS
2979	Illumina-based Analysis of Endophytic Bacterial Diversity of four <i>Allium</i> species. <i>Scientific Reports</i> , 2019, 9, 15271.	1.6	19
2980	<i>Trichinella spiralis</i> infection decreases the diversity of the intestinal flora in the infected mouse. <i>Journal of Microbiology, Immunology and Infection</i> , 2021, 54, 490-500.	1.5	12
2981	Temporal and spatial dynamics of Bacteria, Archaea and protists in equatorial coastal waters. <i>Scientific Reports</i> , 2019, 9, 16390.	1.6	30
2982	Diet is not the primary driver of bacterial community structure in the gut of litter-feeding cockroaches. <i>BMC Microbiology</i> , 2019, 19, 238.	1.3	23
2983	Assessing the potential of culture-independent 16S rRNA microbiome analysis in disease diagnostics: the example of <i>Dianthus gratianopolitanus</i> and <i>Robbsia andropogonis</i> . <i>European Journal of Plant Pathology</i> , 2019, 155, 1211-1223.	0.8	4
2984	Molecular analysis of the endobronchial stent microbial biofilm reveals bacterial communities that associate with stent material and frequent fungal constituents. <i>PLoS ONE</i> , 2019, 14, e0217306.	1.1	16
2985	Variations in the microbiome due to storage preservatives are not large enough to obscure variations due to factors such as host population, host species, body site, and captivity. <i>American Journal of Primatology</i> , 2019, 81, e23045.	0.8	6
2986	Heat-induced shift in coral microbiome reveals several members of the Rhodobacteraceae family as indicator species for thermal stress in <i>Porites lutea</i> . <i>MicrobiologyOpen</i> , 2019, 8, e935.	1.2	76
2987	Dietary supplementation of a fiber-prebiotic and saccharin-eugenol blend in extruded diets fed to dogs. <i>Journal of Animal Science</i> , 2019, 97, 4519-4531.	0.2	34
2988	An Association of Gut Microbiota with Different Phenotypes in Chinese Patients with Rheumatoid Arthritis. <i>Journal of Clinical Medicine</i> , 2019, 8, 1770.	1.0	68
2989	Temperature dependence of parasitic infection and gut bacterial communities in bumble bees. <i>Environmental Microbiology</i> , 2019, 21, 4706-4723.	1.8	34
2990	Effects of florfenicol feeding on diversity and composition of the intestinal microbiota of channel catfish (<i>Ictalurus punctatus</i>). <i>Aquaculture Research</i> , 2019, 50, 3663-3672.	0.9	18
2991	City life alters the gut microbiome and stable isotope profiling of the eastern water dragon (<i>Intellagama lesueurii</i>). <i>Molecular Ecology</i> , 2019, 28, 4592-4607.	2.0	27
2992	Complementary DNA/RNA-Based Profiling: Characterization of Corrosive Microbial Communities and Their Functional Profiles in an Oil Production Facility. <i>Frontiers in Microbiology</i> , 2019, 10, 2587.	1.5	20
2993	Phase Transition and Superconductivity Enhancement in Se-Substituted MoTe ₂ Thin Films. <i>Advanced Materials</i> , 2019, 31, e1904641.	11.1	34
2994	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. <i>MSystems</i> , 2019, 4, .	1.7	23
2995	Characterization of Microbial Communities in a Dairy Farm Matrix in Ningxia, China, by 16S rDNA Analysis. <i>International Journal of Genomics</i> , 2019, 2019, 1-13.	0.8	3
2996	Exact variance component tests for longitudinal microbiome studies. <i>Genetic Epidemiology</i> , 2019, 43, 250-262.	0.6	5

#	ARTICLE	IF	CITATIONS
2997	Effect of the Nursing Mother on the Gut Microbiome of the Offspring During Early Mouse Development. <i>Microbial Ecology</i> , 2019, 78, 517-527.	1.4	17
2998	It's what's on the inside that counts: stress physiology and the bacterial microbiome of a wild urban mammal. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20192111.	1.2	45
2999	The Origin, Succession, and Predicted Metabolism of Bacterial Communities Associated with Leaf Decomposition. <i>MBio</i> , 2019, 10, .	1.8	9
3000	Responses of Microbial Communities and Interaction Networks to Different Management Practices in Tea Plantation Soils. <i>Sustainability</i> , 2019, 11, 4428.	1.6	24
3001	The subgingival microbial community of feline periodontitis and gingivostomatitis: characterization and comparison between diseased and healthy cats. <i>Scientific Reports</i> , 2019, 9, 12340.	1.6	30
3002	Association of dietary patterns with the gut microbiota in older, community-dwelling men. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 1003-1014.	2.2	55
3003	Identification of a Shared Microbiomic and Metabolomic Profile in Systemic Autoimmune Diseases. <i>Journal of Clinical Medicine</i> , 2019, 8, 1291.	1.0	37
3004	Denitrification is the main microbial N loss pathway on the Qinghai-Tibet Plateau above an elevation of 5000m. <i>Science of the Total Environment</i> , 2019, 696, 133852.	3.9	21
3005	Highly Reproducible 16S Sequencing Facilitates Measurement of Host Genetic Influences on the Stickleback Gut Microbiome. <i>MSystems</i> , 2019, 4, .	1.7	8
3006	Effects of water recirculation rate on the microbial community and water quality in relation to the growth and survival of white shrimp (<i>Litopenaeus vannamei</i>). <i>BMC Microbiology</i> , 2019, 19, 192.	1.3	21
3007	Genetic determinants of gut microbiota composition and bile acid profiles in mice. <i>PLoS Genetics</i> , 2019, 15, e1008073.	1.5	75
3008	The Pacific harbor seal gut microbiota in Mexico: Its relationship with diet and functional inferences. <i>PLoS ONE</i> , 2019, 14, e0221770.	1.1	24
3009	Identification of Initial Colonizing Bacteria in Dental Plaques from Young Adults Using Full-Length 16S rRNA Gene Sequencing. <i>MSystems</i> , 2019, 4, .	1.7	22
3010	Maternal supplementation with a synbiotic has distinct outcomes on offspring gut microbiota formation in A/J and C57BL/6 mice, differentially affecting airway inflammatory cell infiltration and mucus production. <i>Journal of Functional Foods</i> , 2019, 61, 103496.	1.6	4
3011	Next-generation sequencing reveals fecal contamination and potentially pathogenic bacteria in a major inflow river of Taihu Lake. <i>Environmental Pollution</i> , 2019, 254, 113108.	3.7	37
3012	Fish oil supplementation to a high-fat diet improves both intestinal health and the systemic obese phenotype. <i>Journal of Nutritional Biochemistry</i> , 2019, 72, 108216.	1.9	26
3013	Soil bacterial communities in the Brazilian Cerrado: Response to vegetation type and management. <i>Acta Oecologica</i> , 2019, 100, 103463.	0.5	16
3014	Alterations to the Esophageal Microbiome Associated with Progression from Barrett's Esophagus to Esophageal Adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1687-1693.	1.1	68

#	ARTICLE	IF	CITATIONS
3015	High-throughput sequencing analysis of microbial community diversity in response to indica and japonica bar-transgenic rice paddy soils. <i>PLoS ONE</i> , 2019, 14, e0222191.	1.1	16
3016	New and Preliminary Evidence on Altered Oral and Gut Microbiota in Individuals with Autism Spectrum Disorder (ASD): Implications for ASD Diagnosis and Subtyping Based on Microbial Biomarkers. <i>Nutrients</i> , 2019, 11, 2128.	1.7	87
3017	Statistical Analysis of Metagenomics Data. <i>Genomics and Informatics</i> , 2019, 17, e6.	0.4	166
3018	Comparative analysis of the fecal microbiota from different species of domesticated and wild suids. <i>Scientific Reports</i> , 2019, 9, 13616.	1.6	30
3019	Conventional and organic soil management as divergent drivers of resident and active fractions of major soil food web constituents. <i>Scientific Reports</i> , 2019, 9, 13521.	1.6	54
3020	Diet-Induced Obese Mice and Leptin-Deficient Lepob/ob Mice Exhibit Increased Circulating GIP Levels Produced by Different Mechanisms. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4448.	1.8	4
3021	Modulation of high fat diet-induced microbiome changes, but not behaviour, by minocycline. <i>Brain, Behavior, and Immunity</i> , 2019, 82, 309-318.	2.0	10
3022	The effect of 2- α -fucosyllactose on simulated infant gut microbiome and metabolites; a pilot study in comparison to GOS and lactose. <i>Scientific Reports</i> , 2019, 9, 13232.	1.6	62
3023	Diversity and functional profile of bacterial communities at Lancaster acid mine drainage dam, South Africa as revealed by 16S rRNA gene high-throughput sequencing analysis. <i>Extremophiles</i> , 2019, 23, 719-734.	0.9	30
3024	The fecal resistome of dairy cattle is associated with diet during nursing. <i>Nature Communications</i> , 2019, 10, 4406.	5.8	100
3025	Stool sampling and DNA isolation kits affect DNA quality and bacterial composition following 16S rRNA gene sequencing using MiSeq Illumina platform. <i>Scientific Reports</i> , 2019, 9, 13837.	1.6	40
3026	Long-Term N Fertilization Decreased Diversity and Altered the Composition of Soil Bacterial and Archaeal Communities. <i>Agronomy</i> , 2019, 9, 574.	1.3	22
3027	Species diversity of fecal microbial flora in <i>Canis lupus familiaris</i> infected with canine parvovirus. <i>Veterinary Microbiology</i> , 2019, 237, 108390.	0.8	10
3028	Influence of hydroxyl-terminated polybutadiene liquid on rheology of fumed silica filled cis-polybutadiene rubber. <i>Polymer</i> , 2019, 180, 121709.	1.8	11
3029	Removal of microorganisms and antibiotic resistance genes from treated urban wastewater: A comparison between aluminium sulphate and tannin coagulants. <i>Water Research</i> , 2019, 166, 115056.	5.3	50
3030	Sugar Beet Pectin Supplementation Did Not Alter Profiles of Fecal Microbiota and Exhaled Breath in Healthy Young Adults and Healthy Elderly. <i>Nutrients</i> , 2019, 11, 2193.	1.7	35
3031	Effect of replacing fishmeal with stickwater hydrolysate on the growth, serum biochemical indexes, immune indexes, intestinal histology and microbiota of rice field eel (<i>monopterus albus</i>). <i>Aquaculture Reports</i> , 2019, 15, 100223.	0.7	26
3032	<i>Prevotella copri</i> is associated with carboplatin-induced gut toxicity. <i>Cell Death and Disease</i> , 2019, 10, 714.	2.7	32

#	ARTICLE	IF	CITATIONS
3033	Microbiome-Transcriptome Interactions Related to Severity of Respiratory Syncytial Virus Infection. <i>Scientific Reports</i> , 2019, 9, 13824.	1.6	30
3034	Geographical location influences the composition of the gut microbiota in wild house mice (<i>Mus</i>) Tj ETQq1 1 0.784314 rgBT /Overloc 1.1 35	1.1	35
3035	Seasonal Changes in Gut Microbiota Diversity and Composition in the Greater Horseshoe Bat. <i>Frontiers in Microbiology</i> , 2019, 10, 2247.	1.5	45
3036	Core gut microbial communities are maintained by beneficial interactions and strain variability in fish. <i>Nature Microbiology</i> , 2019, 4, 2456-2465.	5.9	98
3037	Composition and Drivers of Gut Microbial Communities in Arctic-Breeding Shorebirds. <i>Frontiers in Microbiology</i> , 2019, 10, 2258.	1.5	49
3038	Effects of berberine and metformin on intestinal inflammation and gut microbiome composition in db/db mice. <i>Biomedicine and Pharmacotherapy</i> , 2019, 118, 109131.	2.5	155
3039	Ligand-assisted reduction and reprecipitation synthesis of highly luminescent metal nanoclusters. <i>Nanoscale Advances</i> , 2019, 1, 834-839.	2.2	11
3040	Taxonomic relatedness and environmental pressure synergistically drive the primary succession of biofilm microbial communities in reclaimed wastewater distribution systems. <i>Environment International</i> , 2019, 124, 25-37.	4.8	33
3041	Effects of the captive and wild environment on diversity of the gut microbiome of deer mice (<i>Peromyscus maniculatus</i>). <i>ISME Journal</i> , 2019, 13, 1293-1305.	4.4	84
3042	Biogeographic Distribution Patterns of the Archaeal Communities Across the Black Soil Zone of Northeast China. <i>Frontiers in Microbiology</i> , 2019, 10, 23.	1.5	27
3043	Soil parameters, land use, and geographical distance drive soil bacterial communities along a European transect. <i>Scientific Reports</i> , 2019, 9, 605.	1.6	56
3044	Effects of the long-term storage of human fecal microbiota samples collected in RNAlater. <i>Scientific Reports</i> , 2019, 9, 601.	1.6	36
3045	Role of Probiotics in <i>Mycoplasma pneumoniae</i> Pneumonia in Children: A Short-Term Pilot Project. <i>Frontiers in Microbiology</i> , 2018, 9, 3261.	1.5	7
3046	Analysis of the Pulmonary Microbiome Composition of <i>Legionella pneumophila</i> -Infected Patients. <i>Methods in Molecular Biology</i> , 2019, 1921, 429-443.	0.4	8
3047	Changes in the Active, Dead, and Dormant Microbial Community Structure across a Pleistocene Permafrost Chronosequence. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	63
3048	Microbiome Alteration in Type 2 Diabetes Mellitus Model of Zebrafish. <i>Scientific Reports</i> , 2019, 9, 867.	1.6	30
3049	Comparative study of vulva and abdominal skin microbiota of healthy females with high and average BMI. <i>BMC Microbiology</i> , 2019, 19, 16.	1.3	20
3050	Comparative Evaluation of Microbiota Engraftment Following Fecal Microbiota Transfer in Mice Models: Age, Kinetic and Microbial Status Matter. <i>Frontiers in Microbiology</i> , 2018, 9, 3289.	1.5	77

#	ARTICLE	IF	CITATIONS
3051	Intestinal Morphologic and Microbiota Responses to Dietary <i>Bacillus</i> spp. in a Broiler Chicken Model. <i>Frontiers in Physiology</i> , 2018, 9, 1968.	1.3	77
3052	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. <i>Cancer Medicine</i> , 2019, 8, 617-628.	1.3	71
3053	Green Tea Polyphenols Modify the Gut Microbiome in <i>db/db</i> Mice as Co-Abundance Groups Correlating with the Blood Glucose Lowering Effect. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1801064.	1.5	69
3054	Comparison of hypoglycemic effects of ripened pu-erh tea and raw pu-erh tea in streptozotocin-induced diabetic rats. <i>RSC Advances</i> , 2019, 9, 2967-2977.	1.7	36
3055	Population structure of human gut bacteria in a diverse cohort from rural Tanzania and Botswana. <i>Genome Biology</i> , 2019, 20, 16.	3.8	66
3056	Genomic and metagenomic insights into the microbial community of a thermal spring. <i>Microbiome</i> , 2019, 7, 8.	4.9	40
3057	Multi-locus DNA metabarcoding of zooplankton communities and scat reveal trophic interactions of a generalist predator. <i>Scientific Reports</i> , 2019, 9, 281.	1.6	42
3058	Soil microbial restoration strategies for promoting climate-ready prairie ecosystems. <i>Ecological Applications</i> , 2019, 29, e01858.	1.8	26
3059	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. <i>Environmental Microbiology</i> , 2019, 21, 1331-1343.	1.8	60
3060	Bacterial communities in an optional lichen symbiosis are determined by substrate, not algal photobionts. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	13
3061	Impact of <i>Saccharomyces cerevisiae</i> and <i>Lactobacillus buchneri</i> on microbial communities during ensiling and aerobic spoilage of corn silage1. <i>Journal of Animal Science</i> , 2019, 97, 1273-1285.	0.2	38
3062	Microbial diversity in Huguangyan Maar Lake of China revealed by high-throughput sequencing. <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1245-1257.	0.6	6
3063	Characterization of Fungal nirK-Containing Communities and N ₂ O Emission From Fungal Denitrification in Arable Soils. <i>Frontiers in Microbiology</i> , 2019, 10, 117.	1.5	27
3064	Bacterial communities associated to Chilean altiplanic native plants from the Andean grasslands soils. <i>Scientific Reports</i> , 2019, 9, 1042.	1.6	32
3065	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. <i>Journal of Physiology</i> , 2019, 597, 2361-2378.	1.3	106
3066	Dietary emulsifiers consumption alters anxiety-like and social-related behaviors in mice in a sex-dependent manner. <i>Scientific Reports</i> , 2019, 9, 172.	1.6	60
3067	Diversity of the oral microbiome between dentate and edentulous individuals. <i>Oral Diseases</i> , 2019, 25, 911-918.	1.5	22
3068	Cheatgrass-associated AMF community negatively affects sagebrush root production but not C transfer to the soil. <i>Plant and Soil</i> , 2019, 436, 381-396.	1.8	7

#	ARTICLE	IF	CITATIONS
3069	The Association between Objectively Measured Physical Activity and the Gut Microbiome among Older Community Dwelling Men. <i>Journal of Nutrition, Health and Aging</i> , 2019, 23, 538-546.	1.5	27
3070	Gut microbiome of pre-adolescent children of two ethnicities residing in three distant cities. <i>Scientific Reports</i> , 2019, 9, 7831.	1.6	25
3071	Phycosphere Microbial Succession Patterns and Assembly Mechanisms in a Marine Dinoflagellate Bloom. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	23
3072	Bioinformatics methods. , 2019, , 1-19.		1
3073	High dispersal levels and lake warming are emergent drivers of cyanobacterial community assembly in peri-Alpine lakes. <i>Scientific Reports</i> , 2019, 9, 7366.	1.6	18
3074	Comparison of Bacterial Populations in the Ceca of Swine at Two Different Stages and Their Functional Annotations. <i>Genes</i> , 2019, 10, 382.	1.0	13
3075	Triclosan Alters Microbial Communities in Freshwater Microcosms. <i>Water (Switzerland)</i> , 2019, 11, 961.	1.2	15
3076	Neutral models predict biogeographical patterns of soil microbes at a local scale in Mediterranean heathlands, South Africa. <i>Transactions of the Royal Society of South Africa</i> , 2019, 74, 139-150.	0.8	4
3077	Comparison of 16S rDNA Next Sequencing of Microbiome Communities From Post-scalded and Post-picker Stages in Three Different Commercial Poultry Plants Processing Three Classes of Broilers. <i>Frontiers in Microbiology</i> , 2019, 10, 972.	1.5	16
3078	Changes in stool frequency following chicory inulin consumption, and effects on stool consistency, quality of life and composition of gut microbiota. <i>Food Hydrocolloids</i> , 2019, 96, 688-698.	5.6	33
3079	Comparative microbiomes of ticks collected from a black rhino and its surrounding environment. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2019, 9, 239-243.	0.6	7
3080	Exploring Biodiversity and Arsenic Metabolism of Microbiota Inhabiting Arsenic-Rich Groundwaters in Northern Italy. <i>Frontiers in Microbiology</i> , 2019, 10, 1480.	1.5	26
3081	Gestation alters the gut microbiota of an oviparous lizard. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	25
3082	Relationship between acetaldehyde concentration in mouth air and characteristics of microbiota of tongue dorsum in Japanese healthy adults: a cross-sectional study. <i>Journal of Applied Oral Science</i> , 2019, 27, e20180635.	0.7	4
3083	Community Structure of Bacteria Associated With Drifting <i>Sargassum horneri</i> , the Causative Species of Golden Tide in the Yellow Sea. <i>Frontiers in Microbiology</i> , 2019, 10, 1192.	1.5	22
3084	Actinobacteria and Cyanobacteria Diversity in Terrestrial Antarctic Microenvironments Evaluated by Culture-Dependent and Independent Methods. <i>Frontiers in Microbiology</i> , 2019, 10, 1018.	1.5	50
3085	For common community phylogenetic analyses, go ahead and use synthesis phylogenies. <i>Ecology</i> , 2019, 100, e02788.	1.5	80
3086	Protist diversity and community assembly in surface sediments of the South China Sea. <i>MicrobiologyOpen</i> , 2019, 8, e891.	1.2	24

#	ARTICLE	IF	CITATIONS
3087	Microbiota therapy acts via a regulatory T cell MyD88/ROR γ pathway to suppress food allergy. <i>Nature Medicine</i> , 2019, 25, 1164-1174.	15.2	259
3088	Quantitative and qualitative evaluation of the impact of the G2 enhancer, bead sizes and lysing tubes on the bacterial community composition during DNA extraction from recalcitrant soil core samples based on community sequencing and qPCR. <i>PLoS ONE</i> , 2019, 14, e0200979.	1.1	34
3089	Hass Avocado Inclusion in a Weight-Loss Diet Supported Weight Loss and Altered Gut Microbiota: A 12-Week Randomized, Parallel-Controlled Trial. <i>Current Developments in Nutrition</i> , 2019, 3, nzz068.	0.1	36
3090	Metagenomic assessment of the <i>Cebus apella</i> gut microbiota. <i>American Journal of Primatology</i> , 2019, 81, e23023.	0.8	6
3091	Microbial assemblages and bioindicators as proxies for ecosystem health status: potential and limitations. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6407-6421.	1.7	45
3092	Using carbon substrate as a selection pressure to enhance the potential of aerobic granular sludge microbial communities for removing contaminants of emerging concern. <i>Bioresource Technology</i> , 2019, 290, 121705.	4.8	20
3093	The Successional Changes in the Gut Microbiome of Pasture-Raised Chickens Fed Soy-Containing and Soy-Free Diets. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	1.8	16
3094	Classification of individuals and the potential to detect sexual contact using the microbiome of the pubic region. <i>Forensic Science International: Genetics</i> , 2019, 41, 177-187.	1.6	21
3095	Unveiled feather microcosm: feather microbiota of passerine birds is closely associated with host species identity and bacteriocin-producing bacteria. <i>ISME Journal</i> , 2019, 13, 2363-2376.	4.4	38
3096	Total RNA Analysis of Bacterial Community Structural and Functional Shifts Throughout Vertebrate Decomposition. <i>Journal of Forensic Sciences</i> , 2019, 64, 1707-1719.	0.9	12
3097	FEAST: fast expectation-maximization for microbial source tracking. <i>Nature Methods</i> , 2019, 16, 627-632.	9.0	275
3098	Composition and predictive functional analysis of bacterial communities inhabiting Chinese <i>Cordyceps</i> insight into conserved core microbiome. <i>BMC Microbiology</i> , 2019, 19, 105.	1.3	15
3099	Microbiomeâ€“metabolomics reveals gut microbiota associated with glycine-conjugated metabolites and polyamine metabolism in chronic kidney disease. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4961-4978.	2.4	146
3100	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	13.5	701
3101	Response of Fish Gut Microbiota to Toxin-Containing Cyanobacterial Extracts: A Microcosm Study on the Medaka (<i>Oryzias latipes</i>). <i>Environmental Science and Technology Letters</i> , 2019, 6, 341-347.	3.9	31
3102	Transition of Bacterial Diversity and Composition in Tongue Microbiota during the First Two Years of Life. <i>MSphere</i> , 2019, 4, .	1.3	18
3103	Characterization of Microbiota in Endometrial Fluid and Vaginal Secretions in Infertile Women with Repeated Implantation Failure. <i>Mediators of Inflammation</i> , 2019, 2019, 1-10.	1.4	69
3104	Non-synchronous Structural and Functional Dynamics During the Coalescence of Two Distinct Soil Bacterial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1125.	1.5	13

#	ARTICLE	IF	CITATIONS
3105	Euonymus japonicus phyllosphere microbiome is significantly changed by powdery mildew. Archives of Microbiology, 2019, 201, 1099-1109.	1.0	15
3106	Sociodemographic variation in the oral microbiome. Annals of Epidemiology, 2019, 35, 73-80.e2.	0.9	37
3107	Seasonality overwhelms aquacultural activity in determining the composition and assembly of the bacterial community in Lake Taihu, China. Science of the Total Environment, 2019, 683, 427-435.	3.9	49
3108	The intestinal microbiota and cardiovascular disease. Cardiovascular Research, 2019, 115, 1471-1486.	1.8	33
3109	Is there convergence of gut microbes in blood-feeding vertebrates?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180249.	1.8	21
3110	Dysbiosis of the intestinal microbiota in neurocritically ill patients and the risk for death. Critical Care, 2019, 23, 195.	2.5	84
3111	Spatial differences in bacterial communities preserved in soils archived for a decade. Applied Soil Ecology, 2019, 142, 64-71.	2.1	3
3112	The negative impact of cadmium on nitrogen transformation processes in a paddy soil is greater under non-flooding than flooding conditions. Environment International, 2019, 129, 451-460.	4.8	59
3113	Stages of pregnancy and weaning influence the gut microbiota diversity and function in sows. Journal of Applied Microbiology, 2019, 127, 867-879.	1.4	34
3114	Bovine milk microbiome: a more complex issue than expected. Veterinary Research, 2019, 50, 44.	1.1	67
3115	The Effects of Feeding a Soybean-Based or a Soy-Free Diet on the Gut Microbiome of Pasture-Raised Chickens Throughout Their Lifecycle. Frontiers in Sustainable Food Systems, 2019, 3, .	1.8	9
3116	Daily Sampling Reveals Personalized Diet-Microbiome Associations in Humans. Cell Host and Microbe, 2019, 25, 789-802.e5.	5.1	441
3117	Fecal Microbial Diversity and Structure Are Associated with Diet Quality in the Multiethnic Cohort Adiposity Phenotype Study. Journal of Nutrition, 2019, 149, 1575-1584.	1.3	48
3118	Reduced diversity and stability of coral-associated bacterial communities and suppressed immune function precedes disease onset in corals. Royal Society Open Science, 2019, 6, 190355.	1.1	59
3119	Selenium oxyanion bioconcentration in natural freshwater periphyton. Ecotoxicology and Environmental Safety, 2019, 180, 693-704.	2.9	14
3120	Soil biota composition and the performance of a noxious weed across its invaded range. Ecography, 2019, 42, 1671-1681.	2.1	6
3121	Egg Production in Poultry Farming Is Improved by Probiotic Bacteria. Frontiers in Microbiology, 2019, 10, 1042.	1.5	32
3122	Bacterial Diversity of Anshun Sufu, A Traditional Fermented Tofu in Guizhou Province of China. Transactions of Tianjin University, 2019, 25, 497-503.	3.3	13

#	ARTICLE	IF	CITATIONS
3123	Cut microbiota in ALS: possible role in pathogenesis?. Expert Review of Neurotherapeutics, 2019, 19, 785-805.	1.4	30
3124	The impact of skin care products on skin chemistry and microbiome dynamics. BMC Biology, 2019, 17, 47.	1.7	101
3125	Relative roles of the replacement and richness difference components of beta diversity following the ecological restoration of a mountain meadow, north China. Ecological Informatics, 2019, 52, 159-165.	2.3	7
3126	Shifts in the Composition of the Microbiota of Stored Wheat Grains in Response to Fumigation. Frontiers in Microbiology, 2019, 10, 1098.	1.5	43
3127	Arsenic alleviation in rice by using paddy soil microbial fuel cells. Plant and Soil, 2019, 441, 111-127.	1.8	22
3128	Tobacco exposure associated with oral microbiota oxygen utilization in the New York City Health and Nutrition Examination Study. Annals of Epidemiology, 2019, 34, 18-25.e3.	0.9	27
3129	Short-term and long-term impacts of <i>Helicobacter pylori</i> eradication with reverse hybrid therapy on the gut microbiota. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 1968-1976.	1.4	39
3130	“Balancing” balancing selection? Assortative mating at the major histocompatibility complex despite molecular signatures of balancing selection. Ecology and Evolution, 2019, 9, 5146-5157.	0.8	8
3131	Microbiota and Antibiotic Resistome of Lettuce Leaves and Radishes Grown in Soils Receiving Manure-Based Amendments Derived From Antibiotic-Treated Cows. Frontiers in Sustainable Food Systems, 2019, 3, .	1.8	22
3132	Temperature shapes opposing latitudinal gradients of plant taxonomic and phylogenetic β^2 diversity. Ecology Letters, 2019, 22, 1126-1135.	3.0	54
3133	Longitudinal homogenization of the microbiome between both occupants and the built environment in a cohort of United States Air Force Cadets. Microbiome, 2019, 7, 70.	4.9	33
3134	Impacts of diel temperature variations on nitrogen removal and metacommunity of anammox biofilm reactors. Water Research, 2019, 160, 1-9.	5.3	42
3135	Antimicrobial removal on piglets promotes health and higher bacterial diversity in the nasal microbiota. Scientific Reports, 2019, 9, 6545.	1.6	30
3136	Analysis of the Rumen Microbiota of Beef Calves Supplemented During the Suckling Phase. Frontiers in Microbiology, 2019, 10, 1131.	1.5	15
3137	Effects of clay mineral supplementation on particle-associated and epimural microbiota, and gene expression in the rumen of cows fed high-concentrate diet. Anaerobe, 2019, 59, 38-48.	1.0	53
3138	Bacterial succession and functional diversity during vermicomposting of the white grape marc <i>Vitis vinifera</i> v. Albariño. Scientific Reports, 2019, 9, 7472.	1.6	32
3139	Circulating Microbiota-Based Metagenomic Signature for Detection of Hepatocellular Carcinoma. Scientific Reports, 2019, 9, 7536.	1.6	51
3140	The Variation of Nasal Microbiota Caused by Low Levels of Gaseous Ammonia Exposure in Growing Pigs. Frontiers in Microbiology, 2019, 10, 1083.	1.5	19

#	ARTICLE	IF	CITATIONS
3141	A Distance-Based Kernel Association Test Based on the Generalized Linear Mixed Model for Correlated Microbiome Studies. <i>Frontiers in Genetics</i> , 2019, 10, 458.	1.1	31
3142	Toll-like receptor ϵ 2 and ϵ 4 responses regulate neutrophil infiltration into the junctional epithelium and significantly contribute to the composition of the oral microbiota. <i>Journal of Periodontology</i> , 2019, 90, 1202-1212.	1.7	21
3143	Bacterial community shifts evaluation in the sediments of Puyang River and its nitrogen removal capabilities exploration by resuscitation promoting factor. <i>Ecotoxicology and Environmental Safety</i> , 2019, 179, 188-197.	2.9	54
3144	Navy bean supplemented high-fat diet improves intestinal health, epithelial barrier integrity and critical aspects of the obese inflammatory phenotype. <i>Journal of Nutritional Biochemistry</i> , 2019, 70, 91-104.	1.9	41
3145	Characterizing microbial diversity and community composition of groundwater in a salt-freshwater transition zone. <i>Science of the Total Environment</i> , 2019, 678, 574-584.	3.9	60
3146	Social-Stress-Responsive Microbiota Induces Stimulation of Self-Reactive Effector T Helper Cells. <i>MSystems</i> , 2019, 4, .	1.7	39
3147	Dynamics of archaeal community in soil with application of composted tannery sludge. <i>Scientific Reports</i> , 2019, 9, 7347.	1.6	15
3148	Microbiome: Current Status and Future Applications. <i>Success in Academic Surgery</i> , 2019, , 213-232.	0.1	1
3149	Effects of forest harvest and fertiliser amendment on soil biodiversity and function can persist for decades. <i>Soil Biology and Biochemistry</i> , 2019, 135, 194-205.	4.2	20
3150	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	5.9	491
3151	Molecular detection of microbial colonization in cervical mucus of women with and without endometriosis. <i>American Journal of Reproductive Immunology</i> , 2019, 82, e13147.	1.2	42
3152	Malaria vector species in Amazonian Peru co-occur in larval habitats but have distinct larval microbial communities. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007412.	1.3	22
3153	The Influence of Fungicide Treatments on Mycobiota of Grapes and Its Evolution during Fermentation Evaluated by Metagenomic and Culture-Dependent Methods. <i>Microorganisms</i> , 2019, 7, 114.	1.6	13
3154	Mouse Vendor Influence on the Bacterial and Viral Gut Composition Exceeds the Effect of Diet. <i>Viruses</i> , 2019, 11, 435.	1.5	55
3155	Tree diversity is not always a strong driver of soil microbial diversity: a 7-year-old diversity experiment with trees. <i>Ecosphere</i> , 2019, 10, e02685.	1.0	19
3156	The immune response of the scallop <i>Argopecten purpuratus</i> is associated with changes in the host microbiota structure and diversity. <i>Fish and Shellfish Immunology</i> , 2019, 91, 241-250.	1.6	23
3157	Effects of typical engineered nanomaterials on 4-nonylphenol degradation in river sediment: based on bacterial community and function analysis. <i>Environmental Science: Nano</i> , 2019, 6, 2171-2184.	2.2	8
3158	Diversity and community pattern of sulfate-reducing bacteria in piglet gut. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 40.	2.1	28

#	ARTICLE	IF	CITATIONS
3159	Colonic fermentation of water soluble fiber fraction extracted from sugarcane (<i>Saccharum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 T	4.2	16
3160	The cooling tower water microbiota: Seasonal dynamics and co-occurrence of bacterial and protist phylotypes. <i>Water Research</i> , 2019, 159, 464-479.	5.3	51
3161	An altered composition of the microbiome in microscopic colitis is driven towards the composition in healthy controls by treatment with budesonide. <i>Scandinavian Journal of Gastroenterology</i> , 2019, 54, 446-452.	0.6	25
3162	Comparison of the microbiome, metabolome, and lipidome of obese and non-obese horses. <i>PLoS ONE</i> , 2019, 14, e0215918.	1.1	21
3163	Butyrate Protects Mice from <i>Clostridium difficile</i> -Induced Colitis through an HIF-1-Dependent Mechanism. <i>Cell Reports</i> , 2019, 27, 750-761.e7.	2.9	212
3164	[NiFe]-hydrogenases are constitutively expressed in an enriched <i>Methanobacterium</i> sp. population during electromethanogenesis. <i>PLoS ONE</i> , 2019, 14, e0215029.	1.1	10
3165	Differences in Bacterial Diversity, Composition and Function due to Long-Term Agriculture in Soils in the Eastern Free State of South Africa. <i>Diversity</i> , 2019, 11, 61.	0.7	50
3166	Gamma Irradiation Influences the Survival and Regrowth of Antibiotic-Resistant Bacteria and Antibiotic-Resistance Genes on Romaine Lettuce. <i>Frontiers in Microbiology</i> , 2019, 10, 710.	1.5	11
3167	Supplementation with Sodium Butyrate Modulates the Composition of the Gut Microbiota and Ameliorates High-Fat Diet-Induced Obesity in Mice. <i>Journal of Nutrition</i> , 2019, 149, 747-754.	1.3	99
3168	Multiple stressors interact primarily through antagonism to drive changes in the coral microbiome. <i>Scientific Reports</i> , 2019, 9, 6834.	1.6	64
3169	Diversity and Succession of Microbiota during Fermentation of the Traditional Indian Food Idli. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	25
3170	CCMP: Software-as-a-service approach for fully-automated microbiome profiling. <i>Journal of Biomedical Informatics: X</i> , 2019, 2, 100040.	4.2	3
3171	Metagenomic analysis of isolation methods of a targeted microbe, <i>Campylobacter jejuni</i> , from chicken feces with high microbial contamination. <i>Microbiome</i> , 2019, 7, 67.	4.9	20
3173	Gut microbiota and butyrate level changes associated with the long-term administration of proton pump inhibitors to old rats. <i>Scientific Reports</i> , 2019, 9, 6626.	1.6	29
3174	Impact of Warming on Greenhouse Gas Production and Microbial Diversity in Anoxic Peat From a Sphagnum-Dominated Bog (Grand Rapids, Minnesota, United States). <i>Frontiers in Microbiology</i> , 2019, 10, 870.	1.5	43
3175	Pyrolysis biochar has negligible effects on soil greenhouse gas production, microbial communities, plant germination, and initial seedling growth. <i>Chemosphere</i> , 2019, 228, 565-576.	4.2	30
3176	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. <i>MSphere</i> , 2019, 4, .	1.3	19
3177	Bacterial communities of <i>Aphis gossypii</i> and <i>Myzus persicae</i> (Hemiptera: Aphididae) from pepper crops (<i>Capsicum</i> sp.). <i>Scientific Reports</i> , 2019, 9, 5766.	1.6	22

#	ARTICLE	IF	CITATIONS
3178	Tropical forest conversion to rubber plantation affects soil micro- & mesofaunal community & diversity. <i>Scientific Reports</i> , 2019, 9, 5893.	1.6	33
3179	Progesterone Increases Bifidobacterium Relative Abundance during Late Pregnancy. <i>Cell Reports</i> , 2019, 27, 730-736.e3.	2.9	130
3180	Analysis of oral bacterial communities: comparison of HOMI<i>NGS</i> with a tree-based approach implemented in QIIME. <i>Journal of Oral Microbiology</i> , 2019, 11, 1586413.	1.2	9
3181	Unprecedented bacterial community richness in soybean nodules vary with cultivar and water status. <i>Microbiome</i> , 2019, 7, 63.	4.9	51
3182	Exposure to a Healthy Gut Microbiome Protects Against Reproductive and Metabolic Dysregulation in a PCOS Mouse Model. <i>Endocrinology</i> , 2019, 160, 1193-1204.	1.4	70
3183	Agricultural Risk Factors Influence Microbial Ecology in Honghu Lake. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 76-90.	3.0	31
3184	Characterization of pig saliva as the major natural habitat of <i>Streptococcus suis</i> by analyzing oral, fecal, vaginal, and environmental microbiota. <i>PLoS ONE</i> , 2019, 14, e0215983.	1.1	29
3185	The Vaginal and Urinary Microbiomes in Premenopausal Women With Interstitial Cystitis/Bladder Pain Syndrome as Compared to Unaffected Controls: A Pilot Cross-Sectional Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 92.	1.8	33
3186	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , 2019, 10, 1286.	5.8	46
3187	Bacterial composition of biofilms formed on dairy-processing equipment. <i>Preparative Biochemistry and Biotechnology</i> , 2019, 49, 477-484.	1.0	10
3188	Does evolutionary history determine specificity in broad ecological interactions?. <i>Journal of Ecology</i> , 2019, 107, 1582-1593.	1.9	29
3189	Letrozole treatment of adult female mice results in a similar reproductive phenotype but distinct changes in metabolism and the gut microbiome compared to pubertal mice. <i>BMC Microbiology</i> , 2019, 19, 57.	1.3	31
3190	Characterization of the rumen and fecal microbiome in bloated and non-bloated cattle grazing alfalfa pastures and subjected to bloat prevention strategies. <i>Scientific Reports</i> , 2019, 9, 4272.	1.6	20
3191	Insights gained into activated sludge nitrification through structural and functional profiling of microbial community response to starvation stress. <i>Environmental Science: Water Research and Technology</i> , 2019, 5, 884-896.	1.2	13
3192	Functional Microbiomics in Liver Transplantation: Identifying Novel Targets for Improving Allograft Outcomes. <i>Transplantation</i> , 2019, 103, 668-678.	0.5	25
3193	Regulatory T Cells and Plasmacytoid Dendritic Cells Within the Tumor Microenvironment in Gastric Cancer Are Correlated With Gastric Microbiota Dysbiosis: A Preliminary Study. <i>Frontiers in Immunology</i> , 2019, 10, 533.	2.2	78
3194	Inhibition of urinary stone disease by a multi-species bacterial network ensures healthy oxalate homeostasis. <i>Kidney International</i> , 2019, 96, 180-188.	2.6	77
3195	Heavy metal exposure causes changes in the metabolic health-associated gut microbiome and metabolites. <i>Environment International</i> , 2019, 126, 454-467.	4.8	125

#	ARTICLE	IF	CITATIONS
3196	Using formalin fixed paraffin embedded tissue to characterize the preterm gut microbiota in necrotising enterocolitis and spontaneous isolated perforation using marginal and diseased tissue. <i>BMC Microbiology</i> , 2019, 19, 52.	1.3	24
3197	The <i>Bos taurus</i> maternal microbiome: Role in determining the progeny early-life upper respiratory tract microbiome and health. <i>PLoS ONE</i> , 2019, 14, e0208014.	1.1	31
3198	A Developing Symbiosis: Enabling Cross-Talk Between Ecologists and Microbiome Scientists. <i>Frontiers in Microbiology</i> , 2019, 10, 292.	1.5	50
3199	Health risk of Licorice-Yuanhua combination through induction of colonic H2S metabolism. <i>Journal of Ethnopharmacology</i> , 2019, 236, 136-146.	2.0	14
3200	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1Åmonth. <i>Microbiome</i> , 2019, 7, 34.	4.9	115
3201	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. <i>Frontiers in Immunology</i> , 2019, 10, 69.	2.2	40
3202	Relative abundance of <i>Akkermansia</i> spp. and other bacterial phylotypes correlates with anxiety- and depressive-like behavior following social defeat in mice. <i>Scientific Reports</i> , 2019, 9, 3281.	1.6	85
3203	Fungal-Bacterial Networks in the <i>Populus</i> Rhizobiome Are Impacted by Soil Properties and Host Genotype. <i>Frontiers in Microbiology</i> , 2019, 10, 481.	1.5	71
3204	Incorporating microbial community data with machine learning techniques to predict feed substrates in microbial fuel cells. <i>Biosensors and Bioelectronics</i> , 2019, 133, 64-71.	5.3	60
3205	Research Techniques Made Simple: Profiling the Skin Microbiota. <i>Journal of Investigative Dermatology</i> , 2019, 139, 747-752.e1.	0.3	49
3206	Nonâ€random loss of phylogenetically distinct rare species degrades phylogenetic diversity in semiâ€natural grasslands. <i>Journal of Applied Ecology</i> , 2019, 56, 1419-1428.	1.9	13
3207	Major shifts in gut microbiota during development and its relationship to growth in ostriches. <i>Molecular Ecology</i> , 2019, 28, 2653-2667.	2.0	53
3208	An integrated microbiological and electrochemical approach to determine distributions of Fe metabolism in acid mine drainage-induced â€œiron moundâ€sediments. <i>PLoS ONE</i> , 2019, 14, e0213807.	1.1	6
3209	Insight Into Dynamics of Gut Microbial Community of Broilers Fed With Fructooligosaccharides Supplemented Low Calcium and Phosphorus Diets. <i>Frontiers in Veterinary Science</i> , 2019, 6, 95.	0.9	14
3210	The effects of phytoremediation on soil bacterial communities in an abandoned mine site of rare earth elements. <i>Science of the Total Environment</i> , 2019, 670, 950-960.	3.9	72
3211	Effects of wild blueberry (<i>Vaccinium angustifolium</i>) pomace feeding on gut microbiota and blood metabolites in free-range pastured broiler chickens. <i>Poultry Science</i> , 2019, 98, 3739-3755.	1.5	29
3212	The Gut Microbiome on a Periodized Low-Protein Diet Is Associated With Improved Metabolic Health. <i>Frontiers in Microbiology</i> , 2019, 10, 709.	1.5	14
3213	Effect of green tea and mulberry leaf powders on the gut microbiota of chicken. <i>BMC Veterinary Research</i> , 2019, 15, 77.	0.7	29

#	ARTICLE	IF	CITATIONS
3214	The gut microbiota composition affects dietary polyphenols-mediated cognitive resilience in mice by modulating the bioavailability of phenolic acids. <i>Scientific Reports</i> , 2019, 9, 3546.	1.6	61
3215	Microbial Engraftment and Efficacy of Fecal Microbiota Transplant for <i>Clostridium Difficile</i> in Patients With and Without Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 969-979.	0.9	38
3216	Characterization of the cecum microbiome from wild and captive rock ptarmigans indigenous to Arctic Norway. <i>PLoS ONE</i> , 2019, 14, e0213503.	1.1	18
3217	Gut microbiota in HIV pneumonia patients is related to peripheral CD4 counts, lung microbiota, and in vitro macrophage dysfunction. <i>Microbiome</i> , 2019, 7, 37.	4.9	25
3218	Bioturbation of peanut worms <i>Sipunculus nudus</i> on the composition of prokaryotic communities in a tidal flat as revealed by 16S rRNA gene sequences. <i>MicrobiologyOpen</i> , 2019, 8, e00802.	1.2	14
3219	Contributions of the microbial community to algal biomass and biofuel productivity in a wastewater treatment lagoon system. <i>Algal Research</i> , 2019, 39, 101461.	2.4	8
3220	Discriminating among forest communities based on taxonomic, phylogenetic and trait distances. <i>Forest Ecology and Management</i> , 2019, 440, 40-47.	1.4	15
3221	Three ancient documents solve the jigsaw of the parchment purple spot deterioration and validate the microbial succession model. <i>Scientific Reports</i> , 2019, 9, 1623.	1.6	35
3222	Variations in early gut microbiome are associated with childhood eczema. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	16
3223	Investigating the bacterial microbiota of traditional fermented dairy products using propidium monoazide with single-molecule real-time sequencing. <i>Journal of Dairy Science</i> , 2019, 102, 3912-3923.	1.4	17
3224	Rhizobacterial Community Assembly Patterns Vary Between Crop Species. <i>Frontiers in Microbiology</i> , 2019, 10, 581.	1.5	42
3225	Assessing taxonomic metagenome profilers with OPAL. <i>Genome Biology</i> , 2019, 20, 51.	3.8	67
3226	The fecal, oral, and skin microbiota of children with Chagas disease treated with benznidazole. <i>PLoS ONE</i> , 2019, 14, e0212593.	1.1	21
3227	Fungal Species Diversity in French Bread Sourdoughs Made of Organic Wheat Flour. <i>Frontiers in Microbiology</i> , 2019, 10, 201.	1.5	38
3228	<i>H. pylori</i> eradication with antibiotic treatment causes changes in glucose homeostasis related to modifications in the gut microbiota. <i>PLoS ONE</i> , 2019, 14, e0213548.	1.1	43
3229	Disordered intestinal microbes are associated with the activity of Systemic Lupus Erythematosus. <i>Clinical Science</i> , 2019, 133, 821-838.	1.8	119
3230	Bacterial community in cold and alkaline environments of Hoh Xil basin in Qinghai Tibet Plateau and isolation of potential sources of microbiota. <i>Annals of Microbiology</i> , 2019, 69, 567-576.	1.1	8
3231	Apple consumption is associated with a distinctive microbiota, proteomics and metabolomics profile in the gut of Dawley Sprague rats fed a high-fat diet. <i>PLoS ONE</i> , 2019, 14, e0212586.	1.1	14

#	ARTICLE	IF	CITATIONS
3232	Rainbow trout (<i>Oncorhynchus mykiss</i>) gut microbiota is modulated by insect meal from <i>Hermetia illucens</i> prepupae in the diet. <i>Reviews in Fish Biology and Fisheries</i> , 2019, 29, 465-486.	2.4	136
3233	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of <i>Clostridioides (Clostridium) difficile</i> , despite cellular susceptibility to its toxins. <i>Anaerobe</i> , 2019, 58, 53-72.	1.0	20
3234	Soil bacterial community associated with the dioecious <i>Acanthosicyos horridus</i> in the Namib Desert. <i>Biology and Fertility of Soils</i> , 2019, 55, 393-403.	2.3	5
3235	Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5821.	1.6	414
3236	Diurnal Temperature Variation and Plants Drive Latitudinal Patterns in Seasonal Dynamics of Soil Microbial Community. <i>Frontiers in Microbiology</i> , 2019, 10, 674.	1.5	27
3237	Recovery of Benthic Microalgal Biomass and Community Structure Following Beach Renourishment at Folly Beach, South Carolina. <i>Estuaries and Coasts</i> , 2019, 42, 157-172.	1.0	12
3238	Diel population and functional synchrony of microbial communities on coral reefs. <i>Nature Communications</i> , 2019, 10, 1691.	5.8	28
3239	Antidepressants affect gut microbiota and <i>Ruminococcus flavefaciens</i> is able to abolish their effects on depressive-like behavior. <i>Translational Psychiatry</i> , 2019, 9, 133.	2.4	159
3240	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5755.	1.6	22
3241	Dynamic changes in rumen fermentation and bacterial community following rumen fluid transplantation in a sheep model of rumen acidosis: implications for rumen health in ruminants. <i>FASEB Journal</i> , 2019, 33, 8453-8467.	0.2	23
3242	Impact of Saskatoon berry powder on insulin resistance and relationship with intestinal microbiota in high fat high sucrose diet-induced obese mice. <i>Journal of Nutritional Biochemistry</i> , 2019, 69, 130-138.	1.9	25
3243	NOB suppression in partial nitrification-anammox (PNA) process by discharging aged flocs: Performance and microbial community dynamics. <i>Chemosphere</i> , 2019, 227, 26-33.	4.2	49
3244	Linking shifts in bacterial community with changes in dissolved organic matter pool in a tropical lake. <i>Science of the Total Environment</i> , 2019, 672, 990-1003.	3.9	31
3245	Assessing Microbial Community Patterns During Incipient Soil Formation From Basalt. <i>Journal of Geophysical Research C: Biogeosciences</i> , 2019, 124, 941-958.	1.3	16
3246	Bacterial colonization and antimicrobial resistance genes in neonatal enteral feeding tubes. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	9
3247	<i>Litopenaeus vannamei</i> fed diets with different replacement levels of fish meal by fish silage: A molecular approach on intestinal microbiota. <i>Aquaculture Nutrition</i> , 2019, 25, 721-728.	1.1	10
3248	Low-dimensional representation of genomic sequences. <i>Journal of Mathematical Biology</i> , 2019, 79, 1-29.	0.8	21
3249	Microbiome dynamics during cast ageing in the earthworm <i>Aporrectodea caliginosa</i> . <i>Applied Soil Ecology</i> , 2019, 139, 56-63.	2.1	33

#	ARTICLE	IF	CITATIONS
3250	Unilateral ureteral obstruction causes gut microbial dysbiosis and metabolome disorders contributing to tubulointerstitial fibrosis. <i>Experimental and Molecular Medicine</i> , 2019, 51, 1-18.	3.2	90
3251	Feeding modes shape the acquisition and structure of the initial gut microbiota in newborn lambs. <i>Environmental Microbiology</i> , 2019, 21, 2333-2346.	1.8	45
3252	Bayes-optimal estimation of overlap between populations of fixed size. <i>PLoS Computational Biology</i> , 2019, 15, e1006898.	1.5	10
3253	Protocatechuic acid improved growth performance, meat quality, and intestinal health of Chinese yellow-feathered broilers. <i>Poultry Science</i> , 2019, 98, 3138-3149.	1.5	37
3254	Ceftriaxone and Cefotaxime Have Similar Effects on the Intestinal Microbiota in Human Volunteers Treated by Standard-Dose Regimens. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	41
3255	Oral Administration of Compound Probiotics Improved Canine Feed Intake, Weight Gain, Immunity and Intestinal Microbiota. <i>Frontiers in Immunology</i> , 2019, 10, 666.	2.2	53
3256	Temperature and soil moisture control microbial community composition in an arctic alpine ecosystem along elevational and micro-topographic gradients. <i>ISME Journal</i> , 2019, 13, 2031-2043.	4.4	115
3257	A guide to the application of Hill numbers to DNA-based diversity analyses. <i>Molecular Ecology Resources</i> , 2019, 19, 804-817.	2.2	125
3258	Neighbor urban wastewater treatment plants display distinct profiles of bacterial community and antibiotic resistance genes. <i>Environmental Science and Pollution Research</i> , 2019, 26, 11269-11278.	2.7	25
3259	Neutrophilic proteolysis in the cystic fibrosis lung correlates with a pathogenic microbiome. <i>Microbiome</i> , 2019, 7, 23.	4.9	53
3260	Succession of embryonic and the intestinal bacterial communities of Atlantic salmon (<i>Salmo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.2	68
3261	Replacement of fishmeal by fermented soybean meal could enhance the growth performance but not significantly influence the intestinal microbiota of white shrimp <i>Litopenaeus vannamei</i> . <i>Aquaculture</i> , 2019, 504, 354-360.	1.7	50
3262	Impact of 5 fluorouracil chemotherapy on gut inflammation, functional parameters, and gut microbiota. <i>Brain, Behavior, and Immunity</i> , 2019, 80, 44-55.	2.0	63
3263	Characterization of whole blood transcriptome and early-life fecal microbiota in high and low responder pigs before, and after vaccination for <i>Mycoplasma hyopneumoniae</i> . <i>Vaccine</i> , 2019, 37, 1743-1755.	1.7	16
3264	Offspring Microbiomes Differ Across Breeding Sites in a Panmictic Species. <i>Frontiers in Microbiology</i> , 2019, 10, 35.	1.5	32
3265	Ecological Strategies Behind the Selection of Cultivable Actinomycete Strains from the Yucatan Peninsula for the Discovery of Secondary Metabolites with Antibiotic Activity. <i>Microbial Ecology</i> , 2019, 77, 839-851.	1.4	12
3266	Chinese white truffles shape the ectomycorrhizal microbial communities of <i>Corylus avellana</i> . <i>Annals of Microbiology</i> , 2019, 69, 553-565.	1.1	12
3267	Compositional changes to the ileal microbiome precede the onset of spontaneous ileitis in SHIP deficient mice. <i>Gut Microbes</i> , 2019, 10, 578-598.	4.3	46

#	ARTICLE	IF	CITATIONS
3268	Microbiome-based body fluid identification of samples exposed to indoor conditions. <i>Forensic Science International: Genetics</i> , 2019, 40, 105-113.	1.6	52
3269	Association between rhinovirus species and nasopharyngeal microbiota in infants with severe bronchiolitis. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1925-1928.e7.	1.5	26
3270	The bacterial aetiology of pleural empyema. A descriptive and comparative metagenomic study. <i>Clinical Microbiology and Infection</i> , 2019, 25, 981-986.	2.8	65
3271	Alterations of the Gut Microbiome in Chronic Hepatitis B Virus Infection Associated with Alanine Aminotransferase Level. <i>Journal of Clinical Medicine</i> , 2019, 8, 173.	1.0	27
3272	Helminth-Based Product and the Microbiome of Mice with Lupus. <i>MSystems</i> , 2019, 4, .	1.7	22
3273	Effect of the <i>Lactobacillus rhamnosus</i> strain GG and tagatose as a synbiotic combination in a dextran sulfate sodium-induced colitis murine model. <i>Journal of Dairy Science</i> , 2019, 102, 2844-2853.	1.4	35
3274	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.	0.8	66
3275	No difference in 4-aminquinoline induced tumorigenesis between germ-free and colonized mice. <i>Molecular Carcinogenesis</i> , 2019, 58, 627-632.	1.3	2
3276	Distinct grazing pressure loads generate different impacts on bacterial community in a long-term experiment in Pampa biome. <i>Applied Soil Ecology</i> , 2019, 137, 167-177.	2.1	9
3277	Gut microbiota of the European Brown Hare (<i>Lepus europaeus</i>). <i>Scientific Reports</i> , 2019, 9, 2738.	1.6	14
3278	pdist: ecological dissimilarities for paired and longitudinal microbiome association analysis. <i>Bioinformatics</i> , 2019, 35, 3567-3575.	1.8	21
3279	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019, 4, .	1.7	295
3280	The tea leaf microbiome shows specific responses to chemical pesticides and biocontrol applications. <i>Science of the Total Environment</i> , 2019, 667, 33-40.	3.9	47
3281	Dynamic Development of Fecal Microbiome During the Progression of Diabetes Mellitus in Zucker Diabetic Fatty Rats. <i>Frontiers in Microbiology</i> , 2019, 10, 232.	1.5	73
3282	Phylofactorization: a graph partitioning algorithm to identify phylogenetic scales of ecological data. <i>Ecological Monographs</i> , 2019, 89, e01353.	2.4	52
3283	Computational Resources and Techniques in Enzyme Research. , 2019, , 453-468.		4
3284	The NLRP3 inflammasome mediates DSS-induced intestinal inflammation in <i>Nod2</i> knockout mice. <i>Innate Immunity</i> , 2019, 25, 132-143.	1.1	27
3285	Effects of a <i>Saccharomyces cerevisiae</i> fermentation product on fecal characteristics, nutrient digestibility, fecal fermentative end-products, fecal microbial populations, immune function, and diet palatability in adult dogs. <i>Journal of Animal Science</i> , 2019, 97, 1586-1599.	0.2	43

#	ARTICLE	IF	CITATIONS
3286	Engineering the microbiome for animal health and conservation. <i>Experimental Biology and Medicine</i> , 2019, 244, 494-504.	1.1	65
3287	Composition of gut microbiota in patients with toxigenic <i>Clostridioides (Clostridium) difficile</i> : Comparison between subgroups according to clinical criteria and toxin gene load. <i>PLoS ONE</i> , 2019, 14, e0212626.	1.1	35
3288	Gut Mucosal Proteins and Bacteriome Are Shaped by the Saturation Index of Dietary Lipids. <i>Nutrients</i> , 2019, 11, 418.	1.7	41
3289	Association of Systemic Antibiotic Treatment of Acne With Skin Microbiota Characteristics. <i>JAMA Dermatology</i> , 2019, 155, 425.	2.0	65
3290	Gut microbiota diversity is associated with cardiorespiratory fitness in postâ€primary treatment breast cancer survivors. <i>Experimental Physiology</i> , 2019, 104, 529-539.	0.9	14
3291	Probiotic or synbiotic alters the gut microbiota and metabolism in a randomised controlled trial of weight management in overweight adults. <i>Beneficial Microbes</i> , 2019, 10, 121-135.	1.0	118
3292	Variability in the Response of Bacterial Community Assembly to Environmental Selection and Biotic Factors Depends on the Immigrated Bacteria, as Revealed by a Soil Microcosm Experiment. <i>MSystems</i> , 2019, 4, .	1.7	4
3293	Microbial Population Change in Anaerobic Digestion during Copper Sulfate Inhibition and Recovery. <i>Transactions of the ASABE</i> , 2019, 62, 1231-1241.	1.1	2
3294	Compound- and context-dependent effects of antibiotics on greenhouse gas emissions from livestock. <i>Royal Society Open Science</i> , 2019, 6, 182049.	1.1	3
3295	Bifidogenic and butyrogenic effects of young barely leaf extract in an in vitro human colonic microbiota model. <i>AMB Express</i> , 2019, 9, 182.	1.4	8
3296	Fecal Components Modulate Human Astrovirus Infectivity in Cells and Reconstituted Intestinal Tissues. <i>MSphere</i> , 2019, 4, .	1.3	12
3297	Influence of Gut Microbiota on Behavior and Its Disturbances. , 0, , .		7
3298	Deficiency of Dietary Fiber in <i>Slc5a8</i> -Null Mice Promotes Bacterial Dysbiosis and Alters Colonic Epithelial Transcriptome towards Proinflammatory Milieu. <i>Canadian Journal of Gastroenterology and Hepatology</i> , 2019, 2019, 1-12.	0.8	10
3299	Variation of microbial community structure in a simulated remediation process of BDE-47-contaminated soil. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 344, 012131.	0.2	0
3300	Comparison of Microphototrophic Communities Living in Different Soil Environments in the High Arctic. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	8
3301	5. Metagenomics of extreme environments: methods and applications. , 2019, , 93-126.		0
3302	6. Practical overview of bioinformatics data mining in environmental genomics. , 2019, , 127-150.		0
3303	Microbiome profiling of the onion thrips, <i>Thrips tabaci</i> Lindeman (Thysanoptera: Thripidae). <i>PLoS ONE</i> , 2019, 14, e0223281.	1.1	10

#	ARTICLE	IF	CITATIONS
3304	Fetal exposure to maternal inflammation interrupts murine intestinal development and increases susceptibility to neonatal intestinal injury. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	22
3305	The Earth Is Small for "Leviathans" Long Distance Dispersal of Giant Viruses across Aquatic Environments. <i>Microbes and Environments</i> , 2019, 34, 334-339.	0.7	11
3306	Comparative analysis of microbiota along the length of the gastrointestinal tract of two tree squirrel species (<i>Sciurus aberti</i> and <i>S. niger</i>) living in sympatry. <i>Ecology and Evolution</i> , 2019, 9, 13344-13358.	0.8	5
3307	Songbirds show odour-based discrimination of similarity and diversity at the major histocompatibility complex. <i>Animal Behaviour</i> , 2019, 158, 131-138.	0.8	29
3308	Shift in bacterial taxa precedes morphological plasticity in a larval echinoid. <i>Marine Biology</i> , 2019, 166, 1.	0.7	7
3309	Effects of active dried <i>Saccharomyces cerevisiae</i> on ruminal fermentation and bacterial community during the short-term ruminal acidosis challenge model in Holstein calves. <i>Journal of Dairy Science</i> , 2019, 102, 6518-6531.	1.4	15
3310	High-throughput sequencing reveals the core gut microbiota of the mud crab (<i>Scylla paramamosain</i>) in different coastal regions of southern China. <i>BMC Genomics</i> , 2019, 20, 829.	1.2	24
3311	Temporal evolution of the microbiome, immune system, and epigenome with disease progression in ALS mice. <i>DMM Disease Models and Mechanisms</i> , 2019, 13, .	1.2	50
3312	Effect of C/N on removal of chlorpyrifos in constructed wetland system. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 330, 032085.	0.2	0
3313	Exogenous and endogenous microbiomes of wild-caught <i>Phormia regina</i> (Diptera: Calliphoridae) flies from a suburban farm by 16S rRNA gene sequencing. <i>Scientific Reports</i> , 2019, 9, 20365.	1.6	21
3314	Distinct cellular roles for PDCD10 define a gut-brain axis in cerebral cavernous malformation. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	51
3315	Calorie restriction slows age-related microbiota changes in an Alzheimer's disease model in female mice. <i>Scientific Reports</i> , 2019, 9, 17904.	1.6	86
3316	The Role of the Gut Microbiome in Predicting Response to Diet and the Development of Precision Nutrition Models" Part I: Overview of Current Methods. <i>Advances in Nutrition</i> , 2019, 10, 953-978.	2.9	53
3317	Wild specimens of sand fly phlebotomine <i>Lutzomyia evansi</i> , vector of leishmaniasis, show high abundance of <i>Methylobacterium</i> and natural carriage of <i>Wolbachia</i> and <i>Cardinium</i> types in the midgut microbiome. <i>Scientific Reports</i> , 2019, 9, 17746.	1.6	20
3318	Microbiome and Metabolome Analyses of Milk From Dairy Cows With Subclinical <i>Streptococcus agalactiae</i> Mastitis" Potential Biomarkers. <i>Frontiers in Microbiology</i> , 2019, 10, 2547.	1.5	38
3319	Silicon application and related changes in soil bacterial community dynamics reduced ginseng black spot incidence in <i>Panax ginseng</i> in a short-term study. <i>BMC Microbiology</i> , 2019, 19, 263.	1.3	17
3320	Early life nutrition influences susceptibility to chronic inflammatory colitis in later life. <i>Scientific Reports</i> , 2019, 9, 18111.	1.6	12
3321	The Stain of the Original Salt: Red Heats on Chrome Tanned Leathers and Purple Spots on Ancient Parchments Are Two Sides of the Same Ecological Coin. <i>Frontiers in Microbiology</i> , 2019, 10, 2459.	1.5	16

#	ARTICLE	IF	CITATIONS
3322	Amplicon sequencing and imputed metagenomic analysis of waste soil and sediment microbiome reveals unique bacterial communities and their functional attributes. <i>Environmental Monitoring and Assessment</i> , 2019, 191, 778.	1.3	15
3323	Lactation and menstruation shift the vaginal microbiota in captive rhesus monkeys to be more similar to the male urethral microbiota. <i>Scientific Reports</i> , 2019, 9, 17399.	1.6	9
3324	Parallel changes in gut microbiome composition and function during colonization, local adaptation and ecological speciation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191911.	1.2	41
3325	Modulation of Gut Microbiota by Glucosamine and Chondroitin in a Randomized, Double-Blind Pilot Trial in Humans. <i>Microorganisms</i> , 2019, 7, 610.	1.6	12
3326	Urinary Microbiome Evaluation in Patients Presenting with Hematuria with a Focus on Exposure to Tobacco Smoke. <i>Research and Reports in Urology</i> , 2019, Volume 11, 359-367.	0.6	11
3327	Gut Microbiota Dysbiosis and Increased Plasma LPS and TMAO Levels in Patients With Preeclampsia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 409.	1.8	93
3328	Severe gut microbiota dysbiosis caused by malnourishment can be partly restored during 3 weeks of refeeding with fortified corn-soy-blend in a piglet model of childhood malnutrition. <i>BMC Microbiology</i> , 2019, 19, 277.	1.3	7
3329	Microbiota and Body Composition During the Period of Complementary Feeding. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2019, 69, 726-732.	0.9	6
3330	Impact of Tilapia hepcidin 2-3 dietary supplementation on the gut microbiota profile and immunomodulation in the grouper (<i>Epinephelus lanceolatus</i>). <i>Scientific Reports</i> , 2019, 9, 19047.	1.6	23
3331	Vaginal microbiome transplantation in women with intractable bacterial vaginosis. <i>Nature Medicine</i> , 2019, 25, 1500-1504.	15.2	203
3332	Effects of Long-term Cotton Continuous Cropping on Soil Microbiome. <i>Scientific Reports</i> , 2019, 9, 18297.	1.6	46
3333	The Microbiome and Its Potential for Pharmacology. <i>Handbook of Experimental Pharmacology</i> , 2019, 260, 301-326.	0.9	14
3334	Flagellin-elicited adaptive immunity suppresses flagellated microbiota and vaccinates against chronic inflammatory diseases. <i>Nature Communications</i> , 2019, 10, 5650.	5.8	64
3335	A Prospective Study on Child Morbidity and Gut Microbiota in Rural Malawi. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2019, 69, 431-437.	0.9	8
3336	Low-diversity bacterial microbiota in Southern Ocean representatives of lanternfish genera <i>Electrona</i> , <i>Protomyxophum</i> and <i>Gymnoscopelus</i> (family <i>Myxophidae</i>). <i>PLoS ONE</i> , 2019, 14, e0226159.	1.1	10
3337	Protective effect of <i>Bacillus amyloliquefaciens</i> against <i>Salmonella</i> via polarizing macrophages to M1 phenotype directly and to M2 depended on microbiota. <i>Food and Function</i> , 2019, 10, 7653-7666.	2.1	17
3338	An integrated metabolomics and 16S rRNA gene sequencing approach exploring the molecular pathways and potential targets behind the effects of <i>Radix Scrophulariae</i> . <i>RSC Advances</i> , 2019, 9, 33354-33367.	1.7	3
3339	Related Enteric Viruses Have Different Requirements for Host Microbiota in Mice. <i>Journal of Virology</i> , 2019, 93, .	1.5	30

#	ARTICLE	IF	CITATIONS
3340	Altered Schaedler flora mice: A defined microbiota animal model to study the microbiota-gut-brain axis. <i>Behavioural Brain Research</i> , 2019, 356, 221-226.	1.2	20
3341	Characterisation of the bacterial community in the gastrointestinal tracts of elk (<i>Cervus canadensis</i>). <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 225-235.	0.7	31
3342	Arsenic contamination influences microbial community structure and putative arsenic metabolism gene abundance in iron plaque on paddy rice root. <i>Science of the Total Environment</i> , 2019, 649, 405-412.	3.9	48
3343	Differences in the equine faecal microbiota between horses presenting to a tertiary referral hospital for colic compared with an elective surgical procedure. <i>Equine Veterinary Journal</i> , 2019, 51, 336-342.	0.9	42
3344	Microbiota of eggs revealed by 16S rRNA-based sequencing: From raw materials produced by different suppliers to chilled pasteurized liquid products. <i>Food Control</i> , 2019, 96, 194-204.	2.8	17
3345	Temporal Variability and Stability of the Fecal Microbiome: The Multiethnic Cohort Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 154-162.	1.1	31
3346	Methods for automatic reference trees and multilevel phylogenetic placement. <i>Bioinformatics</i> , 2019, 35, 1151-1158.	1.8	33
3347	Plumage microbiota covaries with the major histocompatibility complex in blue petrels. <i>Molecular Ecology</i> , 2019, 28, 833-846.	2.0	35
3348	Alterations of gastric mucosal microbiota across different stomach microhabitats in a cohort of 276 patients with gastric cancer. <i>EBioMedicine</i> , 2019, 40, 336-348.	2.7	181
3349	Effect of storage temperature on bacterial diversity in chicken skin. <i>Journal of Applied Microbiology</i> , 2019, 126, 854-863.	1.4	7
3350	Disease-modifying therapies alter gut microbial composition in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2019, 6, e517.	3.1	75
3351	Distinctive microbial communities imply the main mechanism in a MEOR trial in high pour-point reservoir. <i>Journal of Petroleum Science and Engineering</i> , 2019, 175, 97-107.	2.1	10
3352	On-board saline black water treatment by bioaugmentation original marine bacteria with <i>Pseudoalteromonas</i> sp. SCSE709-6 and the associated microbial community. <i>Bioresource Technology</i> , 2019, 273, 496-505.	4.8	17
3353	The fecal microbiome and serum concentrations of indoxyl sulfate and p-cresol sulfate in cats with chronic kidney disease. <i>Journal of Veterinary Internal Medicine</i> , 2019, 33, 662-669.	0.6	37
3354	Microbial fermentation of flaxseed fibers modulates the transcriptome of GPR41-expressing enteroendocrine cells and protects mice against diet-induced obesity. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 316, E453-E463.	1.8	29
3355	Novel microbial community composition and carbon biogeochemistry emerge over time following saltwater intrusion in wetlands. <i>Global Change Biology</i> , 2019, 25, 549-561.	4.2	68
3356	Salinity-driven heterogeneity toward anammox distribution and growth kinetics. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1953-1960.	1.7	23
3357	Effect of cropping systems after abandoned salinized farmland reclamation on soil bacterial communities in arid northwest China. <i>Soil and Tillage Research</i> , 2019, 187, 204-213.	2.6	38

#	ARTICLE	IF	CITATIONS
3358	A review of kernel methods for genetic association studies. <i>Genetic Epidemiology</i> , 2019, 43, 122-136.	0.6	24
3359	Soil available phosphorus content drives the spatial distribution of archaeal communities along elevation in acidic terrace paddy soils. <i>Science of the Total Environment</i> , 2019, 658, 723-731.	3.9	17
3360	Mixture of tree species enhances stability of the soil bacterial community through phylogenetic diversity. <i>European Journal of Soil Science</i> , 2019, 70, 644-654.	1.8	11
3361	Organic and inorganic amendments did not affect microbial community composition in the bulk soil differently but did change the relative abundance of selected taxa. <i>European Journal of Soil Science</i> , 2019, 70, 796-806.	1.8	7
3362	A comparison of phylogenetic and species beta diversity measures describing vegetation assemblages along an elevation gradient. <i>Journal of Vegetation Science</i> , 2019, 30, 98-107.	1.1	4
3363	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. <i>Trends in Microbiology</i> , 2019, 27, 105-117.	3.5	652
3364	Microbial communities in local and transplanted soils along a latitudinal gradient. <i>Catena</i> , 2019, 173, 456-464.	2.2	11
3365	The Carbamate Aldicarb Altered the Gut Microbiome, Metabolome, and Lipidome of C57BL/6J Mice. <i>Chemical Research in Toxicology</i> , 2019, 32, 67-79.	1.7	37
3366	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. <i>Journal of Forensic Sciences</i> , 2019, 64, 791-798.	0.9	40
3367	Chronic alcohol exposure induced gut microbiota dysbiosis and its correlations with neuropsychic behaviors and brain BDNF/Gabra1 changes in mice. <i>BioFactors</i> , 2019, 45, 187-199.	2.6	51
3368	The Role of the Mycobiota in the Gut-Liver Axis. , 2019, , 133-145.		1
3369	Community structural differences shape microbial responses to high molecular weight organic matter. <i>Environmental Microbiology</i> , 2019, 21, 557-571.	1.8	40
3370	The evolution of abdominal microbiomes in fungus-growing ants. <i>Molecular Ecology</i> , 2019, 28, 879-899.	2.0	25
3371	Microbiome and its relation to gestational diabetes. <i>Endocrine</i> , 2019, 64, 254-264.	1.1	102
3372	Effect of post-harvest interventions on surficial carrot bacterial community dynamics, pathogen survival, and antibiotic resistance. <i>International Journal of Food Microbiology</i> , 2019, 291, 25-34.	2.1	8
3374	The chirality of imazethapyr herbicide selectively affects the bacterial community in soybean field soil. <i>Environmental Science and Pollution Research</i> , 2019, 26, 2531-2546.	2.7	11
3375	Interleukin-17/interleukin-17 receptor axis elicits intestinal neutrophil migration, restrains gut dysbiosis and lipopolysaccharide translocation in high-fat diet-induced metabolic syndrome model. <i>Immunology</i> , 2019, 156, 339-355.	2.0	52
3376	Highly effective treatment of petrochemical wastewater by a super-sized industrial scale plant with expanded granular sludge bed bioreactor and aerobic activated sludge. <i>Chemical Engineering Journal</i> , 2019, 360, 15-23.	6.6	57

#	ARTICLE	IF	CITATIONS
3377	The microbiome of <i>Escherichia coli</i> and culture-negative nonsevere clinical mastitis: Characterization and associations with linear score and milk production. <i>Journal of Dairy Science</i> , 2019, 102, 578-594.	1.4	12
3378	The Influence of Habitat and Phylogeny on the Skin Microbiome of Amphibians in Guatemala and Mexico. <i>Microbial Ecology</i> , 2019, 78, 257-267.	1.4	34
3379	Bulk tank raw milk microbiota differs within and between farms: A moving goalpost challenging quality control. <i>Journal of Dairy Science</i> , 2019, 102, 1959-1971.	1.4	65
3380	Effects of composted bamboo residue amendments on soil microbial communities in an intensively managed bamboo (<i>Phyllostachys praecox</i>) plantation. <i>Applied Soil Ecology</i> , 2019, 136, 178-183.	2.1	26
3381	The shift of bacterial community composition magnifies over time in response to different sources of soybean residues. <i>Applied Soil Ecology</i> , 2019, 136, 163-167.	2.1	15
3382	Gut microbiome and brain functional connectivity in infants-a preliminary study focusing on the amygdala. <i>Psychopharmacology</i> , 2019, 236, 1641-1651.	1.5	91
3383	Chinese liver fluke <i>Clonorchis sinensis</i> infection changes the gut microbiome and increases probiotic <i>Lactobacillus</i> in mice. <i>Parasitology Research</i> , 2019, 118, 693-699.	0.6	16
3384	Delayed differentiation of vaginal and uterine microbiomes in dairy cows developing postpartum endometritis. <i>PLoS ONE</i> , 2019, 14, e0200974.	1.1	57
3385	Bacterial Communities in the Alpaca Gastrointestinal Tract Vary With Diet and Body Site. <i>Frontiers in Microbiology</i> , 2019, 9, 3334.	1.5	7
3386	Diversity and Composition of Pelagic Prokaryotic and Protist Communities in a Thin Arctic Sea-Ice Regime. <i>Microbial Ecology</i> , 2019, 78, 388-408.	1.4	26
3387	Impact of long-term grazing exclusion on soil microbial community composition and nutrient availability. <i>Biology and Fertility of Soils</i> , 2019, 55, 121-134.	2.3	66
3388	Sex Differences in the Gut Microbiota as Potential Determinants of Gender Predisposition to Disease. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1800870.	1.5	103
3389	Microbiomes of the polychaete <i>Hydroides elegans</i> (Polychaeta: Serpulidae) across its life-history stages. <i>Marine Biology</i> , 2019, 166, 1.	0.7	27
3390	Effects of light intensity on soluble microbial products produced by <i>Synechocystis</i> sp. PCC 6803 and associated heterotrophic communities. <i>Algal Research</i> , 2019, 38, 101409.	2.4	4
3391	Impact of planktonic low nucleic acid-content bacteria to bacterial community structure and associated ecological functions in a shallow lake. <i>Science of the Total Environment</i> , 2019, 658, 868-878.	3.9	28
3392	Seasonal, sub-seasonal and diurnal variation of soil bacterial community composition in a temperate deciduous forest. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	20
3393	Transitions in microbial communities along a 1600 km freshwater trophic gradient. <i>Journal of Great Lakes Research</i> , 2019, 45, 263-276.	0.8	10
3394	Geographic distance and soil microbial biomass carbon drive biogeographical distribution of fungal communities in Chinese Loess Plateau soils. <i>Science of the Total Environment</i> , 2019, 660, 1058-1069.	3.9	36

#	ARTICLE	IF	CITATIONS
3395	Antarctic Krill Are Reservoirs for Distinct Southern Ocean Microbial Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 3226.	1.5	15
3396	T4-type viruses: Important impacts on shaping bacterial community along a chronosequence of 2000-year old paddy soils. <i>Soil Biology and Biochemistry</i> , 2019, 128, 89-99.	4.2	18
3397	Impact of high-grain diet feeding on mucosa-associated bacterial community and gene expression of tight junction proteins in the small intestine of goats. <i>MicrobiologyOpen</i> , 2019, 8, e00745.	1.2	19
3398	Effect of fecal microbiota transplantation route of administration on gut colonization and host response in preterm pigs. <i>ISME Journal</i> , 2019, 13, 720-733.	4.4	59
3399	Promises and pitfalls of using high-throughput sequencing for diet analysis. <i>Molecular Ecology Resources</i> , 2019, 19, 327-348.	2.2	138
3400	Lower perinatal exposure to Proteobacteria is an independent predictor of early childhood wheezing. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 419-421.e5.	1.5	6
3401	Childhood adversity impact on gut microbiota and inflammatory response to stress during pregnancy. <i>Brain, Behavior, and Immunity</i> , 2019, 75, 240-250.	2.0	112
3402	Effect of dietary L-tryptophan on the survival, immune response and gut microbiota of the Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 1007-1017.	1.6	32
3403	Arbuscular mycorrhizal fungi and the associated bacterial community influence the uptake of cadmium in rice. <i>Geoderma</i> , 2019, 337, 749-757.	2.3	88
3404	Prokaryotic Diversity and Distribution in Different Habitats of an Alpine Rock Glacier-Pond System. <i>Microbial Ecology</i> , 2019, 78, 70-84.	1.4	12
3405	Antenatal Microbial Colonization of Mammalian Gut. <i>Reproductive Sciences</i> , 2019, 26, 1045-1053.	1.1	33
3406	Secondary successional forests undergo tightly-coupled changes in soil microbial community structure and soil organic matter. <i>Soil Biology and Biochemistry</i> , 2019, 128, 56-65.	4.2	91
3407	The Mouse Microbiome Is Required for Sex-Specific Diurnal Rhythms of Gene Expression and Metabolism. <i>Cell Metabolism</i> , 2019, 29, 362-382.e8.	7.2	178
3408	The role of gut microbiome and its interaction with arsenic exposure in carotid intima-media thickness in a Bangladesh population. <i>Environment International</i> , 2019, 123, 104-113.	4.8	30
3409	Koumiss consumption modulates gut microbiota, increases plasma high density cholesterol, decreases immunoglobulin G and albumin. <i>Journal of Functional Foods</i> , 2019, 52, 469-478.	1.6	38
3410	Molecular analysis of bacterial contamination on stethoscopes in an intensive care unit. <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 171-177.	1.0	25
3411	Effects of <i>Panax ginseng</i> polysaccharides on the gut microbiota in mice with antibiotic-associated diarrhea. <i>International Journal of Biological Macromolecules</i> , 2019, 124, 931-937.	3.6	94
3412	Danshen can interact with intestinal bacteria from normal and chronic renal failure rats. <i>Biomedicine and Pharmacotherapy</i> , 2019, 109, 1758-1771.	2.5	22

#	ARTICLE	IF	CITATIONS
3413	Resuscitation of anammox bacteria after >10,000 years of dormancy. ISME Journal, 2019, 13, 1098-1109.	4.4	51
3414	Reduced skin bacterial diversity correlates with increased pathogen infection intensity in an endangered amphibian host. Molecular Ecology, 2019, 28, 127-140.	2.0	41
3415	Penicillin Trunk Injection Affects Bacterial Community Structure in Citrus Trees. Microbial Ecology, 2019, 78, 457-469.	1.4	17
3416	Use of autochthonous mesophilic lactic acid bacteria as starter cultures for making Pecorino Crotonese cheese: Effect on compositional, microbiological and biochemical attributes. Food Research International, 2019, 116, 1344-1356.	2.9	35
3417	Mapping the Environmental Microbiome. , 2019, , 17-28.		1
3418	Dibutyl phthalate contamination remolded the fungal community in agro-environmental system. Chemosphere, 2019, 215, 189-198.	4.2	27
3419	Structural and functional profiles of the gut microbial community in polycystic ovary syndrome with insulin resistance (IR-PCOS): a pilot study. Research in Microbiology, 2019, 170, 43-52.	1.0	103
3420	Bacterial community diversity in the rhizosphere of nickel hyperaccumulator species of Halmahera Island (Indonesia). Applied Soil Ecology, 2019, 133, 70-80.	2.1	17
3421	Above and belowground biodiversity in adjacent and distinct serpentine soils. Applied Soil Ecology, 2019, 133, 98-103.	2.1	14
3422	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. Schizophrenia Research, 2019, 204, 23-29.	1.1	157
3423	Metagenomic Achievements in Microbial Diversity Determination in Croplands. , 2019, , 15-35.		16
3424	Assessment of the effects of oxamyl on the bacterial community of an agricultural soil exhibiting enhanced biodegradation. Science of the Total Environment, 2019, 651, 1189-1198.	3.9	25
3425	Parallel phylogeography of <i>Prochlorococcus</i> and <i>Synechococcus</i> . ISME Journal, 2019, 13, 430-441.	4.4	55
3426	Comparison of sampling methods for profiling cervicovaginal microbiome in rhesus macaques. Journal of Medical Primatology, 2019, 48, 54-57.	0.3	2
3427	Soil Characteristics Overwhelm Cultivar Effects on the Structure and Assembly of Root-Associated Microbiomes of Modern Maize. Pedosphere, 2019, 29, 360-373.	2.1	37
3428	Application of a novel amplicon-based sequencing approach reveals the diversity of the <i>Bacillus cereus</i> group in stored raw and pasteurized milk. Food Microbiology, 2019, 81, 32-39.	2.1	16
3429	Computational profiling of the gut-brain axis: microflora dysbiosis insights to neurological disorders. Briefings in Bioinformatics, 2019, 20, 825-841.	3.2	27
3430	Fecal <i>Akkermansia muciniphila</i> Is Associated with Body Composition and Microbiota Diversity in Overweight and Obese Women with Breast Cancer Participating in a Presurgical Weight Loss Trial. Journal of the Academy of Nutrition and Dietetics, 2020, 120, 650-659.	0.4	62

#	ARTICLE	IF	CITATIONS
3431	The Effects of Flue Gas Desulphurization Gypsum on the Properties of Dissolved Organic Matter and Bacterial Community During Composting. <i>Waste and Biomass Valorization</i> , 2020, 11, 2039-2046.	1.8	0
3432	Does birth mode modify associations of maternal pre-pregnancy BMI and gestational weight gain with the infant gut microbiome?. <i>International Journal of Obesity</i> , 2020, 44, 23-32.	1.6	37
3433	Amphibian Host and Skin Microbiota Response to a Common Agricultural Antimicrobial and Internal Parasite. <i>Microbial Ecology</i> , 2020, 79, 175-191.	1.4	15
3434	Modulation of cytokine patterns and microbiome during pregnancy in IBD. <i>Gut</i> , 2020, 69, 473-486.	6.1	64
3435	Infants born to mothers with IBD present with altered gut microbiome that transfers abnormalities of the adaptive immune system to germ-free mice. <i>Gut</i> , 2020, 69, 42-51.	6.1	121
3436	Changes induced by heavy metals in the plant-associated microbiome of <i>Miscanthus x giganteus</i> . <i>Science of the Total Environment</i> , 2020, 711, 134433.	3.9	56
3437	High-throughput sequencing approach to characterize dynamic changes of the fungal and bacterial communities during the production of sufu, a traditional Chinese fermented soybean food. <i>Food Microbiology</i> , 2020, 86, 103340.	2.1	52
3438	Seed-Associated Fungal Diversity and the Molecular Identification of <i>Fusarium</i> with Potential Threat to Ginseng (<i>Panax ginseng</i>) in China. <i>Plant Disease</i> , 2020, 104, 330-339.	0.7	7
3439	Comparative analysis of the gut microbiota of the blue fox (<i>Alopex lagopus</i>) and raccoon dog (<i>Nyctereutes procyonoides</i>). <i>Archives of Microbiology</i> , 2020, 202, 135-142.	1.0	12
3440	The effects of artificial light at night on Eurasian tree sparrow (<i>Passer montanus</i>): Behavioral rhythm disruption, melatonin suppression and intestinal microbiota alterations. <i>Ecological Indicators</i> , 2020, 108, 105702.	2.6	28
3441	Isolation of virulent phages infecting dominant mesophilic aerobic bacteria in cucumber pickle fermentation. <i>Food Microbiology</i> , 2020, 86, 103330.	2.1	29
3442	Ectopic osteogenesis by type I collagen loaded with a novel synthesized PTH-related peptide in vivo. <i>Journal of Biomedical Materials Research - Part A</i> , 2020, 108, 166-177.	2.1	12
3443	Exploration of the Vaginal and Gut Microbiome in African American Women by Body Mass Index, Class of Obesity, and Gestational Weight Gain: A Pilot Study. <i>American Journal of Perinatology</i> , 2020, 37, 1160-1172.	0.6	12
3444	Biochar-based organic fertilizer application rates for <i>Tetrastigma hemsleyanum</i> planted under Moso bamboo. <i>Journal of Forestry Research</i> , 2020, 31, 1813-1821.	1.7	8
3445	Dominance of <i>Wolbachia</i> sp. in the deep-sea sediment bacterial metataxonomic sequencing analysis in the Bay of Bengal, Indian Ocean. <i>Genomics</i> , 2020, 112, 1030-1041.	1.3	10
3446	Endosymbiotic Bacteria Are Prevalent and Diverse in Agricultural Spiders. <i>Microbial Ecology</i> , 2020, 79, 472-481.	1.4	26
3447	Fecal Microbiota Transplantation in Pouchitis: Clinical, Endoscopic, Histologic, and Microbiota Results from a Pilot Study. <i>Digestive Diseases and Sciences</i> , 2020, 65, 1099-1106.	1.1	41
3448	MIMIX: A Bayesian Mixed-Effects Model for Microbiome Data From Designed Experiments. <i>Journal of the American Statistical Association</i> , 2020, 115, 599-609.	1.8	19

#	ARTICLE	IF	CITATIONS
3449	Phosphorus Input Alters the Assembly of Rice (<i>Oryza sativa</i> L.) Root-Associated Communities. <i>Microbial Ecology</i> , 2020, 79, 357-366.	1.4	26
3450	Bacterial Succession in Salt Marsh Soils Along a Short-term Invasion Chronosequence of <i>Spartina alterniflora</i> in the Yellow River Estuary, China. <i>Microbial Ecology</i> , 2020, 79, 644-661.	1.4	33
3451	Culture-independent and dependent evaluation of the equine paranasal sinus microbiota in health and disease. <i>Equine Veterinary Journal</i> , 2020, 52, 455-463.	0.9	11
3452	Diversity and phylogenetic composition of bacterial communities and their association with anthropogenic pollutants in sewage sludge. <i>Chemosphere</i> , 2020, 238, 124629.	4.2	21
3453	Effect of a bioactive product SEL001 from <i>Lactobacillus sakei</i> probio65 on gut microbiota and its anti-colitis effects in a TNBS-induced colitis mouse model. <i>Saudi Journal of Biological Sciences</i> , 2020, 27, 261-270.	1.8	21
3454	Dietary methionyl-methionine supplementation increased growth performance, antioxidant ability, the content of essential amino acids and improved the diversity of intestinal microbiota in Nile tilapia (<i>Oreochromis niloticus</i>). <i>British Journal of Nutrition</i> , 2020, 123, 72-83.	1.2	22
3455	No evidence for phyllosymbiosis in western chipmunk species. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	22
3456	Ambient temperature alters body size and gut microbiota of <i>Xenopus tropicalis</i> . <i>Science China Life Sciences</i> , 2020, 63, 915-925.	2.3	20
3457	Salt is a main factor shaping community composition of arbuscular mycorrhizal fungi along a vegetation successional series in the Yellow River Delta. <i>Catena</i> , 2020, 185, 104318.	2.2	21
3458	eDNA metabarcoding in zooplankton improves the ecological status assessment of aquatic ecosystems. <i>Environment International</i> , 2020, 134, 105230.	4.8	53
3459	Distribution of Protists in the Deep South China Sea Revealed by High-Throughput Sequencing. <i>Journal of Ocean University of China</i> , 2020, 19, 161-170.	0.6	3
3460	Linking rhizosphere soil biochemical and microbial community characteristics across different land use systems in mountainous region in Northeast India. <i>Meta Gene</i> , 2020, 23, 100625.	0.3	12
3461	Composition of the microbial communities in the gastrointestinal tract of perch (<i>Perca</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 Td 2020, 43, 23-38.	0.9	17
3462	Pyrosequencing of the subgingival microbiome in peri-implantitis after non-surgical mechanical debridement therapy. <i>Journal of Periodontal Research</i> , 2020, 55, 238-246.	1.4	10
3463	Dietary Habits of 2- to 9-Year-Old American Children Are Associated with Gut Microbiome Composition. <i>Journal of the Academy of Nutrition and Dietetics</i> , 2020, 120, 517-534.	0.4	34
3464	Locally Adapted <i>Mimulus</i> Ecotypes Differentially Impact Rhizosphere Bacterial and Archaeal Communities in an Environment-Dependent Manner. <i>Phytobiomes Journal</i> , 2020, 4, 53-63.	1.4	6
3465	An adaptive independence test for microbiome community data. <i>Biometrics</i> , 2020, 76, 414-426.	0.8	5
3466	Chemical Modification of Cornstarch by Hydroxypropylation Enhances Cecal Fermentation-Mediated Lipid Metabolism in Rats. <i>Starch/Staerke</i> , 2020, 72, 1900050.	1.1	8

#	ARTICLE	IF	CITATIONS
3467	Long-term exposure of activated sludge in chemostats leads to changes in microbial communities composition and enhanced biodegradation of 4-chloroaniline and N-methylpiperazine. <i>Chemosphere</i> , 2020, 242, 125102.	4.2	12
3468	Diversity and dynamics of microbial communities in brown planthopper at different developmental stages revealed by high-throughput amplicon sequencing. <i>Insect Science</i> , 2020, 27, 883-894.	1.5	28
3469	Pre- and post-serial metagenomic analysis of gut microbiota as a prognostic factor in patients undergoing haematopoietic stem cell transplantation. <i>British Journal of Haematology</i> , 2020, 188, 438-449.	1.2	45
3470	Exercise improves metabolic function and alters the microbiome in rats with gestational diabetes. <i>FASEB Journal</i> , 2020, 34, 1728-1744.	0.2	19
3471	Impact of exogenous nitrogen on the cyanobacterial abundance and community in oil-contaminated sediment: A microcosm study. <i>Science of the Total Environment</i> , 2020, 710, 136296.	3.9	4
3472	DNA sequencing reveals bacterial communities in midgut and other parts of the larvae of <i>Spodoptera exigua</i> Hubner (Lepidoptera: Noctuidae). <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	6
3473	Distinct factors drive the assembly of quinoa-associated microbiomes along elevation. <i>Plant and Soil</i> , 2020, 448, 55-69.	1.8	21
3474	Organic amendment mitigates the negative impacts of mineral fertilization on bacterial communities in Shajiang black soil. <i>Applied Soil Ecology</i> , 2020, 150, 103457.	2.1	24
3475	Superchilling in combination with modified atmosphere packaging resulted in long shelf-life and limited microbial growth in Atlantic cod (<i>Gadus morhua</i> L.) from capture-based-aquaculture in Greenland. <i>Food Microbiology</i> , 2020, 88, 103405.	2.1	28
3476	Altered microbiota composition reflects enhanced communication in 15q11-13 CNV mice. <i>Neuroscience Research</i> , 2020, 161, 59-67.	1.0	8
3477	<i>Bacillus licheniformis</i> fermented products improve growth performance and the fecal microbiota community in broilers. <i>Poultry Science</i> , 2020, 99, 1432-1443.	1.5	67
3478	Altered Fecal Microbiome Years after Traumatic Brain Injury. <i>Journal of Neurotrauma</i> , 2020, 37, 1037-1051.	1.7	60
3479	Disordered cutaneous microbiota in systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2020, 108, 102391.	3.0	35
3480	CXCR3+ T cells in multiple sclerosis correlate with reduced diversity of the gut microbiome. <i>Journal of Translational Autoimmunity</i> , 2020, 3, 100032.	2.0	32
3481	Microbial Community Composition in Deep-Subsurface Reservoir Fluids Reveals Natural Interwell Connectivity. <i>Water Resources Research</i> , 2020, 56, e2019WR025916.	1.7	19
3482	Water quality and associated microbial ecology in selected Alaska Native communities: Challenges in off-the-grid water supplies. <i>Science of the Total Environment</i> , 2020, 711, 134450.	3.9	6
3483	Detection and isolation of protein susceptible indigenous bacteria affected by dietary milk-casein, albumen and soy-protein in the caecum of ICR mice. <i>International Journal of Biological Macromolecules</i> , 2020, 144, 813-820.	3.6	18
3484	Single molecule sequencing reveals response of manganese-oxidizing microbiome to different biofilter media in drinking water systems. <i>Water Research</i> , 2020, 171, 115424.	5.3	26

#	ARTICLE	IF	CITATIONS
3485	High Diversity and Functional Complementation of Alimentary Canal Microbiota Ensure Small Brown Planthopper to Adapt Different Biogeographic Environments. <i>Frontiers in Microbiology</i> , 2020, 10, 2953.	1.5	14
3486	High-throughput sequencing and food microbiology. <i>Advances in Food and Nutrition Research</i> , 2020, 91, 275-300.	1.5	21
3487	Inclusion of the direct-fed microbial <i>Clostridium butyricum</i> in diets for weanling pigs increases growth performance and tends to increase villus height and crypt depth, but does not change intestinal microbial abundance. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	27
3488	Effect of sequestering agents based on a <i>Saccharomyces cerevisiae</i> fermentation product and clay on the ruminal bacterial community of lactating dairy cows challenged with dietary aflatoxin B1. <i>Journal of Dairy Science</i> , 2020, 103, 1431-1447.	1.4	13
3489	Environmental Controls on Microbial Diversity in Arctic Lakes of West Greenland. <i>Microbial Ecology</i> , 2020, 80, 60-72.	1.4	9
3490	Inferential validation and evidence interpretation. , 2020, , 361-380.		0
3491	Sampling, analyzing, and integrating microbiome omics data in a translational clinical setting. , 2020, , 273-279.		0
3492	Influence of terminal electron-accepting conditions on the soil microbial community and degradation of organic contaminants of emerging concern. <i>Science of the Total Environment</i> , 2020, 706, 135327.	3.9	19
3493	The Association Between Smoking and Gut Microbiome in Bangladesh. <i>Nicotine and Tobacco Research</i> , 2020, 22, 1339-1346.	1.4	39
3494	Microbial community dynamics and functional responses that contribute to tolerance of high concentrations of petroleum hydrocarbon. <i>Journal of Chemical Technology and Biotechnology</i> , 2020, 95, 1361-1371.	1.6	3
3495	Reproductive Senescence and Ischemic Stroke Remodel the Gut Microbiome and Modulate the Effects of Estrogen Treatment in Female Rats. <i>Translational Stroke Research</i> , 2020, 11, 812-830.	2.3	36
3496	Response of Rhizobacterial Community to Biochar Amendment in Coal Mining Soils with <i>Brachiaria Decumbens</i> as Pioneer Plant. <i>Soil and Sediment Contamination</i> , 2020, 29, 26-42.	1.1	2
3497	Biogeographical distribution of bacterial communities in saline agricultural soil. <i>Geoderma</i> , 2020, 361, 114095.	2.3	39
3498	Effects of encapsulated cinnamaldehyde and citral on the performance and cecal microbiota of broilers vaccinated or not vaccinated against coccidiosis. <i>Poultry Science</i> , 2020, 99, 936-948.	1.5	43
3499	<i>Clostridium butyricum</i> Modulates the Microbiome to Protect Intestinal Barrier Function in Mice with Antibiotic-Induced Dysbiosis. <i>IScience</i> , 2020, 23, 100772.	1.9	79
3500	Diversity and flexibility of the bacterial communities on <i>Cancer pagurus</i> at different temperatures. <i>Journal of Sea Research</i> , 2020, 156, 101827.	0.6	8
3501	Variation in the Slimy Salamander (<i>Plethodon</i> spp.) Skin and Gut-Microbial Assemblages Is Explained by Geographic Distance and Host Affinity. <i>Microbial Ecology</i> , 2020, 79, 985-997.	1.4	10
3502	Effects of Seasonal Hibernation on the Similarities Between the Skin Microbiota and Gut Microbiota of an Amphibian (<i>Rana dybowskii</i>). <i>Microbial Ecology</i> , 2020, 79, 898-909.	1.4	27

#	ARTICLE	IF	CITATIONS
3503	Optimal Estimation of Wasserstein Distance on a Tree With an Application to Microbiome Studies. <i>Journal of the American Statistical Association</i> , 2021, 116, 1237-1253.	1.8	2
3504	Microbiota associated with the skin, gills, and gut of the fish <i>Parachondrostoma toxostoma</i> from the Rhône basin. <i>Freshwater Biology</i> , 2020, 65, 446-459.	1.2	14
3505	Can fine-scale habitats of limestone outcrops be considered litho-refugia for dry forest tree lineages?. <i>Biodiversity and Conservation</i> , 2020, 29, 1009-1026.	1.2	13
3506	<i>Dynamic Meta-Storms</i> enables comprehensive taxonomic and phylogenetic comparison of shotgun metagenomes at the species level. <i>Bioinformatics</i> , 2020, 36, 2308-2310.	1.8	12
3507	SOD1 deficiency alters gastrointestinal microbiota and metabolites in mice. <i>Experimental Gerontology</i> , 2020, 130, 110795.	1.2	16
3508	Effects of inhaled air pollution on markers of integrity, inflammation, and microbiota profiles of the intestines in Apolipoprotein E knockout mice. <i>Environmental Research</i> , 2020, 181, 108913.	3.7	35
3509	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. <i>Cancer Medicine</i> , 2020, 9, 797-806.	1.3	42
3510	Prenatal low-dose penicillin results in long-term sex-specific changes to murine behaviour, immune regulation, and gut microbiota. <i>Brain, Behavior, and Immunity</i> , 2020, 84, 154-163.	2.0	36
3511	Alteration of Fungal Microbiota After 5-ASA Treatment in UC Patients. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 380-390.	0.9	23
3512	Analysis of Flagellin-Specific Adaptive Immunity Reveals Links to Dysbiosis in Patients With Inflammatory Bowel Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 9, 485-506.	2.3	22
3513	Investigation of direct and indirect transfer of microbiomes between individuals. <i>Forensic Science International: Genetics</i> , 2020, 45, 102212.	1.6	32
3514	Growth performance, immunity and intestinal microbiota of swamp eel (<i>Monopterus albus</i>) fed a diet supplemented with house fly larvae (<i>Musca domestica</i>). <i>Aquaculture Nutrition</i> , 2020, 26, 693-704.	1.1	19
3515	Switching to a Healthy Diet Prevents the Detrimental Effects of Western Diet in a Colitis-Associated Colorectal Cancer Model. <i>Nutrients</i> , 2020, 12, 45.	1.7	12
3516	Gut microbiota degrades toxic isothiocyanates in a flea beetle pest. <i>Molecular Ecology</i> , 2020, 29, 4692-4705.	2.0	39
3517	Gut microbiota composition in obese and non-obese adult relatives from the highlands of Papua New Guinea. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	4
3518	Effects of Sodium Formate and Calcium Propionate Additives on the Fermentation Quality and Microbial Community of Wet Brewers Grains after Short-Term Storage. <i>Animals</i> , 2020, 10, 1608.	1.0	10
3519	You must choose, but choose wisely: Model-based approaches for microbial community analysis. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108042.	4.2	30
3520	Effects of hybrid, kernel maturity, and storage period on the bacterial community in high-moisture and rehydrated corn grain silages. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126131.	1.2	24

#	ARTICLE	IF	CITATIONS
3521	A Diet-Dependent Microbiota Profile Associated with Incident Type 2 Diabetes: From the CORDIOPREV Study. <i>Molecular Nutrition and Food Research</i> , 2020, 64, 2000730.	1.5	7
3522	Sediment-associated bacterial community and predictive functionalities are influenced by choice of 16S ribosomal RNA hypervariable region(s): An amplicon-based diversity study. <i>Genomics</i> , 2020, 112, 4968-4979.	1.3	10
3523	Health and disease markers correlate with gut microbiome composition across thousands of people. <i>Nature Communications</i> , 2020, 11, 5206.	5.8	378
3524	Effects of Dietary Andrographolide Levels on Growth Performance, Antioxidant Capacity, Intestinal Immune Function and Microbioma of Rice Field Eel (<i>Monopterus Albus</i>). <i>Animals</i> , 2020, 10, 1744.	1.0	26
3525	Transfer of environmental microbes to the skin and respiratory tract of humans after urban green space exposure. <i>Environment International</i> , 2020, 145, 106084.	4.8	103
3526	Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. <i>Cell</i> , 2020, 183, 666-683.e17.	13.5	211
3527	Mapping the bacterial metabolic niche space. <i>Nature Communications</i> , 2020, 11, 4887.	5.8	27
3528	Deep insights into the green nitrogen removal by anammox in four full-scale WWTPs treating landfill leachate based on 16S rRNA gene and transcripts by 16S rRNA high-throughput sequencing. <i>Journal of Cleaner Production</i> , 2020, 276, 124176.	4.6	25
3529	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , 2020, 5, .	1.3	20
3530	The <i>Znt7</i> -null mutation has sex dependent effects on the gut microbiota and goblet cell population in the mouse colon. <i>PLoS ONE</i> , 2020, 15, e0239681.	1.1	3
3531	Fecal microbiota transplantation from warthog to pig confirms the influence of the gut microbiota on African swine fever susceptibility. <i>Scientific Reports</i> , 2020, 10, 17605.	1.6	15
3532	Effects of supplementing geese with green sweet sorghum stalks on microbiota in segments of the gastrointestinal tract. <i>South African Journal of Animal Sciences</i> , 2020, 50, 421-433.	0.2	0
3533	Whole kidney bean (<i>Phaseolus vulgaris</i>) and bean hull reduce the total serum cholesterol, modulate the gut microbiota and affect the caecal fermentation in rats. <i>Bioactive Carbohydrates and Dietary Fibre</i> , 2020, 24, 100232.	1.5	16
3534	Preserving Microbial Community Integrity in Oilfield Produced Water. <i>Frontiers in Microbiology</i> , 2020, 11, 581387.	1.5	5
3535	A pioneer calf foetus microbiome. <i>Scientific Reports</i> , 2020, 10, 17712.	1.6	34
3536	The intestinal microbiome, weight, and metabolic changes in women treated by adjuvant chemotherapy for breast and gynecological malignancies. <i>BMC Medicine</i> , 2020, 18, 281.	2.3	19
3537	Dietary Emulsifiers Directly Impact Adherent-Invasive <i>E. Coli</i> Gene Expression to Drive Chronic Intestinal Inflammation. <i>Cell Reports</i> , 2020, 33, 108229.	2.9	66
3538	Evaluating Organism-Wide Changes in the Metabolome and Microbiome following a Single Dose of Antibiotic. <i>MSystems</i> , 2020, 5, .	1.7	6

#	ARTICLE	IF	CITATIONS
3539	Phylogenetic α - and β -diversity elevational gradients reveal consistent patterns of temperate forest community structure. <i>Acta Oecologica</i> , 2020, 109, 103657.	0.5	7
3540	From Sea Surface to Seafloor: A Benthic Allochthonous eDNA Survey for the Abyssal Ocean. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	17
3541	Co-infection of <i>Malassezia sympodialis</i> With Bacterial Pathobionts <i>Pseudomonas aeruginosa</i> or <i>Staphylococcus aureus</i> Leads to Distinct Sinonasal Inflammatory Responses in a Murine Acute Sinusitis Model. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 472.	1.8	15
3542	Maternal influences on oral and faecal microbiota maturation in neonatal calves in beef and dairy production systems. <i>Animal Microbiome</i> , 2020, 2, 31.	1.5	22
3543	Multicenter analysis of sputum microbiota in tuberculosis patients. <i>PLoS ONE</i> , 2020, 15, e0240250.	1.1	10
3544	The effect of protocathechuic acid on the phycosphere in harmful algal bloom species <i>Scrippsiella trochoidea</i> . <i>Aquatic Toxicology</i> , 2020, 227, 105591.	1.9	6
3545	The aging mouse microbiome has obesogenic characteristics. <i>Genome Medicine</i> , 2020, 12, 87.	3.6	29
3546	Early-life gut dysbiosis linked to juvenile mortality in ostriches. <i>Microbiome</i> , 2020, 8, 147.	4.9	30
3547	Temporal dynamics of bacterial communities during seed development and maturation. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	43
3548	Alterations in blood microbiota after colonic cancer surgery. <i>BJS Open</i> , 2020, 4, 1227-1237.	0.7	4
3549	Fermentation profile, microbial populations, taxonomic diversity and aerobic stability of total mixed ration silages based on <i>Cactus</i> and <i>Gliricidia</i> . <i>Journal of Agricultural Science</i> , 2020, 158, 396-405.	0.6	8
3550	The gut microbiome defines social group membership in honey bee colonies. <i>Science Advances</i> , 2020, 6, .	4.7	55
3551	Obesity-induced alterations in the gut microbiome in female mice fed a high-fat diet are antagonized by dietary supplementation with a novel, wax ester-rich, marine oil. <i>Nutrition Research</i> , 2020, 83, 94-107.	1.3	9
3552	Dental black plaque: metagenomic characterization and comparative analysis with white-plaque. <i>Scientific Reports</i> , 2020, 10, 15962.	1.6	5
3553	A novel bioaugmentation technique effectively increases the skin-associated microbial diversity of captive eastern hellbenders. , 2020, 8, coaa040.		3
3554	Impact of <i>PepT1</i> deletion on microbiota composition and colitis requires multiple generations. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 27.	2.9	6
3555	Effects of mixed organic acids and medium chain fatty acids as antibiotic alternatives on the performance, serum immunity, and intestinal health of weaned piglets orally challenged with <i>Escherichia coli</i> K88. <i>Animal Feed Science and Technology</i> , 2020, 269, 114617.	1.1	14
3556	The impact of feed efficiency selection on the ruminal, cecal, and fecal microbiomes of Angus steers from a commercial feedlot. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	23

#	ARTICLE	IF	CITATIONS
3557	Modulation of the bacterial population in commercial cucumber fermentations by brining salt type. <i>Journal of Applied Microbiology</i> , 2020, 128, 1678-1693.	1.4	11
3558	Stochastic Dispersal Rather Than Deterministic Selection Explains the Spatio-Temporal Distribution of Soil Bacteria in a Temperate Grassland. <i>Frontiers in Microbiology</i> , 2020, 11, 1391.	1.5	36
3559	Effects of Zinc Pollution and Compost Amendment on the Root Microbiome of a Metal Tolerant Poplar Clone. <i>Frontiers in Microbiology</i> , 2020, 11, 1677.	1.5	35
3560	Reclamation with organic amendments and plants remodels the diversity and structure of bacterial community in ion-adsorption rare earth element mine tailings. <i>Journal of Soils and Sediments</i> , 2020, 20, 3669-3680.	1.5	14
3561	Gut microbiota in a host-brood parasite system: insights from common cuckoos raised by two warbler species. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9
3562	The sputum microbiome is distinct between COPD and health, independent of smoking history. <i>Respiratory Research</i> , 2020, 21, 183.	1.4	45
3563	Microbiota in the Rhizosphere and Seed of Rice From China, With Reference to Their Transmission and Biogeography. <i>Frontiers in Microbiology</i> , 2020, 11, 995.	1.5	32
3564	The gut microbiota of brood parasite and host nestlings reared within the same environment: disentangling genetic and environmental effects. <i>ISME Journal</i> , 2020, 14, 2691-2702.	4.4	19
3565	Lifestyle preferences drive the structure and diversity of bacterial and archaeal communities in a small riverine reservoir. <i>Scientific Reports</i> , 2020, 10, 11288.	1.6	8
3566	Identification of sulfate-reducing and methanogenic microbial taxa in anaerobic bioreactors from industrial wastewater treatment plants using next-generation sequencing and gene clone library analyses. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2020, 55, 1283-1293.	0.9	5
3567	Oral or Topical Exposure to Glyphosate in Herbicide Formulation Impacts the Gut Microbiota and Survival Rates of Honey Bees. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	78
3568	Host Defense Effectors Expressed by Hemocytes Shape the Bacterial Microbiota From the Scallop Hemolymph. <i>Frontiers in Immunology</i> , 2020, 11, 599625.	2.2	11
3569	Characterization of gut microbiota associated with clinical parameters in intrahepatic cholestasis of pregnancy. <i>BMC Gastroenterology</i> , 2020, 20, 395.	0.8	13
3570	The Response of Estuarine Ammonia-Oxidizing Communities to Constant and Fluctuating Salinity Regimes. <i>Frontiers in Microbiology</i> , 2020, 11, 574815.	1.5	5
3571	Vitamin D metabolites and the gut microbiome in older men. <i>Nature Communications</i> , 2020, 11, 5997.	5.8	88
3572	Highly nutritious diet resists <i>Salmonella Typhimurium</i> infections by improving intestinal microbiota and morphology in broiler chickens. <i>Poultry Science</i> , 2020, 99, 7055-7065.	1.5	20
3573	Effects of dietary fibre and protein content on intestinal fibre degradation, short-chain fatty acid and microbiota composition in a high-fat fructose-rich diet induced obese Göttingen Minipig model. <i>Food and Function</i> , 2020, 11, 10758-10773.	2.1	11
3574	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	1.7	9

#	ARTICLE	IF	CITATIONS
3575	Adjunctive treatment with probiotics partially alleviates symptoms and reduces inflammation in patients with irritable bowel syndrome. <i>European Journal of Nutrition</i> , 2020, 60, 2553-2565.	1.8	31
3576	Phages versus Antibiotics To Treat Infected Diabetic Wounds in a Mouse Model: a Microbiological and Microbiotic Evaluation. <i>MSystems</i> , 2020, 5, .	1.7	14
3577	<i>Saccharomyces cerevisiae</i> Fermentation Product Did Not Attenuate Clinical Signs, but Psyllium Husk Has Protective Effects in a Murine Dextran Sulfate Sodium-Induced Colitis Model. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa159.	0.1	3
3578	Determining Soil Microbial Communities and Their Influence on <i>Ganoderma</i> Disease Incidences in Oil Palm (<i>Elaeis guineensis</i>) via High-Throughput Sequencing. <i>Biology</i> , 2020, 9, 424.	1.3	16
3579	Altitude influences microbial diversity and herbage fermentation in the rumen of yaks. <i>BMC Microbiology</i> , 2020, 20, 370.	1.3	57
3580	Temporal dynamics of the fecal microbiota in veal calves in a 6-month field trial. <i>Animal Microbiome</i> , 2020, 2, 32.	1.5	7
3581	Prokaryotic and Fungal Characterization of the Facilities Used to Assemble, Test, and Launch the OSIRIS-REx Spacecraft. <i>Frontiers in Microbiology</i> , 2020, 11, 530661.	1.5	5
3582	The Domestic Environment and the Lung Mycobiome. <i>Microorganisms</i> , 2020, 8, 1717.	1.6	9
3584	Fine Particulate Matter Exposure Alters Pulmonary Microbiota Composition and Aggravates <i>Pneumococcus</i> -Induced Lung Pathogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 570484.	1.8	23
3585	Microbiome Profiling Reveals Gut Dysbiosis in the Metabotropic Glutamate Receptor 5 Knockout Mouse Model of Schizophrenia. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 582320.	1.8	16
3586	Dynamics of Microbial Community Structure and Ecological Functions in Estuarine Intertidal Sediments. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	17
3587	Chronic G α signaling in AgRP neurons does not cause obesity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20874-20880.	3.3	20
3588	Wastewater treatment and electricity generation from Sugarbeet Processing Wastewater (SBWW) using Microbial Fuel Cell (MFC). , 2020, , .		1
3589	Discovery of Predictors of <i>Mycoplasma hyopneumoniae</i> Vaccine Response Efficiency in Pigs: 16S rRNA Gene Fecal Microbiota Analysis. <i>Microorganisms</i> , 2020, 8, 1151.	1.6	10
3590	Improving Efficiency and Stability of Anammox through Sequentially Coupling Nitritation and Denitritation in a Single-Stage Bioreactor. <i>Environmental Science & Technology</i> , 2020, 54, 10859-10867.	4.6	55
3591	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. <i>Chinese Medical Journal</i> , 2020, 133, 1844-1855.	0.9	55
3592	The Gut Microbiome Associates with Immune Checkpoint Inhibition Outcomes in Patients with Advanced Non-Small Cell Lung Cancer. <i>Cancer Immunology Research</i> , 2020, 8, 1243-1250.	1.6	154
3593	Comparison of microbiota in the cloaca, colon, and magnum of layer chicken. <i>PLoS ONE</i> , 2020, 15, e0237108.	1.1	11

#	ARTICLE	IF	CITATIONS
3594	SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis. BMC Bioinformatics, 2020, 21, 345.	1.2	41
3595	The effects of abiotic and biotic factors on taxonomic and phylogenetic diversity of stream epilithic bacteria around Qiandao Lake. Aquatic Sciences, 2020, 82, 1.	0.6	4
3596	Enhanced biodiversity of gut flora and feed efficiency in pond cultured tilapia under reduced frequency feeding strategies. PLoS ONE, 2020, 15, e0236100.	1.1	16
3597	Changes in sediment microbial diversity following chronic copper-exposure induce community copper-tolerance without increasing sensitivity to arsenic. Journal of Hazardous Materials, 2020, 391, 122197.	6.5	13
3598	Comparative Analysis of Microbial Diversity Across Temperature Gradients in Hot Springs From Yellowstone and Iceland. Frontiers in Microbiology, 2020, 11, 1625.	1.5	48
3599	Evidence of Vent-Adaptation in Sponges Living at the Periphery of Hydrothermal Vent Environments: Ecological and Evolutionary Implications. Frontiers in Microbiology, 2020, 11, 1636.	1.5	15
3600	Spatial Variations in Microbial Compositions in a Karst Critical Zone in Samcheok, Republic of Korea. Applied Sciences (Switzerland), 2020, 10, 4714.	1.3	2
3601	A Shift Pattern of Bacterial Communities Across the Life Stages of the Citrus Red Mite, Panonychus citri. Frontiers in Microbiology, 2020, 11, 1620.	1.5	7
3602	Oral Microbiome Metabarcoding in Two Invasive Small Mammals from New Zealand. Diversity, 2020, 12, 278.	0.7	2
3603	Respiratory microbiota of humpback whales may be reduced in diversity and richness the longer they fast. Scientific Reports, 2020, 10, 12645.	1.6	15
3604	Impact of Glyphosate on the Honey Bee Gut Microbiota: Effects of Intensity, Duration, and Timing of Exposure. MSystems, 2020, 5, .	1.7	55
3605	Schizasterid Heart Urchins Host Microorganisms in a Digestive Symbiosis of Mesozoic Origin. Frontiers in Microbiology, 2020, 11, 1697.	1.5	4
3606	Melatonin Alleviates Neuroinflammation and Metabolic Disorder in DSS-Induced Depression Rats. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-17.	1.9	56
3607	Method development for cross-study microbiome data mining: Challenges and opportunities. Computational and Structural Biotechnology Journal, 2020, 18, 2075-2080.	1.9	27
3608	The meconium microbiota shares more features with the amniotic fluid microbiota than the maternal fecal and vaginal microbiota. Gut Microbes, 2020, 12, 1794266.	4.3	71
3609	Effect of Choline Forms and Gut Microbiota Composition on Trimethylamine-N-Oxide Response in Healthy Men. Nutrients, 2020, 12, 2220.	1.7	38
3610	Glycosidic Linkage Structures Influence Dietary Fiber Fermentability and Propionate Production by Human Colonic Microbiota In Vitro. Biotechnology Journal, 2020, 15, 1900523.	1.8	7
3611	Bacterial Community Structure Dynamics in <i>Meloidogyne incognita</i> -Infected Roots and Its Role in Worm-Microbiome Interactions. MSphere, 2020, 5, .	1.3	14

#	ARTICLE	IF	CITATIONS
3612	The gut bacterial diversity of sheep associated with different breeds in Qinghai province. <i>BMC Veterinary Research</i> , 2020, 16, 254.	0.7	24
3613	The posthatch prophylactic use of ceftiofur affects the cecal microbiota similar to the dietary sanguinarine supplementation in broilers. <i>Poultry Science</i> , 2020, 99, 6013-6021.	1.5	13
3614	An ambient temperature collection and stabilization strategy for canine microbiota studies. <i>Scientific Reports</i> , 2020, 10, 13383.	1.6	10
3615	Enteric parasitic infection disturbs bacterial structure in Mexican children with autoantibodies for type 1 diabetes and/or celiac disease. <i>Gut Pathogens</i> , 2020, 12, 37.	1.6	5
3616	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea. <i>PLoS ONE</i> , 2020, 15, e0236703.	1.1	28
3617	Associations between Diet, the Gut Microbiome, and Short-Chain Fatty Acid Production among Older Caribbean Latino Adults. <i>Journal of the Academy of Nutrition and Dietetics</i> , 2020, 120, 2047-2060.e6.	0.4	28
3618	Characterization of Cutaneous Bacterial Microbiota from Superficial Pyoderma Forms in Atopic Dogs. <i>Pathogens</i> , 2020, 9, 638.	1.2	31
3619	Mucosal-Associated Microbiota Other Than Luminal Microbiota Has a Close Relationship With Diarrhea-Predominant Irritable Bowel Syndrome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 515614.	1.8	20
3622	Bacterial composition and community structure of the oropharynx of adults with asthma are associated with environmental factors. <i>Microbial Pathogenesis</i> , 2020, 149, 104505.	1.3	7
3623	Bio-priming with a hypovirulent phytopathogenic fungus enhances the connection and strength of microbial interaction network in rapeseed. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 45.	2.9	33
3624	Guiqi Baizhu Decoction Alleviates Radiation Inflammation in Rats by Modulating the Composition of the Gut Microbiota. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	3
3625	Inhibitory Effect of a Microecological Preparation on Azoxymethane/Dextran Sodium Sulfate-Induced Inflammatory Colorectal Cancer in Mice. <i>Frontiers in Oncology</i> , 2020, 10, 562189.	1.3	8
3626	Microbiota profile and efficacy of probiotic supplementation on laxation in adults affected by Prader-Willi Syndrome: A randomized, double-blind, crossover trial. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1535.	0.6	10
3628	Gut dysbiosis associated with the rats' responses in methamphetamine-induced conditioned place preference. <i>Addiction Biology</i> , 2021, 26, e12975.	1.4	22
3629	Strong effects of lab-to-field environmental transitions on the bacterial intestinal microbiota of <i>Mus musculus</i> are modulated by <i>Trichuris muris</i> infection. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	17
3630	Animal and Cellular Studies Demonstrate Some of the Beneficial Impacts of Herring Milt Hydrolysates on Obesity-Induced Glucose Intolerance and Inflammation. <i>Nutrients</i> , 2020, 12, 3235.	1.7	11
3631	Teaching Microbiome Analysis: From Design to Computation Through Inquiry. <i>Frontiers in Microbiology</i> , 2020, 11, 528051.	1.5	2
3632	<i>Streptococcus thermophilus</i> DMST-H2 Promotes Recovery in Mice with Antibiotic-Associated Diarrhea. <i>Microorganisms</i> , 2020, 8, 1650.	1.6	18

#	ARTICLE	IF	CITATIONS
3633	Compositional and Functional Comparisons of the Microbiota in the Colostrum and Mature Milk of Dairy Goats. <i>Animals</i> , 2020, 10, 1955.	1.0	9
3634	Parallel and non-parallel changes of the gut microbiota during trophic diversification in repeated young adaptive radiations of sympatric cichlid fish. <i>Microbiome</i> , 2020, 8, 149.	4.9	13
3635	Prebiotic effects of yeast mannan, which selectively promotes <i>Bacteroides thetaiotaomicron</i> and <i>Bacteroides ovatus</i> in a human colonic microbiota model. <i>Scientific Reports</i> , 2020, 10, 17351.	1.6	37
3636	The entomophagous caterpillar fungus <i>Ophiocordyceps sinensis</i> is consumed by its lepidopteran host as a plant endophyte. <i>Fungal Ecology</i> , 2020, 47, 100989.	0.7	26
3637	Gut microbiome adaptation to extreme cold winter in wild plateau pika (<i>Ochotona curzoniae</i>) on the Qinghai-Tibet Plateau. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	14
3638	Host Genetic Background and Gut Microbiota Contribute to Differential Metabolic Responses to Fructose Consumption in Mice. <i>Journal of Nutrition</i> , 2020, 150, 2716-2728.	1.3	15
3639	Effects of metronidazole on the fecal microbiome and metabolome in healthy dogs. <i>Journal of Veterinary Internal Medicine</i> , 2020, 34, 1853-1866.	0.6	103
3640	Effects of eradication of <i>Helicobacter pylori</i> on oral malodor and the oral environment: a single-center observational study. <i>BMC Research Notes</i> , 2020, 13, 406.	0.6	4
3641	Crab shell amendments enhance the abundance and diversity of key microbial groups in sulfate-reducing columns treating acid mine drainage. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 8505-8516.	1.7	3
3642	Nutrient Capture from Aqueous Waste and Photocontrolled Fertilizer Delivery to Tomato Plants Using Fe(III)-Polysaccharide Hydrogels. <i>ACS Omega</i> , 2020, 5, 23009-23020.	1.6	7
3643	Influences of claywater and greenwater on the skin microbiome of cultured larval sablefish (<i>Anoplopoma fimbria</i>). <i>Animal Microbiome</i> , 2020, 2, 27.	1.5	5
3644	Gut bacterial communities and their contribution to performance of specialist <i>Altica</i> flea beetles. <i>Microbial Ecology</i> , 2020, 80, 946-959.	1.4	6
3645	Poorly known microbial taxa dominate the microbiome of hypersaline Sambhar Lake salterns in India. <i>Extremophiles</i> , 2020, 24, 875-885.	0.9	15
3646	Laboratory Analysis Techniques for the Perinatal Microbiome. <i>Journal of Perinatal and Neonatal Nursing</i> , 2020, 34, 239-250.	0.5	2
3647	Fungal diversity in deep-sea sediments from the Magellan seamounts as revealed by a metabarcoding approach targeting the ITS2 regions. <i>Mycology</i> , 2020, 11, 214-229.	2.0	16
3648	Modulation of gut mucosal microbiota as a mechanism of probiotics-based adjunctive therapy for ulcerative colitis. <i>Microbial Biotechnology</i> , 2020, 13, 2032-2043.	2.0	45
3649	Dysbiosis of Gut Microbiota and Short-Chain Fatty Acids in Encephalitis: A Chinese Pilot Study. <i>Frontiers in Immunology</i> , 2020, 11, 1994.	2.2	21
3650	Multiple omics analysis reveals that high fiber diets promote gluconeogenesis and inhibit glycolysis in muscle. <i>BMC Genomics</i> , 2020, 21, 660.	1.2	10

#	ARTICLE	IF	CITATIONS
3651	<i>Lactiplantibacillus plantarum</i> WJL administration during pregnancy and lactation improves lipid profile, insulin sensitivity and gut microbiota diversity in dyslipidemic dams and protects male offspring against cardiovascular dysfunction in later life. <i>Food and Function</i> , 2020, 11, 8939-8950.	2.1	27
3652	Composition and assembly of bacterial communities in surface and deeper sediments from aquaculture-influenced sites in Eastern Lake Taihu, China. <i>Aquatic Sciences</i> , 2020, 82, 1.	0.6	10
3653	Multi-omics Approaches To Decipher the Impact of Diet and Host Physiology on the Mammalian Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	24
3654	Antifungal Potential of the Skin Microbiota of Hibernating Big Brown Bats (<i>Eptesicus fuscus</i>) Infected With the Causal Agent of White-Nose Syndrome. <i>Frontiers in Microbiology</i> , 2020, 11, 1776.	1.5	12
3655	Applying the Anna Karenina principle for wild animal gut microbiota: Temporal stability of the bank vole gut microbiota in a disturbed environment. <i>Journal of Animal Ecology</i> , 2020, 89, 2617-2630.	1.3	28
3656	Assessing the Pyloric Caeca and Distal Gut Microbiota Correlation with Flesh Color in Atlantic Salmon (<i>Salmo salar</i> L., 1758). <i>Microorganisms</i> , 2020, 8, 1244.	1.6	15
3657	Assessing the strength and sensitivity of the core microbiota approach on a highly diverse sponge reef. <i>Environmental Microbiology</i> , 2020, 22, 3985-3999.	1.8	12
3658	Root Fungal Endophytes and Microbial Extracellular Enzyme Activities Show Patterned Responses in Tall Fescues under Drought Conditions. <i>Agronomy</i> , 2020, 10, 1076.	1.3	9
3659	Widespread Pig Farming Practice Linked to Shifts in Skin Microbiomes and Disease in Pond-Breeding Amphibians. <i>Environmental Science & Technology</i> , 2020, 54, 11301-11312.	4.6	15
3660	Comparative analysis of racial differences in breast tumor microbiome. <i>Scientific Reports</i> , 2020, 10, 14116.	1.6	37
3661	Strain Structure and Dynamics Revealed by Targeted Deep Sequencing of the Honey Bee Gut Microbiome. <i>MSphere</i> , 2020, 5, .	1.3	19
3662	Characterization of Microbiota in Cancerous Lung and the Contralateral Non-Cancerous Lung Within Lung Cancer Patients. <i>Frontiers in Oncology</i> , 2020, 10, 1584.	1.3	15
3663	The Impact of the Postpartum "Doing-the-Month" Practice on Human Milk Microbiota: A Pilot Study in Taiwan. <i>Microorganisms</i> , 2020, 8, 1283.	1.6	2
3664	Systemically-delivered biodegradable PLGA alters gut microbiota and induces transcriptomic reprogramming in the liver in an obesity mouse model. <i>Scientific Reports</i> , 2020, 10, 13786.	1.6	10
3665	Mining the Microbiome of Key Species from African Savanna Woodlands: Potential for Soil Health Improvement and Plant Growth Promotion. <i>Microorganisms</i> , 2020, 8, 1291.	1.6	11
3666	A Statistical Method for Association Analysis of Cell Type Compositions. <i>Statistics in Biosciences</i> , 2021, 13, 373-385.	0.6	0
3667	Effects of Smoking and Smoking Cessation on the Intestinal Microbiota. <i>Journal of Clinical Medicine</i> , 2020, 9, 2963.	1.0	25
3668	The Effects of Metformin on the Gut Microbiota of Patients with Type 2 Diabetes: A Two-Center, Quasi-Experimental Study. <i>Life</i> , 2020, 10, 195.	1.1	20

#	ARTICLE	IF	CITATIONS
3669	Microbial diversity of the glass sponge <i>Vazella pourtalesii</i> in response to anthropogenic activities. <i>Conservation Genetics</i> , 2020, 21, 1001-1010.	0.8	11
3670	Impact and consequences of intensive chemotherapy on intestinal barrier and microbiota in acute myeloid leukemia: the role of mucosal strengthening. <i>Gut Microbes</i> , 2020, 12, 1800897.	4.3	38
3671	Rumen Microbiome and Metabolome of Tibetan Sheep (<i>Ovis aries</i>) Reflect Animal Age and Nutritional Requirement. <i>Frontiers in Veterinary Science</i> , 2020, 7, 609.	0.9	25
3672	Integration of molecular profiles in a longitudinal wellness profiling cohort. <i>Nature Communications</i> , 2020, 11, 4487.	5.8	66
3673	Genomic Sequencing Reveals the Diversity of Seminal Bacteria and Relationships to Reproductive Potential in Boar Sperm. <i>Frontiers in Microbiology</i> , 2020, 11, 1873.	1.5	17
3674	Maternal gut microbes shape the early-life assembly of gut microbiota in passerine chicks via nests. <i>Microbiome</i> , 2020, 8, 129.	4.9	40
3675	Belowground impacts of alpine woody encroachment are determined by plant traits, local climate, and soil conditions. <i>Global Change Biology</i> , 2020, 26, 7112-7127.	4.2	26
3676	An intact gut microbiome protects genetically predisposed mice against leukemia. <i>Blood</i> , 2020, 136, 2003-2017.	0.6	64
3677	Abrupt dietary changes between grass and hay alter faecal microbiota of ponies. <i>PLoS ONE</i> , 2020, 15, e0237869.	1.1	16
3678	Learning machine approach reveals microbial signatures of diet and sex in dog. <i>PLoS ONE</i> , 2020, 15, e0237874.	1.1	18
3679	Oral administration of <i>Flavonifractor plautii</i> attenuates inflammatory responses in obese adipose tissue. <i>Molecular Biology Reports</i> , 2020, 47, 6717-6725.	1.0	30
3680	Spider phyllosymbiosis: divergence of widow spider species and their tissues' microbiomes. <i>BMC Evolutionary Biology</i> , 2020, 20, 104.	3.2	14
3681	Microbe-Metabolite Associations Linked to the Rebounding Murine Gut Microbiome Postcolonization with Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>MSystems</i> , 2020, 5, .	1.7	3
3682	Dietary Supplementation with Sugar Beet Fructooligosaccharides and Garlic Residues Promotes Growth of Beneficial Bacteria and Increases Weight Gain in Neonatal Lambs. <i>Biomolecules</i> , 2020, 10, 1179.	1.8	4
3683	Dietary prebiotics promote intestinal <i>Prevotella</i> in association with a low-responding phenotype in a murine oxazolone-induced model of atopic dermatitis. <i>Scientific Reports</i> , 2020, 10, 21204.	1.6	17
3684	Compositional Shift of Oral Microbiota Following Surgical Resection of Tongue Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 600884.	1.8	13
3685	Comparative Analysis of the Gut Microbial Communities of the Eurasian Kestrel (<i>Falco tinnunculus</i>) at Different Developmental Stages. <i>Frontiers in Microbiology</i> , 2020, 11, 592539.	1.5	15
3686	Taxonomic and phylogenetic beta diversity of cricetid rodents in Oaxaca, southern Mexico. <i>Journal of Mammalogy</i> , 2020, 101, 1451-1462.	0.6	1

#	ARTICLE	IF	CITATIONS
3687	Characterization of <i>Clostridioides difficile</i> Strains, the Disease Severity, and the Microbial Changes They Induce. <i>Journal of Clinical Medicine</i> , 2020, 9, 4099.	1.0	5
3688	Gut Microbial Dysbiosis and Plasma Metabolic Profile in Individuals With Vitiligo. <i>Frontiers in Microbiology</i> , 2020, 11, 592248.	1.5	22
3689	Austrian Raw-Milk Hard-Cheese Ripening Involves Successional Dynamics of Non-Inoculated Bacteria and Fungi. <i>Foods</i> , 2020, 9, 1851.	1.9	13
3690	Comparative Microbiome and Metabolome Analyses of the Marine Tunicate <i>Ciona intestinalis</i> from Native and Invaded Habitats. <i>Microorganisms</i> , 2020, 8, 2022.	1.6	17
3691	The Role of Symbiotic Microorganisms, Nutrient Uptake and Rhizosphere Bacterial Community in Response of Pea (<i>Pisum sativum</i> L.) Genotypes to Elevated Al Concentrations in Soil. <i>Plants</i> , 2020, 9, 1801.	1.6	12
3692	Exopolysaccharide Producing <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Strains Modify the Intestinal Microbiota and the Plasmatic Cytokine Levels of BALB/c Mice According to the Type of Polymer Synthesized. <i>Frontiers in Microbiology</i> , 2020, 11, 601233.	1.5	5
3693	Alterations in the Gut Microbiota of Zebrafish (<i>Danio rerio</i>) in Response to Water-Soluble Crude Oil Components and Its Mixture With a Chemical Dispersant. <i>Frontiers in Public Health</i> , 2020, 8, 584953.	1.3	11
3694	Microbiome Analysis from Paired Mucosal and Fecal Samples of a Colorectal Cancer Biobank. <i>Cancers</i> , 2020, 12, 3702.	1.7	15
3695	Host-Specificity and Core Taxa of Seagrass Leaf Microbiome Identified Across Tissue Age and Geographical Regions. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	12
3696	Vitamin A Deficiency in the Early-Life Periods Alters a Diversity of the Colonic Mucosal Microbiota in Rats. <i>Frontiers in Nutrition</i> , 2020, 7, 580780.	1.6	11
3697	Microbiota Features Associated With a High-Fat/Low-Fiber Diet in Healthy Adults. <i>Frontiers in Nutrition</i> , 2020, 7, 583608.	1.6	67
3698	The Effects of a Ketogenic Medium-Chain Triglyceride Diet on the Feces in Dogs With Idiopathic Epilepsy. <i>Frontiers in Veterinary Science</i> , 2020, 7, 541547.	0.9	14
3699	Gut microbiota composition and metabolomic profiles of wild and captive Chinese monals (<i>Lophophorus lhuysii</i>). <i>Frontiers in Zoology</i> , 2020, 17, 36.	0.9	6
3700	Characterization of Bacterial Community, Ammonia-Oxidizing Bacteria, and <i>Nitrospira</i> During the Operation of a Commercial-Scale Recirculating Aquaculture System for Culturing Pufferfish <i>Takifugu rubripes</i> . <i>Journal of Ocean University of China</i> , 2020, 19, 1399-1408.	0.6	2
3701	Microbial community structure across grazing treatments and environmental gradients in the Serengeti. <i>Soil Ecology Letters</i> , 2020, , 1.	2.4	2
3702	The microbiota of the <i>Lasius fuliginosus</i> – <i>Pella laticollis</i> myrmecophilous interaction. , 2020, 87, 754-769.		2
3703	Social isolation alters behavior, the gut-immune-brain axis, and neurochemical circuits in male and female prairie voles. <i>Neurobiology of Stress</i> , 2020, 13, 100278.	1.9	42
3704	Stratification of athletes' gut microbiota: the multifaceted hubs associated with dietary factors, physical characteristics and performance. <i>Gut Microbes</i> , 2020, 12, 1842991.	4.3	40

#	ARTICLE	IF	CITATIONS
3705	Short-Chain Fatty Acid-Producing Gut Microbiota Is Decreased in Parkinson's Disease but Not in Rapid-Eye-Movement Sleep Behavior Disorder. <i>MSystems</i> , 2020, 5, .	1.7	63
3706	Comparison of peri-implant submucosal microbiota in arches with zirconia or titanium implant-supported fixed complete dental prostheses: a study protocol for a randomized controlled trial. <i>Trials</i> , 2020, 21, 979.	0.7	3
3707	Identification of the gut microbiota biomarkers associated with heat cycle and failure to enter oestrus in gilts. <i>Microbial Biotechnology</i> , 2021, 14, 1316-1330.	2.0	9
3708	Organic Matter Composition at Ocean Station Papa Affects Its Bioavailability, Bacterioplankton Growth Efficiency and the Responding Taxa. <i>Frontiers in Marine Science</i> , 2021, 7, .	1.2	17
3709	Coral Microbiomes Demonstrate Flexibility and Resilience Through a Reduction in Community Diversity Following a Thermal Stress Event. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	34
3710	Inoculation With the Plant-Growth-Promoting Rhizobacterium <i>Pseudomonas fluorescens</i> LBUM677 Impacts the Rhizosphere Microbiome of Three Oilseed Crops. <i>Frontiers in Microbiology</i> , 2020, 11, 569366.	1.5	23
3711	Effect of polyphenols isolated from purple sweet potato (<i>Ipomoea batatas</i> cv. Ayamurasaki) on the microbiota and the biomarker of colonic fermentation in rats fed with cellulose or inulin. <i>Food and Function</i> , 2020, 11, 10182-10192.	2.1	16
3712	Effect of the similarity of gut microbiota composition between donor and recipient on graft function after living donor kidney transplantation. <i>Scientific Reports</i> , 2020, 10, 18881.	1.6	8
3713	The Southern Bluefin Tuna Mucosal Microbiome Is Influenced by Husbandry Method, Net Pen Location, and Anti-parasite Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 2015.	1.5	12
3714	Vaginal Microbiota Is Stable throughout the Estrous Cycle in Arabian Mares. <i>Animals</i> , 2020, 10, 2020.	1.0	27
3715	Diet Influences the Oral Microbiota of Infants during the First Six Months of Life. <i>Nutrients</i> , 2020, 12, 3400.	1.7	25
3716	Clustering on Human Microbiome Sequencing Data: A Distance-Based Unsupervised Learning Model. <i>Microorganisms</i> , 2020, 8, 1612.	1.6	4
3717	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.	1.2	16
3718	The relationship between cigarette smoking and the tongue microbiome in an East Asian population. <i>Journal of Oral Microbiology</i> , 2020, 12, 1742527.	1.2	18
3719	Gut microbiota dysbiosis in preeclampsia patients in the second and third trimesters. <i>Chinese Medical Journal</i> , 2020, 133, 1057-1065.	0.9	31
3720	Temporal Dynamics of Bacterial Communities in a Pilot-Scale Vermireactor Fed with Distilled Grape Marc. <i>Microorganisms</i> , 2020, 8, 642.	1.6	14
3721	The effects of waste sorting in environmental microbiome, THP-1 cell viability and inflammatory responses. <i>Environmental Research</i> , 2020, 185, 109450.	3.7	15
3722	Planting <i>Spartina alterniflora</i> in a salt marsh denuded of vegetation by an oil spill induces a rapid response in the soil microbial community. <i>Ecological Engineering</i> , 2020, 151, 105815.	1.6	15

#	ARTICLE	IF	CITATIONS
3723	The microbiome of alpine snow algae shows a specific inter-kingdom connectivity and algae-bacteria interactions with supportive capacities. <i>ISME Journal</i> , 2020, 14, 2197-2210.	4.4	46
3724	Stable and transient structural variation in lemur vaginal, labial and axillary microbiomes: patterns by species, body site, ovarian hormones and forest access. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	10
3725	Digital Proxy of a Bio-Reactor (DIYBOT) combines sensor data and data analytics to improve greywater treatment and wastewater management systems. <i>Scientific Reports</i> , 2020, 10, 8015.	1.6	7
3726	Synergistic depletion of gut microbial consortia, but not individual antibiotics, reduces amyloidosis in APPPS1-21 Alzheimer's transgenic mice. <i>Scientific Reports</i> , 2020, 10, 8183.	1.6	51
3727	Continental-Scale Microbiome Study Reveals Different Environmental Characteristics Determining Microbial Richness, Composition, and Quantity in Hotel Rooms. <i>MSystems</i> , 2020, 5, .	1.7	20
3728	Influence of the FIV Status and Chronic Gingivitis on Feline Oral Microbiota. <i>Pathogens</i> , 2020, 9, 383.	1.2	14
3729	Contrasting Patterns in Diversity and Community Assembly of <i>Phragmites australis</i> Root-Associated Bacterial Communities from Different Seasons. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	39
3730	Antibiotic exposure postweaning disrupts the neurochemistry and function of enteric neurons mediating colonic motor activity. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 318, G1042-G1053.	1.6	27
3731	Dietary Soluble and Insoluble Fiber With or Without Enzymes Altered the Intestinal Microbiota in Weaned Pigs Challenged With Enterotoxigenic <i>E. coli</i> F18. <i>Frontiers in Microbiology</i> , 2020, 11, 1110.	1.5	31
3732	Effects of carbon source addition on microbial community and water quality in recirculating aquaculture systems for <i>Litopenaeus vannamei</i> . <i>Fisheries Science</i> , 2020, 86, 507-517.	0.7	11
3733	Microbial diversity analysis of jiaoke from Xilingol, Inner Mongolia. <i>Journal of Dairy Science</i> , 2020, 103, 5893-5905.	1.4	1
3734	Traditional rice beer depletes butyric acid-producing gut bacteria <i>Faecalibacterium</i> and <i>Roseburia</i> along with fecal butyrate levels in the ethnic groups of Northeast India. <i>3 Biotech</i> , 2020, 10, 283.	1.1	9
3735	Effect of <i>Ganoderma lucidum</i> extract on growth performance, fecal microbiota, and bursal transcriptome of broilers. <i>Animal Feed Science and Technology</i> , 2020, 267, 114551.	1.1	10
3736	Analysis of immune, microbiota and metabolome maturation in infants in a clinical trial of <i>Lactobacillus paracasei</i> CBAÄL74-fermented formula. <i>Nature Communications</i> , 2020, 11, 2703.	5.8	45
3737	Gut Microbial Metabolites Induce Donor-Specific Tolerance of Kidney Allografts through Induction of T Regulatory Cells by Short-Chain Fatty Acids. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 1445-1461.	3.0	50
3738	C:N:P stoichiometry regulates soil organic carbon mineralization and concomitant shifts in microbial community composition in paddy soil. <i>Biology and Fertility of Soils</i> , 2020, 56, 1093-1107.	2.3	112
3739	Greenhouse gas emissions and soil bacterial community as affected by biochar amendments after periodic mineral fertilizer applications. <i>Biology and Fertility of Soils</i> , 2020, 56, 907-925.	2.3	33
3740	Modeling microbial growth in carpet dust exposed to diurnal variations in relative humidity using the 'Time-of-Wetness' framework. <i>Indoor Air</i> , 2020, 30, 978-992.	2.0	15

#	ARTICLE	IF	CITATIONS
3741	Esophageal microbiome signature in patients with Barrett's esophagus and esophageal adenocarcinoma. <i>PLoS ONE</i> , 2020, 15, e0231789.	1.1	58
3742	Intensive land uses modify assembly process and potential metabolic function of edaphic bacterial communities in the Yellow River Delta, China. <i>Science of the Total Environment</i> , 2020, 720, 137713.	3.9	11
3743	Insights into the Function and Horizontal Transfer of Isoproturon Degradation Genes (<i>pdmAB</i>) in <i>Enterobacteriaceae</i> from the Overlook 10 T	1.4	5
3744	Prokaryotic Diversity and Composition of Sediments From Prydz Bay, the Antarctic Peninsula Region, and the Ross Sea, Southern Ocean. <i>Frontiers in Microbiology</i> , 2020, 11, 783.	1.5	5
3745	Effects of polysaccharide from <i>Pueraria lobata</i> on gut microbiota in mice. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 740-749.	3.6	40
3746	MiDAS 3: An ecosystem-specific reference database, taxonomy and knowledge platform for activated sludge and anaerobic digesters reveals species-level microbiome composition of activated sludge. <i>Water Research</i> , 2020, 182, 115955.	5.3	175
3747	Gut microbiota of invasive bullfrog tadpoles responds more rapidly to temperature than a noninvasive congener. <i>Molecular Ecology</i> , 2020, 29, 2449-2462.	2.0	25
3748	Vaginal Microbiota Changes During Estrous Cycle in Dairy Heifers. <i>Frontiers in Veterinary Science</i> , 2020, 7, 371.	0.9	41
3749	Investigation of the Impacts of Antibiotic Exposure on the Diversity of the Gut Microbiota in Chicks. <i>Animals</i> , 2020, 10, 896.	1.0	18
3750	Anti-atherosclerotic effects of <i>Lactobacillus plantarum</i> ATCC 14917 in ApoE ^{-/-} mice through modulation of proinflammatory cytokines and oxidative stress. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6337-6350.	1.7	32
3751	Spatial heterogeneity of the shorebird gastrointestinal microbiome. <i>Royal Society Open Science</i> , 2020, 7, 191609.	1.1	17
3752	Gut microbiome associations with breast cancer risk factors and tumor characteristics: a pilot study. <i>Breast Cancer Research and Treatment</i> , 2020, 182, 451-463.	1.1	48
3753	Characteristics of spatial and seasonal bacterial community structures in a river under anthropogenic disturbances. <i>Environmental Pollution</i> , 2020, 264, 114818.	3.7	51
3754	The Effects of Tetracycline Residues on the Microbial Community Structure of Tobacco Soil in Pot Experiment. <i>Scientific Reports</i> , 2020, 10, 8804.	1.6	19
3755	Detection and isolation of the typical gut indigenous bacteria from ddY mice fed a casein-beef tallow-based or egg yolk-based diet. <i>Journal of Food Biochemistry</i> , 2020, 44, e13246.	1.2	5
3756	Environmental DNA surveys detect distinct metazoan communities across abyssal plains and seamounts in the western Clarion Clipperton Zone. <i>Molecular Ecology</i> , 2020, 29, 4588-4604.	2.0	50
3757	Fecal microbiota responses to rice RS3 are specific to amylose molecular structure. <i>Carbohydrate Polymers</i> , 2020, 243, 116475.	5.1	52
3758	A practical assessment of nano-phosphate on soybean (<i>Glycine max</i>) growth and microbiome establishment. <i>Scientific Reports</i> , 2020, 10, 9151.	1.6	18

#	ARTICLE	IF	CITATIONS
3759	Impacts of a novel defensive symbiosis on the nematode host microbiome. <i>BMC Microbiology</i> , 2020, 20, 159.	1.3	8
3760	Recovery of Vaginal Microbiota after Standard Treatment for Bacterial Vaginosis Infection: An Observational Study. <i>Microorganisms</i> , 2020, 8, 875.	1.6	17
3761	Characterization of the microbiota of commercially traded finfish fillets. <i>Food Research International</i> , 2020, 137, 109373.	2.9	14
3762	Fat, oil, and grease (FOG) deposits yield higher methane than FOG in anaerobic co-digestion with waste activated sludge. <i>Journal of Environmental Management</i> , 2020, 268, 110708.	3.8	19
3763	Diagnosing bioremediation of crude oil-contaminated soil and related geochemical processes at the field scale through microbial community and functional genes. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	19
3764	Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, <i>Scomber japonicus</i> . <i>MSphere</i> , 2020, 5, .	1.3	49
3765	One year cross-sectional study in adult and neonatal intensive care units reveals the bacterial and antimicrobial resistance genes profiles in patients and hospital surfaces. <i>PLoS ONE</i> , 2020, 15, e0234127.	1.1	18
3766	Human microbiota-transplanted C57BL/6 mice and offspring display reduced establishment of key bacteria and reduced immune stimulation compared to mouse microbiota-transplantation. <i>Scientific Reports</i> , 2020, 10, 7805.	1.6	36
3767	Could the gut microbiota community in the coral trout <i>Plectropomus leopardus</i> (Lacepède) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	11
3768	Effects of Inulin Propionate Ester on Obesity-Related Metabolic Syndrome and Intestinal Microbial Homeostasis in Diet-Induced Obese Mice. <i>ACS Omega</i> , 2020, 5, 12865-12876.	1.6	15
3769	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. <i>Molecular Ecology</i> , 2020, 29, 2521-2534.	2.0	58
3770	GenePiper, a Graphical User Interface Tool for Microbiome Sequence Data Mining. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
3771	Alterations in the Gut Microbiome in the Progression of Cirrhosis to Hepatocellular Carcinoma. <i>MSystems</i> , 2020, 5, .	1.7	55
3772	Taxonomic diversity of sputum microbiome in lung cancer patients and its relationship with chromosomal aberrations in blood lymphocytes. <i>Scientific Reports</i> , 2020, 10, 9681.	1.6	17
3773	Microbiota Composition of Breast Milk from Women of Different Ethnicity from the Manawatu-Wanganui Region of New Zealand. <i>Nutrients</i> , 2020, 12, 1756.	1.7	10
3774	Microbial diversity from the continental shelf regions of the Eastern Arabian Sea: A metagenomic approach. <i>Saudi Journal of Biological Sciences</i> , 2020, 27, 2065-2075.	1.8	15
3775	In vitro fermentation potential of the residue of Korean red ginseng root in a mixed culture of swine faecal bacteria. <i>Food and Function</i> , 2020, 11, 6202-6214.	2.1	8
3776	Investigation of Intestinal Microbiota and Fecal Calprotectin in Non-Toxigenic and Toxigenic <i>Clostridioides difficile</i> Colonization and Infection. <i>Microorganisms</i> , 2020, 8, 882.	1.6	8

#	ARTICLE	IF	CITATIONS
3777	Habitat Disturbances Modulate the Barrier Effect of Resident Soil Microbiota on <i>Listeria monocytogenes</i> Invasion Success. <i>Frontiers in Microbiology</i> , 2020, 11, 927.	1.5	14
3778	Microbial Communities in Partially and Fully Treated Effluent of Three Nitrogen-Removing Biofilters. <i>Journal of Sustainable Water in the Built Environment</i> , 2020, 6, 04020010.	0.9	7
3779	Growth performance, breast yield, gastrointestinal ecology and plasma biochemical profile in broiler chickens fed multiple doses of a blend of red, brown and green seaweeds. <i>British Poultry Science</i> , 2020, 61, 590-598.	0.8	12
3780	The protective effect of <i>Bifidobacterium bifidum</i> G9-1 against mucus degradation by <i>Akkermansia muciniphila</i> following small intestine injury caused by a proton pump inhibitor and aspirin. <i>Gut Microbes</i> , 2020, 11, 1385-1404.	4.3	40
3781	Spatial Compartmentalization of the Microbiome between the Lumen and Crypts Is Lost in the Murine Cecum following the Process of Surgery, Including Overnight Fasting and Exposure to Antibiotics. <i>MSystems</i> , 2020, 5, .	1.7	21
3782	Biotic and Environmental Drivers of Plant Microbiomes Across a Permafrost Thaw Gradient. <i>Frontiers in Microbiology</i> , 2020, 11, 796.	1.5	20
3783	Persistence of a Core Microbiome Through the Ontogeny of a Multi-Host Parasite. <i>Frontiers in Microbiology</i> , 2020, 11, 954.	1.5	26
3784	Effect of Alfalfa Hay and Starter Feeding Intervention on Gastrointestinal Microbial Community, Growth and Immune Performance of Yak Calves. <i>Frontiers in Microbiology</i> , 2020, 11, 994.	1.5	27
3785	Contrasting Community Composition of Active Microbial Eukaryotes in Melt Ponds and Sea Water of the Arctic Ocean Revealed by High Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 1170.	1.5	13
3786	Association of the Salivary Microbiome With Animal Contact During Early Life and Stress-Induced Immune Activation in Healthy Participants. <i>Frontiers in Psychiatry</i> , 2020, 11, 353.	1.3	3
3787	Puffer Fish Gut Microbiota Studies Revealed Unique Bacterial Co-Occurrence Patterns and New Insights on Tetrodotoxin Producers. <i>Marine Drugs</i> , 2020, 18, 278.	2.2	12
3788	New Soil, Old Plants, and Ubiquitous Microbes: Evaluating the Potential of Incipient Basaltic Soil to Support Native Plant Growth and Influence Belowground Soil Microbial Community Composition. <i>Sustainability</i> , 2020, 12, 4209.	1.6	2
3789	Seasonal contamination of well-water in flood-prone colonias and other unincorporated U.S. communities. <i>Science of the Total Environment</i> , 2020, 740, 140111.	3.9	14
3790	The day-to-day stability of the ruminal and fecal microbiota in lactating dairy cows. <i>MicrobiologyOpen</i> , 2020, 9, e990.	1.2	30
3791	Short-term effects of biochar and <i>Bacillus pumilus</i> TUAT-1 on the growth of forage rice and its associated soil microbial community and soil properties. <i>Biology and Fertility of Soils</i> , 2020, 56, 481-497.	2.3	23
3792	Joining Illumina paired-end reads for classifying phylogenetic marker sequences. <i>BMC Bioinformatics</i> , 2020, 21, 105.	1.2	18
3793	Alterations in Gut Microbiota of Gestational Diabetes Patients During the First Trimester of Pregnancy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 58.	1.8	64
3794	In situ Linkage of Fungal and Bacterial Proliferation to Microbiologically Influenced Corrosion in B20 Biodiesel Storage Tanks. <i>Frontiers in Microbiology</i> , 2020, 11, 167.	1.5	24

#	ARTICLE	IF	CITATIONS
3795	Physiological and gut microbiome changes associated with low dietary protein level in genetically improved farmed tilapia (GIFT, <i>Oreochromis niloticus</i>) determined by 16S rRNA sequence analysis. <i>MicrobiologyOpen</i> , 2020, 9, e1000.	1.2	22
3796	16S rRNA Gene-Based Analysis Reveals the Effects of Gestational Diabetes on the Gut Microbiota of Mice During Pregnancy. <i>Indian Journal of Microbiology</i> , 2020, 60, 239-245.	1.5	8
3797	A bird's-eye view of phyllosymbiosis: weak signatures of phyllosymbiosis among all 15 species of cranes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192988.	1.2	31
3798	High Diversity of Testate Amoebae (Amoebozoa, Arcellinida) Detected by HTS Analyses in a New England Fen using Newly Designed Taxon-specific Primers. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 450-462.	0.8	9
3799	Fecal microbiota transplantation for the improvement of metabolism in obesity: The FMT-TRIM double-blind placebo-controlled pilot trial. <i>PLoS Medicine</i> , 2020, 17, e1003051.	3.9	177
3800	Exploring intestinal microbiome composition in three Indian major carps under polyculture system: A high-throughput sequencing based approach. <i>Aquaculture</i> , 2020, 524, 735206.	1.7	18
3801	Disrupted tongue microbiota and detection of nonindigenous bacteria on the day of allogeneic hematopoietic stem cell transplantation. <i>PLoS Pathogens</i> , 2020, 16, e1008348.	2.1	22
3802	Optimization of Preservation Methods Allows Deeper Insights into Changes of Raw Milk Microbiota. <i>Microorganisms</i> , 2020, 8, 368.	1.6	9
3803	Impact of global PTP1B deficiency on the gut barrier permeability during NASH in mice. <i>Molecular Metabolism</i> , 2020, 35, 100954.	3.0	11
3804	Long-term CO ₂ enrichment alters the diversity and function of the microbial community in soils with high organic carbon. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107780.	4.2	33
3805	Bacterial community structure correlates with <i>Legionella pneumophila</i> colonization of New York City high rise building premises plumbing systems. <i>Environmental Science: Water Research and Technology</i> , 2020, 6, 1324-1335.	1.2	6
3806	Carbonate facies-specific stable isotope data record climate, hydrology, and microbial communities in Great Salt Lake, UT. <i>Geobiology</i> , 2020, 18, 566-593.	1.1	27
3807	Under the Christmas Tree: Belowground Bacterial Associations With <i>Abies nordmanniana</i> Across Production Systems and Plant Development. <i>Frontiers in Microbiology</i> , 2020, 11, 198.	1.5	9
3808	Microbiome Profile of Deep Endometriosis Patients: Comparison of Vaginal Fluid, Endometrium and Lesion. <i>Diagnostics</i> , 2020, 10, 163.	1.3	57
3809	Soil Microbial Diversity Affects the Plant-Root Colonization by Arbuscular Mycorrhizal Fungi. <i>Microbial Ecology</i> , 2021, 82, 100-103.	1.4	25
3810	Microbiologically influenced corrosion as a function of environmental conditions: A laboratory study using oilfield multispecies biofilms. <i>Corrosion Science</i> , 2020, 169, 108595.	3.0	27
3811	Microbiomes in the insectivorous bat species <i>Mops condylurus</i> rapidly converge in captivity. <i>PLoS ONE</i> , 2020, 15, e0223629.	1.1	17
3812	Maternal exposure to a human relevant mixture of persistent organic pollutants reduces colorectal carcinogenesis in A/J Min/+ mice. <i>Chemosphere</i> , 2020, 252, 126484.	4.2	8

#	ARTICLE	IF	CITATIONS
3813	Cultivating the Macroalgal Holobiont: Effects of Integrated Multi-Trophic Aquaculture on the Microbiome of <i>Ulva rigida</i> (Chlorophyta). <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	61
3814	Probiotic-directed modulation of gut microbiota is basal microbiome dependent. <i>Gut Microbes</i> , 2020, 12, 1736974.	4.3	69
3815	Microbiota Stability and Gastrointestinal Tolerance in Response to a High-Protein Diet with and without a Prebiotic, Probiotic, and Synbiotic: A Randomized, Double-Blind, Placebo-Controlled Trial in Older Women. <i>Journal of the Academy of Nutrition and Dietetics</i> , 2020, 120, 500-516.e10.	0.4	39
3816	Biochars improve tomato and sweet pepper performance and shift bacterial composition in a peat-based growing medium. <i>Applied Soil Ecology</i> , 2020, 153, 103579.	2.1	23
3817	An introduction to phyllosymbiosis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192900.	1.2	163
3818	Blueberry proanthocyanidins and anthocyanins improve metabolic health through a gut microbiota-dependent mechanism in diet-induced obese mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2020, 318, E965-E980.	1.8	58
3819	Cover Crop Diversity as a Tool to Mitigate Vine Decline and Reduce Pathogens in Vineyard Soils. <i>Diversity</i> , 2020, 12, 128.	0.7	16
3820	The impact of ventilation rate on the fungal and bacterial ecology of home indoor air. <i>Building and Environment</i> , 2020, 177, 106800.	3.0	35
3821	Effects of a Diet Supplemented with Exogenous Catalase from <i>Penicillium notatum</i> on Intestinal Development and Microbiota in Weaned Piglets. <i>Microorganisms</i> , 2020, 8, 391.	1.6	14
3822	Egyptian Mongoose (<i>Herpestes ichneumon</i>) Gut Microbiota: Taxonomical and Functional Differences across Sex and Age Classes. <i>Microorganisms</i> , 2020, 8, 392.	1.6	8
3823	Movement ecology and sex are linked to barn owl microbial community composition. <i>Molecular Ecology</i> , 2020, 29, 1358-1371.	2.0	33
3824	Differential Colonization and Succession of Microbial Communities in Rock and Soil Substrates on a Maritime Antarctic Glacier Forefield. <i>Frontiers in Microbiology</i> , 2020, 11, 126.	1.5	65
3825	Alpha-Glucosidase Inhibitors Alter Gut Microbiota and Ameliorate Collagen-Induced Arthritis. <i>Frontiers in Pharmacology</i> , 2019, 10, 1684.	1.6	22
3826	Microbial Diversity Responding to Changes in Depositional Conditions during the Last Glacial and Interglacial Period: NE Ulleung Basin, East Sea (Sea of Japan). <i>Minerals (Basel, Switzerland)</i> , 2020, 10, 208.	0.8	2
3827	Composition, diversity, and activity of aerobic ammonia-oxidizing <i>Bacteria</i> and <i>Archaea</i> in the intertidal sands of a grand strand South Carolina beach. <i>MicrobiologyOpen</i> , 2020, 9, e1011.	1.2	8
3828	Mild changes in the mucosal microbiome during terminal ileum inflammation. <i>Microbial Pathogenesis</i> , 2020, 142, 104104.	1.3	8
3829	Distinct Characteristics of Bacterial Community in the Soil of Nanshazhou Island, South China Sea. <i>Current Microbiology</i> , 2020, 77, 1292-1300.	1.0	3
3830	Modulation of the intestinal microbiota and the metabolites produced by the administration of ice cream and a dietary supplement containing the same probiotics. <i>British Journal of Nutrition</i> , 2020, 124, 57-68.	1.2	20

#	ARTICLE	IF	CITATIONS
3831	Effects of multiple implantations of titanium healing abutments: Surface characteristics and microbial colonization. <i>Dental Materials</i> , 2020, 36, e279-e291.	1.6	10
3832	Identifying mechanisms that predict weight trajectory after bariatric surgery: rationale and design of the biobehavioral trial. <i>Surgery for Obesity and Related Diseases</i> , 2020, 16, 1816-1826.	1.0	20
3833	Seasonal Dynamics of Pelagic Mycoplanktonic Communities: Interplay of Taxon Abundance, Temporal Occurrence, and Biotic Interactions. <i>Frontiers in Microbiology</i> , 2020, 11, 1305.	1.5	23
3834	Water management impact on denitrifier community and denitrification activity in a paddy soil at different growth stages of rice. <i>Agricultural Water Management</i> , 2020, 241, 106354.	2.4	13
3835	The distinct microbial community in <i>Aurelia coerulea</i> polyps versus medusae and its dynamics after exposure to $^{60}\text{Co-}\beta$ radiation. <i>Environmental Research</i> , 2020, 188, 109843.	3.7	3
3836	Gut Microbiota and Liver Fibrosis: One Potential Biomarker for Predicting Liver Fibrosis. <i>BioMed Research International</i> , 2020, 2020, 1-15.	0.9	12
3837	The bacterial communities of <i>Tuber aestivum</i> : preliminary investigations in Molise region, Southern Italy. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	11
3838	Evaluation of the bacterial ocular surface microbiome in ophthalmologically normal dogs prior to and following treatment with topical neomycin-polymyxin-bacitracin. <i>PLoS ONE</i> , 2020, 15, e0234313.	1.1	20
3839	Diazotroph Diversity Associated With Scleractinian Corals and Its Relationships With Environmental Variables in the South China Sea. <i>Frontiers in Physiology</i> , 2020, 11, 615.	1.3	8
3840	Dietary organic cranberry pomace influences multiple blood biochemical parameters and cecal microbiota in pasture-raised broiler chickens. <i>Journal of Functional Foods</i> , 2020, 72, 104053.	1.6	21
3841	Vitamin D Receptor Protects Against Dysbiosis and Tumorigenesis via the JAK/STAT Pathway in Intestine. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 10, 729-746.	2.3	52
3842	Subspecies Niche Specialization in the Oral Microbiome Is Associated with Nasopharyngeal Carcinoma Risk. <i>MSystems</i> , 2020, 5, .	1.7	21
3843	Chemical structure predicts the effect of plant-derived low-molecular weight compounds on soil microbiome structure and pathogen suppression. <i>Functional Ecology</i> , 2020, 34, 2158-2169.	1.7	34
3844	Fungal communities living within leaves of native Hawaiian dicots are structured by landscape-scale variables as well as by host plants. <i>Molecular Ecology</i> , 2020, 29, 3102-3115.	2.0	20
3845	A dietary intervention to improve the microbiome composition of pregnant women with Crohn's disease and their offspring: The MELODY (Modulating Early Life Microbiome through Dietary) Trial. <i>Frontiers in Microbiology</i> , 2020, 11, 100573.	0.5	24
3846	Bed bugs shape the indoor microbial community composition of infested homes. <i>Science of the Total Environment</i> , 2020, 743, 140704.	3.9	15
3847	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020, 5, .	1.7	47
3848	Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. <i>Frontiers in Psychiatry</i> , 2020, 11, 518.	1.3	19

#	ARTICLE	IF	CITATIONS
3849	Environmental Factors, More Than Spatial Distance, Explain Community Structure of Soil Ammonia-Oxidizers in Wetlands on the Qinghai-Tibetan Plateau. <i>Microorganisms</i> , 2020, 8, 933.	1.6	12
3850	Effects of Fermented Soybean Meal Supplementation on the Growth Performance and Cecal Microbiota Community of Broiler Chickens. <i>Animals</i> , 2020, 10, 1098.	1.0	42
3851	Association of microbiota in the stomach of <i>Sinanodonta woodiana</i> and its cultured soil. <i>3 Biotech</i> , 2020, 10, 319.	1.1	1
3852	Distribution and diversity of endophytic fungi in <i>Gentiana rigescens</i> and cytotoxic activities. <i>Chinese Herbal Medicines</i> , 2020, 12, 297-302.	1.2	4
3853	Nutrient enrichment increases size of <i>Zostera marina</i> shoots and enriches for sulfur and nitrogen cycling bacteria in root-associated microbiomes. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	22
3854	Effect of 2- α -fucosyllactose supplementation on intestinal flora in mice with intestinal inflammatory diseases. <i>International Dairy Journal</i> , 2020, 110, 104797.	1.5	20
3855	Comparison of Rumen Microbiota and Serum Biochemical Indices in White Cashmere Goats Fed Ensiled or Sun-Dried Mulberry Leaves. <i>Microorganisms</i> , 2020, 8, 981.	1.6	16
3856	Urbanisation reduces the abundance and diversity of airborne microbes - but what does that mean for our health? A systematic review. <i>Science of the Total Environment</i> , 2020, 738, 140337.	3.9	45
3857	Dysbiosis individualizes the fitness effect of antibiotic resistance in the mammalian gut. <i>Nature Ecology and Evolution</i> , 2020, 4, 1268-1278.	3.4	18
3858	Comparative evaluation of peptidome and microbiota in different types of saliva samples. <i>Annals of Translational Medicine</i> , 2020, 8, 686-686.	0.7	2
3859	Comparing Analytical Methods for the Gut Microbiome and Aging: Gut Microbial Communities and Body Weight in the Osteoporotic Fractures in Men (MrOS) Study. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 1267-1275.	1.7	12
3860	Evaluation of the effects of anthelmintic administration on the fecal microbiome of healthy dogs with and without subclinical <i>Giardia</i> spp. and <i>Cryptosporidium canis</i> infections. <i>PLoS ONE</i> , 2020, 15, e0228145.	1.1	13
3861	Biogeographic pattern of the nirS gene-targeted anammox bacterial community and composition in the northern South China Sea and a coastal Mai Po mangrove wetland. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 3167-3181.	1.7	3
3862	Amplicon sequencing reveals the bacterial diversity in milk, dairy premises and Serra da Canastra artisanal cheeses produced by three different farms. <i>Food Microbiology</i> , 2020, 89, 103453.	2.1	38
3863	Constraints on microbial communities, decomposition and methane production in deep peat deposits. <i>PLoS ONE</i> , 2020, 15, e0223744.	1.1	13
3864	Succession and Colonization Dynamics of Endolithic Phototrophs within Intertidal Carbonates. <i>Microorganisms</i> , 2020, 8, 214.	1.6	12
3865	Combining Citizen Science and Genomics to Investigate Tick, Pathogen, and Commensal Microbiome at Single-Tick Resolution. <i>Frontiers in Genetics</i> , 2020, 10, 1322.	1.1	26
3866	Ocular bacterial signatures of exophthalmic disease in farmed turbot (<i>Scophthalmus maximus</i>) Tj ETQq1 1 0,784314 0,9 4gBT /Ov	0,9	4gBT

#	ARTICLE	IF	CITATIONS
3867	First Insight into Microbiome Profiles of Myrmecophilous Beetles and Their Host, Red Wood Ant <i>Formica polyctena</i> (Hymenoptera: Formicidae) – A Case Study. <i>Insects</i> , 2020, 11, 134.	1.0	9
3868	Bacterioplankton metabolism of phytoplankton lysates across a cyclone–anticyclone eddy dipole impacts the cycling of semi-labile organic matter in the photic zone. <i>Limnology and Oceanography</i> , 2020, 65, 1608-1622.	1.6	7
3869	Dysbiosis-Induced Secondary Bile Acid Deficiency Promotes Intestinal Inflammation. <i>Cell Host and Microbe</i> , 2020, 27, 659-670.e5.	5.1	404
3870	Spatial variations in bacterial and archaeal abundance and community composition in boreal forest pine mycorrhizospheres. <i>European Journal of Soil Biology</i> , 2020, 97, 103168.	1.4	4
3871	Insect pollination: an ecological process involved in the assembly of the seed microbiota. <i>Scientific Reports</i> , 2020, 10, 3575.	1.6	34
3872	Bacterial and Archaeal Diversity in Sulfide-Bearing Waste Rock at Faro Mine Complex, Yukon Territory, Canada. <i>Geomicrobiology Journal</i> , 2020, 37, 511-519.	1.0	15
3873	Alpine headwaters emerging from glaciers and rock glaciers host different bacterial communities: Ecological implications for the future. <i>Science of the Total Environment</i> , 2020, 717, 137101.	3.9	25
3874	Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 8.	2.9	68
3875	Age-Related Differences in the Gut Microbiome of Rhesus Macaques. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 1293-1298.	1.7	31
3876	Response of sediment bacterial communities to the drainage of wastewater from aquaculture ponds in different seasons. <i>Science of the Total Environment</i> , 2020, 717, 137180.	3.9	29
3877	Responses of soil microbiota and nematodes to application of organic and inorganic fertilizers in grassland columns. <i>Biology and Fertility of Soils</i> , 2020, 56, 647-662.	2.3	32
3878	A phylogenetic model for the recruitment of species into microbial communities and application to studies of the human microbiome. <i>ISME Journal</i> , 2020, 14, 1359-1368.	4.4	21
3879	A probiotic treatment increases the immune response induced by the nasal delivery of spore-adsorbed TTFC. <i>Microbial Cell Factories</i> , 2020, 19, 42.	1.9	22
3880	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. <i>PLoS ONE</i> , 2020, 15, e0229001.	1.1	56
3881	Integrated assessment of west coast of South Korea by use of benthic bacterial community structure as determined by eDNA, concentrations of contaminants, and in vitro bioassays. <i>Environment International</i> , 2020, 137, 105569.	4.8	5
3882	Nicotianamine-chelated iron positively affects iron status, intestinal morphology and microbial populations in vivo (<i>Gallus gallus</i>). <i>Scientific Reports</i> , 2020, 10, 2297.	1.6	24
3883	Enrichment of potentially beneficial bacteria from the consistent microbial community confers canker resistance on tomato. <i>Microbiological Research</i> , 2020, 234, 126446.	2.5	4
3884	Microbial community structure shows differing levels of temporal stability in intertidal beach sands of the grand strand region of South Carolina. <i>PLoS ONE</i> , 2020, 15, e0229387.	1.1	7

#	ARTICLE	IF	CITATIONS
3885	Pesticides Decrease Bacterial Diversity and Abundance of Irrigated Rice Fields. <i>Microorganisms</i> , 2020, 8, 318.	1.6	27
3886	Assembly and shifts of the bacterial rhizobiome of field grown transgenic maize line carrying mcr1Ab and mcr2Ab genes at different developmental stages. <i>Plant Growth Regulation</i> , 2020, 91, 113-126.	1.8	8
3887	Microbiota composition modulates inflammation and neointimal hyperplasia after arterial angioplasty. <i>Journal of Vascular Surgery</i> , 2020, 71, 1378-1389.e3.	0.6	4
3888	Impact of acid mine drainage chemistry and microbiology on the development of efficient Fe removal activities. <i>Chemosphere</i> , 2020, 249, 126117.	4.2	11
3889	Investigation of the impact of gut microbiotas on fertility of stored sperm by types of hens. <i>Poultry Science</i> , 2020, 99, 1174-1184.	1.5	5
3890	Rain induces temporary shifts in epiphytic bacterial communities of cucumber and tomato fruit. <i>Scientific Reports</i> , 2020, 10, 1765.	1.6	25
3891	Bacterial Exposure Mediates Developmental Plasticity and Resistance to Lethal <i>Vibrio lentus</i> Infection in Purple Sea Urchin (<i>Strongylocentrotus purpuratus</i>) Larvae. <i>Frontiers in Immunology</i> , 2019, 10, 3014.	2.2	16
3892	Poor nutrient availability in opencast coalmine influences microbial community composition and diversity in exposed and underground soil profiles. <i>Applied Soil Ecology</i> , 2020, 152, 103544.	2.1	12
3893	OGG1 deficiency alters the intestinal microbiome and increases intestinal inflammation in a mouse model. <i>PLoS ONE</i> , 2020, 15, e0227501.	1.1	18
3894	Prenatal Transfer of Gut Bacteria in Rock Pigeon. <i>Microorganisms</i> , 2020, 8, 61.	1.6	19
3895	Atlantic Salmon (<i>Salmo salar</i> L., 1758) Gut Microbiota Profile Correlates with Flesh Pigmentation: Cause or Effect?. <i>Marine Biotechnology</i> , 2020, 22, 786-804.	1.1	24
3896	Antibiotic Treatment Does Not Ameliorate the Metabolic Changes in Rats Presenting Dysbiosis After Consuming a High Fructose Diet. <i>Nutrients</i> , 2020, 12, 203.	1.7	10
3897	Potential probiotic salami with dietary fiber modulates metabolism and gut microbiota in a human intervention study. <i>Journal of Functional Foods</i> , 2020, 66, 103790.	1.6	30
3898	Effect of wheat bran derived prebiotic supplementation on gastrointestinal transit, gut microbiota, and metabolic health: a randomized controlled trial in healthy adults with a slow gut transit. <i>Gut Microbes</i> , 2020, 12, 1704141.	4.3	46
3899	Legacy effects of 8-year nitrogen inputs on bacterial assemblage in wheat rhizosphere. <i>Biology and Fertility of Soils</i> , 2020, 56, 583-596.	2.3	35
3900	Gut bacteria of field-collected larvae of <i>Spodoptera frugiperda</i> undergo selection and are more diverse and active in metabolizing multiple insecticides than laboratory-selected resistant strains. <i>Journal of Pest Science</i> , 2020, 93, 833-851.	1.9	57
3901	Selectived and Reshaped Early Dominant Microbial Community in the Cecum With Similar Proportions and Better Homogenization and Species Diversity Due to Organic Acids as AGP Alternatives Mediate Their Effects on Broilers Growth. <i>Frontiers in Microbiology</i> , 2019, 10, 2948.	1.5	42
3902	Integrating hydrochemical and biological approaches to investigate the surface water and groundwater interactions in the hyporheic zone of the Liuxi River basin, southern China. <i>Journal of Hydrology</i> , 2020, 583, 124622.	2.3	29

#	ARTICLE	IF	CITATIONS
3903	Tools for Analysis of the Microbiome. <i>Digestive Diseases and Sciences</i> , 2020, 65, 674-685.	1.1	70
3904	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020, 11, .	1.8	204
3905	Deficiency of Gankyrin in the small intestine is associated with augmented colitis accompanied by altered bacterial composition of intestinal microbiota. <i>BMC Gastroenterology</i> , 2020, 20, 12.	0.8	3
3906	Light Pollution Changes the Toxicological Effects of Cadmium on Microbial Community Structure and Function Associated with Leaf Litter Decomposition. <i>International Journal of Molecular Sciences</i> , 2020, 21, 422.	1.8	10
3907	Impact of earthquake on the communities of bacteria and archaea in groundwater ecosystems. <i>Journal of Hydrology</i> , 2020, 583, 124563.	2.3	9
3908	Evolutionary signal in the gut microbiomes of 74 bird species from Equatorial Guinea. <i>Molecular Ecology</i> , 2020, 29, 829-847.	2.0	56
3909	Dissecting the factors shaping fish skin microbiomes in a heterogeneous inland water system. <i>Microbiome</i> , 2020, 8, 9.	4.9	52
3910	Impact of TCR Diversity on the Development of Transplanted or Chemically Induced Tumors. <i>Cancer Immunology Research</i> , 2020, 8, 192-202.	1.6	15
3911	Gut-host Crosstalk: Methodological and Computational Challenges. <i>Digestive Diseases and Sciences</i> , 2020, 65, 686-694.	1.1	2
3912	Cheating in arbuscular mycorrhizal mutualism: a network and phylogenetic analysis of mycoheterotrophy. <i>New Phytologist</i> , 2020, 226, 1822-1835.	3.5	30
3913	Variation in Snow Algae Blooms in the Coast Range of British Columbia. <i>Frontiers in Microbiology</i> , 2020, 11, 569.	1.5	26
3914	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
3915	Microbiome and biological blood marker changes in hens at different laying stages in conventional and cage free housings. <i>Poultry Science</i> , 2020, 99, 2362-2374.	1.5	24
3916	A Primer for Microbiome Time-Series Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 310.	1.1	47
3917	Effect of Salinity on the Gut Microbiome of Pike Fry (<i>Esox lucius</i>). <i>Applied Sciences (Switzerland)</i> , 2020, 10, 2506.	1.3	16
3918	Effects of an Eco-Friendly Sanitizing Wash on Spinach Leaf Bacterial Community Structure and Diversity. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 2986.	1.3	4
3919	Response of Tomato Rhizosphere Bacteria to Root-Knot Nematodes, Fenamiphos and Sampling Time Shows Differential Effects on Low Level Taxa. <i>Frontiers in Microbiology</i> , 2020, 11, 390.	1.5	5
3920	A Commercial Probiotic Induces Tolerogenic and Reduces Pathogenic Responses in Experimental Autoimmune Encephalomyelitis. <i>Cells</i> , 2020, 9, 906.	1.8	31

#	ARTICLE	IF	CITATIONS
3921	Microbiota stratification and succession of amylase-producing <i>Bacillus</i> in traditional Chinese Jiuqu (fermentation starters). <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 3544-3553.	1.7	18
3922	Sub-Arctic Field Degradation of Methylsulfonyl-Methyl in Two Alaskan Soils and Microbial Community Composition Effects. <i>Water, Air, and Soil Pollution</i> , 2020, 231, 1.	1.1	4
3923	Effects of corn starch level on growth performance, antioxidant capacity, gut morphology and intestinal microflora of juvenile golden pompano, <i>Trachinotus ovatus</i> . <i>Aquaculture</i> , 2020, 524, 735197.	1.7	50
3924	Detection and isolation of low molecular weight alginate- and laminaran-susceptible gut indigenous bacteria from ICR mice. <i>Carbohydrate Polymers</i> , 2020, 238, 116205.	5.1	34
3925	Vancomycin exposure caused opportunistic pathogens bloom in intestinal microbiome by simulator of the human intestinal microbial ecosystem (SHIME). <i>Environmental Pollution</i> , 2020, 265, 114399.	3.7	30
3926	A non-invasive method to monitor marine pollution from bacterial DNA present in fish skin mucus. <i>Environmental Pollution</i> , 2020, 263, 114438.	3.7	15
3927	Evaluation of haplotype callers for next-generation sequencing of viruses. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104277.	1.0	29
3928	Habitat and seasonality shape the structure of tench (<i>Tinca tinca</i> L.) gut microbiome. <i>Scientific Reports</i> , 2020, 10, 4460.	1.6	46
3929	Site-specific molecular analysis of the bacteriota on worn spectacles. <i>Scientific Reports</i> , 2020, 10, 5577.	1.6	4
3930	The cutaneous microbiome in hospitalized patients with pressure ulcers. <i>Scientific Reports</i> , 2020, 10, 5963.	1.6	15
3931	Phylogenetic clustering and rarity imply risk of local species extinction in prospective deep-sea mining areas of the Clarion-Clipperton Fracture Zone. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192666.	1.2	19
3932	Reintroducing mothur: 10 Years Later. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	160
3933	Diazotrophs Show Signs of Restoration in Amazon Rain Forest Soils with Ecosystem Rehabilitation. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	11
3934	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	1.7	81
3935	Harvesting Mango Fruit with a Short Stem-End Altered Endophytic Microbiome and Reduce Stem-End Rot. <i>Microorganisms</i> , 2020, 8, 558.	1.6	24
3936	Impact of feeding regimens on the composition of gut microbiota and metabolite profiles of plasma and feces from Mongolian sheep. <i>Journal of Microbiology</i> , 2020, 58, 472-482.	1.3	19
3937	Associations between respiratory infections and bacterial microbiome in student dormitories in Northern China. <i>Indoor Air</i> , 2020, 30, 816-826.	2.0	20
3938	Epithelium intrinsic vitamin A signaling co-ordinates pathogen clearance in the gut via IL-18. <i>PLoS Pathogens</i> , 2020, 16, e1008360.	2.1	20

#	ARTICLE	IF	CITATIONS
3939	aPCoA: covariate adjusted principal coordinates analysis. <i>Bioinformatics</i> , 2020, 36, 4099-4101.	1.8	18
3940	Gut Microbiota, Blood Metabolites, and Spleen Immunity in Broiler Chickens Fed Berry Pomaces and Phenolic-Enriched Extractives. <i>Frontiers in Veterinary Science</i> , 2020, 7, 150.	0.9	29
3941	Microbial Ecology of Atlantic Salmon (<i>Salmo salar</i>) Hatcheries: Impacts of the Built Environment on Fish Mucosal Microbiota. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	71
3942	Closely Located but Totally Distinct: Highly Contrasting Prokaryotic Diversity Patterns in Raised Bogs and Eutrophic Fens. <i>Microorganisms</i> , 2020, 8, 484.	1.6	25
3943	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. <i>Evolutionary Applications</i> , 2020, 13, 1984-1999.	1.5	17
3944	Characterization and optimization of abamectinâ€”a powerful antiparasitic from a local <i>Streptomyces avermitilis</i> isolate. <i>Folia Microbiologica</i> , 2020, , 1.	1.1	1
3945	Wildfire effects on diversity and composition in soil bacterial communities. <i>Science of the Total Environment</i> , 2020, 726, 138636.	3.9	52
3946	Distinct successional patterns and processes of freeâ€”living and particleâ€”attached bacterial communities throughout a phytoplankton bloom. <i>Freshwater Biology</i> , 2020, 65, 1363-1375.	1.2	17
3947	From Maternal Grazing to Barn Feeding During Pre-weaning Period: Altered Gastrointestinal Microbiota Contributes to Change the Development and Function of the Rumen and Intestine of Yak Calves. <i>Frontiers in Microbiology</i> , 2020, 11, 485.	1.5	27
3948	Effect of different starch sources in a raw meat-based diet on fecal microbiome in dogs housed in a shelter. <i>Animal Nutrition</i> , 2020, 6, 353-361.	2.1	9
3949	Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. <i>Nature Communications</i> , 2020, 11, 1801.	5.8	153
3950	Nutrient Level Determines Biofilm Characteristics and Subsequent Impact on Microbial Corrosion and Biocide Effectiveness. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	55
3951	Metabolome-Informed Microbiome Analysis Refines Metadata Classifications and Reveals Unexpected Medication Transfer in Captive Cheetahs. <i>MSystems</i> , 2020, 5, .	1.7	12
3952	Effects of hydrolyzed fish protein and autolyzed yeast as substitutes of fishmeal in the gilthead sea bream (<i>Sparus aurata</i>) diet, on fish intestinal microbiome. <i>BMC Veterinary Research</i> , 2020, 16, 118.	0.7	33
3953	The effect of acupuncture on tumor growth and gut microbiota in mice inoculated with osteosarcoma cells. <i>Chinese Medicine</i> , 2020, 15, 33.	1.6	16
3954	Assessment of dietary supplementation with galactomannan oligosaccharides and phytogenics on gut microbiota of European sea bass (<i>Dicentrarchus Labrax</i>) fed low fishmeal and fish oil based diet. <i>PLoS ONE</i> , 2020, 15, e0231494.	1.1	62
3955	Mucins and the Microbiome. <i>Annual Review of Biochemistry</i> , 2020, 89, 769-793.	5.0	184
3956	Metabolic versatility of freshwater sedimentary archaea feeding on different organic carbon sources. <i>PLoS ONE</i> , 2020, 15, e0231238.	1.1	6

#	ARTICLE	IF	CITATIONS
3957	Soybean Oil Modulates the Gut Microbiota Associated with Atherogenic Biomarkers. <i>Microorganisms</i> , 2020, 8, 486.	1.6	5
3958	Prevalent root-derived phenolics drive shifts in microbial community composition and prime decomposition in forest soil. <i>Soil Biology and Biochemistry</i> , 2020, 145, 107797.	4.2	69
3959	Biogeographic patterns of abundant and rare bacterial and microeukaryotic subcommunities in connected freshwater lake zones subjected to different levels of nutrient loading. <i>Journal of Applied Microbiology</i> , 2021, 130, 123-132.	1.4	6
3960	Individual and Site-Specific Variation in a Biogeographical Profile of the Coyote Gastrointestinal Microbiota. <i>Microbial Ecology</i> , 2021, 81, 240-252.	1.4	17
3961	House dust microbiota in relation to adult asthma and atopy in a US farming population. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 910-920.	1.5	21
3962	Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2021, 27, 366-379.	1.4	24
3963	Changes in Bacterial and Fungal Microbiomes Associated with Tomatoes of Healthy and Infected by <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> . <i>Microbial Ecology</i> , 2021, 81, 1004-1017.	1.4	39
3964	Meta-Prism: Ultra-fast and highly accurate microbial community structure search utilizing dual indexing and parallel computation. <i>Briefings in Bioinformatics</i> , 2021, 22, 557-567.	3.2	10
3965	Unlocking the phylogenetic diversity, primary habitats, and abundances of free-living Symbiodiniaceae on a coral reef. <i>Molecular Ecology</i> , 2021, 30, 343-360.	2.0	33
3966	Food or just a free ride? A meta-analysis reveals the global diversity of the Plastisphere. <i>ISME Journal</i> , 2021, 15, 789-806.	4.4	110
3967	Community structure, taxonomic diversity and spatio-temporal variation of sediment and water bacteria in Bhitarkanika mangrove ecosystem, India. <i>International Journal of Environmental Science and Technology</i> , 2021, 18, 1147-1166.	1.8	7
3968	Quantitative profiling of built environment bacterial and fungal communities reveals dynamic material dependent growth patterns and microbial interactions. <i>Indoor Air</i> , 2021, 31, 188-205.	2.0	10
3969	Hypothesis testing for phylogenetic composition: a minimum-cost flow perspective. <i>Biometrika</i> , 2021, 108, 17-36.	1.3	6
3970	Ciliate Diversity From Aquatic Environments in the Brazilian Atlantic Forest as Revealed by High-Throughput DNA Sequencing. <i>Microbial Ecology</i> , 2021, 81, 630-643.	1.4	11
3971	The fungal community associated with the ambrosia beetle <i>Xylosandrus compactus</i> invading the mediterranean maquis in central Italy reveals high biodiversity and suggests environmental acquisitions. <i>Fungal Biology</i> , 2021, 125, 12-24.	1.1	24
3972	Epiphytic and Endophytic Fungal Communities of Tomato Plants. <i>Horticultural Plant Journal</i> , 2021, 7, 38-48.	2.3	26
3973	Influence of stormwater infiltration systems on the structure and the activities of groundwater biofilms: Are the effects restricted to rainy periods?. <i>Science of the Total Environment</i> , 2021, 755, 142451.	3.9	1
3974	Comparison of the microbial communities of alpacas and sheep fed diets with three different ratios of corn stalk to concentrate. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2021, 105, 26-34.	1.0	6

#	ARTICLE	IF	CITATIONS
3975	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 603-616.	0.9	25
3976	Association between indoor microbiome exposure and sick building syndrome (SBS) in junior high schools of Johor Bahru, Malaysia. <i>Science of the Total Environment</i> , 2021, 753, 141904.	3.9	27
3977	Evaluation of plant microbial fuel cells for urban green roofs in a subtropical metropolis. <i>Science of the Total Environment</i> , 2021, 765, 142786.	3.9	20
3978	Long-term organic and inorganic fertilization alters the diazotrophic abundance, community structure, and co-occurrence patterns in a vertisol. <i>Science of the Total Environment</i> , 2021, 766, 142441.	3.9	25
3979	Temporal succession of water microbiomes and resistomes during carcass decomposition in a fish model. <i>Journal of Hazardous Materials</i> , 2021, 403, 123795.	6.5	26
3980	Microbiota Effects on Carcinogenesis: Initiation, Promotion, and Progression. <i>Annual Review of Medicine</i> , 2021, 72, 243-261.	5.0	40
3981	Effect of Calcium-Fortified Potato Starch on Cecal Fermentation and Fat Accumulation in Rats. <i>Starch/Staerke</i> , 2021, 73, 2000097.	1.1	0
3982	Radiation Therapy-Induced Changes of the Nasopharyngeal Commensal Microbiome in Nasopharyngeal Carcinoma Patients. <i>International Journal of Radiation Oncology Biology Physics</i> , 2021, 109, 145-150.	0.4	9
3983	SCRAPP: A tool to assess the diversity of microbial samples from phylogenetic placements. <i>Molecular Ecology Resources</i> , 2021, 21, 340-349.	2.2	5
3984	Characterization of the bacterial microbiomes of social amoebae and exploration of the roles of host and environment on microbiome composition. <i>Environmental Microbiology</i> , 2021, 23, 126-142.	1.8	14
3985	Quantitative estimation of stochastic and deterministic processes for soil prokaryotic community assembly in the Yellow River floodplain. <i>European Journal of Soil Science</i> , 2021, 72, 1462-1477.	1.8	11
3986	Enhanced N ₂ O emission rate in field soil undergoing conventional intensive fertilization is attributed to the shifts of denitrifying guilds. <i>Pedosphere</i> , 2021, 31, 145-156.	2.1	13
3987	Episodic Aspiration with Oral Commensals Induces a MyD88-dependent, Pulmonary T-Helper Cell Type 17 Response that Mitigates Susceptibility to <i>Streptococcus pneumoniae</i> . <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 1099-1111.	2.5	55
3988	Host plant diet affects growth and induces altered gene expression and microbiome composition in the wood white (<i>Leptidea sinapis</i>) butterfly. <i>Molecular Ecology</i> , 2021, 30, 499-516.	2.0	17
3989	Monthly distribution of ammonia-oxidizing microbes in a tropical bay. <i>Journal of Microbiology</i> , 2021, 59, 10-19.	1.3	1
3990	On-farm soil resistome is modified after treating dairy calves with the antibiotic florfenicol. <i>Science of the Total Environment</i> , 2021, 750, 141694.	3.9	11
3991	Derived habitats of indoor microbes are associated with asthma symptoms in Chinese university dormitories. <i>Environmental Research</i> , 2021, 194, 110501.	3.7	18
3992	Gut microbiomes of bigheaded carps and hybrids provide insights into invasion: A hologenome perspective. <i>Evolutionary Applications</i> , 2021, 14, 735-745.	1.5	16

#	ARTICLE	IF	CITATIONS
3993	<i>Clostridium boltea</i> is elevated in neuromyelitis optica spectrum disorder in India and shares sequence similarity with AQP4. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2021, 8, .	3.1	26
3994	Nitrogen and phosphorus additions accelerate decomposition of slow carbon pool and lower total soil organic carbon pool in alpine meadows. <i>Land Degradation and Development</i> , 2021, 32, 1761-1772.	1.8	25
3995	A sustainable approach by using microalgae to minimize the eutrophication process of Mar Menor lagoon. <i>Science of the Total Environment</i> , 2021, 758, 143613.	3.9	12
3996	Fecal microbiota transplant promotes response in immunotherapy-refractory melanoma patients. <i>Science</i> , 2021, 371, 602-609.	6.0	784
3997	Gut Microbiome Components Predict Response to Neoadjuvant Chemoradiotherapy in Patients with Locally Advanced Rectal Cancer: A Prospective, Longitudinal Study. <i>Clinical Cancer Research</i> , 2021, 27, 1329-1340.	3.2	82
3998	Microbiological, immunological, and histological changes in the gut of <i>Salmonella</i> Enteritidis-challenged rats fed goat cheese containing <i>Lactobacillus rhamnosus</i> EM1107. <i>Journal of Dairy Science</i> , 2021, 104, 179-197.	1.4	3
3999	<i>Spartina alterniflora</i> invasions reduce soil fungal diversity and simplify co-occurrence networks in a salt marsh ecosystem. <i>Science of the Total Environment</i> , 2021, 758, 143667.	3.9	28
4000	Bacterial epibiont communities of panmictic Antarctic krill are spatially structured. <i>Molecular Ecology</i> , 2021, 30, 1042-1052.	2.0	6
4001	Alterations in Gut Microbiota Do Not Play a Causal Role in Diet-independent Weight Gain Caused by Ovariectomy. <i>Journal of the Endocrine Society</i> , 2021, 5, bvaa173.	0.1	6
4002	Network-directed isolation of the cooperator <i>Pseudomonas aeruginosa</i> ZM03 enhanced the dibutyl phthalate degradation capacity of <i>Arthrobacter nicotianae</i> ZM05 under pH stress. <i>Journal of Hazardous Materials</i> , 2021, 410, 124667.	6.5	19
4003	IFAA: Robust Association Identification and Inference for Absolute Abundance in Microbiome Analyses. <i>Journal of the American Statistical Association</i> , 2021, 116, 1595-1608.	1.8	2
4004	Wide distribution of <i>Phycisphaera</i> -like planctomycetes from <i>WD2101</i> soil group in peatlands and genome analysis of the first cultivated representative. <i>Environmental Microbiology</i> , 2021, 23, 1510-1526.	1.8	32
4005	Patterns of phylogenetic beta diversity measured at deep evolutionary histories across geographical and ecological spaces for angiosperms in China. <i>Journal of Biogeography</i> , 2021, 48, 773-784.	1.4	19
4006	Diminished rhizosphere and bulk soil microbial abundance and diversity across succession stages in Karst area, southwest China. <i>Applied Soil Ecology</i> , 2021, 158, 103799.	2.1	20
4007	<i>microeco</i> : an R package for data mining in microbial community ecology. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	398
4008	Morphological complexity affects the diversity of marine microbiomes. <i>ISME Journal</i> , 2021, 15, 1372-1386.	4.4	18
4009	Genomic investigations of acute munitions exposures on the health and skin microbiome composition of leopard frog (<i>Rana pipiens</i>) tadpoles. <i>Environmental Research</i> , 2021, 192, 110245.	3.7	8
4010	Efficient treatment of a preclinical inflammatory bowel disease model with engineered bacteria. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 20, 218-226.	1.8	11

#	ARTICLE	IF	CITATIONS
4011	Bacillus subtilisâ€“fermented products ameliorate the growth performance and alter cecal microbiota community in broilers under lipopolysaccharide challenge. Poultry Science, 2021, 100, 875-886.	1.5	28
4012	Endangerment of <i>Ostrya rehderiana</i> Chun and its relationship with rhizosphere soil microflora. Agronomy Journal, 2021, 113, 746-759.	0.9	5
4013	Invasive freshwater snails form novel microbial relationships. Evolutionary Applications, 2021, 14, 770-780.	1.5	9
4014	Methamphetamine exposure and its cessation alter gut microbiota and induce depressive-like behavioral effects on rats. Psychopharmacology, 2021, 238, 281-292.	1.5	25
4015	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. Brain, Behavior, and Immunity, 2021, 91, 245-256.	2.0	44
4016	Comparing DNA Extraction and 16S rRNA Gene Amplification Methods for Plant-Associated Bacterial Communities. Phytobiomes Journal, 2021, 5, 190-201.	1.4	5
4017	Microbiome diversity and dysbiosis in aquaculture. Reviews in Aquaculture, 2021, 13, 1077-1096.	4.6	74
4018	Effects of fermented Aphanizomenon flos-aquae on the caecal microbiome of mice fed a high-sucrose and low-dietary fibre diet. Journal of Applied Phycology, 2021, 33, 397-407.	1.5	5
4019	Effects of Urbanization and Landscape on Gut Microbiomes in White-Crowned Sparrows. Microbial Ecology, 2021, 81, 253-266.	1.4	24
4020	Metagenome Across a Geochemical Gradient of Indian Stone Ruins Found at Historic Sites in Tamil Nadu, India. Microbial Ecology, 2021, 81, 385-395.	1.4	15
4021	Feline conjunctival microbiota in a shelter: effects of time, upper respiratory disease and famciclovir administration. Journal of Feline Medicine and Surgery, 2021, 23, 316-330.	0.6	4
4022	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. Nature Biotechnology, 2021, 39, 165-168.	9.4	61
4023	Metagenomics Approaches to Investigate the Gut Microbiome of COVID-19 Patients. Bioinformatics and Biology Insights, 2021, 15, 117793222199942.	1.0	8
4024	Identification of bacterial isolates from commercial poultry feed via 16S rDNA. Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes, 2021, 56, 272-281.	0.7	4
4025	Analysis of sex differences in dietary copper-fructose interaction-induced alterations of gut microbial activity in relation to hepatic steatosis. Biology of Sex Differences, 2021, 12, 3.	1.8	7
4026	Transient-rare Bacterial Taxa Are Assembled Neutrally across Temporal Scales. Microbes and Environments, 2021, 36, n/a.	0.7	5
4027	Wine Terroir and the Soil Bacteria: An Amplicon Sequencingâ€“Based Assessment of the Barossa Valley and Its Sub-Regions. Frontiers in Microbiology, 2020, 11, 597944.	1.5	13
4028	Signatures of landscape and captivity in the gut microbiota of Southern Hairy-nosed Wombats (<i>Lasiorchinus latifrons</i>). Animal Microbiome, 2021, 3, 4.	1.5	9

#	ARTICLE	IF	CITATIONS
4029	The Impact of Introducing Patient-Reported Inflammatory Bowel Disease Symptoms via Electronic Survey on Clinic Visit Length, Patient and Provider Satisfaction, and the Environment Microbiome. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 746-750.	0.9	1
4031	Geography as non-genetic modulation factor of chicken cecal microbiota. <i>PLoS ONE</i> , 2021, 16, e0244724.	1.1	9
4032	Change in gut histomorphology and microbiota in Chinese striped-necked turtle hatchlings. <i>Aquaculture Research</i> , 2021, 52, 2685-2696.	0.9	3
4033	Impact of long-term fertilizer and summer warming treatments on bulk soil and birch rhizosphere microbial communities in mesic arctic tundra. <i>Arctic, Antarctic, and Alpine Research</i> , 2021, 53, 196-211.	0.4	2
4034	Biosynthesis and prebiotic activity of a linear levan from a new <i>Paenibacillus</i> isolate. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 769-787.	1.7	11
4035	Effect of Nora virus infection on native gut bacterial communities of <i>Drosophila melanogaster</i> . <i>AIMS Microbiology</i> , 2021, 7, 216-237.	1.0	2
4036	Kernel and Dissimilarity Methods for Exploratory Analysis in a Social Context. , 2021, , 669-690.		0
4038	Linking Bacterial Communities Associated with the Environment and the Ecosystem Engineer <i>Orchestia gammarellus</i> at Contrasting Salt Marsh Elevations. <i>Microbial Ecology</i> , 2021, 82, 537-548.	1.4	3
4039	Gut microbiome is affected by inter-sexual and inter-seasonal variation in diet for thick-billed murres (<i>Uria lomvia</i>). <i>Scientific Reports</i> , 2021, 11, 1200.	1.6	40
4040	Specificity of assemblage, not fungal partner species, explains mycorrhizal partnerships of mycoheterotrophic <i>Burmannia</i> plants. <i>ISME Journal</i> , 2021, 15, 1614-1627.	4.4	8
4041	Research on Remediation Effect of Paddy in Film-Bottomed Sandy Land Technology on Microbial Diversity in Desertification Soil. <i>Advances in Geosciences</i> , 2021, 11, 435-448.	0.0	0
4042	Live and ultrasound-inactivated <i>Lactobacillus casei</i> modulate the intestinal microbiota and improve biochemical and cardiovascular parameters in male rats fed a high-fat diet. <i>Food and Function</i> , 2021, 12, 5287-5300.	2.1	15
4043	Natural Bacterial Assemblages in <i>Arabidopsis thaliana</i> Tissues Become More Distinguishable and Diverse during Host Development. <i>MBio</i> , 2021, 12, .	1.8	18
4044	Comparison of clinicopathological parameters, prognosis, micro-ecological environment and metabolic function of Gastric Cancer with or without <i>Fusobacterium</i> sp. <i>Infection. Journal of Cancer</i> , 2021, 12, 1023-1032.	1.2	15
4045	Analyzing Forest Ecosystems. <i>Managing Forest Ecosystems</i> , 2021, , 81-158.	0.4	2
4046	Fecal Fungal Dysbiosis in Chinese Patients With Alzheimer's Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 631460.	1.8	23
4047	Genetic damage in lymphocytes of lung cancer patients is correlated to the composition of the respiratory tract microbiome. <i>Mutagenesis</i> , 2021, 36, 143-153.	1.0	12
4048	Comparisons of oral, intestinal, and pancreatic bacterial microbiomes in patients with pancreatic cancer and other gastrointestinal diseases. <i>Journal of Oral Microbiology</i> , 2021, 13, 1887680.	1.2	17

#	ARTICLE	IF	CITATIONS
4049	Temporal Changes of the Epiphytic Bacteria Community From the Marine Macroalga <i>Ulva lactuca</i> (Santa Marta, Colombian-Caribbean). <i>Current Microbiology</i> , 2021, 78, 534-543.	1.0	21
4050	Effects of vegetation type and soil horizon on soil bacterial and fungal communities in a dry "hot valley. <i>Circular Agricultural Systems</i> , 2021, 1, 1-8.	0.5	1
4051	Transition of microbiota in chicken cecal droppings from commercial broiler farms. <i>BMC Veterinary Research</i> , 2021, 17, 10.	0.7	12
4052	Soil bacterial communities vary more by season than with over two decades of experimental warming in Arctic tussock tundra. <i>Elementa</i> , 2021, 9, .	1.1	5
4053	Assessment of Bacterial Community Structure in Saline Sediment Microcosms Exposed for the First Time to the Ionic Liquid 1-Ethyl-3-Methylimidazolium Chloride. <i>Water, Air, and Soil Pollution</i> , 2021, 232, 1.	1.1	3
4054	Bacterial Diversity Analysis and Evaluation Proteins Hydrolysis during the Acid Whey and Fish Waste Fermentation. <i>Microorganisms</i> , 2021, 9, 100.	1.6	6
4055	Phylogenetic beta diversity of Odonata assemblages in the extreme condition of Central Iran. <i>Journal of Insect Conservation</i> , 2021, 25, 175-187.	0.8	3
4056	Comparative Analysis of the Microbiota Between Rumen and Duodenum of Twin Lambs Based on Diets of <i>Ceratoides</i> or Alfalfa. <i>Polish Journal of Microbiology</i> , 2021, 70, 175-187.	0.6	2
4057	Microbiome dynamics during the HI-SEAS IV mission, and implications for future crewed missions beyond Earth. <i>Microbiome</i> , 2021, 9, 27.	4.9	21
4058	Decrease in acetyl-CoA pathway utilizing butyrate-producing bacteria is a key pathogenic feature of alcohol-induced functional gut microbial dysbiosis and development of liver disease in mice. <i>Gut Microbes</i> , 2021, 13, 1946367.	4.3	34
4059	From taxonomy to metabolic output: what factors define gut microbiome health?. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	19
4060	Composition and Potential Function of Fecal Bacterial Microbiota from Six Bird Species. <i>Birds</i> , 2021, 2, 42-59.	0.6	3
4061	Engraftment of strictly anaerobic oxygen-sensitive bacteria in irritable bowel syndrome patients following fecal microbiota transplantation does not improve symptoms. <i>Gut Microbes</i> , 2021, 13, 1-16.	4.3	8
4062	The Microbiome of Size-Fractionated Airborne Particles from the Sahara Region. <i>Environmental Science & Technology</i> , 2021, 55, 1487-1496.	4.6	12
4064	Microbial diversity of co-occurring heterotrophs in cultures of marine picocyanobacteria. <i>Environmental Microbiomes</i> , 2021, 16, 1.	2.2	28
4065	Gut Microbiota Condition the Therapeutic Efficacy of Trastuzumab in HER2-Positive Breast Cancer. <i>Cancer Research</i> , 2021, 81, 2195-2206.	0.4	63
4066	Blueberry polyphenols alter gut microbiota & phenolic metabolism in rats. <i>Food and Function</i> , 2021, 12, 2442-2456.	2.1	21
4067	Effects of Immunization With the Soil-Derived Bacterium <i>Mycobacterium vaccae</i> on Stress Coping Behaviors and Cognitive Performance in a "Two Hit" Stressor Model. <i>Frontiers in Physiology</i> , 2020, 11, 524833.	1.3	9

#	ARTICLE	IF	CITATIONS
4068	Beyond samples: A metric revealing more connections of gut microbiota between individuals. Computational and Structural Biotechnology Journal, 2021, 19, 3930-3937.	1.9	3
4070	Mucosal microbiome dysbiosis associated with duodenum bulb inflammation. Microbial Pathogenesis, 2021, 150, 104711.	1.3	4
4071	The effects of feeding ferric citrate on ruminal bacteria, methanogenic archaea and methane production in growing beef steers. Access Microbiology, 2021, 3, acmi000180.	0.2	1
4072	The Alteration of Intestinal Microbiota Profile and Immune Response in Epinephelus coioides during Pathogen Infection. Life, 2021, 11, 99.	1.1	16
4073	Wheat-durum pasta added of inactivated <i>Bifidobacterium animalis</i> decreases glucose and total cholesterol levels and modulates gut microbiota in healthy rats. International Journal of Food Sciences and Nutrition, 2021, 72, 781-793.	1.3	12
4074	Elevation Correlates With Significant Changes in Relative Abundance in Hummingbird Fecal Microbiota, but Composition Changes Little. Frontiers in Ecology and Evolution, 2021, 8, .	1.1	13
4075	Typical gut indigenous bacteria in ICR mice fed a soy protein-based normal or low-protein diet. Current Research in Food Science, 2021, 4, 295-300.	2.7	11
4076	Comparison of Blood Bacterial Communities in Periodontal Health and Periodontal Disease. Frontiers in Cellular and Infection Microbiology, 2020, 10, 577485.	1.8	36
4077	Gut microbiome analysis as a predictive marker for the gastric cancer patients. Applied Microbiology and Biotechnology, 2021, 105, 803-814.	1.7	38
4078	Host reproductive cycle influences the pouch microbiota of wild southern hairy-nosed wombats (<i>Lasiorhinus latifrons</i>). Animal Microbiome, 2021, 3, 13.	1.5	11
4079	Efficacy of <i>Bifidobacterium bifidum</i> G9-1 in improving quality of life in patients with chronic constipation: a prospective intervention study. Bioscience of Microbiota, Food and Health, 2021, 40, 105-114.	0.8	5
4080	The Human Gut Microbiota in all its States: From Disturbance to Resilience. , 2022, , 161-178.		4
4081	Environmental DNA simultaneously informs hydrological and biodiversity characterization of an Alpine catchment. Hydrology and Earth System Sciences, 2021, 25, 735-753.	1.9	5
4083	Gut Microbial Profile Is Associated With Residential Settings and Not Nutritional Status in Adults in Karnataka, India. Frontiers in Nutrition, 2021, 8, 595756.	1.6	1
4085	Influence of Enzyme Supplementation in the Diets of Broiler Chickens Formulated with Different Corn Hybrids Dried at Various Temperatures. Animals, 2021, 11, 643.	1.0	4
4086	High-Intensity Interval Training and $\hat{\pm}$ -Linolenic Acid Supplementation Improve DHA Conversion and Increase the Abundance of Gut Mucosa-Associated Oscillospira Bacteria. Nutrients, 2021, 13, 788.	1.7	11
4089	Gut microbiota comparison of vaginally and cesarean born infants exclusively breastfed by mothers secreting $\hat{\pm}$ fucosylated oligosaccharides in breast milk. PLoS ONE, 2021, 16, e0246839.	1.1	13
4090	Ingestion of probiotic (<i>Lactobacillus helveticus</i> and <i>Bifidobacterium longum</i>) alters intestinal microbial structure and behavioral expression following social defeat stress. Scientific Reports, 2021, 11, 3763.	1.6	31

#	ARTICLE	IF	CITATIONS
4091	The dysbiosis of ovine foot microbiome during the development and treatment of contagious ovine digital dermatitis. <i>Animal Microbiome</i> , 2021, 3, 19.	1.5	18
4092	Human impacts on global freshwater fish biodiversity. <i>Science</i> , 2021, 371, 835-838.	6.0	262
4093	Gut microbiota alterations associated with antibody-mediated rejection after kidney transplantation. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2473-2484.	1.7	12
4094	Shifts in marine invertebrate bacterial assemblages associated with tissue necrosis during a heat wave. <i>Coral Reefs</i> , 2021, 40, 395-404.	0.9	12
4097	Data Analysis Strategies for Microbiome Studies in Human Populations—a Systematic Review of Current Practice. <i>MSystems</i> , 2021, 6, .	1.7	14
4098	Outdoor Atmospheric Microbial Diversity Is Associated With Urban Landscape Structure and Differs From Indoor-Transit Systems as Revealed by Mobile Monitoring and Three-Dimensional Spatial Analysis. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	10
4099	The Gut Microbial Composition Is Species-Specific and Individual-Specific in Two Species of Estrildid Finches, the Bengalese Finch and the Zebra Finch. <i>Frontiers in Microbiology</i> , 2021, 12, 619141.	1.5	13
4100	Ecosystem engineers drive differing microbial community composition in intertidal estuarine sediments. <i>PLoS ONE</i> , 2021, 16, e0240952.	1.1	12
4101	Decade-scale stability and change in a marine bivalve microbiome. <i>Molecular Ecology</i> , 2021, 30, 1237-1250.	2.0	15
4102	Intestinal mucosal microbiota composition of patients with acquired immune deficiency syndrome in Guangzhou, China. <i>Experimental and Therapeutic Medicine</i> , 2021, 21, 391.	0.8	4
4103	Gut Microbiome of Children and Adolescents With Primary Sclerosing Cholangitis in Association With Ulcerative Colitis. <i>Frontiers in Immunology</i> , 2020, 11, 598152.	2.2	18
4104	The amphibian microbiome exhibits poor resilience following pathogen-induced disturbance. <i>ISME Journal</i> , 2021, 15, 1628-1640.	4.4	38
4105	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. <i>Nature Metabolism</i> , 2021, 3, 274-286.	5.1	278
4106	<i>Helicobacter pylori</i> infection worsens impaired glucose regulation in high-fat diet mice in association with an altered gut microbiome and metabolome. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2081-2095.	1.7	16
4107	Conducting research on diet-microbiome interactions: A review of current challenges, essential methodological principles, and recommendations for best practice in study design. <i>Journal of Human Nutrition and Dietetics</i> , 2021, 34, 631-644.	1.3	23
4108	Structural and Functional Dysbiosis of Fecal Microbiota in Chinese Patients With Alzheimer's Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 634069.	1.8	91
4109	Hindgut Microbiota Reflects Different Digestive Strategies in Dung Beetles (Coleoptera: Scarabaeidae:). <i>Tj ETQq0 0 0 rgBT /Overlock 10</i>	1.4	22
4110	Allium-Based Phytobiotic Enhances Egg Production in Laying Hens through Microbial Composition Changes in Ileum and Cecum. <i>Animals</i> , 2021, 11, 448.	1.0	21

#	ARTICLE	IF	CITATIONS
4112	Adults with Prader-Willi syndrome exhibit a unique microbiota profile. BMC Research Notes, 2021, 14, 51.	0.6	4
4113	Changes in the gut microbial community of the eastern newt (<i>Notophthalmus viridescens</i>) across its three distinct life stages. FEMS Microbiology Ecology, 2021, 97, .	1.3	7
4114	Changes in Bacterial and Chemical Components and Growth Prediction for <i>Lactobacillus sakei</i> during Kimoto-Style Fermentation Starter Preparation in Sake Brewing: a Comprehensive Analysis. Applied and Environmental Microbiology, 2021, 87, .	1.4	14
4115	Organic Waste Substrates Induce Important Shifts in Gut Microbiota of Black Soldier Fly (<i>Hermetia</i>) Tj ETQq1 1 0.784314 rgBT /Overl Microbiology, 2021, 12, 635881.	1.5	46
4116	Spatially explicit depiction of a floral epiphytic bacterial community reveals role for environmental filtering within petals. MicrobiologyOpen, 2021, 10, e1158.	1.2	16
4117	Alpha-Gal Syndrome. TÃ¼rkiye KalÃ§a Cerrahisi Dergisi, 2021, 1, 102-106.	0.1	0
4118	Characterization of Bacterial Communities of Cold-Smoked Salmon during Storage. Foods, 2021, 10, 362.	1.9	19
4119	Metagenomic analysis of the gut microbiome composition associated with vitamin D supplementation in Taiwanese infants. Scientific Reports, 2021, 11, 2856.	1.6	14
4120	Land Use Effects on Airborne Bacterial Communities Are Evident in Both Near-Surface and Higher-Altitude Air. Diversity, 2021, 13, 85.	0.7	5
4121	Microbiomes of different ages in Rendzic Leptosols in the Crimean Peninsula. PeerJ, 2021, 9, e10871.	0.9	2
4122	Soil microbial composition and carbon mineralization are associated with vegetation type and temperature regime in mesocosms of a semiarid ecosystem. FEMS Microbiology Letters, 2021, 368, .	0.7	3
4123	Development of a novel model of cholecystectomy in subsequently ovariectomized mice and characterization of metabolic and gastrointestinal phenotypes: a pilot study. BMC Gastroenterology, 2021, 21, 62.	0.8	1
4124	Airflow limitation and tongue microbiota in community-dwelling elderly individuals. ERJ Open Research, 2021, 7, 00616-2020.	1.1	0
4125	Microbial Community Dynamics of Soybean (<i>Glycine max</i>) Is Affected by Cropping Sequence. Frontiers in Microbiology, 2021, 12, 632280.	1.5	11
4126	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature Microbiology, 2021, 6, 499-511.	5.9	116
4127	Deep-Sea Nematodes of the Mozambique Channel: Evidence of Random Community Assembly Dynamics in Seep Sediments. Frontiers in Marine Science, 2021, 8, .	1.2	3
4129	Alterations in Gut Microbial Communities Across Anatomical Locations in Inflammatory Bowel Diseases. Frontiers in Nutrition, 2021, 8, 615064.	1.6	14
4130	The microbial dimension of submarine groundwater discharge: current challenges and future directions. FEMS Microbiology Reviews, 2021, 45, .	3.9	38

#	ARTICLE	IF	CITATIONS
4131	Microbial community compositions and sulfate-reducing bacterial profiles in malodorous urban canal sediments. <i>Archives of Microbiology</i> , 2021, 203, 1981-1993.	1.0	7
4132	Prostaglandin E ₂ promotes intestinal inflammation via inhibiting microbiota-dependent regulatory T cells. <i>Science Advances</i> , 2021, 7, .	4.7	44
4133	Resource aromaticity affects bacterial community successions in response to different sources of dissolved organic matter. <i>Water Research</i> , 2021, 190, 116776.	5.3	101
4134	Effects of cotton-maize rotation on soil microbiome structure. <i>Molecular Plant Pathology</i> , 2021, 22, 673-682.	2.0	17
4135	Ancient grains as novel dietary carbohydrate sources in canine diets. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	5
4136	A Statistical Perspective on the Challenges in Molecular Microbial Biology. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2021, 26, 131-160.	0.7	10
4137	Weaning Age Affects the Development of the Ruminal Bacterial and Archaeal Community in Hu Lambs During Early Life. <i>Frontiers in Microbiology</i> , 2021, 12, 636865.	1.5	10
4138	Effect of stocking density on performance, meat quality and cecal bacterial communities of yellow feather broilers. <i>Animal Biotechnology</i> , 2022, 33, 1322-1332.	0.7	6
4139	Longitudinal metabarcoding analysis of karst bacterioplankton microbiomes provide evidence of epikarst to cave transport and community succession. <i>PeerJ</i> , 2021, 9, e10757.	0.9	9
4140	Cottonseed Press Cake as a Potential Diet for Industrially Farmed Black Soldier Fly Larvae Triggers Adaptations of Their Bacterial and Fungal Gut Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 634503.	1.5	30
4142	Comparative Analysis of Gut Microbiota in Captive and Wild Oriental White Storks: Implications for Conservation Biology. <i>Frontiers in Microbiology</i> , 2021, 12, 649466.	1.5	17
4143	A zero-inflated non-negative matrix factorization for the deconvolution of mixed signals of biological data. <i>International Journal of Biostatistics</i> , 2022, 18, 203-218.	0.4	2
4144	Effects of Clinical Wastewater on the Bacterial Community Structure from Sewage to the Environment. <i>Microorganisms</i> , 2021, 9, 718.	1.6	8
4145	Relative contributions of egg-associated and substrate-associated microorganisms to black soldier fly larval performance and microbiota. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	12
4147	Distance-Based Analysis with Quantile Regression Models. <i>Statistics in Biosciences</i> , 2021, 13, 291-312.	0.6	0
4148	Gut microbial ecology of the Critically Endangered Fijian crested iguana (<i>Brachylophus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Ecology and Evolution, 2021, 11, 4731-4743.	0.8	12
4149	Gut microbiota determines the social behavior of mice and induces metabolic and inflammatory changes in their adipose tissue. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 28.	2.9	35
4150	Climate change alters the haemolymph microbiome of oysters. <i>Marine Pollution Bulletin</i> , 2021, 164, 111991.	2.3	35

#	ARTICLE	IF	CITATIONS
4151	Lactulose significantly increased the relative abundance of <i>Bifidobacterium</i> and <i>Blautia</i> in mice feces as revealed by 16S rRNA amplicon sequencing. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 5721-5729.	1.7	6
4152	Soil Metagenomics Reveals Effects of Continuous Sugarcane Cropping on the Structure and Functional Pathway of Rhizospheric Microbial Community. <i>Frontiers in Microbiology</i> , 2021, 12, 627569.	1.5	80
4153	Different Effects of Mineral Versus Vegetal Granular Activated Carbon Filters on the Microbial Community Composition of a Drinking Water Treatment Plant. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	3
4155	Consumption of Select Dietary Emulsifiers Exacerbates the Development of Spontaneous Intestinal Adenoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2602.	1.8	16
4156	Gut microbiota dysbiosis is associated with worse emotional states in HIV infection. <i>Journal of NeuroVirology</i> , 2021, 27, 228-238.	1.0	7
4157	Influence of Temperature and Sulfate Concentration on the Sulfate/Sulfite Reduction Prokaryotic Communities in the Tibetan Hot Springs. <i>Microorganisms</i> , 2021, 9, 583.	1.6	8
4158	Gut microbiota in patients with newly diagnosed acromegaly: a pilot cross-sectional study. <i>Pituitary</i> , 2021, 24, 600-610.	1.6	9
4159	Livestock Manure Type Affects Microbial Community Composition and Assembly During Composting. <i>Frontiers in Microbiology</i> , 2021, 12, 621126.	1.5	52
4160	Biomat Resilience to Desiccation and Flooding Within a Shallow, Unit Process Open Water Engineered Wetland. <i>Water (Switzerland)</i> , 2021, 13, 815.	1.2	5
4161	Changes in physicochemical properties, enzymatic activities, and the microbial community of soil significantly influence the continuous cropping of <i>Panax quinquefolius</i> L. (American ginseng). <i>Plant and Soil</i> , 2021, 463, 427-446.	1.8	66
4162	Identification of microorganisms responsible for foam formation in mesophilic anaerobic digesters treating surplus activated sludge. <i>Water Research</i> , 2021, 191, 116779.	5.3	18
4163	Analysis of Soil Fungal and Bacterial Communities in Tianchi Volcano Crater, Northeast China. <i>Life</i> , 2021, 11, 280.	1.1	11
4164	Rapid enrichment of anammox bacteria linked to floc aggregates in a single-stage partial nitrification-anammox process: Providing the initial carrier and anaerobic microenvironment. <i>Water Research</i> , 2021, 191, 116807.	5.3	60
4165	Bacterial community analysis of purulent material from liver abscesses of crossbred cattle and Holstein steers fed finishing diets with or without tylosin. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	14
4166	Association of maternal gut microbiota and plasma metabolism with congenital heart disease in offspring: a multi-omic analysis. <i>Scientific Reports</i> , 2021, 11, 5339.	1.6	11
4167	Evaluation of the gut microbiome in association with biological signatures of inflammation in murine polytrauma and shock. <i>Scientific Reports</i> , 2021, 11, 6665.	1.6	7
4170	Characteristics of soil bacterial and fungal communities on interval seawater covering Linchang Island, China. <i>Archives of Microbiology</i> , 2021, 203, 2453-2461.	1.0	1
4171	Associations between the gut microbiome and fatigue in cancer patients. <i>Scientific Reports</i> , 2021, 11, 5847.	1.6	24

#	ARTICLE	IF	CITATIONS
4172	Nonlinear machine learning pattern recognition and bacteria-metabolite multilayer network analysis of perturbed gastric microbiome. <i>Nature Communications</i> , 2021, 12, 1926.	5.8	22
4173	Biocultural Drivers of Salivary Microbiota in Australian Aboriginal and Torres Strait Islander Children. <i>Frontiers in Oral Health</i> , 2021, 2, 641328.	1.2	6
4174	Long-term storage of feces at 80 °C versus 20 °C is negligible for 16S rRNA amplicon profiling of the equine bacterial microbiome. <i>PeerJ</i> , 2021, 9, e10837.	0.9	7
4175	Microbial community structure in a host-parasite system: the case of Prussian carp and its parasitic crustaceans. <i>Journal of Applied Microbiology</i> , 2021, 131, 1722-1741.	1.4	10
4176	Enterolignan Production in a Flaxseed Intervention Study in Postmenopausal US Women of African Ancestry and European Ancestry. <i>Nutrients</i> , 2021, 13, 919.	1.7	9
4177	Dental chews positively shift the oral microbiota of adult dogs. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	9
4178	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
4179	Compositional and Functional Changes in the Gut Microbiota in Irritable Bowel Syndrome Patients. <i>Gut and Liver</i> , 2021, 15, 253-261.	1.4	25
4180	Effects of phenylbutazone alone or in combination with a nutritional therapeutic on gastric ulcers, intestinal permeability, and fecal microbiota in horses. <i>Journal of Veterinary Internal Medicine</i> , 2021, 35, 1121-1130.	0.6	8
4181	<i>Verticillium dahliae</i> Inoculation and in vitro Propagation Modify the Xylem Microbiome and Disease Reaction to <i>Verticillium</i> Wilt in a Wild Olive Genotype. <i>Frontiers in Plant Science</i> , 2021, 12, 632689.	1.7	14
4182	Evaluation of Established Methods for DNA Extraction and Primer Pairs Targeting 16S rRNA Gene for Bacterial Microbiota Profiling of Olive Xylem Sap. <i>Frontiers in Plant Science</i> , 2021, 12, 640829.	1.7	14
4183	Allium Extract Implements Weaned Piglet's Productive Parameters by Modulating Distal Gut Microbiota. <i>Antibiotics</i> , 2021, 10, 269.	1.5	14
4185	mSphere of Influence: Drivers of Host-Associated Microbial Community Structure and Change. <i>MSphere</i> , 2021, 6, .	1.3	1
4186	Rootstocks Shape Their Microbiome's Bacterial Communities in the Rhizosphere of Different Grapevine Rootstocks. <i>Microorganisms</i> , 2021, 9, 822.	1.6	18
4187	Traffic generated emissions alter the lung microbiota by promoting the expansion of Proteobacteria in C57Bl/6 mice placed on a high-fat diet. <i>Ecotoxicology and Environmental Safety</i> , 2021, 213, 112035.	2.9	11
4188	Identification of new eligible indicator organisms for combined sewer overflow via 16S rRNA gene amplicon sequencing in Kanda River, Tokyo. <i>Journal of Environmental Management</i> , 2021, 284, 112059.	3.8	10
4189	<i>Macrobodella decora</i> : Old World Leech Gut Microbial Community Structure Conserved in a New World Leech. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	4
4190	Nutraceuticals Induced Changes in the Broiler Gastrointestinal Tract Microbiota. <i>MSystems</i> , 2021, 6, .	1.7	10

#	ARTICLE	IF	CITATIONS
4191	Gut Structure and Microbial Communities in <i>Sirex noctilio</i> (Hymenoptera: Siricidae) and Their Predicted Contribution to Larval Nutrition. <i>Frontiers in Microbiology</i> , 2021, 12, 641141.	1.5	12
4192	Diversity and composition of pollen loads carried by pollinators are primarily driven by insect traits, not floral community characteristics. <i>Oecologia</i> , 2021, 196, 131-143.	0.9	25
4193	Effect of Bovine Milk Fat Globule Membrane and Lactoferrin in Infant Formula on Gut Microbiome and Metabolome at 4 Months of Age. <i>Current Developments in Nutrition</i> , 2021, 5, nzab027.	0.1	9
4194	Ecological and Evolutionary responses to Antibiotic Treatment in the Human Gut Microbiota. <i>FEMS Microbiology Reviews</i> , 2021, 45, .	3.9	21
4195	Divergent airway microbiomes in lung transplant recipients with or without pulmonary infection. <i>Respiratory Research</i> , 2021, 22, 118.	1.4	8
4197	Metagenomic Analysis of Microbial Composition Revealed Cross-Contamination Pathway of Bacteria at a Foodservice Facility. <i>Frontiers in Microbiology</i> , 2021, 12, 636329.	1.5	11
4198	The Bacterial Community Diversity of Bathroom Hot Tap Water Was Significantly Lower Than That of Cold Tap and Shower Water. <i>Frontiers in Microbiology</i> , 2021, 12, 625324.	1.5	8
4200	<i>Streptomyces</i> strains modulate dynamics of soil bacterial communities and their efficacy in disease suppression caused by <i>Phytophthora capsici</i> . <i>Scientific Reports</i> , 2021, 11, 9317.	1.6	25
4201	Orange Juice and Yogurt Carrying Probiotic <i>Bacillus coagulans</i> GBI-30 6086: Impact of Intake on Wistar Male Rats Health Parameters and Gut Bacterial Diversity. <i>Frontiers in Microbiology</i> , 2021, 12, 623951.	1.5	13
4202	The microbial diversity following antibiotic treatment of <i>Clostridioides difficile</i> infection. <i>BMC Gastroenterology</i> , 2021, 21, 166.	0.8	8
4203	Tonsillar Microbiota: a Cross-Sectional Study of Patients with Chronic Tonsillitis or Tonsillar Hypertrophy. <i>MSystems</i> , 2021, 6, .	1.7	7
4204	Oral administration of <i>Lactobacillus crispatus</i> M247 to papillomavirus-infected women: results of a preliminary, uncontrolled, open trial. <i>Minerva Obstetrics and Gynecology</i> , 2021, 73, 621-631.	0.5	11
4205	Loss of Interleukin-10 (IL-10) Signaling Promotes IL-22-Dependent Host Defenses against Acute <i>Clostridioides difficile</i> Infection. <i>Infection and Immunity</i> , 2021, 89, .	1.0	6
4206	Presence of Bromotyrosine Alkaloids in Marine Sponges Is Independent of Metabolomic and Microbiome Architectures. <i>MSystems</i> , 2021, 6, .	1.7	18
4207	Adherent-invasive <i>E. coli</i> metabolism of propanediol in Crohn's disease regulates phagocytes to drive intestinal inflammation. <i>Cell Host and Microbe</i> , 2021, 29, 607-619.e8.	5.1	60
4208	Sea urchin microbiomes vary with habitat and resource availability. <i>Limnology and Oceanography Letters</i> , 2021, 6, 119-126.	1.6	4
4209	Next generation sequencing, insect microbiomes, and the confounding effect of <i>Wolbachia</i> : a case study using <i>Drosophila suzukii</i> Matsumura (Diptera: Drosophilidae). <i>Canadian Journal of Zoology</i> , 0, , .	0.4	4
4210	Prediction, enrichment and isolation identify a responsive, competitive community of cellulolytic microorganisms from a municipal landfill. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	3

#	ARTICLE	IF	CITATIONS
4211	Paraprobiotics obtained by six different inactivation processes: impacts on the biochemical parameters and intestinal microbiota of Wistar male rats. <i>International Journal of Food Sciences and Nutrition</i> , 2021, 72, 1057-1070.	1.3	10
4212	Diet-ruminal microbiome-host crosstalk contributes to differential effects of calf starter and alfalfa hay on rumen epithelial development and pancreatic \pm -amylase activity in yak calves. <i>Journal of Dairy Science</i> , 2021, 104, 4326-4340.	1.4	11
4213	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021, 6, .	1.7	22
4214	Bacterial Microbiota of Field-Collected <i>Helicoverpa zea</i> (Lepidoptera: Noctuidae) from Transgenic Bt and Non-Bt Cotton. <i>Microorganisms</i> , 2021, 9, 878.	1.6	10
4215	Brassica napus phyllosphere bacterial composition changes with growth stage. <i>Plant and Soil</i> , 2021, 464, 501-516.	1.8	13
4216	A Substrate-Independent Benthic Sampler (SIBS) for Hard and Mixed-Bottom Marine Habitats: A Proof-of-Concept Study. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	10
4217	Evaluation of sublethal and transgenerational effects of sulfoxaflor on <i>Aphis gossypii</i> via life table parameters and 16S rRNA sequencing. <i>Pest Management Science</i> , 2021, 77, 3406-3418.	1.7	19
4218	Prokaryotic community diversity during bioremediation of crude oil contaminated oilfield soil: effects of hydrocarbon concentration and salinity. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 787-800.	0.8	4
4219	Measuring change in biological communities: multivariate analysis approaches for temporal datasets with low sample size. <i>PeerJ</i> , 2021, 9, e11096.	0.9	12
4220	Effects of phytonutrient-supplemented diets on the intestinal microbiota of <i>Cyprinus carpio</i> . <i>PLoS ONE</i> , 2021, 16, e0248537.	1.1	10
4222	Inter-site and interpersonal diversity of salivary and tongue microbiomes, and the effect of oral care tablets. <i>F1000Research</i> , 2020, 9, 1477.	0.8	5
4224	Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. <i>Microbiome</i> , 2021, 9, 92.	4.9	40
4225	Tongue Microbiota Composition and Dental Caries Experience in Primary School Children. <i>MSphere</i> , 2021, 6, .	1.3	10
4226	When your host shuts down: larval diapause impacts host-microbiome interactions in <i>Nasonia vitripennis</i> . <i>Microbiome</i> , 2021, 9, 85.	4.9	18
4227	White and Red Sorghum as Primary Carbohydrate Sources in Extruded Diets of Felines. <i>Frontiers in Veterinary Science</i> , 2021, 8, 668255.	0.9	1
4228	Metabolic capabilities mute positive response to direct and indirect impacts of warming throughout the soil profile. <i>Nature Communications</i> , 2021, 12, 2089.	5.8	36
4229	Beneficial Effects of Natural Mineral Waters on Intestinal Inflammation and the Mucosa-Associated Microbiota. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4336.	1.8	10
4231	Metagenomic Geolocation Prediction Using an Adaptive Ensemble Classifier. <i>Frontiers in Genetics</i> , 2021, 12, 642282.	1.1	5

#	ARTICLE	IF	CITATIONS
4232	Response to Holmes " practical considerations for vector microbiome studies. <i>Molecular Ecology</i> , 2021, 30, 2214-2219.	2.0	1
4233	Reshaping of the gastrointestinal microbiome alters atherosclerotic plaque inflammation resolution in mice. <i>Scientific Reports</i> , 2021, 11, 8966.	1.6	11
4234	Changes in the ceca microbiota of broilers vaccinated for coccidiosis or supplemented with salinomycin. <i>Poultry Science</i> , 2021, 100, 100969.	1.5	20
4235	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
4236	The Gut Microbiome in Autism: Study-Site Effects and Longitudinal Analysis of Behavior Change. <i>MSystems</i> , 2021, 6, .	1.7	28
4238	Microbiota populations in supragingival plaque, subgingival plaque, and saliva habitats of adult dogs. <i>Animal Microbiome</i> , 2021, 3, 38.	1.5	13
4239	Long- and short-read metabarcoding technologies reveal similar spatiotemporal structures in fungal communities. <i>Molecular Ecology Resources</i> , 2021, 21, 1833-1849.	2.2	16
4240	A semiparametric model for between-subject attributes: Applications to beta-diversity of microbiome data. <i>Biometrics</i> , 2022, 78, 950-962.	0.8	5
4241	Oral administration of <i>Moringa oleifera</i> leaf powder relieves oxidative stress, modulates mucosal immune response and cecal microbiota after exposure to heat stress in New Zealand White rabbits. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 66.	2.1	17
4242	Effects of Vancomycin on Persistent Pain-Stimulated and Pain-Depressed Behaviors in Female Fischer Rats With or Without Voluntary Access to Running Wheels. <i>Journal of Pain</i> , 2021, 22, 1530-1544.	0.7	0
4243	Gut microbiome variation modulates the effects of dietary fiber on host metabolism. <i>Microbiome</i> , 2021, 9, 117.	4.9	61
4244	A combination of <i>Lactobacillus buchneri</i> and <i>Pediococcus pentosaceus</i> extended the aerobic stability of conventional and brown midrib mutants corn hybrids ensiled at low dry matter concentrations by causing a major shift in their bacterial and fungal community. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	8
4245	The Abundance of the <i>nifH</i> Gene Became Higher and the <i>nifH</i> -Containing Diazotrophic Bacterial Communities Changed During Primary Succession in the Hailuoguo Glacier Chronosequence, China. <i>Frontiers in Microbiology</i> , 2021, 12, 672656.	1.5	3
4246	Microbiological Activity during Co-Composting of Food and Agricultural Waste for Soil Amendment. <i>Agronomy</i> , 2021, 11, 928.	1.3	17
4247	Eukaryotic Biodiversity and Spatial Patterns in the Clarion-Clipperton Zone and Other Abyssal Regions: Insights From Sediment DNA and RNA Metabarcoding. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	33
4249	Glycan-based shaping of the microbiota during primate evolution. <i>ELife</i> , 2021, 10, .	2.8	8
4250	Effect of an intramammary lipopolysaccharide challenge on the hindgut microbial composition and fermentation of dairy cattle experiencing intermittent subacute ruminal acidosis. <i>Journal of Dairy Science</i> , 2021, 104, 5417-5431.	1.4	12
4251	Rumen Microbiota of Tibetan Sheep (<i>Ovis aries</i>) Adaptation to Extremely Cold Season on the Qinghai-Tibetan Plateau. <i>Frontiers in Veterinary Science</i> , 2021, 8, 673822.	0.9	18

#	ARTICLE	IF	CITATIONS
4252	Comparative Analysis of Milk Microbiomes and Their Association with Bovine Mastitis in Two Farms in Central Russia. <i>Animals</i> , 2021, 11, 1401.	1.0	9
4253	Sex differences in gut microbiota modulation of aversive conditioning, open field activity, and basolateral amygdala dendritic spine density. <i>Journal of Neuroscience Research</i> , 2021, 99, 1780-1801.	1.3	12
4254	Characterization of Microbiome on Feces, Blood and Milk in Dairy Cows with Different Milk Leucocyte Pattern. <i>Animals</i> , 2021, 11, 1463.	1.0	14
4255	Shiftwork, functional bowel symptoms, and the microbiome. <i>PeerJ</i> , 2021, 9, e11406.	0.9	5
4256	Different enzymatic associations in diets of broiler chickens formulated with corn dried at various temperatures. <i>Poultry Science</i> , 2021, 100, 101013.	1.5	5
4257	Comparison of the effects of acetic acid bacteria and lactic acid bacteria on the microbial diversity of and the functional pathways in dough as revealed by high-throughput metagenomics sequencing. <i>International Journal of Food Microbiology</i> , 2021, 346, 109168.	2.1	14
4258	The Investigation of the Connections Among Hydrogeological Factors and the Emissions of Two Greenhouse Gases in Lake Sediment. <i>Water Resources Research</i> , 2021, 57, e2020WR029375.	1.7	7
4259	Phylogeny- and Abundance-Based Metrics Allow for the Consistent Comparison of Core Gut Microbiome Diversity Indices Across Host Species. <i>Frontiers in Microbiology</i> , 2021, 12, 659918.	1.5	14
4260	The role of intestinal microbiota of the marine fish (<i>Acanthopagrus latus</i>) in mercury biotransformation. <i>Environmental Pollution</i> , 2021, 277, 116768.	3.7	22
4261	Comparison of Gut Microbiota Between Infants with Atopic Dermatitis and Healthy Controls in Guangzhou, China. <i>Journal of Asthma and Allergy</i> , 2021, Volume 14, 493-500.	1.5	6
4262	Co-exposure to inorganic arsenic and fluoride prominently disrupts gut microbiota equilibrium and induces adverse cardiovascular effects in offspring rats. <i>Science of the Total Environment</i> , 2021, 767, 144924.	3.9	18
4263	Land use intensification destabilizes stream microbial biodiversity and decreases metabolic efficiency. <i>Science of the Total Environment</i> , 2021, 767, 145440.	3.9	6
4264	Chestnut Shell Tannins: Effects on Intestinal Inflammation and Dysbiosis in Zebrafish. <i>Animals</i> , 2021, 11, 1538.	1.0	16
4265	Antibiotic resistance, antimicrobial residues and bacterial community diversity in pasture-raised poultry, swine and beef cattle manures. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	13
4266	Insights into the taxonomic and functional characterization of agricultural crop core rhizobiomes and their potential microbial drivers. <i>Scientific Reports</i> , 2021, 11, 10068.	1.6	15
4267	Altered Nasal Microbiota Composition Associated with Development of Polyserositis by <i>Mycoplasma hyorhinis</i> . <i>Pathogens</i> , 2021, 10, 603.	1.2	10
4268	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
4269	Different Non-Structural Carbohydrates/Crude Proteins (NCS/CP) Ratios in Diet Shape the Gastrointestinal Microbiota of Water Buffalo. <i>Veterinary Sciences</i> , 2021, 8, 96.	0.6	2

#	ARTICLE	IF	CITATIONS
4272	Effects of Dietary Inclusion of Dry Hydrastis canadensis on Laying Performance, Egg Quality, Serum Biochemical Parameters and Cecal Microbiota in Laying Hens. <i>Animals</i> , 2021, 11, 1381.	1.0	2
4273	Binary Metabolic Phenotypes and Phenotype Diversity Metrics for the Functional Characterization of Microbial Communities. <i>Frontiers in Microbiology</i> , 2021, 12, 653314.	1.5	5
4274	Soil characteristics and microbial community response in rare earth mining areas in southern Jiangxi Province, China. <i>Environmental Science and Pollution Research</i> , 2021, 28, 56418-56431.	2.7	12
4276	In situ rumen degradation characteristics and bacterial colonization of whole cottonseed, cottonseed hull and cottonseed meal with different gossypol content. <i>AMB Express</i> , 2021, 11, 91.	1.4	9
4277	Nationality and body location alter human skin microbiome. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5241-5256.	1.7	18
4278	Dysbiosis exacerbates colitis by promoting ubiquitination and accumulation of the innate immune adaptor STING in myeloid cells. <i>Immunity</i> , 2021, 54, 1137-1153.e8.	6.6	46
4280	Evaluation of the Fecal Bacterial Communities of Angus Steers With Divergent Feed Efficiencies Across the Lifespan From Weaning to Slaughter. <i>Frontiers in Veterinary Science</i> , 2021, 8, 597405.	0.9	21
4281	Host Phylogeny and Diet Shape Gut Microbial Communities Within Bamboo-Feeding Insects. <i>Frontiers in Microbiology</i> , 2021, 12, 633075.	1.5	27
4282	Shifts in gut and vaginal microbiomes are associated with cancer recurrence time in women with ovarian cancer. <i>PeerJ</i> , 2021, 9, e11574.	0.9	16
4283	Characterization of salivary microbiota in elderly patients with type 2 diabetes mellitus: a matched case-control study. <i>Clinical Oral Investigations</i> , 2021, , 1.	1.4	14
4284	Sow Contact Is a Major Driver in the Development of the Nasal Microbiota of Piglets. <i>Pathogens</i> , 2021, 10, 697.	1.2	12
4285	Mediterranean Diet to Prevent the Development of Colon Diseases: A Meta-Analysis of Gut Microbiota Studies. <i>Nutrients</i> , 2021, 13, 2234.	1.7	42
4286	Microbiota regulate social behaviour via stress response neurons in the brain. <i>Nature</i> , 2021, 595, 409-414.	18.7	142
4287	Infant gut microbiome composition is associated with non-social fear behavior in a pilot study. <i>Nature Communications</i> , 2021, 12, 3294.	5.8	36
4288	Alterations in the Fecal Microbiome and Metabolome of Horses with Antimicrobial-Associated Diarrhea Compared to Antibiotic-Treated and Non-Treated Healthy Case Controls. <i>Animals</i> , 2021, 11, 1807.	1.0	20
4289	Effects of dietary lipid levels on growth performance, hepatic health, lipid metabolism and intestinal microbiota on <i>Trachinotus ovatus</i> . <i>Aquaculture Nutrition</i> , 2021, 27, 1554-1568.	1.1	16
4290	Habitat environmental factors influence intestinal microbial diversity of the short-faced moles (<i>Scaptochirus moschata</i>). <i>AMB Express</i> , 2021, 11, 93.	1.4	4
4291	Coffee Consumption Modulates Amoxicillin-Induced Dysbiosis in the Murine Gut Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 637282.	1.5	5

#	ARTICLE	IF	CITATIONS
4292	Responses of juvenile fathead minnow (<i>Pimephales promelas</i>) gut microbiome to a chronic dietary exposure of benzo[a]pyrene. <i>Environmental Pollution</i> , 2021, 278, 116821.	3.7	12
4293	Microbial ecology of alfalfa, radish, and rapeseed sprouts based on culture methods and 16S rRNA microbiome sequencing. <i>Food Research International</i> , 2021, 144, 110316.	2.9	15
4295	Microbial Profile Evaluation of Beef Steaks From Different Packaging and Retail Lighting Display Conditions. <i>Meat and Muscle Biology</i> , 2021, 5, .	0.7	3
4296	Miscanthus Grass as a Novel Functional Fiber Source in Extruded Feline Diets. <i>Frontiers in Veterinary Science</i> , 2021, 8, 668288.	0.9	4
4297	Natural genetic variation drives microbiome selection in the <i>Caenorhabditis elegans</i> gut. <i>Current Biology</i> , 2021, 31, 2603-2618.e9.	1.8	48
4298	Human encroachment into wildlife gut microbiomes. <i>Communications Biology</i> , 2021, 4, 800.	2.0	36
4300	Detection and isolation of Î²-conglycinin-susceptible gut indigenous bacteria from ICR mice fed high-sucrose diet. <i>Food Bioscience</i> , 2021, 41, 100994.	2.0	8
4301	Characterization of the microbiome of the invasive Asian toad in Madagascar across the expansion range and comparison with a native co-occurring species. <i>PeerJ</i> , 2021, 9, e11532.	0.9	7
4302	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	1.5	2
4304	Sex- and age-specific variation of gut microbiota in Brandt's voles. <i>PeerJ</i> , 2021, 9, e11434.	0.9	12
4305	Habitual Dietary Intake Affects the Altered Pattern of Gut Microbiome by Acarbose in Patients with Type 2 Diabetes. <i>Nutrients</i> , 2021, 13, 2107.	1.7	16
4306	Microbiomes of commercially-available pine nuts and sesame seeds. <i>PLoS ONE</i> , 2021, 16, e0252605.	1.1	2
4307	Supersaturated-oxygen aeration effects on a high-loaded membrane bioreactor (HL-MBR): Biological performance and microbial population dynamics. <i>Science of the Total Environment</i> , 2021, 771, 144847.	3.9	7
4308	Gut Microbiome Composition and Serum Metabolome Profile Among Individuals With Spinal Cord Injury and Normal Glucose Tolerance or Prediabetes/Type 2 Diabetes. <i>Archives of Physical Medicine and Rehabilitation</i> , 2022, 103, 702-710.	0.5	8
4309	The impact of propagule pressure on whole community invasions in biomethane-producing communities. <i>IScience</i> , 2021, 24, 102659.	1.9	7
4310	Social environment and genetics underlie body site-specific microbiomes of Yellowstone National Park gray wolves (<i>Canis lupus</i>). <i>Ecology and Evolution</i> , 2021, 11, 9472-9488.	0.8	10
4311	Quality of phytoplankton deposition structures bacterial communities at the water-sediment interface. <i>Molecular Ecology</i> , 2021, 30, 3515-3529.	2.0	6
4312	Optimized bacterial DNA isolation method for microbiome analysis of human tissues. <i>MicrobiologyOpen</i> , 2021, 10, e1191.	1.2	21

#	ARTICLE	IF	CITATIONS
4313	Gastric microbiota composition in patients with corpus atrophic gastritis. <i>Digestive and Liver Disease</i> , 2021, 53, 1580-1587.	0.4	10
4314	The effects of psyllium husk on gut microbiota composition and function in chronically constipated women of reproductive age using 16S rRNA gene sequencing analysis. <i>Aging</i> , 2021, 13, 15366-15383.	1.4	11
4315	Fecal Mycobiota Combined With Host Immune Factors Distinguish <i>Clostridioides difficile</i> Infection From Asymptomatic Carriage. <i>Gastroenterology</i> , 2021, 160, 2328-2339.e6.	0.6	22
4316	Shifts in the structure of rhizosphere bacterial communities of avocado after <i>Fusarium dieback</i> . <i>Rhizosphere</i> , 2021, 18, 100333.	1.4	11
4317	Probiotic Effects of <i>Lactobacillus fermentum</i> ZJUIDS06 and <i>Lactobacillus plantarum</i> ZY08 on Hypercholesteremic Golden Hamsters. <i>Frontiers in Nutrition</i> , 2021, 8, 705763.	1.6	26
4318	Identification of Microbiological Activities in Wet Flue Gas Desulfurization Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 675628.	1.5	1
4319	Comparison of bacterial communities in roots of selected trees with and without summer truffle (<i>Tuber aestivum</i>) ectomycorrhiza. <i>Folia Forestalia Polonica, Series A</i> , 2021, 63, 97-111.	0.1	2
4320	Composition and Associations of the Infant Gut Fungal Microbiota with Environmental Factors and Childhood Allergic Outcomes. <i>MBio</i> , 2021, 12, e0339620.	1.8	31
4321	Effect of Fungicide Application on Lowbush Blueberries Soil Microbiome. <i>Microorganisms</i> , 2021, 9, 1366.	1.6	8
4322	A probiotic has differential effects on allergic airway inflammation in A/J and C57BL/6 mice and is correlated with the gut microbiome. <i>Microbiome</i> , 2021, 9, 134.	4.9	14
4323	Oral Ferric Maltol Does Not Adversely Affect the Intestinal Microbiome of Patients or Mice, but Ferrous Sulphate Does. <i>Nutrients</i> , 2021, 13, 2269.	1.7	10
4324	Use of Legumes and Yeast as Novel Dietary Protein Sources in Extruded Canine Diets. <i>Frontiers in Veterinary Science</i> , 2021, 8, 667642.	0.9	9
4325	Consistency of Bacterial Communities in a Parasitic Worm: Variation Throughout the Life Cycle and Across Geographic Space. <i>Microbial Ecology</i> , 2022, 83, 724-738.	1.4	8
4326	Longitudinal Survey of Fecal Microbiota in Healthy Dogs Administered a Commercial Probiotic. <i>Frontiers in Veterinary Science</i> , 2021, 8, 664318.	0.9	4
4327	A pilot experiment to assess the efficiency of pharmaceutical plant wastewater treatment and the decreasing effluent toxicity to periphytic biofilms. <i>Journal of Hazardous Materials</i> , 2021, 411, 125121.	6.5	11
4328	Microbial community dynamics in a hatchery recirculating aquaculture system (RAS) of sole (<i>Solea</i>) Tj ETQq1 1 0.784314 rgBT ₁₇ /Overlo	1.7	17
4329	Control of <i>Streptomyces alfalfae</i> XY25T Over Clubroot Disease and Its Effect on Rhizosphere Microbial Community in Chinese Cabbage Field Trials. <i>Frontiers in Microbiology</i> , 2021, 12, 641556.	1.5	11
4330	Evaluation of different materials used for sealing of implant abutment access channel and the peri-implant sulcus microbiota: A 6-month, randomized controlled trial. <i>Clinical Oral Implants Research</i> , 2021, 32, 941-950.	1.9	3

#	ARTICLE	IF	CITATIONS
4332	Remodeling of the maternal gut microbiome during pregnancy is shaped by parity. <i>Microbiome</i> , 2021, 9, 146.	4.9	36
4333	Exploring the Potential of <i>Micrococcus luteus</i> Culture Supernatant With Resuscitation-Promoting Factor for Enhancing the Culturability of Soil Bacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 685263.	1.5	12
4334	A Phylogeny-Informed Analysis of the Global Coral-Symbiodiniaceae Interaction Network Reveals that Traits Correlated with Thermal Bleaching Are Specific to Symbiont Transmission Mode. <i>MSystems</i> , 2021, 6, .	1.7	5
4335	Changes in physico-chemical characteristics and viable bacterial communities during fermentation of alfalfa silages inoculated with <i>Lactobacillus plantarum</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 127.	1.7	11
4336	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. <i>ISME Communications</i> , 2021, 1, .	1.7	60
4337	Disentangling the syntrophic electron transfer mechanisms of <i>Candidatus geobacter eutrophica</i> through electrochemical stimulation and machine learning. <i>Scientific Reports</i> , 2021, 11, 15140.	1.6	8
4339	Gut Microbiota Regulates the Interaction between Diet and Genetics to Influence Glucose Tolerance. <i>Medicines (Basel, Switzerland)</i> , 2021, 8, 34.	0.7	4
4340	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. <i>Nature Medicine</i> , 2021, 27, 1432-1441.	15.2	216
4341	Culture-enriched community profiling improves resolution of the vertebrate gut microbiota. <i>Molecular Ecology Resources</i> , 2022, 22, 122-136.	2.2	12
4342	Resilience of Microbial Communities after Hydrogen Peroxide Treatment of a Eutrophic Lake to Suppress Harmful Cyanobacterial Blooms. <i>Microorganisms</i> , 2021, 9, 1495.	1.6	20
4344	Roux-en-Y Gastric Bypass Improved Insulin Resistance via Alteration of the Human Gut Microbiome and Alleviation of Endotoxemia. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	5
4345	Responses of cucumber (<i>Cucumis sativus</i> L.) rhizosphere microbial community to some agronomic management practices. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	4
4346	Data analysis workflow for the detection of canine vector-borne pathogens using 16S rRNA Next-Generation Sequencing. <i>BMC Veterinary Research</i> , 2021, 17, 262.	0.7	2
4347	Changes in the Microbial Community in Soybean Plots Treated with Biochar and Poultry Litter. <i>Agronomy</i> , 2021, 11, 1428.	1.3	6
4348	Side-by-side and exo-pitting degradation mechanism revealed from in vitro human fecal fermentation of granular starches. <i>Carbohydrate Polymers</i> , 2021, 263, 118003.	5.1	30
4350	Comparison of Preservation and Extraction Methods on Five Taxonomically Disparate Coral Microbiomes. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
4351	Comparative Analysis of Fecal Microbiomes From Wild Waterbirds to Poultry, Cattle, Pigs, and Wastewater Treatment Plants for a Microbial Source Tracking Approach. <i>Frontiers in Microbiology</i> , 2021, 12, 697553.	1.5	20
4353	In-vivo impact of common cosmetic preservative systems in full formulation on the skin microbiome. <i>PLoS ONE</i> , 2021, 16, e0254172.	1.1	9

#	ARTICLE	IF	CITATIONS
4354	Oral infection with a periodontal pathogen alters oral and gut microbiomes. <i>Anaerobe</i> , 2021, 71, 102399.	1.0	16
4355	Compositional and functional succession of bacterial and fungal communities is associated with changes in abiotic properties during pig manure composting. <i>Waste Management</i> , 2021, 131, 350-358.	3.7	30
4356	Molecular characterization of the bacterial communities present in sheep's milk and cheese produced in South Brazilian Region via 16S rRNA gene metabarcoding sequencing. <i>LWT - Food Science and Technology</i> , 2021, 147, 111579.	2.5	11
4357	Tree-aggregated predictive modeling of microbiome data. <i>Scientific Reports</i> , 2021, 11, 14505.	1.6	13
4358	Metabarcoding under Brine: Microbial Ecology of Five Hypersaline Lakes at Rottneest Island (WA, Australia). <i>Frontiers in Microbiology</i> , 2021, 12, 698674.	1.2	6
4359	The Mechanism Underlying of Long-Term Stable Indigo Reduction State in Indigo Fermentation Using Sukumo (Composted <i>Polygonum tinctorium</i> Leaves). <i>Frontiers in Microbiology</i> , 2021, 12, 698674.	1.5	6
4361	<i>Helicobacter pylori</i> infection-induced changes in the intestinal microbiota of 14-year-old or 15-year-old Japanese adolescents: a cross-sectional study. <i>BMJ Open</i> , 2021, 11, e047941.	0.8	3
4362	<i>Clostridium butyricum</i> enhances colonization resistance against <i>Clostridioides difficile</i> by metabolic and immune modulation. <i>Scientific Reports</i> , 2021, 11, 15007.	1.6	23
4363	Rhamnan sulphate from green algae <i>Monostroma nitidum</i> improves constipation with gut microbiome alteration in double-blind placebo-controlled trial. <i>Scientific Reports</i> , 2021, 11, 13384.	1.6	13
4364	Spatiotemporal variation in the fecal microbiota of mule deer is associated with proximate and future measures of host health. <i>BMC Veterinary Research</i> , 2021, 17, 258.	0.7	1
4365	The role of plant-pollinator interactions in structuring nectar microbial communities. <i>Journal of Ecology</i> , 2021, 109, 3379-3395.	1.9	22
4366	Diverse Profile of Fermentation Byproducts From Thin Stillage. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 695306.	2.0	16
4367	Dynamic Changes in the Nasal Microbiome Associated With Disease Activity in Patients With Granulomatosis With Polyangiitis. <i>Arthritis and Rheumatology</i> , 2021, 73, 1703-1712.	2.9	14
4368	The Nexus between Fire and Soil Bacterial Diversity in the African Miombo Woodlands of Niassa Special Reserve, Mozambique. <i>Microorganisms</i> , 2021, 9, 1562.	1.6	6
4369	Antibiotic-Induced Dysbiosis of Microbiota Promotes Chicken Lipogenesis by Altering Metabolomics in the Cecum. <i>Metabolites</i> , 2021, 11, 487.	1.3	18
4370	<i>Wolbachia</i> Strain wGri From the Tea Geometrid Moth <i>Ectropis grisescens</i> Contributes to Its Host's Fecundity. <i>Frontiers in Microbiology</i> , 2021, 12, 694466.	1.5	5
4371	Environmentally enriched housing conditions affect pig welfare, immune system and gut microbiota in early life. <i>Animal Microbiome</i> , 2021, 3, 52.	1.5	24
4372	Prokaryotic community diversity in the sediments of saline lagoons and its resistance to seasonal disturbances by water level cycles. <i>Journal of Soils and Sediments</i> , 2021, 21, 3169-3184.	1.5	5

#	ARTICLE	IF	CITATIONS
4373	Prokaryotic diversity and potentially pathogenic bacteria in vended foods and environmental samples. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	5
4374	Composition of the Fecal Microbiota of Piglets at Various Growth Stages. <i>Frontiers in Veterinary Science</i> , 2021, 8, 661671.	0.9	17
4375	Reduction of <i>Salmonella Infantis</i> on skin-on, bone-in chicken thighs by cetylpyridinium chloride application and the impact on the skin microbiota. <i>Poultry Science</i> , 2022, 101, 101409.	1.5	5
4376	Impact of Dietary Isoflavone Supplementation on the Fecal Microbiota and Its Metabolites in Postmenopausal Women. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 7939.	1.2	7
4377	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.	2.7	9
4379	Southwestern Bats and Their External Bacteria. <i>Western North American Naturalist</i> , 2021, 81, .	0.2	1
4380	Production and diversity of microorganisms associated with sinking particles in the subtropical North Pacific Ocean. <i>Limnology and Oceanography</i> , 2021, 66, 3255-3270.	1.6	12
4381	Strong host-specific selection and over-dominance characterize arbuscular mycorrhizal fungal root colonizers of coastal sand dune plants of the Mediterranean region. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
4382	Interactions between <i>Teladorsagia circumcincta</i> Infections and Microbial Composition of Sheep with or without Successful Monepantel Treatment—A Preliminary Study. <i>Ruminants</i> , 2021, 1, 31-45.	0.4	2
4383	Clinically Healthy Human Gingival Tissues Show Significant Inter-individual Variability in GCF Chemokine Expression and Subgingival Plaque Microbial Composition. <i>Frontiers in Oral Health</i> , 2021, 2, 689475.	1.2	7
4384	An Exploratory Study for the Association of Gut Microbiome with Efficacy of Immune Checkpoint Inhibitor in Patients with Hepatocellular Carcinoma. <i>Journal of Hepatocellular Carcinoma</i> , 2021, Volume 8, 809-822.	1.8	17
4385	Land use and season drive changes in soil microbial communities and related functions in agricultural soils. <i>Environmental DNA</i> , 2021, 3, 1214-1228.	3.1	14
4386	Differential Effects of Western and Mediterranean-Type Diets on Gut Microbiota: A Metagenomics and Metabolomics Approach. <i>Nutrients</i> , 2021, 13, 2638.	1.7	32
4387	Prolonged drought imparts lasting compositional changes to the rice root microbiome. <i>Nature Plants</i> , 2021, 7, 1065-1077.	4.7	111
4388	Measuring the absolute abundance of the microbiome by adding yeast containing 16S rRNA gene from a hyperthermophile. <i>MicrobiologyOpen</i> , 2021, 10, e1220.	1.2	3
4389	Response of Fecal Bacterial Flora to the Exposure of Fumonisin B1 in BALB/c Mice. <i>Toxins</i> , 2021, 13, 612.	1.5	3
4390	Gut microbiome is affected by gut region but robust to host physiological changes in captive active-season ground squirrels. <i>Animal Microbiome</i> , 2021, 3, 56.	1.5	5
4391	The microbial population structure and function of peanut peanut and their effects on aflatoxin contamination. <i>LWT - Food Science and Technology</i> , 2021, 148, 111285.	2.5	4

#	ARTICLE	IF	CITATIONS
4392	Plant- <i>β</i> -bacteria associations are phylogenetically structured in the phyllosphere. <i>Molecular Ecology</i> , 2021, 30, 5572-5587.	2.0	15
4393	Intercropping improves heavy metal phytoremediation efficiency through changing properties of rhizosphere soil in bamboo plantation. <i>Journal of Hazardous Materials</i> , 2021, 416, 125898.	6.5	60
4394	Spatial analysis of the root system coupled to microbial community inoculation shed light on rhizosphere bacterial community assembly. <i>Biology and Fertility of Soils</i> , 2021, 57, 973-989.	2.3	12
4396	Characterizing the Cattle Gut Microbiome in Farms with a High and Low Prevalence of Shiga Toxin Producing <i>Escherichia coli</i> . <i>Microorganisms</i> , 2021, 9, 1737.	1.6	8
4397	Oxidized Milk Induces Spatial Learning and Memory Impairment by Altering Gut Microbiota in Offspring Mice during Pregnancy and Lactation. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 9934-9946.	2.4	3
4398	Aboveground and belowground responses to cyanobacterial biofertilizer supplement in a semi-arid, perennial bioenergy cropping system. <i>GCB Bioenergy</i> , 2021, 13, 1908-1923.	2.5	4
4399	Resistance, resilience, and functional redundancy of freshwater bacterioplankton communities facing a gradient of agricultural stressors in a mesocosm experiment. <i>Molecular Ecology</i> , 2021, 30, 4771-4788.	2.0	12
4400	Biogeographic history and habitat specialization shape floristic and phylogenetic composition across Amazonian forests. <i>Ecological Monographs</i> , 2021, 91, e01473.	2.4	10
4401	Multi-Omics Analysis Reveals a Dependent Relationship Between Rumen Bacteria and Diet of Grass- and Grain-Fed Yaks. <i>Frontiers in Microbiology</i> , 2021, 12, 642959.	1.5	9
4402	Shifts in arbuscular mycorrhizal fungal community composition and edaphic variables during reclamation chronosequence of an open-cast coal mining dump. <i>Catena</i> , 2021, 203, 105301.	2.2	8
4403	Nutrient pollution alters the gut microbiome of a territorial reef fish. <i>Marine Pollution Bulletin</i> , 2021, 169, 112522.	2.3	15
4404	Truffle Microbiome Is Driven by Fruit Body Compartmentalization Rather than Soils Conditioned by Different Host Trees. <i>MSphere</i> , 2021, 6, e0003921.	1.3	10
4405	Infection Heterogeneity and Microbiota Differences in Chicks Infected by <i>Salmonella enteritidis</i> . <i>Microorganisms</i> , 2021, 9, 1705.	1.6	8
4406	Bacterial Community Patterns in the <i>Agaricus bisporus</i> Cultivation System, from Compost Raw Materials to Mushroom Caps. <i>Microbial Ecology</i> , 2022, 84, 20-32.	1.4	17
4407	Potential for Passive Treatment of Coal Mine-derived Acid Mine Drainage in Abandoned Stream Channels. <i>Mine Water and the Environment</i> , 0, , 1.	0.9	1
4408	Gut microbiome is associated with multiple sclerosis activity in children. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 1867-1883.	1.7	21
4409	A New Non-invasive Method for Collecting DNA From Small Mammals in the Field, and Its Application in Simultaneous Vector and Disease Monitoring in Brushtail Possums. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	4
4410	Lipocalin 2 Deficiency Restrains Aging-Related Reshaping of Gut Microbiota Structure and Metabolism. <i>Biomolecules</i> , 2021, 11, 1286.	1.8	3

#	ARTICLE	IF	CITATIONS
4411	Nodal immune flare mimics nodal disease progression following neoadjuvant immune checkpoint inhibitors in non-small cell lung cancer. <i>Nature Communications</i> , 2021, 12, 5045.	5.8	42
4412	Healthcare-Associated Infections-Related Bacteriome and Antimicrobial Resistance Profiling: Assessing Contamination Hotspots in a Developing Country Public Hospital. <i>Frontiers in Microbiology</i> , 2021, 12, 711471.	1.5	4
4413	Larvae of Deep-Sea Invertebrates Harbor Low-Diversity Bacterial Communities. <i>Biological Bulletin</i> , 2021, 241, 65-76.	0.7	0
4414	Do host-associated microbes show a contrarian latitudinal diversity gradient? Insights from <i>Mytilus californianus</i> , an intertidal foundation host. <i>Journal of Biogeography</i> , 2021, 48, 2839-2852.	1.4	6
4415	Alterations of gut microbiota in gestational diabetes patients during the second trimester of pregnancy in the Shanghai Han population. <i>Journal of Translational Medicine</i> , 2021, 19, 366.	1.8	14
4416	Diverse and abundant arbuscular mycorrhizal fungi in ecological floating beds used to treat eutrophic water. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 6959-6975.	1.7	6
4417	Establishment of Gut Microbiome During Early Life and Its Relationship With Growth in Endangered Crested Ibis (<i>Nipponia nippon</i>). <i>Frontiers in Microbiology</i> , 2021, 12, 723682.	1.5	14
4418	Temporal changes in total and metabolically active ruminal methanogens in dairy cows supplemented with 3-nitrooxypropanol. <i>Journal of Dairy Science</i> , 2021, 104, 8721-8735.	1.4	18
4419	Combined effects of BARLEYmax and cocoa polyphenols on colonic microbiota and bacterial metabolites in vitro. <i>Food Science and Biotechnology</i> , 2021, 30, 1417-1425.	1.2	3
4420	Changes in Bacterial Communities During Treatment of Municipal Wastewater in Arctic Wastewater Stabilization Ponds. <i>Frontiers in Water</i> , 2021, 3, .	1.0	2
4421	Maternal cecal microbiota transfer rescues early-life antibiotic-induced enhancement of type 1 diabetes in mice. <i>Cell Host and Microbe</i> , 2021, 29, 1249-1265.e9.	5.1	32
4422	Increase in carbohydrate content and variation in microbiome are related to the drought tolerance of <i>Codonopsis pilosula</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 165, 19-35.	2.8	12
4423	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	2.2	37
4424	Effects of dietary macronutrient profile on apparent total tract macronutrient digestibility and fecal microbiota, fermentative metabolites, and bile acids of female dogs after spay surgery. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	4
4425	Dietary and Pharmacologic Manipulations of Host Lipids and Their Interaction With the Gut Microbiome in Non-human Primates. <i>Frontiers in Medicine</i> , 2021, 8, 646710.	1.2	6
4426	Association of Increased Serum Lipopolysaccharide, But Not Microbial Dysbiosis, With Obesity-Related Osteoarthritis. <i>Arthritis and Rheumatology</i> , 2022, 74, 227-236.	2.9	21
4427	Administration of <i>Bifidobacterium bifidum</i> BGN4 and <i>Bifidobacterium longum</i> BORI Improves Cognitive and Memory Function in the Mouse Model of Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 709091.	1.7	29
4428	Individuals with substance use disorders have a distinct oral microbiome pattern. <i>Brain, Behavior, & Immunity - Health</i> , 2021, 15, 100271.	1.3	11

#	ARTICLE	IF	CITATIONS
4429	High Taxonomic Diversity in Ship Bilges Presents Challenges for Monitoring Microbial Corrosion and Opportunity To Utilize Community Functional Profiling. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0089021.	1.4	1
4430	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. <i>MSphere</i> , 2021, 6, e0045521.	1.3	12
4431	Colonization by the Red Imported Fire Ant, <i>Solenopsis invicta</i> , Modifies Soil Bacterial Communities. <i>Microbial Ecology</i> , 2022, 84, 240-256.	1.4	6
4434	Comparative analysis of the gut microbiota in bighead carp under different culture patterns. <i>Journal of Applied Microbiology</i> , 2022, 132, 1357-1369.	1.4	7
4436	Oral microbiota in xerostomia patients - A preliminary study. <i>Journal of Dental Sciences</i> , 2022, 17, 324-330.	1.2	7
4437	Exploring Changes in the Host Gut Microbiota During a Controlled Human Infection Model for <i>Campylobacter jejuni</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 702047.	1.8	6
4438	Effects of Inhaled Corticosteroid/Long-Acting β_2 -Agonist Combination on the Airway Microbiome of Patients with Chronic Obstructive Pulmonary Disease: A Randomized Controlled Clinical Trial (DISARM). <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 204, 1143-1152.	2.5	44
4439	Thermal discharge-induced seawater warming alters richness, community composition and interactions of bacterioplankton assemblages in a coastal ecosystem. <i>Scientific Reports</i> , 2021, 11, 17341.	1.6	10
4440	Characterization of gut microbiome and metabolome in <i>Helicobacter pylori</i> patients in an underprivileged community in the United States. <i>World Journal of Gastroenterology</i> , 2021, 27, 5575-5594.	1.4	16
4441	Next Generation Microbiome Research: Identification of Keystone Species in the Metabolic Regulation of Host-Gut Microbiota Interplay. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 719072.	1.8	21
4442	Effect of replacing barley silage with calcium oxide-treated barley straw on rumen fermentation, rumen microbiota, nutrient digestibility, and growth performance of finishing beef cattle. <i>Canadian Journal of Animal Science</i> , 2021, 101, 493-506.	0.7	3
4443	Gut microbiota alterations in response to sleep length among African-origin adults. <i>PLoS ONE</i> , 2021, 16, e0255323.	1.1	18
4444	Effect of Dietary Inulin Supplementation on the Gut Microbiota Composition and Derived Metabolites of Individuals Undergoing Hemodialysis: A Pilot Study. , 2021, 31, 512-522.		29
4445	Composition of the microbial communities at different body sites in women with preterm birth and their newborns. <i>Medicine in Microecology</i> , 2021, 9, 100046.	0.7	3
4446	Oscillating dietary crude protein concentrations increase N retention of calves by affecting urea-N recycling and nitrogen metabolism of rumen bacteria and epithelium. <i>PLoS ONE</i> , 2021, 16, e0257417.	1.1	4
4447	Biogeography rather than substrate type determines bacterial colonization dynamics of marine plastics. <i>PeerJ</i> , 2021, 9, e12135.	0.9	15
4448	Pumping supplies alter the microbiome of pumped human milk: An in-home, randomized, crossover trial. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 1960-1970.	2.2	5
4449	Bridging the Gap between Analytical and Microbial Sciences in Microbiome Research. <i>MSystems</i> , 2021, 6, e0058521.	1.7	4

#	ARTICLE	IF	CITATIONS
4450	Learning, visualizing and exploring 16S rRNA structure using an attention-based deep neural network. <i>PLoS Computational Biology</i> , 2021, 17, e1009345.	1.5	13
4452	Patterns of bacterial diversity in embryonic capsules of the spotted salamander <i>Ambystoma maculatum</i> : an expanding view of a symbiosis. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	8
4453	Geography-dependent symbiont communities in two oligophagous aphid species. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
4454	Regime transition Shapes the Composition, Assembly Processes, and Co-occurrence Pattern of Bacterioplankton Community in a Large Eutrophic Freshwater Lake. <i>Microbial Ecology</i> , 2022, 84, 336-350.	1.4	4
4455	Rumen bacteria influence milk protein yield of yak grazing on the Qinghai-Tibet plateau. <i>Animal Bioscience</i> , 2021, 34, 1466-1478.	0.8	8
4456	Limitation and Potential Effects of Different Levels of Aging Corn on Performance, Antioxidative Capacity, Intestinal Health, and Microbiota in Broiler Chickens. <i>Animals</i> , 2021, 11, 2832.	1.0	2
4457	Breeding Strategy Shapes the Composition of Bacterial Communities in Female Nile Tilapia Reared in a Recirculating Aquaculture System. <i>Frontiers in Microbiology</i> , 2021, 12, 709611.	1.5	2
4458	Effects of <i>Helicobacter pylori</i> Infection on the Oral Microbiota of Reflux Esophagitis Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 732613.	1.8	8
4459	Community response of arbuscular mycorrhizal fungi to extreme drought in a cold-temperate grassland. <i>New Phytologist</i> , 2022, 234, 2003-2017.	3.5	35
4460	Altered fecal microbiota composition in individuals who abuse methamphetamine. <i>Scientific Reports</i> , 2021, 11, 18178.	1.6	23
4461	Symbiotic germination and development of fully mycoheterotrophic plants convergently targeting similar Glomeraceae taxa. <i>Environmental Microbiology</i> , 2021, 23, 6328-6343.	1.8	3
4462	The value of gut microbiota to predict feed efficiency and growth of rabbits under different feeding regimes. <i>Scientific Reports</i> , 2021, 11, 19495.	1.6	13
4463	Extensive sex-specific and regional variations observed in the microbiome of <i>Dermacentor reticulatus</i> . <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101767.	1.1	4
4464	Study on the diversity of epiphytic bacteria on corn and alfalfa using Illumina MiSeq/NovaSeq high-throughput sequencing system. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	3
4465	Spatial distribution of sediment archaeal and bacterial communities relates to the source of organic matter and hypoxia – a biogeographical study on Lake Remoray (France). <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	2
4466	Full-Scale Clinical Data and Reshaped Intestinal Microbiome on a Short-Term Low-Phosphorus Diet among Healthy Adults. , 2021, 31, 448-458.		2
4467	Longitudinal patterns in the skin microbiome of wild, individually marked frogs from the Sierra Nevada, California. <i>ISME Communications</i> , 2021, 1, .	1.7	5
4468	Longitudinal patterns in sediment type and quality during daily flow regimes and following natural hazards in an urban estuary: a Hurricane Harvey retrospective. <i>Environmental Science and Pollution Research</i> , 2021, , 1.	2.7	1

#	ARTICLE	IF	CITATIONS
4469	Relative Importance of Deterministic and Stochastic Processes on Soil Microbial Community Assembly in Temperate Grasslands. <i>Microorganisms</i> , 2021, 9, 1929.	1.6	22
4470	Chemical, biochemical, and microbiological properties of Technosols produced from urban inorganic and organic wastes. <i>Journal of Soils and Sediments</i> , 2022, 22, 146-161.	1.5	3
4471	Gammaproteobacteria, a core taxon in the guts of soil fauna, are potential responders to environmental concentrations of soil pollutants. <i>Microbiome</i> , 2021, 9, 196.	4.9	46
4472	Microbiome of the Successful Freshwater Invader, the Signal Crayfish, and Its Changes along the Invasion Range. <i>Microbiology Spectrum</i> , 2021, 9, e0038921.	1.2	11
4473	Diversity and characteristics of raw milk microbiota from Korean dairy farms using metagenomic and culturomic analysis. <i>Food Control</i> , 2021, 127, 108160.	2.8	12
4474	Analyzing Type 2 Diabetes Associations with the Gut Microbiome in Individuals from Two Ethnic Backgrounds Living in the Same Geographic Area. <i>Nutrients</i> , 2021, 13, 3289.	1.7	17
4475	Colorectal Tumour Mucosa Microbiome Is Enriched in Oral Pathogens and Defines Three Subtypes That Correlate with Markers of Tumour Progression. <i>Cancers</i> , 2021, 13, 4799.	1.7	8
4476	Serra da Estrela PDO Cheese Microbiome as Revealed by Next Generation Sequencing. <i>Microorganisms</i> , 2021, 9, 2007.	1.6	9
4477	Agricultural Management Affects the Active Rhizosphere Bacterial Community Composition and Nitrification. <i>MSystems</i> , 2021, 6, e0065121.	1.7	15
4478	Free threonine in human breast milk is related to infant intestinal microbiota composition. <i>Amino Acids</i> , 2022, 54, 365-383.	1.2	4
4479	Characterization of oral and cloacal microbial communities of wild and rehabilitated loggerhead sea turtles (<i>Caretta caretta</i>). <i>Animal Microbiome</i> , 2021, 3, 59.	1.5	11
4480	Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. <i>Cell Reports Medicine</i> , 2021, 2, 100393.	3.3	39
4482	Salt tolerance of halotolerant bacteria from coastal soils and sediments near saltern field of Hainan Island, China. <i>Archives of Microbiology</i> , 2021, 203, 5921-5930.	1.0	2
4483	Diversity of <i>Treponema denticola</i> and Other Oral Treponeme Lineages in Subjects with Periodontitis and Gingivitis. <i>Microbiology Spectrum</i> , 2021, 9, e0070121.	1.2	19
4484	The Bacterial Diversity of Spontaneously Fermented Dairy Products Collected in Northeast Asia. <i>Foods</i> , 2021, 10, 2321.	1.9	14
4485	Effects 10Âyears elevated atmospheric CO2 on soil bacterial community structure in Sanjiang Plain, Northeastern China. <i>Plant and Soil</i> , 2022, 471, 73-87.	1.8	3
4486	Unexpected diversity of Endozoicomonas in deep-sea corals. <i>Marine Ecology - Progress Series</i> , 2021, 673, 1-15.	0.9	12
4487	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16

#	ARTICLE	IF	CITATIONS
4488	Intermittent aeration improving activated granular sludge granulation for nitrogen and phosphorus removal from domestic wastewater. <i>Bioresource Technology Reports</i> , 2021, 15, 100739.	1.5	5
4489	Low Diversity in Nasal Microbiome Associated With <i>Staphylococcus aureus</i> Colonization and Bloodstream Infections in Hospitalized Neonates. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab475.	0.4	6
4490	Microbiome and Metabolic Changes of Milk in Response to Dietary Supplementation With Bamboo Leaf Extract in Dairy Cows. <i>Frontiers in Nutrition</i> , 2021, 8, 723446.	1.6	6
4491	Sinomenine hydrochloride ameliorates dextran sulfate sodium-induced colitis in mice by modulating the gut microbiota composition whilst suppressing the activation of the NLRP3 inflammasome. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 1287.	0.8	14
4492	Relationship between airway dysbiosis, inflammation and lung function in adults with cystic fibrosis. <i>Journal of Cystic Fibrosis</i> , 2021, 20, 754-760.	0.3	25
4493	Metagenomic analysis of individually analyzed ticks from Eastern Europe demonstrates regional and sex-dependent differences in the microbiota of <i>Ixodes ricinus</i> . <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101768.	1.1	11
4494	Analysis of Matched Skin and Gut Microbiome of Patients with Vitiligo Reveals Deep Skin Dysbiosis: Link with Mitochondrial and Immune Changes. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2280-2290.	0.3	26
4495	Microbial diversity and physicochemical characteristics of tropical karst soils in the northeastern Yucatan peninsula, Mexico. <i>Applied Soil Ecology</i> , 2021, 165, 103969.	2.1	6
4496	Analysis of Stored Wheat Grain-Associated Microbiota Reveals Biocontrol Activity among Microorganisms against Mycotoxigenic Fungi. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 781.	1.5	8
4497	Microbiome Associated with the Mycangia of Female and Male Adults of the Ambrosia Beetle <i>Platypus cylindrus</i> Fab. (Coleoptera: Curculionidae). <i>Insects</i> , 2021, 12, 881.	1.0	4
4498	Carcass decay deteriorates water quality and modifies the nirS denitrifying communities in different degradation stages. <i>Science of the Total Environment</i> , 2021, 785, 147185.	3.9	16
4500	Diversity and Co-Occurrence Patterns of Fungal and Bacterial Communities from Alkaline Sediments and Water of Julong High-Altitude Hot Springs at Tianchi Volcano, Northeast China. <i>Biology</i> , 2021, 10, 894.	1.3	7
4501	Guadipyr, a new insecticide, induces microbiota dysbiosis and immune disorders in the midgut of silkworms (<i>Bombyx mori</i>). <i>Environmental Pollution</i> , 2021, 286, 117531.	3.7	11
4502	The diversity of soil mesofauna declines after bamboo invasion in subtropical China. <i>Science of the Total Environment</i> , 2021, 789, 147982.	3.9	14
4503	Effects of feed ration and temperature on Chinook salmon (<i>Oncorhynchus tshawytscha</i>) microbiota in freshwater recirculating aquaculture systems. <i>Aquaculture</i> , 2021, 543, 736965.	1.7	23
4504	Low-level environmental metal pollution is associated with altered gut microbiota of a wild rodent, the bank vole (<i>Myodes glareolus</i>). <i>Science of the Total Environment</i> , 2021, 790, 148224.	3.9	15
4505	Impacts of PBDE-47 exposure before, during and after pregnancy on the maternal gut microbiome and its association with host metabolism. <i>Ecotoxicology and Environmental Safety</i> , 2021, 222, 112530.	2.9	10
4506	Deciphering the colonic fermentation characteristics of agavin and digestion-resistant maltodextrin in a simulated batch fermentation system. <i>International Journal of Biological Macromolecules</i> , 2021, 189, 151-159.	3.6	5

#	ARTICLE	IF	CITATIONS
4507	eDNA metabarcoding revealed differential structures of aquatic communities in a dynamic freshwater ecosystem shaped by habitat heterogeneity. <i>Environmental Research</i> , 2021, 201, 111602.	3.7	28
4508	<i>Ruminiclostridium 5</i> , <i>Parabacteroides distasonis</i> , and bile acid profile are modulated by prebiotic diet and associate with facilitated sleep/clock realignment after chronic disruption of rhythms. <i>Brain, Behavior, and Immunity</i> , 2021, 97, 150-166.	2.0	34
4509	Effects of ShenLing BaiZhu San Supplementation on Gut Microbiota and Oxidative Stress in Rats with Ulcerative Colitis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-8.	0.5	10
4510	Microbiological assessment of ecological status in the Pearl River Estuary, China. <i>Ecological Indicators</i> , 2021, 130, 108084.	2.6	8
4511	The Alteration human of gut microbiota and metabolites before and after renal transplantation. <i>Microbial Pathogenesis</i> , 2021, 160, 105191.	1.3	4
4512	<i>Rhizobium alarii</i> improves water stress tolerance in a non-legume. <i>Science of the Total Environment</i> , 2021, 797, 148895.	3.9	17
4513	Assessment of the fungal community associated with cocoa bean fermentation from two regions in Colombia. <i>Food Research International</i> , 2021, 149, 110670.	2.9	4
4514	Effects of design parameters, microbial community and nitrogen removal on the field-scale multi-pond constructed wetlands. <i>Science of the Total Environment</i> , 2021, 797, 148989.	3.9	14
4515	In vitro fecal fermentation outcomes of starch-lipid complexes depend on starch assembles more than lipid type. <i>Food Hydrocolloids</i> , 2021, 120, 106941.	5.6	28
4516	Characterization of the blood microbiota in children with Celiac disease. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100069.	1.4	0
4517	Influence of compost and biochar on soil biological properties under turfgrass supplied deficit irrigation. <i>Applied Soil Ecology</i> , 2021, 168, 104134.	2.1	17
4518	Localized reshaping of the fungal community in response to a forest fungal pathogen reveals resilience of Mediterranean mycobiota. <i>Science of the Total Environment</i> , 2021, 800, 149582.	3.9	7
4519	Oral seeding and niche-adaptation of middle ear biofilms in health. <i>Biofilm</i> , 2021, 3, 100041.	1.5	4
4520	Perfluorinated compounds (PFCs) in regional industrial rivers: Interactions between pollution flux and eukaryotic community phylosymbiosis. <i>Environmental Research</i> , 2022, 203, 111876.	3.7	10
4521	Temperature dependence of sequential chlorinated ethenes dechlorination and the dynamics of dechlorinating microorganisms. <i>Chemosphere</i> , 2022, 287, 131989.	4.2	13
4522	Hydrogen-rich water ameliorates neuropathological impairments in a mouse model of Alzheimer's disease through reducing neuroinflammation and modulating intestinal microbiota. <i>Neural Regeneration Research</i> , 2022, 17, 409.	1.6	12
4523	The response of sediment microbial communities to temporal and site-specific variations of pollution in interconnected aquaculture pond and ditch systems. <i>Science of the Total Environment</i> , 2022, 806, 150498.	3.9	24
4524	Impact of polypropylene microplastics and chemical pollutants on European sea bass (<i>Dicentrarchus labrax</i>) Tj ETQq1 1 0.784314 rgBT /Ove	3.9	39

#	ARTICLE	IF	CITATIONS
4525	Effects of environmental factors on soil bacterial community structure and diversity in different contaminated districts of Southwest China mine tailings. <i>Science of the Total Environment</i> , 2022, 802, 149899.	3.9	69
4526	The alteration of gut microbiome community play an important role in mercury biotransformation in largemouth bass. <i>Environmental Research</i> , 2022, 204, 112026.	3.7	14
4527	Response of soil bacterial community to agricultural reclamation in the Tengger desert, northwestern China. <i>Applied Soil Ecology</i> , 2022, 169, 104189.	2.1	6
4528	Microbial characteristics of the leachate contaminated soil of an informal landfill site. <i>Chemosphere</i> , 2022, 287, 132155.	4.2	42
4529	Straw return promoted the simultaneous elimination of sulfamethoxazole and related antibiotic resistance genes in the paddy soil. <i>Science of the Total Environment</i> , 2022, 806, 150525.	3.9	5
4531	MB-GAN: Microbiome Simulation via Generative Adversarial Network. <i>GigaScience</i> , 2021, 10, .	3.3	14
4532	Responses of soil microbiome to steel corrosion. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 6.	2.9	28
4534	Alterations of bacterial communities of vocal cord mucous membrane increases the risk for glottic laryngeal squamous cell carcinoma. <i>Journal of Cancer</i> , 2021, 12, 4049-4063.	1.2	8
4535	Spatial analysis of gut microbiome reveals a distinct ecological niche associated with the mucus layer. <i>Gut Microbes</i> , 2021, 13, 1874815.	4.3	40
4536	Pectin supplement significantly enhanced the anti-PD-1 efficacy in tumor-bearing mice humanized with gut microbiota from patients with colorectal cancer. <i>Theranostics</i> , 2021, 11, 4155-4170.	4.6	84
4537	A rarefaction-based extension of the LDM for testing presenceâ€“absence associations in the microbiome. <i>Bioinformatics</i> , 2021, 37, 1652-1657.	1.8	18
4538	Neonatal antibiotic exposure impairs child growth during the first six years of life by perturbing intestinal microbial colonization. <i>Nature Communications</i> , 2021, 12, 443.	5.8	113
4539	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. <i>Nature Genetics</i> , 2021, 53, 147-155.	9.4	101
4540	Yeast diversity in the vineyard: how it is defined, measured and influenced by fungicides. <i>Australian Journal of Grape and Wine Research</i> , 2021, 27, 169-193.	1.0	7
4541	Insights into Bacterial Community Involved in Bioremediation of Aged Oil-Contaminated Soil in Arid Environment. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110168.	0.6	4
4542	Machine learning applications in microbial ecology, human microbiome studies, and environmental monitoring. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1092-1107.	1.9	111
4543	Comparison and interpretation of characteristics of Rhizosphere microbiomes of three blueberry varieties. <i>BMC Microbiology</i> , 2021, 21, 30.	1.3	12
4546	Dysbiosis of urine microbiota in obstructive urinary retention patients revealed by next-generation sequencing. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 2.	1.7	5

#	ARTICLE	IF	CITATIONS
4547	DOCA salt hypertension and the role of the OVL sympathetic gut microbiome axis. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2021, 48, 490-497.	0.9	0
4548	Gut Microbiome Changes in Captive Plateau Zokors (<i>Eospalax baileyi</i>). <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432199635.	0.6	4
4549	Taxonomic Composition and Diversity of the Gut Microbiota in Relation to Habitual Dietary Intake in Korean Adults. <i>Nutrients</i> , 2021, 13, 366.	1.7	19
4550	Characterization of Salivary Microbiota in Patients with Atherosclerotic Cardiovascular Disease: A Case-Control Study. <i>Journal of Atherosclerosis and Thrombosis</i> , 2022, 29, 403-421.	0.9	16
4551	Parkinson's Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4552	A double-blind, 377-subject randomized study identifies <i>Ruminococcus</i> , <i>Coprococcus</i> , <i>Christensenella</i> , and <i>Collinsella</i> as long-term potential key players in the modulation of the gut microbiome of lactose intolerant individuals by galacto-oligosaccharides. <i>Gut Microbes</i> , 2021, 13, 1957536.	4.3	12
4553	Characterization of the marine aquaculture microbiome: A seasonal survey in a seabass farm. <i>Aquaculture</i> , 2021, 531, 735987.	1.7	11
4554	Comparison of microbial diversity in rumen and small intestine of Xinong Saanen dairy goats using 16S rRNA gene high-throughput sequencing. <i>Animal Production Science</i> , 2022, 62, 1379-1390.	0.6	5
4555	Development of a Flow-through Biofilm Reactor for Anammox Startup and Operation: Nitrogen Removal and Metacommunity. <i>ACS ES&T Water</i> , 2021, 1, 573-583.	2.3	6
4556	Grapevine Microbiota Reflect Diversity among Compartments and Complex Interactions within and among Root and Shoot Systems. <i>Microorganisms</i> , 2021, 9, 92.	1.6	29
4557	Intestinal microbial communities of rainbow trout (<i>Oncorhynchus mykiss</i>) may be improved by feeding a <i>Hermetia illucens</i> meal/low-fishmeal diet. <i>Fish Physiology and Biochemistry</i> , 2021, 47, 365-380.	0.9	60
4558	Immunoglobulin A Targets a Unique Subset of the Microbiota in Inflammatory Bowel Disease. <i>Cell Host and Microbe</i> , 2021, 29, 83-93.e3.	5.1	53
4561	Microbiome of Barrier Organs in Allergy: Who Runs the World? Germs!. <i>Handbook of Experimental Pharmacology</i> , 2021, 268, 53-65.	0.9	6
4562	Kernel Methods for Regression Analysis of Microbiome Compositional Data. <i>Springer Proceedings in Mathematics and Statistics</i> , 2013, , 191-201.	0.1	18
4564	Accurate Profiling of Microbial Communities from Massively Parallel Sequencing Using Convex Optimization. <i>Lecture Notes in Computer Science</i> , 2013, , 279-297.	1.0	1
4565	Microbiota and Lipotoxicity. <i>Advances in Experimental Medicine and Biology</i> , 2017, 960, 247-260.	0.8	1
4566	Compost Microbial Populations and Interactions with Plants. , 2010, , 231-251.		9
4567	The Genus <i>Bacteroides</i> . , 2014, , 459-484.		8

#	ARTICLE	IF	CITATIONS
4568	Intra-Field Variation of Prokaryotic Communities On and Below the Seafloor in the Back-Arc Hydrothermal System of the Southern Mariana Trough. , 2015, , 301-311.		3
4569	Large nitrogen oxide emission pulses from desert soils and associated microbiomes. Biogeochemistry, 2020, 149, 239-250.	1.7	20
4570	Dietary sanguinarine supplementation on the growth performance, immunity and intestinal health of grass carp (<i>Ctenopharyngodon idellus</i>) fed cottonseed and rapeseed meal diets. Aquaculture, 2020, 528, 735521.	1.7	28
4571	Bacterial community shifts in decomposing cowpats and the subsequent impacts on fecal source indicators for water quality monitoring. Ecological Indicators, 2020, 113, 106239.	2.6	6
4572	Abiotic processes dominate soil organic matter mineralization: Investigating the regulatory gate hypothesis by inoculating a previously fumigated soil with increasing fresh soil inocula. Geoderma, 2020, 373, 114400.	2.3	6
4573	Temporal analysis of the microbial communities in a nitrate-contaminated aquifer and the co-occurrence of anammox, n-damo and nitrous-oxide reducing bacteria. Journal of Contaminant Hydrology, 2020, 234, 103657.	1.6	13
4574	Effect of elevated temperature on cis-1,2-dichloroethene dechlorination and microbial community structure in contaminated soilsâ€”A biostimulation approach. Journal of Environmental Chemical Engineering, 2020, 8, 103682.	3.3	9
4575	Women's multisite microbial modulation during pregnancy. Microbial Pathogenesis, 2020, 147, 104230.	1.3	10
4576	Effects of laying breeder hens dietary Î²-carotene, curcumin, allicin, and sodium butyrate supplementation on the jejunal microbiota and immune response of their offspring chicks. Poultry Science, 2020, 99, 3807-3816.	1.5	13
4577	Shifts in a Phenanthrene-Degrading Microbial Community are Driven by Carbohydrate Metabolism Selection in a Ryegrass Rhizosphere. Environmental Science & Technology, 2021, 55, 962-973.	4.6	37
4578	Warming drives ecological community changes linked to host-associated microbiome dysbiosis. Nature Climate Change, 2020, 10, 1057-1061.	8.1	45
4579	Grain-rich diets altered the colonic fermentation and mucosa-associated bacterial communities and induced mucosal injuries in goats. Scientific Reports, 2016, 6, 20329.	1.6	74
4580	Altered Mucosal Microbiome Diversity and Disease Severity in Sjögren Syndrome. Scientific Reports, 2016, 6, 23561.	1.6	268
4581	Estimating diversity in networked ecological communities. Biostatistics, 2022, 23, 207-222.	0.9	92
4582	Stream sediment bacterial communities exhibit temporally-consistent and distinct thresholds to land use change in a mixed-use watershed. FEMS Microbiology Ecology, 2021, 97, .	1.3	9
4583	Graded dietary resistant starch concentrations on apparent total tract macronutrient digestibility and fecal fermentative end products and microbial populations of healthy adult dogs. Journal of Animal Science, 2021, 99, .	0.2	9
4584	Streptococcus and Prevotella are associated with the prognosis of oesophageal squamous cell carcinoma. Journal of Medical Microbiology, 2018, 67, 1058-1068.	0.7	49
4585	First insight into the faecal microbiota of the high Arctic muskoxen (<i>Ovibos moschatus</i>). Microbial Genomics, 2016, 2, e000066.	1.0	18

#	ARTICLE	IF	CITATIONS
4586	Increased productivity in poultry birds by sub-lethal dose of antibiotics is arbitrated by selective enrichment of gut microbiota, particularly short-chain fatty acid producers. <i>Microbiology (United Kingdom)</i> , 2020, 51, 505-526.	1.9	51
4668	Systematic review: the effects of proton pump inhibitors on the microbiome of the digestive tract—evidence from next-generation sequencing studies. <i>Alimentary Pharmacology and Therapeutics</i> , 2020, 51, 505-526.	1.9	51
4669	Microbial Biogeography: Patterns in Microbial Diversity across Space and Time. <i>Microbiology (United Kingdom)</i> , 2020, 51, 505-526.	1.9	51
4670	Genomic and Expression Analyses of Cold-Adapted Microorganisms. <i>Microbiology (United Kingdom)</i> , 2020, 51, 505-526.	1.9	51
4671	The Generalized Matrix Decomposition Biplot and Its Application to Microbiome Data. <i>MSystems</i> , 2019, 4, .	1.7	6
4672	Age matters: Submersion period shapes community composition of lake biofilms under glyphosate stress. <i>Facets</i> , 2018, 3, 934-951.	1.1	13
4673	Eventually consistent cardinality estimation with applications in biodata mining. <i>Microbiology (United Kingdom)</i> , 2020, 51, 505-526.	1.9	51
4674	Microbiota-dependent signals are required to sustain TLR-mediated immune responses. <i>JCI Insight</i> , 2019, 4, .	2.3	36
4675	Î²-Klotho deficiency protects against obesity through a crosstalk between liver, microbiota, and brown adipose tissue. <i>JCI Insight</i> , 2017, 2, .	2.3	41
4676	Gut microbiota modulates adoptive cell therapy via CD8 ⁺ dendritic cells and IL-12. <i>JCI Insight</i> , 2018, 3, .	2.3	111
4677	Gut microbiota modulate dendritic cell antigen presentation and radiotherapy-induced antitumor immune response. <i>Journal of Clinical Investigation</i> , 2019, 130, 466-479.	3.9	159
4678	The composition of the microbiota modulates allograft rejection. <i>Journal of Clinical Investigation</i> , 2016, 126, 2736-2744.	3.9	86
4679	Dynamics of Clostridium genus and hard-cheese spoiling Clostridium species in anaerobic digesters treating agricultural biomass. <i>AMB Express</i> , 2020, 10, 102.	1.4	8
4680	Microbiome and metabolic changes in milk in response to artemisinin supplementation in dairy cows. <i>AMB Express</i> , 2020, 10, 154.	1.4	13
4682	Analysis of Mucosa-Associated Microbiota in Colorectal Cancer. <i>Medical Science Monitor</i> , 2017, 23, 4422-4430.	0.5	71
4683	Health and saliva microbiomes of a semi-urbanized indigenous tribe in Peninsular Malaysia. <i>F1000Research</i> , 2019, 8, 175.	0.8	9
4684	Health and saliva microbiomes of a semi-urbanized indigenous tribe in Peninsular Malaysia. <i>F1000Research</i> , 2019, 8, 175.	0.8	8
4685	The influence of host genetics on the microbiome. <i>F1000Research</i> , 2020, 9, 84.	0.8	32

#	ARTICLE	IF	CITATIONS
4686	Inter-site and interpersonal diversity of salivary and tongue microbiomes, and the effect of oral care tablets. <i>F1000Research</i> , 2020, 9, 1477.	0.8	7
4687	NG-Tax, a highly accurate and validated pipeline for analysis of 16S rRNA amplicons from complex biomes. <i>F1000Research</i> , 2016, 5, 1791.	0.8	140
4688	NG-Tax, a highly accurate and validated pipeline for analysis of 16S rRNA amplicons from complex biomes. <i>F1000Research</i> , 2016, 5, 1791.	0.8	121
4689	Exploited Application of Pyrosequencing in Microbial Diversity of Activated Sludge System of Common Effluent Treatment Plants. <i>American Journal of Microbiological Research</i> , 2014, 2, 157-165.	0.2	2
4690	Phylosymbiosis: Relationships and Functional Effects of Microbial Communities across Host Evolutionary History. <i>PLoS Biology</i> , 2016, 14, e2000225.	2.6	475
4691	Antibiotic exposure perturbs the gut microbiota and elevates mortality in honeybees. <i>PLoS Biology</i> , 2017, 15, e2001861.	2.6	367
4692	Comprehensive Meta-analysis of Ontology Annotated 16S rRNA Profiles Identifies Beta Diversity Clusters of Environmental Bacterial Communities. <i>PLoS Computational Biology</i> , 2015, 11, e1004468.	1.5	23
4693	ESPRIT-Forest: Parallel clustering of massive amplicon sequence data in subquadratic time. <i>PLoS Computational Biology</i> , 2017, 13, e1005518.	1.5	16
4694	Amino acid metabolic signaling influences <i>Aedes aegypti</i> midgut microbiome variability. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005677.	1.3	67
4695	An Automated Phylogenetic Tree-Based Small Subunit rRNA Taxonomy and Alignment Pipeline (STAP). <i>PLoS ONE</i> , 2008, 3, e2566.	1.1	44
4696	Characterization of Coastal Urban Watershed Bacterial Communities Leads to Alternative Community-Based Indicators. <i>PLoS ONE</i> , 2010, 5, e11285.	1.1	66
4697	Characteristic Male Urine Microbiomes Associate with Asymptomatic Sexually Transmitted Infection. <i>PLoS ONE</i> , 2010, 5, e14116.	1.1	234
4698	Disordered Microbial Communities in the Upper Respiratory Tract of Cigarette Smokers. <i>PLoS ONE</i> , 2010, 5, e15216.	1.1	350
4699	High Genetic Diversity and Different Distributions of Glycosyl Hydrolase Family 10 and 11 Xylanases in the Goat Rumen. <i>PLoS ONE</i> , 2011, 6, e16731.	1.1	17
4700	Nitrogenase Gene Amplicons from Global Marine Surface Waters Are Dominated by Genes of Non-Cyanobacteria. <i>PLoS ONE</i> , 2011, 6, e19223.	1.1	176
4701	Comparison of Microbial Community Compositions of Injection and Production Well Samples in a Long-Term Water-Flooded Petroleum Reservoir. <i>PLoS ONE</i> , 2011, 6, e23258.	1.1	67
4702	Microbial Biogeography of Public Restroom Surfaces. <i>PLoS ONE</i> , 2011, 6, e28132.	1.1	222
4703	Prokaryotic and Eukaryotic Community Structure in Field and Cultured Microbialites from the Alkaline Lake Alchichica (Mexico). <i>PLoS ONE</i> , 2011, 6, e28767.	1.1	111

#	ARTICLE	IF	CITATIONS
4704	Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. PLoS ONE, 2012, 7, e30126.	1.1	653
4705	Composition and Similarity of Bovine Rumen Microbiota across Individual Animals. PLoS ONE, 2012, 7, e33306.	1.1	508
4706	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. PLoS ONE, 2012, 7, e36466.	1.1	572
4707	Office Space Bacterial Abundance and Diversity in Three Metropolitan Areas. PLoS ONE, 2012, 7, e37849.	1.1	114
4708	Dramatic Shifts in Benthic Microbial Eukaryote Communities following the Deepwater Horizon Oil Spill. PLoS ONE, 2012, 7, e38550.	1.1	139
4709	Metagenomics of the Svalbard Reindeer Rumen Microbiome Reveals Abundance of Polysaccharide Utilization Loci. PLoS ONE, 2012, 7, e38571.	1.1	190
4710	Exposure of Soil Microbial Communities to Chromium and Arsenic Alters Their Diversity and Structure. PLoS ONE, 2012, 7, e40059.	1.1	238
4711	The Cervical Microbiome over 7 Years and a Comparison of Methodologies for Its Characterization. PLoS ONE, 2012, 7, e40425.	1.1	101
4712	Soil Bacterial Diversity Screening Using Single 16S rRNA Gene V Regions Coupled with Multi-Million Read Generating Sequencing Technologies. PLoS ONE, 2012, 7, e42671.	1.1	92
4713	Compositional Stability of a Salivary Bacterial Population against Supragingival Microbiota Shift following Periodontal Therapy. PLoS ONE, 2012, 7, e42806.	1.1	66
4714	Phylogenetic Diversity and Environment-Specific Distributions of Glycosyl Hydrolase Family 10 Xylanases in Geographically Distant Soils. PLoS ONE, 2012, 7, e43480.	1.1	15
4715	Implications of Pyrosequencing Error Correction for Biological Data Interpretation. PLoS ONE, 2012, 7, e44357.	1.1	17
4716	Characterization of the Fecal Microbiota Using High-Throughput Sequencing Reveals a Stable Microbial Community during Storage. PLoS ONE, 2012, 7, e46953.	1.1	190
4717	Habitat-Associated Phylogenetic Community Patterns of Microbial Ammonia Oxidizers. PLoS ONE, 2012, 7, e47330.	1.1	55
4718	Sponge-Microbe Associations Survive High Nutrients and Temperatures. PLoS ONE, 2012, 7, e52220.	1.1	72
4719	Short-Read Assembly of Full-Length 16S Amplicons Reveals Bacterial Diversity in Subsurface Sediments. PLoS ONE, 2013, 8, e56018.	1.1	153
4720	Edge Principal Components and Squash Clustering: Using the Special Structure of Phylogenetic Placement Data for Sample Comparison. PLoS ONE, 2013, 8, e56859.	1.1	79
4721	In-situ Effects of Eutrophication and Overfishing on Physiology and Bacterial Diversity of the Red Sea Coral <i>Acropora hemprichii</i> . PLoS ONE, 2013, 8, e62091.	1.1	94

#	ARTICLE	IF	CITATIONS
4722	Invasion Is a Community Affair: Clandestine Followers in the Bacterial Community Associated to Green Algae, <i>Caulerpa racemosa</i> , Track the Invasion Source. PLoS ONE, 2013, 8, e68429.	1.1	63
4723	NaOH-Debitting Induces Changes in Bacterial Ecology during Table Olives Fermentation. PLoS ONE, 2013, 8, e69074.	1.1	75
4724	Change in Phylogenetic Community Structure during Succession of Traditionally Managed Tropical Rainforest in Southwest China. PLoS ONE, 2013, 8, e71464.	1.1	26
4725	Bacterial Community Mapping of the Mouse Gastrointestinal Tract. PLoS ONE, 2013, 8, e74957.	1.1	363
4726	Multilocus Sequence Analysis of Nectar Pseudomonads Reveals High Genetic Diversity and Contrasting Recombination Patterns. PLoS ONE, 2013, 8, e75797.	1.1	18
4727	Fecal Protease Activity Is Associated with Compositional Alterations in the Intestinal Microbiota. PLoS ONE, 2013, 8, e78017.	1.1	48
4728	Allelic Differences within and among Sister Spores of the Arbuscular Mycorrhizal Fungus <i>Glomus etunicatum</i> Suggest Segregation at Sporulation. PLoS ONE, 2013, 8, e83301.	1.1	19
4729	Impact of Technical Sources of Variation on the Hand Microbiome Dynamics of Healthcare Workers. PLoS ONE, 2014, 9, e88999.	1.1	20
4730	Age and Microenvironment Outweigh Genetic Influence on the Zucker Rat Microbiome. PLoS ONE, 2014, 9, e100916.	1.1	40
4731	Distribution and Diversity of Planktonic Fungi in the West Pacific Warm Pool. PLoS ONE, 2014, 9, e101523.	1.1	46
4732	Carbohydrate-Free Peach (<i>Prunus persica</i>) and Plum (<i>Prunus domestica</i>) Juice Affects Fecal Microbial Ecology in an Obese Animal Model. PLoS ONE, 2014, 9, e101723.	1.1	40
4733	Shift in the Microbial Ecology of a Hospital Hot Water System following the Introduction of an On-Site Monochloramine Disinfection System. PLoS ONE, 2014, 9, e102679.	1.1	62
4734	16S rRNA Gene Survey of Microbial Communities in Winogradsky Columns. PLoS ONE, 2014, 9, e104134.	1.1	32
4735	A Systems Biology Approach Investigating the Effect of Probiotics on the Vaginal Microbiome and Host Responses in a Double Blind, Placebo-Controlled Clinical Trial of Post-Menopausal Women. PLoS ONE, 2014, 9, e104511.	1.1	55
4736	Phylobetadiversity among Forest Types in the Brazilian Atlantic Forest Complex. PLoS ONE, 2014, 9, e105043.	1.1	63
4737	Amphibian Beta Diversity in the Brazilian Atlantic Forest: Contrasting the Roles of Historical Events and Contemporary Conditions at Different Spatial Scales. PLoS ONE, 2014, 9, e109642.	1.1	37
4738	Characterization of Egg Laying Hen and Broiler Fecal Microbiota in Poultry Farms in Croatia, Czech Republic, Hungary and Slovenia. PLoS ONE, 2014, 9, e110076.	1.1	70
4739	Bacterial Diversity Dynamics Associated with Different Diets and Different Primer Pairs in the Rumen of Kankrej Cattle. PLoS ONE, 2014, 9, e111710.	1.1	71

#	ARTICLE	IF	CITATIONS
4740	Bacterial Endophytic Communities in the Grapevine Depend on Pest Management. PLoS ONE, 2014, 9, e112763.	1.1	125
4741	Environmentally Determined Differences in the Murine Lung Microbiota and Their Relation to Alveolar Architecture. PLoS ONE, 2014, 9, e113466.	1.1	116
4742	Gut Microbiota and Tacrolimus Dosing in Kidney Transplantation. PLoS ONE, 2015, 10, e0122399.	1.1	133
4743	New Perspectives on Microbial Community Distortion after Whole-Genome Amplification. PLoS ONE, 2015, 10, e0124158.	1.1	35
4744	Biochar in Co-Contaminated Soil Manipulates Arsenic Solubility and Microbiological Community Structure, and Promotes Organochlorine Degradation. PLoS ONE, 2015, 10, e0125393.	1.1	45
4745	Chamber Bioaerosol Study: Outdoor Air and Human Occupants as Sources of Indoor Airborne Microbes. PLoS ONE, 2015, 10, e0128022.	1.1	168
4746	Land Use History Shifts In Situ Fungal and Bacterial Successions following Wheat Straw Input into the Soil. PLoS ONE, 2015, 10, e0130672.	1.1	81
4747	Comparison of the Oral Microbiomes of Canines and Their Owners Using Next-Generation Sequencing. PLoS ONE, 2015, 10, e0131468.	1.1	75
4748	Composition and Diversity of the Fecal Microbiome and Inferred Fecal Metagenome Does Not Predict Subsequent Pneumonia Caused by <i>Rhodococcus equi</i> in Foals. PLoS ONE, 2015, 10, e0136586.	1.1	15
4749	Cloacal Microbiome Structure in a Long-Distance Migratory Bird Assessed Using Deep 16sRNA Pyrosequencing. PLoS ONE, 2015, 10, e0137401.	1.1	70
4750	Methanosarcina Play an Important Role in Anaerobic Co-Digestion of the Seaweed <i>Ulva lactuca</i> : Taxonomy and Predicted Metabolism of Functional Microbial Communities. PLoS ONE, 2015, 10, e0142603.	1.1	33
4751	Ribosomal DNA and Plastid Markers Used to Sample Fungal and Plant Communities from Wetland Soils Reveals Complementary Biotas. PLoS ONE, 2016, 11, e0142759.	1.1	16
4752	Linking the Composition of Bacterial and Archaeal Communities to Characteristics of Soil and Flora Composition in the Atlantic Rainforest. PLoS ONE, 2016, 11, e0146566.	1.1	18
4753	Microbial Community Profile and Water Quality in a Protected Area of the Caatinga Biome. PLoS ONE, 2016, 11, e0148296.	1.1	20
4754	Deletion of the Toll-Like Receptor 5 Gene Per Se Does Not Determine the Gut Microbiome Profile That Induces Metabolic Syndrome: Environment Trumps Genotype. PLoS ONE, 2016, 11, e0150943.	1.1	20
4755	Effects of Host Plant Factors on the Bacterial Communities Associated with Two Whitefly Sibling Species. PLoS ONE, 2016, 11, e0152183.	1.1	15
4756	Intestinal Microbiota Is Influenced by Gender and Body Mass Index. PLoS ONE, 2016, 11, e0154090.	1.1	511
4757	Variability of Bacterial Communities in the Moth <i>Heliothis virescens</i> Indicates Transient Association with the Host. PLoS ONE, 2016, 11, e0154514.	1.1	89

#	ARTICLE	IF	CITATIONS
4758	Effects of Isoflavone-Enriched Feed on the Rumen Microbiota in Dairy Cows. PLoS ONE, 2016, 11, e0154642.	1.1	43
4759	Bacterial Community Diversity Harboured by Interacting Species. PLoS ONE, 2016, 11, e0155392.	1.1	25
4760	Dietary Regulation of the Gut Microbiota Engineered by a Minimal Defined Bacterial Consortium. PLoS ONE, 2016, 11, e0155620.	1.1	16
4761	Bacterial and Archaeal Diversity in the Gastrointestinal Tract of the North American Beaver (Castor) Tj ETQq1 1 0.784314 rgBJ /Overl	1.1	35
4762	GUTSS: An Alignment-Free Sequence Comparison Method for Use in Human Intestinal Microbiome and Fecal Microbiota Transplantation Analysis. PLoS ONE, 2016, 11, e0158897.	1.1	8
4763	Effects of Arabinoxylan and Resistant Starch on Intestinal Microbiota and Short-Chain Fatty Acids in Subjects with Metabolic Syndrome: A Randomised Crossover Study. PLoS ONE, 2016, 11, e0159223.	1.1	123
4764	MixMC: A Multivariate Statistical Framework to Gain Insight into Microbial Communities. PLoS ONE, 2016, 11, e0160169.	1.1	139
4765	Dysbiosis of the Fecal Microbiota in Cattle Infected with Mycobacterium avium subsp. paratuberculosis. PLoS ONE, 2016, 11, e0160353.	1.1	44
4766	Metagenomic Analysis of Fungal Diversity on Strawberry Plants and the Effect of Management Practices on the Fungal Community Structure of Aerial Organs. PLoS ONE, 2016, 11, e0160470.	1.1	76
4767	Disturbance in the Mucosa-Associated Commensal Bacteria Is Associated with the Exacerbation of Chronic Colitis by Repeated Psychological Stress; Is That the New Target of Probiotics?. PLoS ONE, 2016, 11, e0160736.	1.1	13
4768	Distinct Bacterial Microbiomes in Sexual and Asexual Potamopyrgus antipodarum, a New Zealand Freshwater Snail. PLoS ONE, 2016, 11, e0161050.	1.1	26
4769	Expanding the UniFrac Toolbox. PLoS ONE, 2016, 11, e0161196.	1.1	58
4770	Urinary Microbiota Associated with Preterm Birth: Results from the Conditions Affecting Neurocognitive Development and Learning in Early Childhood (CANDLE) Study. PLoS ONE, 2016, 11, e0162302.	1.1	18
4771	Comparative Metagenomics Reveal Phylum Level Temporal and Spatial Changes in Mycobiome of Belowground Parts of Crocus sativus. PLoS ONE, 2016, 11, e0163300.	1.1	26
4772	Limited Bacterial Diversity within a Treatment Plant Receiving Antibiotic-Containing Waste from Bulk Drug Production. PLoS ONE, 2016, 11, e0165914.	1.1	9
4773	Initial Characterization of the Pig Skin Bacteriome and Its Effect on In Vitro Models of Wound Healing. PLoS ONE, 2016, 11, e0166176.	1.1	35
4774	Common Lung Microbiome Identified among Mechanically Ventilated Surgical Patients. PLoS ONE, 2016, 11, e0166313.	1.1	9
4775	K-shuff: A Novel Algorithm for Characterizing Structural and Compositional Diversity in Gene Libraries. PLoS ONE, 2016, 11, e0167634.	1.1	8

#	ARTICLE	IF	CITATIONS
4776	Alterations in Gut Microbiome Composition and Barrier Function Are Associated with Reproductive and Metabolic Defects in Women with Polycystic Ovary Syndrome (PCOS): A Pilot Study. PLoS ONE, 2017, 12, e0168390.	1.1	253
4777	Bacterial Communities Associated with Houseflies (<i>Musca domestica</i> L.) Sampled within and between Farms. PLoS ONE, 2017, 12, e0169753.	1.1	69
4778	Changes in bacterial community composition of <i>Escherichia coli</i> O157:H7 super-shedder cattle occur in the lower intestine. PLoS ONE, 2017, 12, e0170050.	1.1	25
4779	Betel nut chewing, oral premalignant lesions, and the oral microbiome. PLoS ONE, 2017, 12, e0172196.	1.1	111
4780	Archaeal and bacterial communities in deep-sea hydrogenetic ferromanganese crusts on old seamounts of the northwestern Pacific. PLoS ONE, 2017, 12, e0173071.	1.1	30
4781	Seasonal changes in the digesta-adherent rumen bacterial communities of dairy cattle grazing pasture. PLoS ONE, 2017, 12, e0173819.	1.1	35
4782	The preservation of microbial DNA in archived soils of various genetic types. PLoS ONE, 2017, 12, e0173901.	1.1	17
4783	The rhizospheric microbial community structure and diversity of deciduous and evergreen forests in Taihu Lake area, China. PLoS ONE, 2017, 12, e0174411.	1.1	49
4784	Relative abundance of total subgingival plaque-specific bacteria in salivary microbiota reflects the overall periodontal condition in patients with periodontitis. PLoS ONE, 2017, 12, e0174782.	1.1	62
4785	Bacterial diversity of bacteriomes and organs of reproductive, digestive and excretory systems in two cicada species (Hemiptera: Cicadidae). PLoS ONE, 2017, 12, e0175903.	1.1	23
4786	Effects of iron supplementation on growth, gut microbiota, metabolomics and cognitive development of rat pups. PLoS ONE, 2017, 12, e0179713.	1.1	25
4787	A benign helminth alters the host immune system and the gut microbiota in a rat model system. PLoS ONE, 2017, 12, e0182205.	1.1	36
4788	Disruption in the cecal microbiota of chickens challenged with <i>Clostridium perfringens</i> and other factors was alleviated by <i>Bacillus licheniformis</i> supplementation. PLoS ONE, 2017, 12, e0182426.	1.1	74
4789	Microbiota of little penguins and short-tailed shearwaters during development. PLoS ONE, 2017, 12, e0183117.	1.1	23
4790	Exploring the salivary microbiome of children stratified by the oral hygiene index. PLoS ONE, 2017, 12, e0185274.	1.1	59
4791	Phylogenic inference using alignment-free methods for applications in microbial community surveys using 16s rRNA gene. PLoS ONE, 2017, 12, e0187940.	1.1	5
4792	An in vivo assessment of the cholesterol-lowering efficacy of <i>Lactobacillus plantarum</i> ECGC 13110402 in normal to mildly hypercholesterolaemic adults. PLoS ONE, 2017, 12, e0187964.	1.1	99
4793	Impact of genistein on the gut microbiome of humanized mice and its role in breast tumor inhibition. PLoS ONE, 2017, 12, e0189756.	1.1	57

#	ARTICLE	IF	CITATIONS
4794	Fecal microbiota in the female prairie vole (<i>Microtus ochrogaster</i>). PLoS ONE, 2018, 13, e0190648.	1.1	10
4795	Differences in the intestinal microbiota between uninfected piglets and piglets infected with porcine epidemic diarrhea virus. PLoS ONE, 2018, 13, e0192992.	1.1	37
4796	Microbial diversity in two traditional bacterial douchi from Gansu province in northwest China using Illumina sequencing. PLoS ONE, 2018, 13, e0194876.	1.1	26
4797	Variation in the microbiome of the urogenital tract of Chlamydia-free female koalas (<i>Phascolarctos</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	14
4798	Cerumen microbial community shifts between healthy and otitis affected dogs. PLoS ONE, 2020, 15, e0241447.	1.1	10
4799	Soil microbiome of the postmining areas in polar ecosystems in surroundings of Nadym, Western Siberia, Russia. Open Agriculture, 2019, 4, 684-696.	0.7	13
4800	Rumen bacterial community of young and adult of reindeer (<i>Rangifer tarandus</i>) from Yamalo-Nenets Autonomous District of Russia. Open Agriculture, 2020, 5, 10-20.	0.7	6
4801	Microbiome of abandoned agricultural and mature tundra soils in southern Yamal region, Russian Arctic. Open Agriculture, 2020, 5, 335-344.	0.7	4
4802	Maternal Immune Activation Alters Adult Behavior, Gut Microbiome and Juvenile Brain Oscillations in Ferrets. ENeuro, 2018, 5, ENEURO.0313-18.2018.	0.9	19
4803	Effects of triclosan on bacterial community composition and <i>Vibrio</i> populations in natural seawater microcosms. Elementa, 2017, 5, 1-16.	1.1	5
4804	Neonatal exposure to androgens dynamically alters gut microbiota architecture. Journal of Endocrinology, 2020, 247, 69-85.	1.2	12
4805	Coupling of the chemical niche and microbiome in the rhizosphere: implications from watermelon grafting. Frontiers of Agricultural Science and Engineering, 2016, 3, 249.	0.9	8
4806	Immunobiotics are the Novel Biotech Drugs with Antibacterial and Immunomodulatory Properties. MikrobiolohichnyĀ-Zhurnal, 2017, 79, 66-75.	0.2	7
4807	Interplay between gonadal hormones and postnatal overfeeding in defining sex-dependent differences in gut microbiota architecture. Aging, 2020, 12, 19979-20000.	1.4	14
4808	Breast tissue, oral and urinary microbiomes in breast cancer. Oncotarget, 2017, 8, 88122-88138.	0.8	134
4809	EFFECT OF ORGANIC SUBSTRATE COMPOSITION ON MICROBIAL COMMUNITY STRUCTURE OF PILOT-SCALE BIOCHEMICAL REACTORS TREATING MINING INFLUENCED WATER. Journal of the American Society of Mining and Reclamation, 2008, 2008, 878-891.	0.3	4
4810	The alterations of gut microbiota in mice with chronic pancreatitis. Annals of Translational Medicine, 2019, 7, 464-464.	0.7	26
4811	Two-Phase Bioconversion of Greek-Yogurt Waste Into Medium-Chain Carboxylic Acid Oil <i>via</i> Lactic Acid Without External Electron Donor Addition. SSRN Electronic Journal, 0, , .	0.4	1

#	ARTICLE	IF	CITATIONS
4812	Dysbiosis-Induced Secondary Bile Acid Deficiency Promotes Intestinal Inflammation. SSRN Electronic Journal, 0, , .	0.4	1
4813	Construction of autotrophic nitrogen removal system based on zero-valent iron (ZVI): performance and mechanism. Water Science and Technology, 2020, 82, 2990-3002.	1.2	15
4814	Extraction and 16S rRNA Sequence Analysis of Microbiomes Associated with Rice Roots. Bio-protocol, 2018, 8, e2884.	0.2	25
4815	Comparative actinomycete diversity in marine sediments. Aquatic Microbial Ecology, 2008, 52, 1-11.	0.9	42
4816	Bacterial diversity of <i>Gymnodinium catenatum</i> and its relationship to dinoflagellate toxicity. Aquatic Microbial Ecology, 2010, 61, 73-87.	0.9	28
4817	Phylogenetic diversity and community structure of sponge-associated bacteria from mangroves of the Caribbean Sea. Aquatic Microbial Ecology, 2011, 62, 231-240.	0.9	18
4818	Response of heterotrophic stream biofilm communities to a gradient of resources. Aquatic Microbial Ecology, 2011, 64, 149-161.	0.9	51
4819	Phylogeny of cultivable heterotrophic bacteria derived from mixed colonies. Aquatic Microbial Ecology, 2012, 66, 95-106.	0.9	2
4820	Linkage between copepods and bacteria in the North Atlantic Ocean. Aquatic Microbial Ecology, 2014, 72, 215-225.	0.9	41
4821	Effect of short-term, diel changes in environmental conditions on active microbial communities in a salt marsh pond. Aquatic Microbial Ecology, 2017, 80, 29-41.	0.9	12
4822	Spatial variation of bacterial and fungal communities of estuarine seagrass leaf microbiomes. Aquatic Microbial Ecology, 2020, 84, 59-74.	0.9	16
4823	Unearthing the sand microbiome of sea turtle nests with disparate survivorship at a mass-nesting beach in Costa Rica. Aquatic Microbial Ecology, 2020, 85, 71-83.	0.9	3
4824	Bacteria of the genus <i>Endozoicomonas</i> dominate the microbiome of the Mediterranean gorgonian coral <i>Eunicella cavolini</i> . Marine Ecology - Progress Series, 2013, 479, 75-84.	0.9	111
4825	Microbial distribution in different spatial positions within the walls of a black sulfide hydrothermal chimney. Marine Ecology - Progress Series, 2014, 508, 67-85.	0.9	6
4826	Spatio-temporal variability in Mediterranean rocky shore microphytobenthos. Marine Ecology - Progress Series, 2017, 575, 17-29.	0.9	18
4827	Bacterial community dynamics during embryonic and larval development of three confamilial echinoids. Marine Ecology - Progress Series, 2019, 611, 179-188.	0.9	27
4828	Eggs of echinoids separated by the Isthmus of Panama harbor divergent microbiota. Marine Ecology - Progress Series, 2020, 648, 169-177.	0.9	6
4829	Oyster calcifying fluid harbors persistent and dynamic autochthonous bacterial populations that may aid in shell formation. Marine Ecology - Progress Series, 2020, 653, 57-75.	0.9	6

#	ARTICLE	IF	CITATIONS
4830	Microbiome Diversity in Sputum of Nontuberculous Mycobacteria Infected Women with a History of Breast Cancer. <i>Cellular Physiology and Biochemistry</i> , 2019, 52, 263-279.	1.1	16
4831	Alterations of the Fecal Microbiota in Chinese Patients With Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2020, 11, 590783.	2.2	43
4832	Differently Pre-treated Rapeseed Meals Affect in vitro Swine Gut Microbiota Composition. <i>Frontiers in Microbiology</i> , 2020, 11, 570985.	1.5	12
4833	Systematic Comparisons for Composition Profiles, Taxonomic Levels, and Machine Learning Methods for Microbiome-Based Disease Prediction. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 610845.	1.6	11
4834	Gut Microbiome Composition Remains Stable in Individuals with Diabetes-Related Early to Late Stage Chronic Kidney Disease. <i>Biomedicines</i> , 2021, 9, 19.	1.4	11
4835	The Influence of Caerulomycin A on the Intestinal Microbiota in SD Rats. <i>Marine Drugs</i> , 2020, 18, 277.	2.2	5
4836	Multi-Omic Analysis Reveals Different Effects of Sulforaphane on the Microbiome and Metabolome in Old Compared to Young Mice. <i>Microorganisms</i> , 2020, 8, 1500.	1.6	14
4837	Cyanobacterial Mats in Calcite-Precipitating Serpentinite-Hosted Alkaline Springs of the Voltri Massif, Italy. <i>Microorganisms</i> , 2021, 9, 62.	1.6	9
4838	Biofilm feeding: Microbial colonization of food promotes the growth of a detritivorous arthropod. <i>ZooKeys</i> , 2016, 577, 25-41.	0.5	23
4839	Characterisation and comparison of the mucosa-associated bacterial communities across the gastrointestinal tract of stranded green turtles, <i>Chelonia mydas</i> . <i>AIMS Microbiology</i> , 2020, 6, 361-378.	1.0	7
4840	Temporal Dynamics of Air Bacterial Communities in a University Health Centre Using Illumina MiSeq Sequencing. <i>Aerosol and Air Quality Research</i> , 2020, 20, 966-980.	0.9	7
4841	The Potential Role of Environment in Structuring the Microbiota of <i>Camponotus</i> across Parts of the Body. <i>Advances in Entomology (Irvine, Calif)</i> , 2019, 07, 47-70.	0.1	13
4842	Number of PCR Cycles and Magnesium Chloride Concentration Affect Detection of <i>tet</i> Genes Encoding Ribosomal Protection Proteins in Swine Manure. <i>Advances in Microbiology</i> , 2014, 04, 780-787.	0.3	5
4843	Association between Gut Microbiome Composition and Rotavirus Vaccine Response among Nicaraguan Infants. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 102, 213-219.	0.6	35
4844	Evidence of Microbiome-Drug Interaction between the Antimalarial Lumefantrine and Gut Microbiota in Mice. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 103, 1553-1555.	0.6	1
4845	Abundant Indigestible Carbohydrate Fraction in BARLEYmax Influences Colonic Fermentation Properties <i>In Vitro</i> . <i>Nihon EiyÅ•ShokuryÅ•Gakkai Shi = Nippon EiyÅ•ShokuryÅ•Gakkaishi = Journal of Japanese Society of Nutrition and Food Science</i> , 2020, 73, 81-91.	0.2	1
4846	Microbial Community Analysis using RDP II (Ribosomal Database Project II):Methods, Tools and New Advances. <i>Environmental Engineering Research</i> , 2009, 14, 3-9.	1.5	10
4847	Analysis of Microbial Communities in Animal Carcass Disposal Soils. <i>Daehan Hwan'gyeong Gonghag Hoeji</i> , 2013, 35, 503-508.	0.4	5

#	ARTICLE	IF	CITATIONS
4848	Pyrosequencing study of caecal bacterial community of rabbit does and kits from a farm affected by epizootic rabbit enteropathy. <i>World Rabbit Science</i> , 2017, 25, 261.	0.1	3
4849	Association between oropharyngeal microbiome and weight gain in piglets during pre and post weaning life. <i>Journal of Animal Science and Technology</i> , 2020, 62, 247-262.	0.8	9
4856	Next-generation approaches to the microbial ecology of food fermentations. <i>BMB Reports</i> , 2012, 45, 377-389.	1.1	113
4857	Microbial Biodiversity and Biogeography on the Deep Seafloor. , 0, , .		1
4858	Variation of <i>Anaeromyxobacter</i> community structure and abundance in paddy soil slurry over flooding time. <i>African Journal of Agricultural Research Vol Pp</i> , 2011, 6, .	0.2	2
4861	Bidirectional interactions between indomethacin and the murine intestinal microbiota. <i>ELife</i> , 2015, 4, e08973.	2.8	80
4862	Convergence between the microcosms of Southeast Asian and North American pitcher plants. <i>ELife</i> , 2018, 7, .	2.8	29
4863	Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. <i>ELife</i> , 2018, 7, .	2.8	70
4864	Rarity is a more reliable indicator of land-use impacts on soil invertebrate communities than other diversity metrics. <i>ELife</i> , 2020, 9, .	2.8	20
4865	Respiratory tissue-associated commensal bacteria offer therapeutic potential against pneumococcal colonization. <i>ELife</i> , 2020, 9, .	2.8	22
4866	Use of next generation sequencing to compare simple habitat and species level differences in the gut microbiota of an invasive and native freshwater fish species. <i>PeerJ</i> , 2020, 8, e10237.	0.9	4
4867	Different analysis strategies of 16S rRNA gene data from rodent studies generate contrasting views of gut bacterial communities associated with diet, health and obesity. <i>PeerJ</i> , 2020, 8, e10372.	0.9	8
4868	Impact of demographics on human gut microbial diversity in a US Midwest population. <i>PeerJ</i> , 2016, 4, e1514.	0.9	61
4869	A comparison of rumen microbial profiles in dairy cows as retrieved by 454 Roche and Ion Torrent (PGM) sequencing platforms. <i>PeerJ</i> , 2016, 4, e1599.	0.9	17
4870	The impact of freeze-drying infant fecal samples on measures of their bacterial community profiles and milk-derived oligosaccharide content. <i>PeerJ</i> , 2016, 4, e1612.	0.9	13
4871	Responses of microbial community from tropical pristine coastal soil to crude oil contamination. <i>PeerJ</i> , 2016, 4, e1733.	0.9	26
4872	Characterization of microbial associations with methanotrophic archaea and sulfate-reducing bacteria through statistical comparison of nested Magneto-FISH enrichments. <i>PeerJ</i> , 2016, 4, e1913.	0.9	43
4873	Differences in stability of seed-associated microbial assemblages in response to invasion by phytopathogenic microorganisms. <i>PeerJ</i> , 2016, 4, e1923.	0.9	49

#	ARTICLE	IF	CITATIONS
4874	Succession of the turkey gastrointestinal bacterial microbiome related to weight gain. PeerJ, 2013, 1, e237.	0.9	83
4875	PhyloSift: phylogenetic analysis of genomes and metagenomes. PeerJ, 2014, 2, e243.	0.9	633
4876	Environment and host species shape the skin microbiome of captive neotropical bats. PeerJ, 2016, 4, e2430.	0.9	48
4877	Phylogenetic factorization of compositional data yields lineage-level associations in microbiome datasets. PeerJ, 2017, 5, e2969.	0.9	105
4878	Sorghum and wheat differentially affect caecal microbiota and associated performance characteristics of meat chickens. PeerJ, 2017, 5, e3071.	0.9	23
4879	Molecular assessment of the fecal microbiota in healthy cats and dogs before and during supplementation with fructo-oligosaccharides (FOS) and inulin using high-throughput 454-pyrosequencing. PeerJ, 2017, 5, e3184.	0.9	42
4880	Endosymbiont interference and microbial diversity of the Pacific coast tick, <i>Dermacentor occidentalis</i> , in San Diego County, California. PeerJ, 2017, 5, e3202.	0.9	50
4881	Alien vs. predator: bacterial challenge alters coral microbiomes unless controlled by <i>Halobacteriovorax</i> predators. PeerJ, 2017, 5, e3315.	0.9	74
4882	A microbial survey of the International Space Station (ISS). PeerJ, 2017, 5, e4029.	0.9	52
4883	Is there a link between aging and microbiome diversity in exceptional mammalian longevity?. PeerJ, 2018, 6, e4174.	0.9	28
4884	Effect of dark sweet cherry powder consumption on the gut microbiota, short-chain fatty acids, and biomarkers of gut health in obese db/db mice. PeerJ, 2018, 6, e4195.	0.9	39
4885	CoMiniCut™ a small volume <i>in vitro</i> colon model for the screening of gut microbial fermentation processes. PeerJ, 2018, 6, e4268.	0.9	60
4886	16S rRNA gene sequencing reveals effects of photoperiod on cecal microbiota of broiler roosters. PeerJ, 2018, 6, e4390.	0.9	22
4887	Inulin-type fructan improves diabetic phenotype and gut microbiota profiles in rats. PeerJ, 2018, 6, e4446.	0.9	127
4888	Characterization of shifts of koala (<i>Phascolarctos cinereus</i>) intestinal microbial communities associated with antibiotic treatment. PeerJ, 2018, 6, e4452.	0.9	30
4889	The bacterial communities of <i>Drosophila suzukii</i> collected from undamaged cherries. PeerJ, 2014, 2, e474.	0.9	62
4890	Comparative chemical analysis of army ant mandibular gland volatiles (Formicidae: Dorylinae). PeerJ, 2018, 6, e5319.	0.9	11
4891	Effect of a specific composition of short- and medium-chain fatty acid 1-Monoglycerides on growth performances and gut microbiota of gilthead sea bream (<i>Sparus aurata</i>). PeerJ, 2018, 6, e5355.	0.9	63

#	ARTICLE	IF	CITATIONS
4892	Compositional and predicted functional analysis of the gut microbiota of <i>Radix auricularia</i> (Linnaeus) via high-throughput Illumina sequencing. PeerJ, 2018, 6, e5537.	0.9	44
4893	Effects of agricultural management on phyllosphere fungal diversity in vineyards and the association with adjacent native forests. PeerJ, 2018, 6, e5715.	0.9	27
4894	Effects of wine-cap <i>Stropharia</i> cultivation on soil nutrients and bacterial communities in forestlands of northern China. PeerJ, 2018, 6, e5741.	0.9	20
4895	Structure, dynamics and predicted functional role of the gut microbiota of the blue (<i>Haliotis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock e5830.	0.9	26
4896	Skin bacterial diversity is higher on lizards than sympatric frogs in tropical Australia. PeerJ, 2018, 6, e5960.	0.9	25
4897	Regional fresh snowfall microbiology and chemistry are driven by geography in storm-tracked events, Colorado, USA. PeerJ, 2018, 6, e5961.	0.9	16
4898	The gut microbiome correlates with conspecific aggression in a small population of rescued dogs (<i>Canis familiaris</i>). PeerJ, 2019, 7, e6103.	0.9	60
4899	Captivity causes taxonomic and functional convergence of gut microbial communities in bats. PeerJ, 2019, 7, e6844.	0.9	21
4900	The microbiome profiling of fungivorous black tinder fungus beetle <i>Bolitophagus reticulatus</i> reveals the insight into bacterial communities associated with larvae and adults. PeerJ, 2019, 7, e6852.	0.9	4
4901	Oceanographic habitat and the coral microbiomes of urban-impacted reefs. PeerJ, 2019, 7, e7552.	0.9	8
4902	The effect of diet on the structure of gut bacterial community of sympatric pair of whitefishes (<i>Coregonus lavaretus</i>): one story more. PeerJ, 2019, 7, e8005.	0.9	18
4903	The impact of storage conditions on human stool 16S rRNA microbiome composition and diversity. PeerJ, 2019, 7, e8133.	0.9	20
4904	Early-life intestinal microbiome in <i>Trachemys scripta elegans</i> analyzed using 16S rRNA sequencing. PeerJ, 2020, 8, e8501.	0.9	15
4905	Iroki: automatic customization and visualization of phylogenetic trees. PeerJ, 2020, 8, e8584.	0.9	78
4906	Microbiome analysis of healthy and diseased sponges <i>Lubomirskia baicalensis</i> by using cell cultures of primmorphs. PeerJ, 2020, 8, e9080.	0.9	17
4907	An updated genetic marker for detection of Lake Sinai Virus and metagenetic applications. PeerJ, 2020, 8, e9424.	0.9	6
4908	MetaBoot: a machine learning framework of taxonomical biomarker discovery for different microbial communities based on metagenomic data. PeerJ, 2015, 3, e993.	0.9	13
4909	Analysis of Community Structure of Metabolically Active Bacteria in a Rice Field Subjected to Long-Term Fertilization Practices. Han'guk T'oyang Piryo Hakhoe Chi Han'guk T'oyang Piryo Hakhoe, 2013, 46, 585-592.	0.1	4

#	ARTICLE	IF	CITATIONS
4910	Bacterial core community in soybean rhizosphere. Korean Journal of Microbiology, 2015, 51, 347-354.	0.2	9
4911	Comparison of DNA Extraction Methods for Human Oral Microbiome Research. British Journal of Medicine and Medical Research, 2014, 4, 1980-1991.	0.2	14
4912	Fungal lysozyme leverages the gut microbiota to curb DSS-induced colitis. Gut Microbes, 2021, 13, 1988836.	4.3	29
4913	Two ST11 <i>Klebsiella pneumoniae</i> strains exacerbate colorectal tumorigenesis in a colitis-associated mouse model. Gut Microbes, 2021, 13, 1980348.	4.3	12
4914	High-Throughput Sequencing for Examining Salmonella Prevalence and Pathogen-Microbiota Relationships in Barn Swallows. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	3
4915	Arbuscular mycorrhizal fungal communities of a mangrove forest along a salinity gradient on Iriomote Island. Plant and Soil, 2022, 472, 145-159.	1.8	3
4916	A field experiment reveals seasonal variation in the <i>Daphnia</i> gut microbiome. Oikos, 2021, 130, 2191-2201.	1.2	11
4917	Functional Diversity within Gut Microbiomes: Implications for Conserving Biodiversity. Conservation, 2021, 1, 311-326.	0.8	1
4918	Characterizing the breast cancer lipidome and its interaction with the tissue microbiota. Communications Biology, 2021, 4, 1229.	2.0	17
4919	Microbiome of Haemaphysalis longicornis Tick in Korea. Korean Journal of Parasitology, 2021, 59, 489-496.	0.5	8
4920	Migration effects on the intestinal microbiota of Tibetans. PeerJ, 2021, 9, e12036.	0.9	4
4921	Fine-Scale Spatial Structure of Soil Microbial Communities in Burrows of a Keystone Rodent Following Mass Mortality. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	2
4922	Ileal mucosa-associated microbiota overgrowth associated with pathogenesis of primary biliary cholangitis. Scientific Reports, 2021, 11, 19705.	1.6	8
4923	New Insights into the Relationships between Bacterial Dynamics and Water Quality of Aquaculture Systems Supplemented with Carbon Source and Biofilm Substratum. Microorganisms, 2021, 9, 2168.	1.6	0
4924	Lactobacillus rhamnosus Probio-M9 Improves the Quality of Life in Stressed Adults by Gut Microbiota. Foods, 2021, 10, 2384.	1.9	14
4925	Central and Northern European caterpillar assemblages show strong phylogenetic structure. Functional Ecology, 0, , .	1.7	0
4927	Perturbations of the ileal mycobiota by necrotic enteritis in broiler chickens. Journal of Animal Science and Biotechnology, 2021, 12, 107.	2.1	6
4928	16S rRNA Gene Amplicon Sequencing Data of the Iron Quadrangle Ferruginous Caves (Brazil) Shows the Importance of Conserving This Singular and Threatened Geosystem. Diversity, 2021, 13, 494.	0.7	2

#	ARTICLE	IF	CITATIONS
4929	Microbiome of Pukzing Cave in India shows high antimicrobial activity against plant and animal pathogens. <i>Genomics</i> , 2021, 113, 4098-4108.	1.3	5
4930	Cross-Sectional Analysis of the Microbiota of Human Gut and Its Direct Environment in a Household Cohort with High Background of Antibiotic Use. <i>Microorganisms</i> , 2021, 9, 2115.	1.6	2
4931	Does biological rhythm transmit from plants to rhizosphere microbes?. <i>Environmental Microbiology</i> , 2021, 23, 6895-6906.	1.8	8
4932	Yeast β -glucan reduces obesity-associated <i>Bilophila</i> abundance and modulates bile acid metabolism in healthy and high-fat diet mouse models. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 321, G639-G655.	1.6	8
4934	Microbial diversity in tropical marine sediments assessed using culture-dependent and culture-independent techniques. <i>Environmental Microbiology</i> , 2021, 23, 6859-6875.	1.8	8
4935	Effects of dietary zearalenone on the serum biochemistry, hepatic and intestinal histology, and intestinal microbiota of juvenile Dabry's sturgeon (<i>Acipenser dabryanus</i>). <i>Journal of Applied Ichthyology</i> , 2021, 37, 932-941.	0.3	3
4936	Effect of organic acids on growth performance, intestinal morphology, and immunity of broiler chickens with and without coccidial challenge. <i>AMB Express</i> , 2021, 11, 140.	1.4	23
4937	Diversity and Predicted Function of Gut Microbes from Two Species of Viviparid Snails. <i>Freshwater Mollusk Biology and Conservation</i> , 2021, 24, .	0.4	3
4940	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , 2021, 6, e0069121.	1.7	27
4941	Fast and accurate distance-based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	2.2	25
4942	Comparative analysis of the serum microbiome of HIV infected individuals. <i>Genomics</i> , 2021, 113, 4015-4021.	1.3	6
4943	Short-term grazing exclusions reduced soil organic carbon but not bacterial diversity in the sagebrush desert, Northwest China. <i>Global Ecology and Conservation</i> , 2021, 31, e01872.	1.0	9
4945	Increasing ecological inference from high throughput sequencing of fungi in the environment through a tagging approach. <i>Molecular Ecology Resources</i> , 2008, .	2.2	0
4947	Effect of Ocean Acidification on the Coral Microbial Community. , 2012, , 163-173.		0
4949	The faecal flora: a source of healthcare-associated infections and antibiotic resistance. , 2013, , .		0
4950	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
4951	Seasonal Variations in the Bacterial Community of Gwangyang Bay Seawater. <i>Journal of Life Science</i> , 2014, 24, 522-531.	0.2	5
4953	Host Trait Prediction of Metagenomic Data for Topology-Based Visualization. <i>Lecture Notes in Computer Science</i> , 2015, , 134-149.	1.0	3

#	ARTICLE	IF	CITATIONS
4955	The Human Microbiome and Clinical Immunology. , 0, , 19-25.		0
4959	Addition of Sodium Hydroxide to Seawater Inhibits Sulfide Production (Souring) by Microbes in Oil Field Water. Journal of Chemical Engineering of Japan, 2017, 50, 850-856.	0.3	1
4960	Waste Water Microbiology. International Journal of Molecular Biology Open Access, 2017, 2, .	0.2	2
4964	Hospital Microbiomics: Benchmarking from the First Longitudinal Study of Microbiome Dynamics among Patient, Staff and Hospital Habitats. Journal of Bacteriology & Mycology Open Access, 2017, 4, .	0.2	0
4967	Relationships between and formation dynamics of the microbiota of consumers, producers, and the environment in an abalone aquatic system. PLoS ONE, 2017, 12, e0182590.	1.1	0
4971	Study of Periplaneta Americana Microbial Community Structure and Diversity by 16S rRNA High-Throughput Sequencing. Sustainability in Environment, 2017, 2, 350.	0.2	0
4978	Comfrey Mulch Enriches Soil, But Does Not Improve an Indicator Crop within One Season. International Journal of Plant & Soil Science, 2018, 22, 1-9.	0.2	0
4980	Variation of Prokaryotic and Fungal Soil Communities across a Vegetative Transect. Agricultural Research & Technology: Open Access Journal, 2018, 15, .	0.1	1
4982	Bioinformatics Analysis of Microbial Abundance and Diversity in Acid Mine Drainage from the Solomon Mine Near Creede, Colorado. Fine Focus, 2018, 4, 41-65.	0.2	0
5006	Impact of Manure Storage Time and Temperature on Microbial Composition and Stable Fly (Diptera:) Tj ETQq1 1 0.784314 rgBT /Over 0,3 1		
5016	Composition and dynamics of the bacterial communities present in the post-slaughter environment of farmed Atlantic salmon (<i>Salmo salar</i> L.) and correlations to gelatin degrading activity. PeerJ, 2019, 7, e7040.	0.9	1
5023	Simulative Study of Effects of LM Microorganism on Environment: Analyses of Metabolomes and Soil Microbial Communities. Korean Journal of Environmental Agriculture, 2019, 38, 197-204.	0.0	0
5037	Diagnostic potential of gut microbiota in Parkinsonâ€™s disease. Bulletin of Siberian Medicine, 2020, 18, 92-101.	0.1	1
5040	Characterization of the bacterial microbiota composition and evolution at different intestinal tract in wild pigs (<i>Sus scrofa ussuricus</i>). PeerJ, 2020, 8, e9124.	0.9	8
5041	Early-Life Intake of an Isotonic Protein Drink Improves the Gut Microbial Profile of Piglets. Animals, 2020, 10, 879.	1.0	0
5043	<p>Geneâ€™Environment Interactions in Major Mental Disorders in the Czech Republic</p>. Neuropsychiatric Disease and Treatment, 2020, Volume 16, 1147-1156.	1.0	0
5050	Effects of dietary tributyrin and physterol ester supplementation on growth performance, intestinal morphology, microbiota and metabolites in weaned piglets. Journal of Applied Microbiology, 2022, 132, 2293-2305.	1.4	6
5051	Effects of graded inclusion levels of raw garbanzo beans on apparent total tract digestibility, fecal quality, and fecal fermentative end-products and microbiota in extruded feline diets. Journal of Animal Science, 2021, 99, .	0.2	3

#	ARTICLE	IF	CITATIONS
5052	Fungal Metagenome of Chernevaya Taiga Soils: Taxonomic Composition, Differential Abundance and Factors Related to Plant Gigantism. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 908.	1.5	4
5054	A hierarchical Bayesian approach for detecting global microbiome associations. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2021, 20, 85-100.	0.2	0
5055	Context-dependent effects of glucocorticoids on the lizard gut microbiome. <i>Molecular Ecology</i> , 2022, 31, 185-196.	2.0	11
5056	The Concentration of Organic Acids in Cranberry Juice Modulates the Gut Microbiota in Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11537.	1.8	4
5058	Dissolved organic matter production from herder application and in-situ burning of crude oil at high latitudes: Bioavailable molecular composition patterns and microbial community diversity effects. <i>Journal of Hazardous Materials</i> , 2022, 424, 127598.	6.5	7
5059	Vitamin A Deficiency Exacerbates Gut Microbiota Dysbiosis and Cognitive Deficits in Amyloid Precursor Protein/Presenilin 1 Transgenic Mice. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 753351.	1.7	14
5060	Skin inflammation activates intestinal stromal fibroblasts and promotes colitis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	12
5061	Association Between Gut Microbiota and Elevated Serum Urate in Two Independent Cohorts. <i>Arthritis and Rheumatology</i> , 2022, 74, 682-691.	2.9	37
5062	Forestomach fermentation and microbial communities of alpacas (<i>Lama) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 Td (pacos<i> Journal of Animal and Feed Sciences, 2020, 29, 323-329.	0.4	0
5063	Host trait prediction from human microbiome data for Colorectal Cancer. , 2020, , .		1
5065	Milk microbiome: evaluation study on the differences among cows with a different health status classified by leukocyte pattern. <i>Acta Fytotechnica Et Zootechnica</i> , 2020, 23, 67-73.	0.1	0
5066	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. <i>PLoS ONE</i> , 2020, 15, e0243609.	1.1	6
5069	Statistical Methods for Pairwise Comparison of Metagenomic Samples. <i>Frontiers in Probability and the Statistical Sciences</i> , 2021, , 81-99.	0.1	0
5070	Microbiology of a multi-layer biosolid/desulfurized tailings cover on a mill tailings impoundment. <i>Journal of Environmental Management</i> , 2022, 302, 114030.	3.8	7
5071	Microbiomes across root compartments are shaped by inoculation with a fungal biological control agent. <i>Applied Soil Ecology</i> , 2022, 170, 104230.	2.1	4
5072	New insights to the difference in microbial composition and interspecies interactions between fouling layer and mixed liquor in a membrane bioreactor. <i>Journal of Membrane Science</i> , 2022, 643, 120034.	4.1	8
5073	Invention of Artificial Rice Field Soil: A Tool to Study the Effect of Soil Components on the Activity and Community of Microorganisms Involved in Anaerobic Organic Matter Decomposition. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	1
5076	The Gut Microbiome and Antimicrobial Resistance in Companion Animals. , 2020, , 233-245.		1

#	ARTICLE	IF	CITATIONS
5077	Vermicomposts Are Biologically Different: Microbial and Functional Diversity of Green Vermicomposts. , 2020, , 125-140.		2
5081	Patterns of change in $\hat{\alpha}$ and $\hat{\beta}$ taxonomic and phylogenetic diversity in the secondary succession of semi-natural grasslands in the Northern Apennines. PeerJ, 2020, 8, e8683.	0.9	7
5091	Roseburia Abundance Associates With Severity, Evolution and Outcome of Acute Ischemic Stroke. Frontiers in Cellular and Infection Microbiology, 2021, 11, 669322.	1.8	12
5093	Quality and safety aspects in fermentation of winged kelp (<i>Alaria esculenta</i>) and sugar kelp (<i>Saccharina latissima</i>) by the natural microbiota with or without addition of a <i>Lactiplantibacillus plantarum</i> starter culture. Food Research International, 2021, 150, 110800.	2.9	7
5094	Microbial and Geochemical Evidence of Permafrost Formation at Mamontova Gora and Syrdakh, Central Yakutia. Frontiers in Earth Science, 2021, 9, .	0.8	3
5095	Succession of Microbial Communities of Corn Silage Inoculated with Heterofermentative Lactic Acid Bacteria from Ensiling to Aerobic Exposure. Fermentation, 2021, 7, 258.	1.4	15
5099	AMDB: a database of animal gut microbial communities with manually curated metadata. Nucleic Acids Research, 2022, 50, D729-D735.	6.5	11
5100	Effect of exposure to antibiotics on the gut microbiome and biochemical indexes of pregnant women. BMJ Open Diabetes Research and Care, 2021, 9, e002321.	1.2	9
5101	The Dominating Role of Genetic Background in Shaping Gut Microbiota of Honeybee Queen Over Environmental Factors. Frontiers in Microbiology, 2021, 12, 722901.	1.5	3
5102	The oral microbial composition and diversity affect the clinical course of palmoplantar pustulosis patients after dental focal infection treatment. Journal of Dermatological Science, 2021, 104, 193-200.	1.0	4
5103	Dataset complexity impacts both MOTU delimitation and biodiversity estimates in eukaryotic 18S rRNA metabarcoding studies. Environmental DNA, 2022, 4, 363-384.	3.1	7
5111	Porting and optimizing UniFrac for GPUs. , 2020, , .		3
5114	Composition and function of the microbiotas in the different parts of the midgut of <i>Pyrrhocoris sibiricus</i> (Hemiptera: Pyrrhocoridae) revealed using high-throughput sequencing of 16S rRNA. European Journal of Entomology, 0, 117, 352-371.	1.2	4
5117	Colonization of carbapenem-resistant <i>Klebsiella pneumoniae</i> in a sink-drain model biofilm system. Infection Control and Hospital Epidemiology, 2021, 42, 1-9.	1.0	5
5121	The difference between cellulolytic $\hat{\alpha}$ -culturomes TM and microbiomes inhabiting two contrasting soil types. PLoS ONE, 2020, 15, e0242060.	1.1	6
5122	Fungal microbiome of barley grain revealed by NGS and mycological analysis. Foods and Raw Materials, 2020, , 286-297.	0.8	1
5123	River Microbiome Composition Reflects Macroscale Climatic and Geomorphic Differences in Headwater Streams. Frontiers in Water, 2020, 2, .	1.0	8
5124	Goats fed with non-protein nitrogen: ruminal bacterial community and ruminal fermentation, intake, digestibility and nitrogen balance. Journal of Agricultural Science, 2020, 158, 781-790.	0.6	4

#	ARTICLE	IF	CITATIONS
5125	The Hologenome Concept: Human, Animal and Plant Microbiota. , 2013, , .		15
5127	Phyloseq: a bioconductor package for handling and analysis of high-throughput phylogenetic sequence data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 235-46.	0.7	84
5128	TWO APPLICATIONS OF PERMUTATION TESTS IN BIOSTASTICS. Boletines De La Sociedad De CirugÃa De Rosario, 2013, 19, 255-266.	0.0	2
5129	Comparisons of distance methods for combining covariates and abundances in microbiome studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 213-24.	0.7	24
5130	VEGF-C mediated enhancement of lymphatic drainage reduces intestinal inflammation by regulating IL-9/IL-17 balance and improving gut microbiota in experimental chronic colitis. American Journal of Translational Research (discontinued), 2017, 9, 4772-4784.	0.0	17
5131	Lung tissue microbial profile in lung cancer is distinct from emphysema. American Journal of Cancer Research, 2018, 8, 1775-1787.	1.4	24
5132	A common microbial signature is present in the lower airways of interstitial lung diseases including sarcoidosis. Sarcoidosis Vasculitis and Diffuse Lung Diseases, 2018, 35, 354-362.	0.2	4
5133	Estimation of Personal Environment Via Fingertip Microbiome and Mobile Phone Surfaces. Iranian Journal of Biotechnology, 2021, 19, e2696.	0.3	0
5134	Bacterial communities from vagina of dairy healthy heifers and cows with impaired reproductive performance. Research in Veterinary Science, 2022, 142, 15-23.	0.9	11
5135	Advances in sequencing technology, databases, and analyses tools for the assessment of microbial diversity. , 2022, , 317-347.		1
5136	Carbon dioxide to bio-oil in a bioelectrochemical system-assisted microalgae biorefinery process. Sustainable Energy and Fuels, 2021, 6, 150-161.	2.5	22
5137	Microbiome composition resulting from different substrates influences trichloroethene dechlorination performance. Journal of Environmental Management, 2022, 303, 114145.	3.8	9
5138	Discovering naturally-occurring microbiota in disease suppressive soil: Potential role of biological elements in suppressing Ganoderma boninense. Biological Control, 2022, 165, 104787.	1.4	6
5139	Intercropping with Chinese leek decreased Meloidogyne javanica population and shifted microbial community structure in Sacha Inchi plantation. Journal of Agricultural Science, 0, , 1-10.	0.6	2
5140	Power Play of Commensal Bacteria in the Buccal Cavity of Female Nile Tilapia. Frontiers in Microbiology, 2021, 12, 773351.	1.5	3
5141	A Faithful Gut: Core Features of Gastrointestinal Microbiota of Long-Distance Migratory Bats Remain Stable despite Dietary Shifts Driving Differences in Specific Bacterial Taxa. Microbiology Spectrum, 2021, 9, e0152521.	1.2	3
5142	Nasopharyngeal microbiota in hospitalized children with Bordetella pertussis and Rhinovirus infection. Scientific Reports, 2021, 11, 22858.	1.6	8
5143	Infant gut bacterial community composition and food-related manifestation of atopy in early childhood. Pediatric Allergy and Immunology, 2022, 33, .	1.1	13

#	ARTICLE	IF	CITATIONS
5144	Preterm infant meconium microbiota transplant induces growth failure, inflammatory activation, and metabolic disturbances in germ-free mice. <i>Cell Reports Medicine</i> , 2021, 2, 100447.	3.3	13
5145	Microbiome Analysis of Mucosal Ileoanal Pouch in Ulcerative Colitis Patients Revealed Impairment of the Pouches Immunometabolites. <i>Cells</i> , 2021, 10, 3243.	1.8	9
5146	Rhizosphere bacteria community and functions under typical natural halophyte communities in North China salinized areas. <i>PLoS ONE</i> , 2021, 16, e0259515.	1.1	6
5147	Altered Fecal Microbiota Correlated With Systemic Inflammation in Male Subjects With Methamphetamine Use Disorder. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 783917.	1.8	11
5148	Microbial diversity analysis of two full-scale seawater desalination treatment trains provides insights into detrimental biofilm formation. , 2021, 1, 100001.		6
5149	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6
5150	Commensal Bifidobacterium Strains Enhance the Efficacy of Neo-Epitope Based Cancer Vaccines. <i>Vaccines</i> , 2021, 9, 1356.	2.1	10
5151	Cognitive behavioral therapy for irritable bowel syndrome induces bidirectional alterations in the brain-gut-microbiome axis associated with gastrointestinal symptom improvement. <i>Microbiome</i> , 2021, 9, 236.	4.9	34
5153	An integrated host-microbiome response to atrazine exposure mediates toxicity in <i>Drosophila</i> . <i>Communications Biology</i> , 2021, 4, 1324.	2.0	10
5154	Broad Dissemination of Plasmids across Groundwater-Fed Rapid Sand Filter Microbiomes. <i>MBio</i> , 2021, 12, e0306821.	1.8	6
5155	The Baltic Sea methane pockmark microbiome: The new insights into the patterns of relative abundance and ANME niche separation. <i>Marine Environmental Research</i> , 2022, 173, 105533.	1.1	17
5156	Analysing microbiome intervention design studies: Comparison of alternative multivariate statistical methods. <i>PLoS ONE</i> , 2021, 16, e0259973.	1.1	11
5157	Effects of <i>Platycodon grandiflorum</i> on Gut Microbiome and Immune System of Immunosuppressed Mouse. <i>Metabolites</i> , 2021, 11, 817.	1.3	2
5158	The Immune Barrier of Porcine Uterine Mucosa Differs Dramatically at Proliferative and Secretory Phases and Could Be Positively Modulated by Colonizing Microbiota. <i>Frontiers in Immunology</i> , 2021, 12, 750808.	2.2	2
5159	Contents of lobetyolin, syringin, and atractylolide III in <i>Codonopsis pilosula</i> are related to dynamic changes of endophytes under drought stress. <i>Chinese Medicine</i> , 2021, 16, 122.	1.6	8
5160	Spatial and Temporal Constraints on the Composition of Microbial Communities in Subsurface Boreholes of the Edgar Experimental Mine. <i>Microbiology Spectrum</i> , 2021, 9, e0063121.	1.2	2
5161	Revealing the composition of the eukaryotic microbiome of oyster spat by CRISPR-Cas Selective Amplicon Sequencing (CCSAS). <i>Microbiome</i> , 2021, 9, 230.	4.9	6
5162	Unveiling Endophytic Bacterial Community Structures of Different Rice Cultivars Grown in a Cadmium-Contaminated Paddy Field. <i>Frontiers in Microbiology</i> , 2021, 12, 756327.	1.5	13

#	ARTICLE	IF	CITATIONS
5163	Microbial community structure and metabolic potential in the coastal sediments around the Yellow River Estuary. <i>Science of the Total Environment</i> , 2022, 816, 151582.	3.9	6
5164	From DNA sequences to microbial ecology: Wrangling NEON soil microbe data with the neonMicrobe R package. <i>Ecosphere</i> , 2021, 12, e03842.	1.0	3
5165	Effects of Glutathione on Growth, Intestinal Antioxidant Capacity, Histology, Gene Expression, and Microbiota of Juvenile Triploid <i>Oncorhynchus mykiss</i> . <i>Frontiers in Physiology</i> , 2021, 12, 784852.	1.3	8
5166	A holobiont view of island biogeography: Unravelling patterns driving the nascent diversification of a Hawaiian spider and its microbial associates. <i>Molecular Ecology</i> , 2022, 31, 1299-1316.	2.0	5
5167	Clean room microbiome complexity impacts planetary protection bioburden. <i>Microbiome</i> , 2021, 9, 238.	4.9	11
5168	Microbial profiles of peri-implant mucositis and peri-implantitis: Submucosal microbial dysbiosis correlates with disease severity. <i>Clinical Oral Implants Research</i> , 2022, 33, 172-183.	1.9	13
5169	Coral reef biofilm bacterial diversity and successional trajectories are structured by reef benthic organisms and shift under chronic nutrient enrichment. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 84.	2.9	8
5170	Alone Yet Not Alone: <i>Frankia</i> Lives Under the Same Roof With Other Bacteria in Actinorhizal Nodules. <i>Frontiers in Microbiology</i> , 2021, 12, 749760.	1.5	10
5171	Biodiversity and degradation potential of oil-degrading bacteria isolated from sediments of hydrothermal and non-hydrothermal areas of the Southwest Mid-Indian Ocean Ridge. <i>Environmental Science and Pollution Research</i> , 2021, , 1.	2.7	1
5172	Analysis of the relationship between bile duct and duodenal microbiota reveals that potential dysbacteriosis is the main cause of primary common bile duct stones. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 414-428.	1.8	6
5173	Beta Diversity and Distance-Based Analysis of Microbiome Data. <i>Frontiers in Probability and the Statistical Sciences</i> , 2021, , 101-127.	0.1	2
5174	Microbiota associated with echinoid eggs and the implications for maternal provisioning. <i>Marine Ecology - Progress Series</i> , 2022, 683, 67-79.	0.9	3
5175	Initial sample processing can influence the soil microbial metabarcoding surveys, revealed by <i>Leucocalocybe mongolica</i> fairy ring ecosystem. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 1427-1438.	0.5	6
5176	The gut microbiota of <i>Cystidicola farionis</i> parasitizing the swim bladder of the nosed charr morph <i>Salvelinus malma</i> complex in Lake Kronotskoe (Kamchatka, Russia). <i>Journal of Nematology</i> , 2021, 53, 1-15.	0.4	1
5177	A More Diverse Cervical Microbiome Associates with Better Clinical Outcomes in Patients with Endometriosis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5178	Effects of faecal microbiota transplantation on the growth performance, intestinal microbiota, jejunum morphology and immune function of laying-type chicks. <i>Animal Production Science</i> , 2021, , .	0.6	4
5180	Bacterial Diversity, Organic Acid, and Flavor Analysis of Dacha and Ercha Fermented Grains of Fen Flavor Baijiu. <i>Frontiers in Microbiology</i> , 2021, 12, 769290.	1.5	7
5181	Multi-Omics Analysis of the Gut-Liver Axis Reveals the Mechanism of Liver Injury in Colitis Mice. <i>Frontiers in Immunology</i> , 2021, 12, 773070.	2.2	6

#	ARTICLE	IF	CITATIONS
5182	Exosome-like nanoparticles from Mulberry bark prevent DSS-induced colitis via the AhR/COPS8 pathway. <i>EMBO Reports</i> , 2022, 23, e53365.	2.0	56
5183	Vertical distribution patterns and drivers of soil bacterial communities across the continuous permafrost region of northeastern China. <i>Ecological Processes</i> , 2022, 11, .	1.6	4
5184	Reduced calorie diet combined with NNMT inhibition establishes a distinct microbiome in DIO mice. <i>Scientific Reports</i> , 2022, 12, 484.	1.6	0
5185	Metataxonomic, bioactivity and microbiome analysis of Red Sea marine sponges from Egypt. <i>Marine Genomics</i> , 2022, 61, 100920.	0.4	3
5186	Integral approach for the evaluation of poultry manure, compost, and digestate: Amendment characterization, mineralization, and effects on soil and intensive crops. <i>Waste Management</i> , 2022, 139, 124-135.	3.7	19
5187	Abnormal groundwater levels and microbial communities in the Pohang Enhanced Geothermal System site wells pre- and post-Mw 5.5 earthquake in Korea. <i>Science of the Total Environment</i> , 2022, 810, 152305.	3.9	1
5188	Animal corpse degradation enriches antibiotic resistance genes but remains recalcitrant in drinking water microcosm. <i>International Biodeterioration and Biodegradation</i> , 2022, 168, 105372.	1.9	6
5189	Gut Microbiota Regulates the Interplay between Diet and Genetics to Influence Glucose Tolerance . , 2020, 61, .		0
5190	Social overcrowding impacts gut microbiota, promoting stress, inflammation, and dysglycemia. <i>Gut Microbes</i> , 2021, 13, 2000275.	4.3	12
5191	Physical Activity and Dietary Composition Relate to Differences in Gut Microbial Patterns in a Multi-Ethnic Cohort—The HELIUS Study. <i>Metabolites</i> , 2021, 11, 858.	1.3	6
5192	Specialised digestive adaptations within the hindgut of a colobine monkey. <i>Innovation(China)</i> , 2022, 3, 100207.	5.2	6
5193	RfTest: A Robust and Flexible Community-Level Test for Microbiome Data Powerfully Detects Phylogenetically Clustered Signals. <i>Frontiers in Genetics</i> , 2021, 12, 749573.	1.1	5
5194	Innate Type 2 Immunity Controls Hair Follicle Commensalism by <i>Demodex</i> Mites. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5195	Compositional Data Analysis using Kernels in mass cytometry data. <i>Bioinformatics Advances</i> , 2022, 2, vbac003.	0.9	2
5196	Mink (<i>Neovison vison</i>) fecal microbiomes are influenced by sex, temperature, and time postdefecation. <i>Journal of Mammalogy</i> , 2022, 103, 316-327.	0.6	4
5197	Bacterial Communities and Prediction of Microbial Metabolic Pathway in Rice Wine Koji From Different Regions in China. <i>Frontiers in Microbiology</i> , 2021, 12, 748779.	1.5	9
5199	IncH1A plasmids potentially facilitate horizontal flow of antibiotic resistance genes to pathogens in microbial communities of urban residential sewage. <i>Molecular Ecology</i> , 2022, 31, 1595-1608.	2.0	14
5201	Sulfate-dependant microbially induced corrosion of mild steel in the deep sea: a 10-year microbiome study. <i>Microbiome</i> , 2022, 10, 4.	4.9	16

#	ARTICLE	IF	CITATIONS
5202	Integration of intestinal microbiota and metabonomics to elucidate different alleviation impacts of non-saponification and saponification astaxanthin pre-treatment on paracetamol-induced oxidative stress in rats. <i>Food and Function</i> , 2022, 13, 1860-1880.	2.1	11
5204	Increased Microbial Diversity and Decreased Prevalence of Common Pathogens in the Gut Microbiomes of Wild Turkeys Compared to Domestic Turkeys. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0142321.	1.4	8
5205	The gut microbiota of environmentally enriched mice regulates visual cortical plasticity. <i>Cell Reports</i> , 2022, 38, 110212.	2.9	23
5206	16S rRNA Gene-Based Metagenomic Analysis of Rhizosphere Soil Bacteria in Arkansas Rice Crop Fields. <i>Agronomy</i> , 2022, 12, 222.	1.3	8
5207	Chemical composition of selected insect meals and their effect on apparent total tract digestibility, fecal metabolites, and microbiota of adult cats fed insect-based retorted diets. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	3
5208	Cowsâ€™ reproductive performances and parity order influences the cervicovaginal fungal community. <i>Microbial Pathogenesis</i> , 2022, 162, 105351.	1.3	2
5209	A More Diverse Cervical Microbiome Associates with Better Clinical Outcomes in Patients with Endometriosis: A Pilot Study. <i>Biomedicines</i> , 2022, 10, 174.	1.4	15
5210	Incorporating genomeâ€based phylogeny and functional similarity into diversity assessments helps to resolve a global collection of human gut metagenomes. <i>Environmental Microbiology</i> , 2022, 24, 3966-3984.	1.8	2
5211	How microbiomes can help inform conservation: landscape characterisation of gut microbiota helps shed light on additional population structure in a specialist folivore. <i>Animal Microbiome</i> , 2022, 4, 12.	1.5	7
5212	Parkinsonâ€™s Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. <i>MSystems</i> , 2022, 7, e0119121.	1.7	13
5213	In Vivo Evaluation of the Toxicity of Patulin Degradation Products Produced by <i>Lactobacillus Casei</i> Yzu01. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5214	In Vivo Evaluation of the Toxicity of Patulin Degradation Products Produced by <i>Lactobacillus Casei</i> Yzu01. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5215	Effects of Complementary Feeding With Different Protein-Rich Foods on Infant Growth and Gut Health: Study Protocol. <i>Frontiers in Pediatrics</i> , 2021, 9, 793215.	0.9	4
5216	Ketoconazole 2% cream alters the skin fungal microbiome in seborrhoeic dermatitis: a cohort study. <i>Clinical and Experimental Dermatology</i> , 2022, 47, 1088-1096.	0.6	12
5217	Metabarcoding reveals massive species diversity of Diptera in a subtropical ecosystem. <i>Ecology and Evolution</i> , 2022, 12, e8535.	0.8	12
5218	Contrasting Community Composition and Co-Occurrence Relationships of the Active Pico-Sized Haptophytes in the Surface and Subsurface Chlorophyll Maximum Layers of the Arctic Ocean in Summer. <i>Microorganisms</i> , 2022, 10, 248.	1.6	4
5219	An Exploratory Study on the Microbiome of Northern and Southern Populations of <i>Ixodes scapularis</i> Ticks Predicts Changes and Unique Bacterial Interactions. <i>Pathogens</i> , 2022, 11, 130.	1.2	11
5220	Probiotics-induced Changes in Intestinal Structure and Gut Microbiota Are Associated with Reduced Rate of Pimpled Eggs in the Late Laying Period of Hens. <i>Journal of Poultry Science</i> , 2022, 59, 206-222.	0.7	5

#	ARTICLE	IF	CITATIONS
5221	The Role of the Western Diet and Oral Microbiota in Parkinson's Disease. <i>Nutrients</i> , 2022, 14, 355.	1.7	14
5222	Comparison of ready-to-eat organic antimicrobials, sodium bisulfate, and sodium lactate, on <i>Listeria monocytogenes</i> and the indigenous microbiome of organic uncured beef frankfurters stored under refrigeration for three weeks. <i>PLoS ONE</i> , 2022, 17, e0262167.	1.1	3
5223	Salivary Microbial Dysbiosis Is Associated With Peri-Implantitis: A Case-Control Study in a Brazilian Population. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 696432.	1.8	8
5224	Glycan profiling of the gut microbiota by Glycan-seq. <i>ISME Communications</i> , 2022, 2, .	1.7	4
5225	Gut microbiome development in early childhood is affected by day care attendance. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 2.	2.9	17
5226	Niches and Seasonal Changes, Rather Than Transgenic Events, Affect the Microbial Community of <i>Populus euramericana</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 805261.	1.5	3
5227	Establishment and characterization of stable, diverse, fecal-derived <i>in vitro</i> microbial communities that model the intestinal microbiota. <i>Cell Host and Microbe</i> , 2022, 30, 260-272.e5.	5.1	58
5229	Diet-Induced Non-alcoholic Fatty Liver Disease and Associated Gut Dysbiosis Are Exacerbated by Oral Infection. <i>Frontiers in Oral Health</i> , 2021, 2, 784448.	1.2	2
5232	Considerations and best practices in animal science 16S ribosomal RNA gene sequencing microbiome studies. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	36
5233	Longitudinal 16S rRNA gut microbiota data of infant triplets show partial susceptibility to host genetics. <i>IScience</i> , 2022, 25, 103861.	1.9	5
5234	Conceptual strategies for characterizing interactions in microbial communities. <i>IScience</i> , 2022, 25, 103775.	1.9	12
5235	Genetic diversity, gene flow and hybridization in fan-shaped sponges (<i>Phakellia</i> spp.) in the North-East Atlantic deep sea. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 181, 103685.	0.6	6
5236	Biochar mitigation of soil acidification and carbon sequestration is influenced by materials and temperature. <i>Ecotoxicology and Environmental Safety</i> , 2022, 232, 113241.	2.9	29
5237	Horizontal transfer of antibiotic resistance genes within the bacterial communities in aquacultural environment. <i>Science of the Total Environment</i> , 2022, 820, 153286.	3.9	9
5238	Vertical stratification of microbial communities and isotope geochemistry tie groundwater denitrification to sampling location within a nitrate-contaminated aquifer. <i>Science of the Total Environment</i> , 2022, 820, 153092.	3.9	8
5239	Hydrous ferric oxides (HFO's) precipitated from contaminated waters at several abandoned Sb deposits Interdisciplinary assessment. <i>Science of the Total Environment</i> , 2022, 821, 153248.	3.9	8
5240	A Guide to Dietary Pattern's Microbiome Data Integration. <i>Journal of Nutrition</i> , 2022, 152, 1187-1199.	1.3	12
5242	Performance determinants of unsupervised clustering methods for microbiome data. <i>Microbiome</i> , 2022, 10, 25.	4.9	15

#	ARTICLE	IF	CITATIONS
5243	Enterobacter cloacae: a villain in CaOx stone disease?. Urolithiasis, 2022, 50, 177.	1.2	5
5244	Cervicovaginal Microbiota Predicts Neisseria gonorrhoeae Clinical Presentation. Frontiers in Microbiology, 2021, 12, 790531.	1.5	4
5245	Dietary Intake Mediates Ethnic Differences in Gut Microbial Composition. Nutrients, 2022, 14, 660.	1.7	17
5246	Environmental structure impacts microbial composition and secondary metabolism. ISME Communications, 2022, 2, .	1.7	19
5247	Lactobacillus plantarum KLDS1.0386 with antioxidant capacity ameliorates the lipopolysaccharide-induced acute liver injury in mice by NF- κ B and Nrf2 pathway. Food Bioscience, 2022, 47, 101589.	2.0	9
5248	Decreased levels and ecological risks of disinfection by-product chloroform in a field-scale artificial groundwater recharge project by colloid supplement. Environment International, 2022, 161, 107130.	4.8	2
5249	Salmonella phage CKT1 significantly relieves the body weight loss of chicks by normalizing the abnormal intestinal microbiome caused by hypervirulent Salmonella Pullorum. Poultry Science, 2022, 101, 101668.	1.5	13
5250	Inhibition of gut microbial β -glucuronidase effectively prevents carcinogen-induced microbial dysbiosis and intestinal tumorigenesis. Pharmacological Research, 2022, 177, 106115.	3.1	10
5251	Conventional and ohmic heating pasteurization of fresh and thawed sheep milk: Energy consumption and assessment of bacterial microbiota during refrigerated storage. Innovative Food Science and Emerging Technologies, 2022, 76, 102947.	2.7	17
5252	Gut microbiota-driven brain β amyloidosis in mice requires microglia. Journal of Experimental Medicine, 2022, 219, .	4.2	44
5253	Effects of Eimeria tenella on Cecal Luminal and Mucosal Microbiota in Broiler Chickens. Avian Diseases, 2022, 66, .	0.4	8
5254	Immunomodulatory effects of mixed <i>Lactobacillus plantarum</i> on lipopolysaccharide-induced intestinal injury in mice. Food and Function, 2022, 13, 4914-4929.	2.1	5
5255	The Startup of Anaerobic Co-Digestion of Poultry Litter and Wheat Straw in an Asbr by Gradually Increasing Organic Loading Rate: Methane Production and Microbial Community Analysis. SSRN Electronic Journal, 0, , .	0.4	0
5256	An experimental test of disease resistance function in the skin-associated bacterial communities of three tropical amphibian species. FEMS Microbiology Ecology, 2022, 98, .	1.3	2
5257	Preliminary Report on Intestinal Flora Disorder, Faecal Short-Chain Fatty Acid Level Decline and Intestinal Mucosal Tissue Weakening Caused by Litchi Extract to Induce Systemic Inflammation in HFA Mice. Nutrients, 2022, 14, 776.	1.7	2
5258	Dietary supplementation with fiber, α - α biotics, and spray-dried plasma affects apparent total tract macronutrient digestibility and the fecal characteristics, fecal microbiota, and immune function of adult dogs. Journal of Animal Science, 2022, 100, .	0.2	9
5259	RecPD: A Recombination-aware measure of phylogenetic diversity. PLoS Computational Biology, 2022, 18, e1009899.	1.5	4
5260	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. Frontiers in Bioinformatics, 2022, 2, .	1.0	10

#	ARTICLE	IF	CITATIONS
5261	Identification of bovine respiratory disease through the nasal microbiome. <i>Animal Microbiome</i> , 2022, 4, 15.	1.5	14
5262	Metagenetic and Volatilomic Approaches to Elucidate the Effect of <i>Lactiplantibacillus plantarum</i> Starter Cultures on Sicilian Table Olives. <i>Frontiers in Microbiology</i> , 2021, 12, 771636.	1.5	10
5263	Microbial biogeography of the wombat gastrointestinal tract. <i>PeerJ</i> , 2022, 10, e12982.	0.9	2
5264	Colonization and Interaction of Bacteria Associated With Chinese Chives Affected by Ecological Compartments and Growth Conditions. <i>Frontiers in Microbiology</i> , 2022, 13, 775002.	1.5	3
5265	Microbiome Resilience and Health Implications for People in Half-Year Travel. <i>Frontiers in Immunology</i> , 2022, 13, 848994.	2.2	2
5266	To rarefy or not to rarefy: robustness and efficiency trade-offs of rarefying microbiome data. <i>Bioinformatics</i> , 2022, 38, 2389-2396.	1.8	11
5267	Low-Dose Interleukin-2 Altered Gut Microbiota and Ameliorated Collagen-Induced Arthritis. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 1365-1379.	1.6	5
5268	The Leaf Microbiome of Tobacco Plants across Eight Chinese Provinces. <i>Microorganisms</i> , 2022, 10, 450.	1.6	7
5269	Composition and characteristics of soil microbial communities in cotton fields with different incidences of <i>Verticillium</i> wilt. <i>Plant Signaling and Behavior</i> , 2022, 17, 2034271.	1.2	6
5270	The gut microbiota of gibbons across host genus and captive site in China. <i>American Journal of Primatology</i> , 2022, 84, e23360.	0.8	2
5271	Effects of Sodium Hyaluronate Eye Drops With or Without Preservatives on Ocular Surface Bacterial Microbiota. <i>Frontiers in Medicine</i> , 2022, 9, 793565.	1.2	4
5272	Microbiome structure and response to watering in rhizosphere of <i>Nitrosalsola vermiculata</i> and surrounding bulk soil. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2022, 50, 12567.	0.5	1
5273	Network-Based Differences in the Vaginal and Bladder Microbial Communities Between Women With and Without Urgency Urinary Incontinence. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 759156.	1.8	12
5274	Incorporation of Data From Multiple Hypervariable Regions when Analyzing Bacterial 16S rRNA Gene Sequencing Data. <i>Frontiers in Genetics</i> , 2022, 13, 799615.	1.1	10
5275	Spermatic Microbiome Characteristics in Infertile Patients: Impact on Sperm Count, Mobility, and Morphology. <i>Journal of Clinical Medicine</i> , 2022, 11, 1505.	1.0	9
5276	Relationships Between Diurnal Changes of Tongue Coating Microbiota and Intestinal Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 813790.	1.8	3
5277	Encapsulated Fecal Microbiota Transplantation: Development, Efficacy, and Clinical Application. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 826114.	1.8	21
5278	DNA Metabarcoding Enables High-Throughput Detection of Spotted Wing Drosophila (<i>Drosophila</i>) Tj ETQq1 1 0.784314 rgBTg/Overlook	1.1	11

#	ARTICLE	IF	CITATIONS
5279	Development of a novel feeding method for Japanese black calves with thermophile probiotics at postweaning. <i>Journal of Applied Microbiology</i> , 2022, 132, 3870-3882.	1.4	7
5280	Bacterial microbiome of faecal samples of naked mole-rat collected from the toilet chamber. <i>BMC Research Notes</i> , 2022, 15, 107.	0.6	1
5282	Sow vaccination against virulent <i>Glaesserella parasuis</i> shapes the nasal microbiota of their offspring. <i>Scientific Reports</i> , 2022, 12, 3357.	1.6	9
5284	Interaction of bacterial genera associated with therapeutic response to immune checkpoint PD-1 blockade in a United States cohort. <i>Genome Medicine</i> , 2022, 14, 35.	3.6	29
5285	Wild Heterotrophic Nitrifying Strain <i>Pseudomonas</i> BT1 Isolated from Kitchen Waste Sludge Restores Ammonia Nitrogen Removal in a Sewage Treatment Plant Shocked by Thiourea. <i>Applied Biochemistry and Biotechnology</i> , 2022, , 1.	1.4	2
5286	Meteorites as Food Source on Early Earth: Growth, Selection, and Inhibition of a Microbial Community on a Carbonaceous Chondrite. <i>Astrobiology</i> , 2022, 22, 495-508.	1.5	2
5287	Microbial Co-occurrence Network and Fermentation Information of Natural Woody-Plant Silage Prepared With Grass and Crop By-Product in Southern Africa. <i>Frontiers in Microbiology</i> , 2022, 13, 756209.	1.5	9
5288	Multiomic Analysis of the Gut Microbiome in Psoriasis Reveals Distinct Host-Microbe Associations. <i>JID Innovations</i> , 2022, 2, 100115.	1.2	8
5290	Deep sequencing reveals changes in prokaryotic taxonomy and functional diversity of pit muds in different distilleries of China. <i>Annals of Microbiology</i> , 2022, 72, .	1.1	5
5291	Cerebral Intraparenchymal Hemorrhage Changes Patients' Gut Bacteria Composition and Function. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 829491.	1.8	13
5292	Alternations in the gut microbiota and metabolome with newly diagnosed unstable angina. <i>Journal of Genetics and Genomics</i> , 2022, 49, 240-248.	1.7	3
5293	Freeze-drying can replace cold-chains for transport and storage of fecal microbiome samples. <i>PeerJ</i> , 2022, 10, e13095.	0.9	3
5294	Bacterial communities associated with wood rot fungi that use distinct decomposition mechanisms. <i>ISME Communications</i> , 2022, 2, .	1.7	13
5295	Nasal Microbiome Change During and After Exacerbation in Asthmatic Children. <i>Frontiers in Microbiology</i> , 2021, 12, 833726.	1.5	8
5297	The Power of Microbiome Studies: Some Considerations on Which Alpha and Beta Metrics to Use and How to Report Results. <i>Frontiers in Microbiology</i> , 2021, 12, 796025.	1.5	44
5298	<i>Lactobacillus paracasei</i> induced antitumor immunity and synergized with anti-programmed cell death 1 to reduce tumor burden in mice. <i>Gut Microbes</i> , 2022, 14, 2046246.	4.3	27
5299	The Antiviral Effect of Isatis Root Polysaccharide against NADC30-like PRRSV by Transcriptome and Proteome Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3688.	1.8	1
5300	MinION, a portable long-read sequencer, enables rapid vaginal microbiota analysis in a clinical setting. <i>BMC Medical Genomics</i> , 2022, 15, 68.	0.7	12

#	ARTICLE	IF	CITATIONS
5301	Changes in Gut Microbiota by the <i>Lactobacillus casei</i> Anchoring the K88 Fimbrial Protein Prevented Newborn Piglets From Clinical Diarrhea. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 842007.	1.8	12
5302	Dynamics of the normal gut microbiota: A longitudinal one-year population study in Sweden. <i>Cell Host and Microbe</i> , 2022, 30, 726-739.e3.	5.1	64
5303	Gut Mucosal Microbiome Is Perturbed in Rheumatoid Arthritis Mice and Partly Restored after TDAG8 Deficiency or Suppression by Salicylanilide Derivative. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3527.	1.8	8
5304	A global microbiome survey of vineyard soils highlights the microbial dimension of viticultural terroirs. <i>Communications Biology</i> , 2022, 5, 241.	2.0	35
5305	Alteration of barrier properties, stratum corneum ceramides and microbiome composition in response to lotion application on cosmetic dry skin. <i>Scientific Reports</i> , 2022, 12, 5223.	1.6	13
5306	Development of Next-Generation Probiotics by Investigating the Interrelationships between Gastrointestinal Microbiota and Diarrhea in Preruminant Holstein Calves. <i>Animals</i> , 2022, 12, 695.	1.0	5
5307	Bacterial Communities in the Feces of Laboratory Reared <i>Gampsocleis gratiosa</i> (Orthoptera): Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 502	1.0	0
5308	Newly designed foraminifera primers identify habitat-specific lineages through metabarcoding analyses. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12913.	0.8	0
5309	Analysis of the Relationship between the Phylogenetic Diversity of Benthic Communities and Degree of Mineralization of Plain Rivers of the Lower Volga River Basin. <i>Russian Journal of Ecology</i> , 2022, 53, 100-110.	0.3	1
5310	MiRKAT-MC: A Distance-Based Microbiome Kernel Association Test With Multi-Categorical Outcomes. <i>Frontiers in Genetics</i> , 2022, 13, 841764.	1.1	4
5311	The microbial metabolite trimethylamine N-oxide promotes antitumor immunity in triple-negative breast cancer. <i>Cell Metabolism</i> , 2022, 34, 581-594.e8.	7.2	105
5312	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
5313	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	1.7	35
5314	The bacteriology of pleural infection (TORPIDS): an exploratory metagenomics analysis through next generation sequencing. <i>Lancet Microbe</i> , The, 2022, 3, e294-e302.	3.4	22
5315	Effect of dietary honeysuckle (<i>Lonicera caerulea</i> L.) supplementation on lipid metabolism, immunity and intestinal microbiota in grass carp (<i>Ctenopharyngodon idellus</i>). <i>Aquaculture Reports</i> , 2022, 23, 101063.	0.7	8
5316	Effects of Maternal Factors and Postpartum Environment on Early Colonization of Intestinal Microbiota in Piglets. <i>Frontiers in Veterinary Science</i> , 2022, 9, 815944.	0.9	0
5317	Can seagrass modify the effects of ocean acidification on oysters?. <i>Marine Pollution Bulletin</i> , 2022, 177, 113438.	2.3	7
5318	Intrinsic and extrinsic factors influence on an omnivore's gut microbiome. <i>PLoS ONE</i> , 2022, 17, e0266698.	1.1	5

#	ARTICLE	IF	CITATIONS
5319	The Bacterial Microbiota of Edible Insects <i>Acheta domesticus</i> and <i>Gryllus assimilis</i> Revealed by High Content Analysis. <i>Foods</i> , 2022, 11, 1073.	1.9	9
5320	Alterations in the saliva microbiome in patients with gastritis and small bowel inflammation. <i>Microbial Pathogenesis</i> , 2022, 165, 105491.	1.3	8
5321	Strain Identification and Quantitative Analysis in Microbial Communities. <i>Journal of Molecular Biology</i> , 2022, 434, 167582.	2.0	15
5322	Increasing transparency and reproducibility in stroke-microbiota research: A toolbox for microbiota analysis. <i>IScience</i> , 2022, 25, 103998.	1.9	3
5323	Impaired central tolerance induces changes in the gut microbiota that exacerbate autoimmune hepatitis. <i>Journal of Autoimmunity</i> , 2022, 128, 102808.	3.0	3
5324	Human enteric viruses autonomously shape inflammatory bowel disease phenotype through divergent innate immunomodulation. <i>Science Immunology</i> , 2022, 7, eabn6660.	5.6	38
5325	Initial fungal diversity impacts flavor compounds formation in the spontaneous fermentation of Chinese liquor. <i>Food Research International</i> , 2022, 155, 110995.	2.9	13
5326	Evaluation of rain-shelter cultivation mode effects on microbial diversity during Cabernet Sauvignon (<i>Vitis vinifera</i> L.) maturation in Jingyang, Shaanxi, China. <i>Food Research International</i> , 2022, 156, 111165.	2.9	8
5327	In vivo evaluation of the toxicity of patulin degradation products produced by <i>Lactobacillus casei</i> YZU01. <i>Biological Control</i> , 2022, 169, 104878.	1.4	1
5328	Investigating the microbial terroir of fermented foods produced in a professional kitchen. <i>International Journal of Gastronomy and Food Science</i> , 2022, 28, 100509.	1.3	3
5329	Enhanced production of short-chain fatty acids from sludge by thermal hydrolysis and acidogenic fermentation for organic resource recovery. <i>Science of the Total Environment</i> , 2022, 828, 154389.	3.9	17
5330	Altered fecal microbiota, IgA, and fermentative end-products in adult dogs fed prebiotics and a nonviable <i>Lactobacillus acidophilus</i> . <i>Journal of Animal Science</i> , 2021, 99, .	0.2	7
5331	Weight loss and high-protein, high-fiber diet consumption impact blood metabolite profiles, body composition, voluntary physical activity, fecal microbiota, and fecal metabolites of adult dogs. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	13
5332	Fiber mixture-specific effect on distal colonic fermentation and metabolic health in lean but not in prediabetic men. <i>Gut Microbes</i> , 2022, 14, 2009297.	4.3	15
5333	Nitrogen Fertiliser Immobilisation and Uptake in the Rhizospheres of Wheat and Canola. <i>Agronomy</i> , 2021, 11, 2507.	1.3	0
5334	Bacterial Microbiomes in the Sediments of Lotic Systems Ecologic Drivers and Role: A Case Study from the MureÅŸ River, Transylvania, Romania. <i>Water (Switzerland)</i> , 2021, 13, 3518.	1.2	8
5336	Microbiological and clinical evaluation of ultrasonic debridement with/without erythritol air polishing during supportive periodontal therapy in arches with full-arch fixed implant-supported prostheses: protocol for a randomised controlled trial. <i>BMJ Open</i> , 2021, 11, e053286.	0.8	2
5337	Mycobiota of Fine Roots of <i>Pseudotsuga menziesii</i> Introduced to the Native Forest Environment. <i>Forests</i> , 2021, 12, 1766.	0.9	1

#	ARTICLE	IF	CITATIONS
5340	Comparison of Gut Microbiota and Metabolic Status of Sows With Different Litter Sizes During Pregnancy. <i>Frontiers in Veterinary Science</i> , 2021, 8, 793174.	0.9	8
5341	Bacterial Succession during Vermicomposting of Silver Wattle (<i>Acacia dealbata</i> Link). <i>Microorganisms</i> , 2022, 10, 65.	1.6	9
5342	Human-provisioned foods reduce gut microbiome diversity in American black bears (<i>Ursus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	0.6	0
5343	An altered microbiome in a Parkinson's disease model <i>Drosophila melanogaster</i> has a negative effect on development. <i>Scientific Reports</i> , 2021, 11, 23635.	1.6	4
5344	Convergent Microbial Community Formation in Replicate Anaerobic Reactors Inoculated from Different Sources and Treating Ersatz Crew Waste. <i>Life</i> , 2021, 11, 1374.	1.1	1
5345	Long-term acclimation might enhance the growth and competitive ability of <i>Microcystis aeruginosa</i> in warm environments. <i>Freshwater Biology</i> , 2022, 67, 589-602.	1.2	5
5346	Putative Familial Transmissible Bacteria of Various Body Niches Link with Home Environment and Children's Immune Health. <i>Microbiology Spectrum</i> , 2021, 9, e0087221.	1.2	0
5347	The differences between fecal microbiota and intestinal fluid microbiota in colon polyps. <i>Medicine (United States)</i> , 2021, 100, e28028.	0.4	6
5348	The gut microbiota in pediatric multiple sclerosis and demyelinating syndromes. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 2252-2269.	1.7	34
5349	Supplementation with Exogenous Catalase from <i>Penicillium notatum</i> in the Diet Ameliorates Lipopolysaccharide-Induced Intestinal Oxidative Damage through Affecting Intestinal Antioxidant Capacity and Microbiota in Weaned Pigs. <i>Microbiology Spectrum</i> , 2021, 9, e0065421.	1.2	28
5350	Intestinal microbiota disturbance affects the occurrence of African swine fever. <i>Animal Biotechnology</i> , 2021, , 1-10.	0.7	2
5351	<i>Saccharomyces cerevisiae</i> Dehydrated Culture Modulates Fecal Microbiota and Improves Innate Immunity of Adult Dogs. <i>Fermentation</i> , 2022, 8, 2.	1.4	5
5352	Flooding and ecological restoration promote wetland microbial communities and soil functions on former cranberry farmland. <i>PLoS ONE</i> , 2021, 16, e0260933.	1.1	1
5353	Characterization of the Gastrointestinal and Reproductive Tract Microbiota in Fertile and Infertile Pakistani Couples. <i>Biology</i> , 2022, 11, 40.	1.3	4
5354	Analysis of the intestinal microbial community altered during rotavirus infection in suckling mice. <i>Virology Journal</i> , 2021, 18, 254.	1.4	9
5355	Impact of intensive lifestyle intervention on gut microbiota composition in type 2 diabetes: a post-hoc analysis of a randomized clinical trial. <i>Gut Microbes</i> , 2022, 14, 2005407.	4.3	10
5356	Excess Vitamins or Imbalance of Folic Acid and Choline in the Gestational Diet Alter the Gut Microbiota and Obesogenic Effects in Wistar Rat Offspring. <i>Nutrients</i> , 2021, 13, 4510.	1.7	11
5357	Short- and long-term effects of amoxicillin/clavulanic acid or doxycycline on the gastrointestinal microbiome of growing cats. <i>PLoS ONE</i> , 2021, 16, e0253031.	1.1	11

#	ARTICLE	IF	CITATIONS
5359	Fish Diversity Monitored by Environmental DNA in the Yangtze River Mainstream. <i>Fishes</i> , 2022, 7, 1.	0.7	4
5360	Gut Microbiome-Based Diagnostic Model to Predict Diabetes Mellitus. <i>Bioengineered</i> , 2021, 12, 12521-12534.	1.4	16
5362	Differences in the Composition of Gut Microbiota between Patients with Parkinson's Disease and Healthy Controls: A Cohort Study. <i>Journal of Clinical Medicine</i> , 2021, 10, 5698.	1.0	18
5363	Hepatoprotective effects of Cassiae Semen on mice with non-alcoholic fatty liver disease based on gut microbiota. <i>Communications Biology</i> , 2021, 4, 1357.	2.0	26
5364	Different soil salinity imparts clear alteration in rhizospheric bacterial community dynamics in rice and peanut. <i>Archives of Microbiology</i> , 2022, 204, 36.	1.0	3
5366	Community RNA-Seq: multi-kingdom responses to living versus decaying roots in soil. <i>ISME Communications</i> , 2021, 1, .	1.7	8
5367	Marker Genes (16S and ITS) Protocol for Plant Microbiome Analyses. <i>Bio-protocol</i> , 2022, 12, .	0.2	0
5369	The Potential Role of Hypochlorhydria in the Development of Duodenal Dysbiosis: A Preliminary Report. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 854904.	1.8	6
5370	Recently Evolved Francisella-Like Endosymbiont Outcompetes an Ancient and Evolutionarily Associated Coxiella-Like Endosymbiont in the Lone Star Tick (<i>Amblyomma americanum</i>) Linked to the Alpha-Gal Syndrome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 787209.	1.8	9
5371	mbDenoise: microbiome data denoising using zero-inflated probabilistic principal components analysis. <i>Genome Biology</i> , 2022, 23, 94.	3.8	8
5372	The gut microbiome influences host diet selection behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2117537119.	3.3	44
5373	Teasing apart the host-related, nutrient-related and temperature-related effects shaping the phenology and microbiome of the tropical seagrass <i>Halophila stipulacea</i> . <i>Environmental Microbiomes</i> , 2022, 17, 18.	2.2	6
5374	Early-life gut microbiota and attention deficit hyperactivity disorder in preadolescents. <i>Pediatric Research</i> , 2023, 93, 2051-2060.	1.1	5
5375	MEMO: Mass Spectrometry-Based Sample Vectorization to Explore Chemodiverse Datasets. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	7
5376	Compositional and functional features of the gut microbiota of the intertidal snail <i>Nerita yoldii</i> along China's coast. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 0, , 1-8.	0.4	2
5378	<i>Bacillus cereus</i> (EG-Q3) in the Gut of <i>Ectropis grisescens</i> Contributes to Host Response to Starvation Conditions. <i>Frontiers in Microbiology</i> , 2022, 13, 785415.	1.5	1
5379	Analysis of Gut Microbiota and Metabolites in Diannan Small Ear Sows at Diestrus and Metestrus. <i>Frontiers in Microbiology</i> , 2022, 13, 826881.	1.5	3
5380	Enumeration of citrus endophytic bacterial communities based on illumine metagenomics technique. <i>PLoS ONE</i> , 2022, 17, e0263144.	1.1	3

#	ARTICLE	IF	CITATIONS
5381	Novel symbionts and potential human pathogens excavated from argasid tick microbiomes that are shaped by dual or single symbiosis. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1979-1992.	1.9	4
5382	Early microbial markers of periodontal and cardiometabolic diseases in ORIGINS. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 30.	2.9	7
5384	Effects of Soil Acidification on Bacterial and Fungal Communities in the Jiaodong Peninsula, Northern China. <i>Agronomy</i> , 2022, 12, 927.	1.3	6
5385	Effects of red cabbage extract rich in anthocyanins on rumen fermentation, rumen bacterial community, nutrient digestion, and plasma indices in beef bulls. <i>Animal</i> , 2022, 16, 100510.	1.3	1
5386	Precipitation increased the proportion of non-mycorrhizal fungi in <i>Plantathera chlorantha</i> orchid roots. <i>Rhizosphere</i> , 2022, 22, 100522.	1.4	1
5972	Alterations of mucosa-attached microbiome and epithelial cell numbers in the cystic fibrosis small intestine with implications for intestinal disease. <i>Scientific Reports</i> , 2022, 12, 6593.	1.6	10
5975	Composition and Diversity of Soil Microbial Community Associated With Land Use Types in the Agro-Pastoral Area in the Upper Yellow River Basin. <i>Frontiers in Plant Science</i> , 2022, 13, 819661.	1.7	6
5976	Soil Environments Influence Gut Prokaryotic Communities in the Larvae of the Invasive Japanese Beetle <i>Popillia japonica</i> Newman. <i>Frontiers in Microbiology</i> , 2022, 13, 854513.	1.5	4
5977	Ontology-aware deep learning enables ultrafast and interpretable source tracking among sub-million microbial community samples from hundreds of niches. <i>Genome Medicine</i> , 2022, 14, 43.	3.6	9
5978	Drinking Water Supplemented with Acidifiers Improves the Growth Performance of Weaned Pigs and Potentially Regulates Antioxidant Capacity, Immunity, and Gastrointestinal Microbiota Diversity. <i>Antioxidants</i> , 2022, 11, 809.	2.2	8
5980	DEPP: Deep Learning Enables Extending Species Trees using Single Genes. <i>Systematic Biology</i> , 2023, 72, 17-34.	2.7	11
5981	<i>Brassica napus</i> Bacterial Assembly Processes Vary with Plant Compartment and Growth Stage but Not between Lines. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0027322.	1.4	10
5984	Cooked common bean flour, but not its protein hydrolysate, has the potential to improve gut microbiota composition and function in BALB/c mice fed a high-fat diet added with 6-propyl-2-thiouracil. <i>Journal of Nutritional Biochemistry</i> , 2022, 106, 109022.	1.9	4
5985	Assessment of the Endophytic Fungal Composition of <i>Lactobacillus plantarum</i> and <i>Enterococcus faecalis</i> -Fermented <i>Astragalus membranaceus</i> Using Single-Molecule, Real-Time Sequencing Technology. <i>Frontiers in Veterinary Science</i> , 2022, 9, 880152.	0.9	0
5986	Description of non-brachycephalic canine conjunctival microbiome before and after application of an antiseptic preparation. <i>Veterinary Ophthalmology</i> , 2022, 25, 297-306.	0.6	2
5987	Bacterial microbiota analysis demonstrates that ticks can acquire bacteria from habitat and host blood meal. <i>Experimental and Applied Acarology</i> , 2022, 87, 81-95.	0.7	6
5988	<i>Fusobacterium nucleatum</i> promotes colon cancer progression by changing the mucosal microbiota and colon transcriptome in a mouse model. <i>World Journal of Gastroenterology</i> , 2022, 28, 1981-1995.	1.4	13
5989	The Microbiota of a Mite Prey-Predator System on Different Host Plants Are Characterized by Dysbiosis and Potential Functional Redundancy. <i>Microbial Ecology</i> , 2022, , .	1.4	1

#	ARTICLE	IF	CITATIONS
5990	Simulated Leaching of Foliar Applied Copper Bactericides on the Soil Microbiome Utilizing Various Beta Diversity Resemblance Measurements. <i>Microbiology Spectrum</i> , 2022, 10, e0148121.	1.2	2
5991	Decreased Tissue Omega-6/Omega-3 Fatty Acid Ratio Prevents Chemotherapy-Induced Gastrointestinal Toxicity Associated with Alterations of Gut Microbiome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5332.	1.8	6
5992	Tumour immunotherapy: lessons from predator–prey theory. <i>Nature Reviews Immunology</i> , 2022, 22, 765-775.	10.6	41
5993	Diet Fermentation Leads to Microbial Adaptation in Black Soldier Fly (<i>Hermetia illucens</i> ; Linnaeus.) <i>Tj ETQq1 1 0.784314 rgBT₄/Overlook</i>	1.6	4
5994	Application of thifluzamide alters microbial network structure and affects methane cycle genes in rice-paddy soil. <i>Science of the Total Environment</i> , 2022, 838, 155769.	3.9	1
5995	Study on manipulation of ruminal fermentation using a bioelectrochemical system. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2022, , .	1.0	0
5996	Black Soldier Fly Larvae Influence Internal and Substrate Bacterial Community Composition Depending on Substrate Type and Larval Density. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0008422.	1.4	10
5997	A randomization-based causal inference framework for uncovering environmental exposure effects on human gut microbiota. <i>PLoS Computational Biology</i> , 2022, 18, e1010044.	1.5	8
5998	Land-Use Driven Changes in Soil Microbial Community Composition and Soil Fertility in the Dry-Hot Valley Region of Southwestern China. <i>Microorganisms</i> , 2022, 10, 956.	1.6	3
5999	Composition, Structure and Diversity of Soil Bacterial Communities before, during and after Transit through the Gut of the Earthworm <i>Aporrectodea caliginosa</i> . <i>Microorganisms</i> , 2022, 10, 1025.	1.6	12
6000	Gut Lignocellulose Activity and Microbiota in Asian Longhorned Beetle and Their Predicted Contribution to Larval Nutrition. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	10
6001	Large-herbivore nemabiomes: patterns of parasite diversity and sharing. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20212702.	1.2	6
6002	Start-up of co-digestion of poultry litter and wheat straw in anaerobic sequencing batch reactor by gradually increasing organic loading rate: Methane production and microbial community analysis. <i>Bioresource Technology</i> , 2022, 354, 127232.	4.8	16
6003	The synergy of Fe(III) and NO ₂ ⁻ drives the anaerobic oxidation of methane. <i>Science of the Total Environment</i> , 2022, 837, 155766.	3.9	7
6004	Suppression of Berberine and Probiotics (in vitro and in vivo) on the Growth of Colon Cancer With Modulation of Gut Microbiota and Butyrate Production. <i>Frontiers in Microbiology</i> , 2022, 13, 869931.	1.5	8
6005	Primer Choice and Xylem-Microbiome-Extraction Method Are Important Determinants in Assessing Xylem Bacterial Community in Olive Trees. <i>Plants</i> , 2022, 11, 1320.	1.6	4
6006	Intergenerational Transfer of Persistent Bacterial Communities in Female Nile Tilapia. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
6007	A high-fibre personalised dietary advice given via a web tool reduces constipation complaints in adults. <i>Journal of Nutritional Science</i> , 2022, 11, e31.	0.7	1

#	ARTICLE	IF	CITATIONS
6008	Plant growth-promoting rhizobacteria <i>Burkholderia vietnamiensis</i> B418 inhibits root-knot nematode on watermelon by modifying the rhizosphere microbial community. <i>Scientific Reports</i> , 2022, 12, 8381.	1.6	14
6009	Gut Microbial Ecology of Five Species of Sympatric Desert Rodents in Relation to Herbivorous and Insectivorous Feeding Strategies. <i>Integrative and Comparative Biology</i> , 2022, 62, 237-251.	0.9	4
6010	<i>Brassicaceae</i> host plants mask the feedback from the previous year's soil history on bacterial communities, except when they experience drought. <i>Environmental Microbiology</i> , 2022, 24, 3529-3548.	1.8	5
6011	Dynamic Distribution of Gut Microbiota in Pigs at Different Growth Stages: Composition and Contribution. <i>Microbiology Spectrum</i> , 2022, 10, e0068821.	1.2	36
6012	Large Comparative Analyses of Primate Body Site Microbiomes Indicate that the Oral Microbiome Is Unique among All Body Sites and Conserved among Nonhuman Primates. <i>Microbiology Spectrum</i> , 2022, 10, e0164321.	1.2	5
6013	Effect of antibiotics in the first week of life on faecal microbiota development. <i>Archives of Disease in Childhood: Fetal and Neonatal Edition</i> , 2022, 107, 603-610.	1.4	9
6014	Extension of PERMANOVA to Testing the Mediation Effect of the Microbiome. <i>Genes</i> , 2022, 13, 940.	1.0	3
6015	Single-molecule real-time sequencing reveals differences in bacterial diversity in raw milk in different regions and seasons in China. <i>Journal of Dairy Science</i> , 2022, 105, 5669-5684.	1.4	6
6016	Distribution of Vaginal and Gut Microbiome in Advanced Maternal Age. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	3
6017	Gut Microbiota Associated with Clinical Relapse in Patients with Quiescent Ulcerative Colitis. <i>Microorganisms</i> , 2022, 10, 1044.	1.6	1
6018	Fine scale transitions of the microbiota and metabolome along the gastrointestinal tract of herbivorous fishes. <i>Animal Microbiome</i> , 2022, 4, .	1.5	11
6019	An Altered Microbiota in the Lower and Upper Female Reproductive Tract of Women with Recurrent Spontaneous Abortion. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	10
6020	Quercetin Reduces Inflammation and Protects Gut Microbiota in Broilers. <i>Molecules</i> , 2022, 27, 3269.	1.7	19
6021	Mechanism of Electron Acceptor Promoting Propionic Acid Transformation in Anaerobic Fermentation. <i>Energies</i> , 2022, 15, 3947.	1.6	1
6023	Effects of captivity and rewilding on amphibian skin microbiomes. <i>Biological Conservation</i> , 2022, 271, 109576.	1.9	25
6024	Diagnosing microbiologically influenced corrosion at a crude oil pipeline facility leak site – A multiple lines of evidence approach. <i>International Biodeterioration and Biodegradation</i> , 2022, 172, 105438.	1.9	7
6025	Tillage management exerts stronger controls on soil microbial community structure and organic matter molecular composition than N fertilization. <i>Agriculture, Ecosystems and Environment</i> , 2022, 336, 108028.	2.5	3
6026	Niche differentiation of denitrifying anaerobic methane oxidation microbes in Taihu Lake of China. <i>Environmental Technology and Innovation</i> , 2022, 28, 102670.	3.0	2

#	ARTICLE	IF	CITATIONS
6027	Biodiversity risk assessment of genetically modified <i>Chaetoceros gracilis</i> for outdoor cultivation. <i>Journal of General and Applied Microbiology</i> , 2022, 68, 151-162.	0.4	1
6028	Association between gut microbiota and prediabetes in people living with HIV. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100143.	1.4	4
6029	The Impact of Probiotic Supplementation on Cognitive, Pathological and Metabolic Markers in a Transgenic Mouse Model of Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 2022, 16, .	1.4	13
6030	Response of Gut Microbiota, Digestive Enzyme Ability, and Immune Function to Starvation in the Oriental River Prawn <i>Macrobrachium nipponense</i> . <i>Aquaculture Nutrition</i> , 2022, 2022, 1-15.	1.1	1
6031	Bacterial colonisation dynamics of household plastics in a coastal environment. <i>Science of the Total Environment</i> , 2022, 838, 156199.	3.9	12
6032	Cloaca and feather-associated bacteria communities in common waxbills <i>Estrilda astrild</i>. <i>Journal of Avian Biology</i> , 2022, 2022, .	0.6	1
6037	Rationale and study design of Randomized Controlled Trial of Dietary Supplementation with prune (dried plums) on bone density, geometry, and estimated bone strength in postmenopausal women: The Prune study. <i>Contemporary Clinical Trials Communications</i> , 2022, 28, 100941.	0.5	6
6039	High-throughput sequencing to evaluate the effects of methamphetamine on the succession of the bacterial community to estimate the postmortem interval. <i>Forensic Sciences Research</i> , 0, , 1-12.	0.9	3
6040	Metagenomic Analysis Using Phylogenetic Placement—A Review of the First Decade. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	17
6042	Using microbiome information to understand and improve animal performance. <i>Italian Journal of Animal Science</i> , 2022, 21, 899-913.	0.8	4
6043	DNA Barcoding to Enhance Conservation of Sunshine Coast Heathlands. <i>Diversity</i> , 2022, 14, 436.	0.7	5
6044	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	1.7	2
6045	Fecal Microbiota Signatures Are Not Consistently Related to Symptom Severity in Irritable Bowel Syndrome. <i>Digestive Diseases and Sciences</i> , 2022, 67, 5137-5148.	1.1	10
6046	Sputum Microbiota in Coal Workers Diagnosed with Pneumoconiosis as Revealed by 16S rRNA Gene Sequencing. <i>Life</i> , 2022, 12, 830.	1.1	2
6047	Fecal Dysbiosis and Immune Dysfunction in Chinese Elderly Patients With Schizophrenia: An Observational Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	12
6048	Caffeic acid phenethyl ester suppresses intestinal FXR signaling and ameliorates nonalcoholic fatty liver disease by inhibiting bacterial bile salt hydrolase activity. <i>Acta Pharmacologica Sinica</i> , 2023, 44, 145-156.	2.8	12
6049	Microbial and genes diversity analysis: Relationship between starch conversion and carbohydrate metabolism during Niandoubao fermentation via the glutinous proso millet (GPM) process. <i>Food Control</i> , 2022, 140, 109154.	2.8	4
6050	Bacterial diversity and community composition in the gut and rearing water of Pacific White shrimp <i>Penaeus vannamei</i> during an outbreak of white feces disease. <i>Aquaculture</i> , 2022, 559, 738431.	1.7	7

#	ARTICLE	IF	CITATIONS
6052	<i>fast.adonis</i> : a computationally efficient non-parametric multivariate analysis of microbiome data for large-scale studies. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	2
6053	Efficacy of Utilization of All-Plant-Based and Commercial Low-Fishmeal Feeds in Two Divergently Selected Strains of Rainbow Trout (<i>Oncorhynchus mykiss</i>): Focus on Growth Performance, Whole-Body Proximate Composition, and Intestinal Microbiome. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	5
6054	Comparison of the gastric microbiome in Billroth I and Roux-en-Y reconstructions after distal gastrectomy. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
6055	Signatures of functional bacteriome structure in a tropical direct-developing amphibian species. <i>Animal Microbiome</i> , 2022, 4, .	1.5	6
6056	A rarefaction-without-resampling extension of PERMANOVA for testing presenceâ€“absence associations in the microbiome. <i>Bioinformatics</i> , 2022, 38, 3689-3697.	1.8	6
6057	Microbial community response to a bioaugmentation test to degrade trichloroethylene in a fractured rock aquifer, Trenton, N.J. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	6
6058	The impact of <i>Rhodiola rosea</i> on biomarkers of diabetes, inflammation, and microbiota in a leptin receptor-knockout mouse model. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
6059	Infection and antibiotic treatment have prolonged effects on gut microbiota, muscle and hepatic fatty acids in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Journal of Applied Microbiology</i> , 2022, 133, 1709-1724.	1.4	3
6060	A potential oral microbiome signature associated with coronary artery disease in Tunisia. <i>Bioscience Reports</i> , 2022, 42, .	1.1	6
6061	Saponification with calcium enhanced methane yield in anaerobic digestion of fat, oil, and grease: The essential role of calcium. <i>Renewable Energy</i> , 2022, 195, 1103-1112.	4.3	3
6062	Altered skin fungal and bacterial community compositions in tinea capitis. <i>Mycoses</i> , 2022, 65, 834-840.	1.8	3
6063	Using PacBio SMRT Sequencing Technology and Metabolomics to Explore the Microbiota-Metabolome Interaction Related to Silage Fermentation of Woody Plant. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
6064	Heat stress impacts the multi-domain ruminal microbiota and some of the functional features independent of its effect on feed intake in lactating dairy cows. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	3
6065	Selective Probiotic Treatment Positively Modulates the Microbiotaâ€“Gutâ€“Brain Axis in the BTBR Mouse Model of Autism. <i>Brain Sciences</i> , 2022, 12, 781.	1.1	10
6066	Historic Wooden Shipwrecks Influence Dispersal of Deep-Sea Biofilms. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	5
6067	More persistent bacterial than fungal associations in the microbiota of a pest insect. <i>Journal of Pest Science</i> , 2023, 96, 785-796.	1.9	2
6069	Characteristics of Gut Microbiome and Its Metabolites, Short-Chain Fatty Acids, in Children With Idiopathic Short Stature. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	6
6070	Influence of <i>Agaricus bisporus</i> establishment and fungicidal treatments on casing soil metataxonomy during mushroom cultivation. <i>BMC Genomics</i> , 2022, 23, .	1.2	1

#	ARTICLE	IF	CITATIONS
6071	Dietary Moringa oleifera leaf powder improves jejunal permeability and digestive function by modulating the microbiota composition and mucosal immunity in heat stressed rabbits. Environmental Science and Pollution Research, 2022, 29, 80952-80967.	2.7	7
6072	The Gut Mycobiome Characterization of Gestational Diabetes Mellitus and Its Association With Dietary Intervention. Frontiers in Microbiology, 0, 13, .	1.5	7
6073	Super-taxon in human microbiome are identified to be associated with colorectal cancer. BMC Bioinformatics, 2022, 23, .	1.2	4
6075	Adherence to Gluten-Free Diet Restores Alpha Diversity in Celiac People but the Microbiome Composition Is Different to Healthy People. Nutrients, 2022, 14, 2452.	1.7	10
6076	Fecal microbiome of horses transitioning between warm-season and cool-season grass pasture within integrated rotational grazing systems. Animal Microbiome, 2022, 4, .	1.5	5
6078	Saccharomyces Boulardii Ameliorates Non-alcoholic Steatohepatitis in Mice Induced by a Methionine-Choline-Deficient Diet Through Gut-Liver Axis. Frontiers in Microbiology, 0, 13, .	1.5	3
6079	Escherichia/Shigella, SCFAs, and Metabolic Pathways—The Triad That Orchestrates Intestinal Dysbiosis in Patients with Decompensated Alcoholic Cirrhosis from Western Mexico. Microorganisms, 2022, 10, 1231.	1.6	22
6081	Antidepressant Shugan Jieyu Capsule Alters Gut Microbiota and Intestinal Microbiome Function in Rats With Chronic Unpredictable Mild Stress -Induced Depression. Frontiers in Pharmacology, 0, 13, .	1.6	9
6082	Vacuum-enhanced anaerobic fermentation: Achieving process intensification, thickening and improved hydrolysis and VFA yields in a single treatment step. Water Research, 2022, 220, 118719.	5.3	7
6083	Protocol for correlation analysis of the murine gut microbiome and meta-metabolome using 16S rDNA sequencing and UPLC-MS. STAR Protocols, 2022, 3, 101494.	0.5	0
6084	Gut Microbiota Ecology and Inferred Functions in Children With ASD Compared to Neurotypical Subjects. Frontiers in Microbiology, 0, 13, .	1.5	16
6085	Gut Commensal Parabacteroides goldsteinii MTS01 Alters Gut Microbiota Composition and Reduces Cholesterol to Mitigate Helicobacter pylori-Induced Pathogenesis. Frontiers in Immunology, 0, 13, .	2.2	11
6086	Divergent gut microbiota in two closely related house mouse subspecies under common garden conditions. FEMS Microbiology Ecology, 2022, 98, .	1.3	5
6087	Organohalide respiration potential in marine sediments from Aarhus Bay. FEMS Microbiology Ecology, 2022, 98, .	1.3	6
6088	Extracellular DNA: A Critical Aspect of Marine Biofilms. Microorganisms, 2022, 10, 1285.	1.6	2
6089	<i>In vitro</i> colonic fermentation characteristics of barley-koji differ from those of barley. Bioscience, Biotechnology and Biochemistry, 0, , .	0.6	0
6090	Wuwei Qingzhuo San Ameliorates Hyperlipidemia in Mice Fed With HFD by Regulating Metabolomics and Intestinal Flora Composition. Frontiers in Pharmacology, 0, 13, .	1.6	4
6091	Schoolyard Biodiversity Determines Short-Term Recovery of Disturbed Skin Microbiota in Children. Microbial Ecology, 2023, 86, 658-669.	1.4	5

#	ARTICLE	IF	CITATIONS
6093	Impacts of Gadolinium and Yttrium on the Performance and Microbial Community Composition of a Bench-Scale-Activated Sludge System. <i>ACS ES&T Water</i> , 2022, 2, 1370-1379.	2.3	2
6094	Dietary Utilization Drives the Differentiation of Gut Bacterial Communities between Specialist and Generalist Drosophilid Flies. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
6095	Prebiotic potential of apple pomace and pectins from different apple varieties: Modulatory effects on key target commensal microbial populations. <i>Food Hydrocolloids</i> , 2022, 133, 107958.	5.6	18
6097	Community structure and co-occurrence network analysis of bacteria and fungi in wheat fields vs fruit orchards. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	5
6099	Effects of Salinity on the Growth, Physiological Characteristics, and Intestinal Microbiota of the Echiura Worm (<i>Urechis unicinctus</i>). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
6100	The Relationship Between Pediatric Gut Microbiota and SARS-CoV-2 Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	29
6101	Fecal bacterial microbiota in constipated patients before and after eight weeks of daily <i>Bifidobacterium infantis</i> 35624 administration. <i>Revista De Gastroenterología De México (English)</i> Tj ETQq0 0 0 0 0 BT /Overlock 10 Tf		
6103	Environmental Selection Shapes Bacterial Community Composition in Traditionally Fermented Maize-Based Foods from Benin, Tanzania and Zambia. <i>Microorganisms</i> , 2022, 10, 1354.	1.6	2
6104	A single respiratory tract infection early in life reroutes healthy microbiome development and affects adult metabolism in a preclinical animal model. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	1
6105	Habitat and Host Species Drive the Structure of Bacterial Communities of Two Neotropical Trap-Jaw <i>Odontomachus</i> Ants. <i>Microbial Ecology</i> , 0, , .	1.4	1
6106	Analysis of Intestinal Mycobiota of Patients with <i>Clostridioides difficile</i> Infection among a Prospective Inpatient Cohort. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	9
6107	Morphology, microbiota, and metabolome along the intestinal tract of female turkeys. <i>Poultry Science</i> , 2022, 101, 102046.	1.5	0
6108	Populational and metabolic shifts induced by acetate, butyrate and lactate in dark fermentation. <i>International Journal of Hydrogen Energy</i> , 2022, 47, 28385-28398.	3.8	4
6110	MicrobiomeGWAS: A Tool for Identifying Host Genetic Variants Associated with Microbiome Composition. <i>Genes</i> , 2022, 13, 1224.	1.0	9
6111	Optimal growth temperature of Arctic soil bacterial communities increases under experimental warming. <i>Global Change Biology</i> , 2022, 28, 6050-6064.	4.2	16
6112	<i>Bifidobacterium longum</i> BL-10 with Antioxidant Capacity Ameliorates Lipopolysaccharide-Induced Acute Liver Injury in Mice by the Nuclear Factor- κ B Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 8680-8692.	2.4	7
6113	Spatial variations of bacterial communities associated with biological soil crusts along a climatic gradient in alpine grassland ecosystems. <i>Plant and Soil</i> , 2022, 480, 493-506.	1.8	4
6114	Microbiome composition of the marine sponge <i>Cliona</i> variants at the neotropical southern Caribbean Sea displays a predominant core of Rhizobiales and Nitrosopumilaceae. <i>Journal of Applied Microbiology</i> , 2022, 133, 2027-2038.	1.4	0

#	ARTICLE	IF	CITATIONS
6115	Beneficial Shifts in the Gut Bacterial Community of Gilthead Seabream (<i>Sparus aurata</i>) Juveniles Supplemented with Allium-Derived Compound Propyl Propane Thiosulfonate (PTSO). <i>Animals</i> , 2022, 12, 1821.	1.0	5
6116	Phylogenies of the 16S rRNA gene and its hypervariable regions lack concordance with core genome phylogenies. <i>Microbiome</i> , 2022, 10, .	4.9	43
6117	Relationship between inflammatory status and microbial composition in severe asthma and during exacerbation. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 3362-3376.	2.7	7
6118	<i>Fusobacterium</i> is enriched in oral cancer and promotes induction of programmed death-ligand 1 (PD-L1). <i>Neoplasia</i> , 2022, 31, 100813.	2.3	14
6119	Grass-legume mixtures enhance forage production via the bacterial community. <i>Agriculture, Ecosystems and Environment</i> , 2022, 338, 108087.	2.5	21
6120	High salt stress increases archaeal abundance and network connectivity in saline agricultural soils. <i>Catena</i> , 2022, 217, 106520.	2.2	10
6121	Exploiting 16S rRNA-based metagenomics to reveal neglected microorganisms associated with infertility in breeding bulls in Spanish extensive herds. <i>Research in Veterinary Science</i> , 2022, 150, 52-57.	0.9	2
6122	Dental plaque-inspired versatile nanosystem for caries prevention and tooth restoration. <i>Bioactive Materials</i> , 2023, 20, 418-433.	8.6	24
6123	The Application of Tomato Plant Residue Compost and Plant Growth-Promoting Rhizobacteria Improves Soil Quality and Enhances the Ginger Field Soil Bacterial Community. <i>Agronomy</i> , 2022, 12, 1741.	1.3	6
6124	Promotion of nitrogen removal in a zero-valent iron-mediated nitrogen removal system operated in co-substrate mode. <i>Chemosphere</i> , 2022, 307, 135779.	4.2	2
6125	The Common and Unique Pattern of Microbiome Profiles among Saliva, Tissue, and Stool Samples in Patients with Crohn's Disease. <i>Microorganisms</i> , 2022, 10, 1467.	1.6	5
6126	Response of Bacterial Community to the Occurrence of Clubroot Disease in Chinese Cabbage. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
6127	Disentangling the assembly mechanisms of bacterial communities in a transition zone between the alpine steppe and alpine meadow ecosystems on the Tibetan Plateau. <i>Science of the Total Environment</i> , 2022, 847, 157446.	3.9	5
6128	Impacts of Rotation-Fallow Practices on Bacterial Community Structure in Paddy Fields. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
6129	Was the decline of saltmarsh tabanid populations after the 2010 oil spill associated with change in the larval food web?. <i>Ecosphere</i> , 2022, 13, .	1.0	1
6130	Exploring fine-scale assembly of ectomycorrhizal fungal communities through phylogenetic and spatial distribution analyses. <i>Mycorrhiza</i> , 2022, 32, 439-449.	1.3	3
6131	Bringing pharmacomicrobiomics to the clinic through well-designed studies. <i>Clinical and Translational Science</i> , 2022, 15, 2303-2315.	1.5	4
6132	Unlocking the Potential of the Human Microbiome for Identifying Disease Diagnostic Biomarkers. <i>Diagnostics</i> , 2022, 12, 1742.	1.3	16

#	ARTICLE	IF	CITATIONS
6133	Hair Microbiome Diversity within and across Primate Species. <i>MSystems</i> , 0, , .	1.7	0
6134	Dirichlet-tree multinomial mixtures for clustering microbiome compositions. <i>Annals of Applied Statistics</i> , 2022, 16, .	0.5	2
6135	Emerging tools for understanding the human microbiome. <i>Progress in Molecular Biology and Translational Science</i> , 2022, , .	0.9	0
6136	Illuminating protist diversity in pitcher plants and bromeliad tanks. <i>PLoS ONE</i> , 2022, 17, e0270913.	1.1	1
6137	Bacterial composition and colony structure of the lower respiratory tract in infants and children with recurrent wheezing: a caseâ€“control study. <i>Italian Journal of Pediatrics</i> , 2022, 48, .	1.0	2
6138	MOCHI: a comprehensive cross-platform tool for amplicon-based microbiota analysis. <i>Bioinformatics</i> , 2022, 38, 4286-4292.	1.8	2
6139	Evaluation of Full-Length Versus V4-Region 16S rRNA Sequencing for Phylogenetic Analysis of Mouse Intestinal Microbiota After a Dietary Intervention. <i>Current Microbiology</i> , 2022, 79, .	1.0	10
6140	Low abundance members of the gut microbiome exhibit high immunogenicity. <i>Gut Microbes</i> , 2022, 14, .	4.3	8
6141	Islands Within Islands: Bacterial Phylogenetic Structure and Consortia in Hawaiian Lava Caves and Fumaroles. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	10
6142	Microbial and Planktonic Community Characteristics of <i>Eriocheir sinensis</i> Culture Ponds Experiencing Harmful Algal Blooms. <i>Fishes</i> , 2022, 7, 180.	0.7	4
6143	Differences in gut microbiota correlate with symptoms and regional brain volumes in patients with late-life depression. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	14
6144	<i>Hermetia illucens</i> L. larvaeâ€“associated intestinal microbes reduce the transmission risk of zoonotic pathogens in pig manure. <i>Microbial Biotechnology</i> , 2022, 15, 2631-2644.	2.0	11
6145	Effects of Decreasing Fishmeal as Main Source of Protein on Growth, Digestive Physiology, and Gut Microbiota of Olive Flounder (<i>Paralichthys olivaceus</i>). <i>Animals</i> , 2022, 12, 2043.	1.0	3
6146	Saliva microbiome changes in thyroid cancer and thyroid nodules patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	6
6147	Pigmentation biosynthesis influences the microbiome in sea urchins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	3
6148	Microbial risk score for capturing microbial characteristics, integrating multi-omics data, and predicting disease risk. <i>Microbiome</i> , 2022, 10, .	4.9	10
6149	Global patterns and rates of habitat transitions across the eukaryotic tree of life. <i>Nature Ecology and Evolution</i> , 2022, 6, 1458-1470.	3.4	19
6150	A Pilot Study: the Development of a Facility-Associated Microbiome and Its Association with the Presence of <i>Listeria</i> Spp. in One Small Meat Processing Facility. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5

#	ARTICLE	IF	CITATIONS
6151	Comparative analysis of bacterial communities in the sediment and seawater environments from marine large yellow croaker cages (Zhejiang coast, China). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
6153	Gut microbiomes of cyprinid fish exhibit host-species symbiosis along gut trait and diet. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6154	Microbiota differences of skin and pharyngeal microbiota between patients with plaque and guttate psoriasis in China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
6155	Cecal microbiota of feedlot cattle fed a four-species <i>Bacillus</i> supplement. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	4
6156	Cronos: A Machine Learning Pipeline for Description and Predictive Modeling of Microbial Communities Over Time. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	1
6157	Alterations in the vaginal microbiota of patients with preterm premature rupture of membranes. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	7
6158	Colony self-shading facilitates Symbiodiniaceae cohabitation in a South Pacific coral community. <i>Coral Reefs</i> , 0, , .	0.9	2
6159	Bacterial Community and Chemical Composition of Mixed Fresh Cactus Forage and Buffel Grass Hay during Aerobic Exposure. <i>Agronomy</i> , 2022, 12, 1927.	1.3	1
6161	Investigation of Gut Bacterial Communities of Asian Citrus Psyllid (<i>Diaphorina citri</i>) Reared on Different Host Plants. <i>Insects</i> , 2022, 13, 694.	1.0	6
6162	Experimental methods modestly impact interpretation of the effect of environmental exposures on the larval zebrafish gut microbiome. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
6163	Comparing the potential of <i>Bacillus amyloliquefaciens</i> CGMCC18230 with antimicrobial growth promoters for growth performance, bone development, expression of phosphorus transporters, and excreta microbiome in broiler chickens. <i>Poultry Science</i> , 2022, 101, 102126.	1.5	5
6164	Argentine Navy Icebreaker Ship "Almirante Irizar" Sludge Microbial Composition Analysis for Biohydrogen Production. <i>Bioenergy Research</i> , 2023, 16, 1217-1228.	2.2	2
6165	Microbiome alterations associated with phthalate exposures in a US-based sample of Latino workers. <i>Environmental Research</i> , 2022, 214, 114126.	3.7	3
6166	Differential Susceptibility of the Gut Microbiota to DSS Treatment Interferes in the Conserved Microbiome Association in Mouse Models of Colitis and Is Related to the Initial Gut Microbiota Difference. , 2022, 2022, 1-20.		10
6167	Namco: a microbiome explorer. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
6168	Changes in the composition of bacterial communities and pathogen levels during wastewater treatment. <i>Environmental Science and Pollution Research</i> , 2023, 30, 1232-1243.	2.7	3
6169	Metabolic responses of thermophilic endospores to sudden heat-induced perturbation in marine sediment samples. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6170	A comparison of faecal glucocorticoid metabolite concentration and gut microbiota diversity in bonobos (<i>Pan paniscus</i>). <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	1

#	ARTICLE	IF	CITATIONS
6171	Genomic reconstruction of short-chain fatty acid production by the human gut microbiota. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	18
6172	Impact of Microbiota Depletion by Antibiotics on SARS-CoV-2 Infection of K18-hACE2 Mice. <i>Cells</i> , 2022, 11, 2572.	1.8	3
6173	Methane seepage intensity distinguish microbial communities in sediments at the Mid-Okinawa Trough. <i>Science of the Total Environment</i> , 2022, 851, 158213.	3.9	4
6174	Metataxonomic Mapping of the Microbial Diversity of Irish and Eastern Mediterranean Cheeses. <i>Foods</i> , 2022, 11, 2483.	1.9	11
6175	Intraamniotic Administration (Gallus gallus) of Genistein Alters Mineral Transport, Intestinal Morphology, and Gut Microbiota. <i>Nutrients</i> , 2022, 14, 3473.	1.7	8
6176	Distance-Based Phylogenetic Placement with Statistical Support. <i>Biology</i> , 2022, 11, 1212.	1.3	0
6178	The microbiome of fly organs and fly-human microbial transfer during decomposition. <i>Forensic Science International</i> , 2022, 340, 111425.	1.3	4
6179	Association between parasite microbiomes and caste development and colony structure in a social trematode. <i>Molecular Ecology</i> , 2022, 31, 5608-5617.	2.0	4
6180	Age as a primary driver of the gut microbial composition and function in wild harbor seals. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
6182	Integrating microbial DNA community analyses into time-integrated suspended sediment sampling methods. <i>Journal of Soils and Sediments</i> , 0, , .	1.5	2
6183	Liver abscess microbiota of feedlot steers finished in natural and traditional management programs. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	3
6184	Different Intestinal Microbiota with Growth Stages of Three-Breed Hybrid Pig. <i>BioMed Research International</i> , 2022, 2022, 1-9.	0.9	2
6185	MiCloud: A unified web platform for comprehensive microbiome data analysis. <i>PLoS ONE</i> , 2022, 17, e0272354.	1.1	6
6187	Microbiota and mobile genetic elements influence antibiotic resistance genes in dust from dense urban public places. <i>Environmental Pollution</i> , 2022, 311, 119991.	3.7	8
6188	Female reproductive dysfunctions and the gut microbiota. <i>Journal of Molecular Endocrinology</i> , 2022, 69, R81-R94.	1.1	24
6189	Composition of gastrointestinal microbiota in association with treatment response in individuals with metastatic castrate resistant prostate cancer progressing on enzalutamide and initiating treatment with anti-PD-1 (pembrolizumab). <i>Neoplasia</i> , 2022, 32, 100822.	2.3	17
6190	Microbiome alterations from volatile organic compounds (VOC) exposures among workers in salons primarily serving women of color. <i>Environmental Research</i> , 2022, 214, 114125.	3.7	3
6191	Uncovering the Fecal Bacterial Communities of Sympatric Sika Deer (<i>Cervus nippon</i>) and Wapiti (<i>Cervus canadensis</i>). <i>Animals</i> , 2022, 12, 2468.	1.0	1

#	ARTICLE	IF	CITATIONS
6192	Exploring bacterioplankton communities and their temporal dynamics in the rearing water of a biofloc-based shrimp (<i>Litopenaeus vannamei</i>) aquaculture system. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
6194	Protective effect of methionine on the intestinal oxidative stress and microbiota change induced by nickel. <i>Ecotoxicology and Environmental Safety</i> , 2022, 244, 114037.	2.9	2
6195	Microbiome Changes during Regenerative Endodontic Treatment Using Different Methods of Disinfection. <i>Journal of Endodontics</i> , 2022, 48, 1273-1284.	1.4	16
6196	Altered gut microbiota correlates with behavioral problems but not gastrointestinal symptoms in individuals with autism. <i>Brain, Behavior, and Immunity</i> , 2022, 106, 161-178.	2.0	17
6197	Exploration of rumen microbial and carbohydrate-active enzyme profiles in cattle fed coir a lignin-rich diet using a metagenomic approach. <i>Gene</i> , 2022, 846, 146868.	1.0	2
6198	Identification of the biomethanation pathways during biological CO ₂ fixation with exogenous H ₂ addition. <i>Fuel Processing Technology</i> , 2022, 238, 107478.	3.7	11
6199	The effect of sheep grazing abandonment on soil bacterial communities in productive mountain grasslands. <i>Science of the Total Environment</i> , 2022, 851, 158398.	3.9	3
6200	Anthropogenic degradation alter surface soil biogeochemical pools and microbial communities in an Andean temperate forest. <i>Science of the Total Environment</i> , 2023, 854, 158508.	3.9	4
6201	Responses of microbial community composition and respiration to soil moisture in eroded soil. <i>Applied Soil Ecology</i> , 2023, 181, 104662.	2.1	10
6202	Meta-Prism 2.0: Enabling algorithm and web server for ultra-fast, memory-efficient, and accurate analysis among millions of microbial community samples. <i>GigaScience</i> , 2022, 11, .	3.3	0
6203	Dysbiosis of human microbiome and infectious diseases. <i>Progress in Molecular Biology and Translational Science</i> , 2022, , 33-51.	0.9	8
6204	<i>Lycium barbarum</i> polysaccharides and capsaicin modulate inflammatory cytokines and colonic microbiota in colitis rats induced by dextran sulfate sodium. <i>Journal of Clinical Biochemistry and Nutrition</i> , 2022, 71, 229-237.	0.6	1
6205	Heritage-specific oral microbiota in Indigenous Australian dental calculus. <i>Evolution, Medicine and Public Health</i> , 2022, 10, 352-362.	1.1	7
6206	Tools to Study Gut Microbiome. , 2022, , 253-270.		0
6207	Effects of Early Antiretroviral Therapy on the Composition and Diversity of the Fecal Microbiome of SIV-infected Rhesus Macaques (<i>Macaca mulatta</i>). <i>Comparative Medicine</i> , 2022, , .	0.4	0
6208	Integrated Kinetic Modelling and Microbial Profiling Provide Insights Into Biological Sulfate-Reducing Reactor Design and Operation. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	1
6209	Shifts in uterine bacterial communities associated with endogenous progesterone and 17 β -estradiol concentrations in beef cattle. <i>Domestic Animal Endocrinology</i> , 2023, 82, 106766.	0.8	5
6210	Innate type 2 immunity controls hair follicle commensalism by <i>Demodex</i> mites. <i>Immunity</i> , 2022, 55, 1891-1908.e12.	6.6	10

#	ARTICLE	IF	CITATIONS
6211	Crowdsourced benchmarking of taxonomic metagenome profilers: lessons learned from the sbv IMPROVER Microbiomics challenge. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
6212	Host Species and Captivity Distinguish the Microbiome Compositions of a Diverse Zoo-Resident Non-Human Primate Population. <i>Diversity</i> , 2022, 14, 715.	0.7	1
6213	The Lung Allograft Microbiome Associates with Pepsin, Inflammation, and Primary Graft Dysfunction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 1508-1521.	2.5	5
6214	Polysaccharide from <i>Salviae miltiorrhizae Radix et Rhizoma</i> Attenuates the Progress of Obesity-Induced Non-Alcoholic Fatty Liver Disease through Modulating Intestinal Microbiota-Related Gutâ€™Liver Axis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10620.	1.8	8
6216	Two modes of evolution shape bacterial strain diversity in the mammalian gut for thousands of generations. <i>Nature Communications</i> , 2022, 13, .	5.8	19
6217	A large-scale, multi-year microbial community survey of a freshwater trout aquaculture facility. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
6218	Gut microbiome of multiple sclerosis patients and paired household healthy controls reveal associations with disease risk and course. <i>Cell</i> , 2022, 185, 3467-3486.e16.	13.5	72
6219	Intramammary infusion of matrine-chitosan hydrogels for treating subclinical bovine mastitis â€™effects on milk microbiome and metabolites. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
6220	Effect of sex on the gut microbiota characteristics of passerine migratory birds. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6221	Compost Microcosms as Microbially Diverse, Natural-like Environments for Microbiome Research in <i>Caenorhabditis elegans</i> . <i>Journal of Visualized Experiments</i> , 2022, , .	0.2	3
6222	The impact of protozoa addition on the survivability of <i>Bacillus</i> inoculants and soil microbiome dynamics. <i>ISME Communications</i> , 2022, 2, .	1.7	6
6223	The combined impact of low temperatures and shifting phosphorus availability on the competitive ability of cyanobacteria. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
6224	Study of gut microbiota alterations in Alzheimer's dementia patients from Kazakhstan. <i>Scientific Reports</i> , 2022, 12, .	1.6	32
6225	Comparison of Microbial Profiling and Tracer Testing for the Characterization of Injector-Producer Interwell Connectivities. <i>Water (Switzerland)</i> , 2022, 14, 2921.	1.2	1
6226	The Relationship of Tumor Microbiome and Oral Bacteria and Intestinal Dysbiosis in Canine Mammary Tumor. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10928.	1.8	12
6227	Study of Wetland Soils of the Salar de Atacama with Different Azonal Vegetative Formations Reveals Changes in the Microbiota Associated with Hygrophile Plant Type on the Soil Surface. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
6228	Old climatically-buffered infertile landscapes (OCBILs): more than harsh habitats, Atlantic Forest inselbergs can be drivers of evolutionary diversity. <i>Journal of Mountain Science</i> , 2022, 19, 2528-2543.	0.8	2
6230	Complexities of Inferring Symbiont Function: <i>Paraburkholderia</i> Symbiont Dynamics in Social Amoeba Populations and Their Impacts on the Amoeba Microbiota. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	4

#	ARTICLE	IF	CITATIONS
6231	The Effect of Microbial Diversity and Biomass on Microbial Respiration in Two Soils along the Soil Chronosequence. <i>Microorganisms</i> , 2022, 10, 1920.	1.6	6
6232	More than just hitchhikers: a survey of bacterial communities associated with diatoms originating from sea turtles. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	2
6233	The Metabolome and the Gut Microbiota for the Prediction of Necrotizing Enterocolitis and Spontaneous Intestinal Perforation: A Systematic Review. <i>Nutrients</i> , 2022, 14, 3859.	1.7	9
6234	Bowel habits, faecal microbiota and faecal bile acid composition of healthy adults consuming fruit pomace fibres: two-arm, randomised, double-blinded, placebo-controlled trials. <i>British Journal of Nutrition</i> , 2023, 130, 42-55.	1.2	2
6236	Gut microbiome associations with host genotype vary across ethnicities and potentially influence cardiometabolic traits. <i>Cell Host and Microbe</i> , 2022, 30, 1464-1480.e6.	5.1	13
6237	EXPERT: transfer learning-enabled context-aware microbial community classification. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	3
6238	Hepatic cytochrome P450 8B1 and cholic acid potentiate intestinal epithelial injury in colitis by suppressing intestinal stem cell renewal. <i>Cell Stem Cell</i> , 2022, 29, 1366-1381.e9.	5.2	37
6239	Altered microbial biogeography in an innate model of colitis. <i>Gut Microbes</i> , 2022, 14, .	4.3	9
6240	Testing microbiome associations with survival times at both the community and individual taxon levels. <i>PLoS Computational Biology</i> , 2022, 18, e1010509.	1.5	5
6241	Correlating gut microbial membership to brown bear health metrics. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
6242	Sustained Drought, but Not Short-Term Warming, Alters the Gut Microbiomes of Wild <i>Anolis</i> Lizards. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	10
6244	Selection, drift and community interactions shape microbial biogeographic patterns in the Pacific Ocean. <i>ISME Journal</i> , 2022, 16, 2653-2665.	4.4	27
6245	Diversity of the gut, vaginal and oral microbiome among pregnant women in South Africa with and without pre-eclampsia. <i>Frontiers in Global Women S Health</i> , 0, 3, .	1.1	2
6246	Sources of variation in community composition of the hindgut microbiota in two tropical <i>Kyphosus</i> species. <i>Coral Reefs</i> , 2022, 41, 1523-1535.	0.9	3
6247	Impact of Skin Disinfection on Cutaneous Microbiota, before and after Peripheral Venous Catheter Insertion. <i>Antibiotics</i> , 2022, 11, 1209.	1.5	0
6248	The core bacterial microbiome of banana (<i>Musa</i> spp.). <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	5
6249	Axial spondyloarthritis patients have altered mucosal IgA response to oral and fecal microbiota. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
6251	Combined IgE neutralization and <i>Bifidobacterium longum</i> supplementation reduces the allergic response in models of food allergy. <i>Nature Communications</i> , 2022, 13, .	5.8	8

#	ARTICLE	IF	CITATIONS
6252	Feeding up to 91% concentrate to Holstein and Jersey dairy cows: Effects on enteric methane emission, rumen fermentation and bacterial community, digestibility, production, and feeding behavior. <i>Journal of Dairy Science</i> , 2022, 105, 9523-9541.	1.4	18
6253	Random sampling associated with microbial profiling leads to overestimated stochasticity inference in community assembly. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
6254	Microbial communities associated with epilithic algal matrix with different morphological characters in Luhuitou fringing reef. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
6255	Microecosystem of yak rumen on the Qinghai-Tibetan Plateau is stable and is unaffected by soil or grass microbiota. <i>Environmental Microbiology</i> , 2022, 24, 5760-5773.	1.8	2
6256	A new monocomponent xylanase improves performance, ileal digestibility of energy and nutrients, intestinal morphology, and intestinal microbiota in young broilers. <i>Journal of Applied Poultry Research</i> , 2023, 32, 100301.	0.6	3
6258	The Use of Raw Poultry Waste as Soil Amendment Under Field Conditions Caused a Loss of Bacterial Genetic Diversity Together with an Increment of Eutrophic Risk and Phytotoxic Effects. <i>Microbial Ecology</i> , 2023, 86, 1082-1095.	1.4	1
6259	Evolutionary opportunity and the limits of community similarity in replicate radiations of island lizards. <i>Ecology Letters</i> , 2022, 25, 2384-2396.	3.0	1
6260	Variations in fungal and bacterial microbiome and chemical composition among fermenting Kishu-Narezushi batches. <i>Bioscience, Biotechnology and Biochemistry</i> , 2022, 86, 1705-1717.	0.6	3
6261	Effect of Environmental Heterogeneity and Trophic Status in Sampling Strategy on Estimation of Small-Scale Regional Biodiversity of Microorganisms. <i>Microorganisms</i> , 2022, 10, 2119.	1.6	1
6262	Glacial Legacies: Microbial Communities of Antarctic Refugia. <i>Biology</i> , 2022, 11, 1440.	1.3	3
6263	Effects of dietary Bopu powder supplementation on intestinal development and microbiota in broiler chickens. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
6264	Succession of the microbial communities and metabolic functions in composting or deep burial processing of dead chickens. <i>British Poultry Science</i> , 2023, 64, 185-194.	0.8	0
6265	Toxic effects of naproxen on the intestine of the goldfish, <i>Carassius auratus</i> . <i>Molecular and Cellular Toxicology</i> , 0, , .	0.8	0
6266	Oral administration of human carbonic anhydrase I suppresses colitis in a murine inflammatory bowel disease model. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
6267	Effects of trunk injection with emamectin benzoate on arthropod diversity. <i>Pest Management Science</i> , 2023, 79, 935-946.	1.7	4
6268	Phylogenetic diversity of eastern Asia-eastern North America disjunct plants is mainly associated with divergence time. <i>Plant Diversity</i> , 2023, 45, 27-35.	1.8	1
6270	The Changes of Microbial Communities and Key Metabolites after Early Bursaphelenchus xylophilus Invasion of Pinus massoniana. <i>Plants</i> , 2022, 11, 2849.	1.6	4
6271	Indoor microbiome and allergic diseases: From theoretical advances to prevention strategies. , 2022, 1, 133-146.		14

#	ARTICLE	IF	CITATIONS
6272	Association between Gut Microbiota and Emotional-Behavioral Symptoms in Children with Attention-Deficit/Hyperactivity Disorder. <i>Journal of Personalized Medicine</i> , 2022, 12, 1634.	1.1	3
6273	Mortality by ribosomal sequencing (MoRS) provides a window into taxon-specific cell lysis. <i>ISME Journal</i> , 2023, 17, 105-116.	4.4	6
6274	Association of body mass index and intestinal (faecal) <i>Streptococcus</i> in adults in Xining city, China P.R.. <i>Beneficial Microbes</i> , 2022, 13, 465-471.	1.0	5
6275	Elemental sulphur recovery from a sulphate-rich aqueous stream in a single hybrid linear flow channel reactor is mediated through microbial community dynamics and adaptation to reactor zones. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	0
6276	Diversities in the Gut Microbial Patterns in Patients with Atherosclerotic Cardiovascular Diseases and Certain Heart Failure Phenotypes. <i>Biomedicines</i> , 2022, 10, 2762.	1.4	4
6279	Cell size is a key ecological trait associated with biogeographic patterns of microbial eukaryotes in coastal waters. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
6280	TangNaiKang, herbal formulation, alleviates obesity in diabetic SHR/cp rats through modulation of gut microbiota and related metabolic functions. <i>Pharmaceutical Biology</i> , 2022, 60, 2002-2010.	1.3	1
6281	Infant behavioral state and stool microbiome in infants receiving <i>Lactocaseibacillus rhamnosus</i> GG in formula: randomized controlled trial. <i>BMC Pediatrics</i> , 2022, 22, .	0.7	2
6282	Baat Gene Knockout Alters Post-Natal Development, the Gut Microbiome, and Reveals Unusual Bile Acids in Mice. <i>Journal of Lipid Research</i> , 2022, 63, 100297.	2.0	9
6283	Gut microbial ecology of Philippine gekkonids: ecoevolutionary effects on microbiome compositions. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	2
6284	Single Seed Microbiota: Assembly and Transmission from Parent Plant to Seedling. <i>MBio</i> , 2022, 13, .	1.8	13
6285	Dynamic trophic shifts in bacterial and eukaryotic communities during the first 30 years of microbial succession following retreat of an Antarctic glacier. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
6286	Species-level respiratory microbiome profiling for etiologic diagnosis of children pneumonia using full length 16S rRNA gene sequencing. <i>Indian Journal of Medical Microbiology</i> , 2023, 43, 11-17.	0.3	1
6288	Gut Microbiota and Transcriptome Analysis Reveals a Genetic Component to Dropping Moisture in Chickens. <i>Poultry Science</i> , 2022, , 102242.	1.5	0
6290	Effects of heat stress on 16S rDNA, metagenome and metabolome in Holstein cows at different growth stages. <i>Scientific Data</i> , 2022, 9, .	2.4	1
6291	An ecological and evolutionary perspective of the historical US nursery flora. <i>Plants People Planet</i> , 0, , .	1.6	1
6293	<i>Gracilaria gracilis</i> and <i>Nannochloropsis oceanica</i> , singly or in combination, in diets alter the intestinal microbiota of European seabass (<i>Dicentrarchus labrax</i>). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	7
6294	Effect of Diet on the Midgut Microbial Composition and Host Immunity of the Fall Armyworm, <i>Spodoptera frugiperda</i> . <i>Biology</i> , 2022, 11, 1602.	1.3	2

#	ARTICLE	IF	CITATIONS
6295	Methanogen Levels Are Significantly Associated with Fecal Microbiota Composition and Alpha Diversity in Healthy Adults and Irritable Bowel Syndrome Patients. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
6296	Effect of Resistant Dextrin on Intestinal Gas Homeostasis and Microbiota. <i>Nutrients</i> , 2022, 14, 4611.	1.7	6
6297	The gut microbiome of wild American marten in the Upper Peninsula of Michigan. <i>PLoS ONE</i> , 2022, 17, e0275850.	1.1	1
6298	Impact of COVID-19 and Antibiotic Treatments on Gut Microbiome: A Role for <i>Enterococcus</i> spp.. <i>Biomedicines</i> , 2022, 10, 2786.	1.4	8
6299	Lake sediments from littoral and profundal zones are heterogeneous but equivalent sources of methane produced by distinct methanogenic communities – a case study from Lake Remoray. <i>Journal of Geophysical Research G: Biogeosciences</i> , 0, , .	1.3	0
6300	Sampling from four geographically divergent young female populations demonstrates forensic geolocation potential in microbiomes. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
6301	Effect of chia flour associated with high fat diet on intestinal health in female ovariectomized Wistar rats. <i>European Journal of Nutrition</i> , 0, , .	1.8	3
6302	<i>Lactobacillus paracasei</i> IMC 502 ameliorates type 2 diabetes by mediating gut microbiota – SCFA – hormone/inflammation pathway in mice. <i>Journal of the Science of Food and Agriculture</i> , 2023, 103, 2949-2959.	1.7	10
6303	Maternal anxiety, depression and stress affects offspring gut microbiome diversity and bifidobacterial abundances. <i>Brain, Behavior, and Immunity</i> , 2023, 107, 253-264.	2.0	30
6304	Prune supplementation for 12 months alters the gut microbiome in postmenopausal women. <i>Food and Function</i> , 2022, 13, 12316-12329.	2.1	5
6305	GUT BACTERIAL DIVERSITY BETWEEN POLYGRID LAND SNAILS REFLECT ENVIRONMENTAL DIFFERENCES. <i>Texas Journal of Science</i> , 2022, 74, .	0.3	0
6306	Impacts of iron amendments and per-fluoroalkyl substances – bio-availability to the soil microbiome in wheat ecosystem. <i>Chemosphere</i> , 2023, 311, 137140.	4.2	2
6307	The impact of alternating drainage and inundation cycles on geochemistry and microbiology of intact peat cores. <i>Science of the Total Environment</i> , 2023, 858, 159664.	3.9	3
6310	Rapid detection and online analysis of microbial changes through flow cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 0, , .	1.1	1
6311	The Functional Characteristics of Goat Cheese Microbiota from a One-Health Perspective. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14131.	1.8	4
6312	Sociability in a non-captive macaque population is associated with beneficial gut bacteria. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
6313	Unraveling the effects of sulfamethoxazole on the composition of gut microbiota and immune responses in <i>Stichopus variegatus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
6314	High throughput method of 16S rRNA gene sequencing library preparation for plant root microbial community profiling. <i>Scientific Reports</i> , 2022, 12, .	1.6	2

#	ARTICLE	IF	CITATIONS
6315	Chlorogenic acid improves growth performance of weaned rabbits via modulating the intestinal epithelium functions and intestinal microbiota. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
6316	Homeostasis of the Intestinal Mucosa in Healthy HorsesâCorrelation between the Fecal Microbiome, Secretory Immunoglobulin A and Fecal Egg Count. <i>Animals</i> , 2022, 12, 3094.	1.0	1
6317	Developmental stage variation in the gut microbiome of South China tigers. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6318	Proof of principle study replicating microbial clusters in connection to birth mode and diet in the early life intestine. <i>PLoS ONE</i> , 2022, 17, e0277502.	1.1	1
6319	BioâFunctionalized Manganese Nanoparticles Suppress Fusarium Wilt in Watermelon (<i>Citrullus</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf Community Modulation. <i>Small</i> , 2023, 19, .	5.2	22
6320	Agr2-associated ER stress promotes adherent-invasive E.Âcoli dysbiosis and triggers CD103+ dendritic cell IL-23-dependent ileocolitis. <i>Cell Reports</i> , 2022, 41, 111637.	2.9	3
6321	Evaluation of the Ecological Environment Affected by Cry1Ah1 in Poplar. <i>Life</i> , 2022, 12, 1830.	1.1	1
6322	Linking Bacterial Rhizosphere Communities of Two Pioneer Species, <i>Brachystegia boehmii</i> and <i>B. spiciformis</i> , to the Ecological Processes of Miombo Woodlands. <i>Forests</i> , 2022, 13, 1840.	0.9	1
6323	Host biology, ecology and the environment influence microbial biomass and diversity in 101 marine fish species. <i>Nature Communications</i> , 2022, 13, .	5.8	21
6324	High polyphenolic cranberry beverage alters specific fecal microbiota but not gut permeability following aspirin challenge in healthy obese adults: A randomized, double-blind, crossover trial. <i>Journal of Functional Foods</i> , 2022, 99, 105332.	1.6	3
6325	Airway Bacterial Biodiversity in Exhaled Breath Condensates of Asthmatic ChildrenâDoes It Differ from the Healthy Ones?. <i>Journal of Clinical Medicine</i> , 2022, 11, 6774.	1.0	3
6327	Germinated Millet (<i>Pennisetum glaucum</i> (L.) R. Br.) Flour Improved the Gut Function and Its Microbiota Composition in Rats Fed with High-Fat High-Fructose Diet. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 15217.	1.2	1
6328	Arsenic-triggered bacterial minorities correlate with arsenic accumulation in cabbage. <i>Geoderma</i> , 2023, 429, 116278.	2.3	0
6329	A novel approach to enhance CO biomethanation by semi-disaggregation of anaerobic granular sludge. <i>Energy Conversion and Management</i> , 2023, 276, 116551.	4.4	1
6330	End-of-life MoS₂-enabled device and material transformation in landfill leachate and its effect on the landfill microbiome. <i>Environmental Science: Nano</i> , 2023, 10, 203-214.	2.2	1
6331	Transgenerational transfer of the microbiome is altered by ocean acidification in oyster larvae. <i>Aquaculture</i> , 2023, 565, 739153.	1.7	2
6332	New insights into microbial community coalescence in the land-sea continuum. <i>Microbiological Research</i> , 2023, 267, 127259.	2.5	2
6333	Insights into the phenol disinfectant on the methane performance from wastewater by mesophilic anaerobic digestion: Single and two stages analysis. <i>Chemical Engineering Research and Design</i> , 2023, 170, 19-27.	2.7	4

#	ARTICLE	IF	CITATIONS
6334	Low diversity and microdiversity of comammox bacteria in wastewater systems suggest specific adaptations within the Ca. Nitrospira nitrosa cluster. <i>Water Research</i> , 2023, 229, 119497.	5.3	8
6335	Stronger effects of environmental factors than denitrifying genes on soil denitrification under a subtropical land use change. <i>Catena</i> , 2023, 222, 106876.	2.2	3
6336	Skeletal muscle insulin resistance and adipose tissue hypertrophy persist beyond the reshaping of gut microbiota in young rats fed a fructose-rich diet. <i>Journal of Nutritional Biochemistry</i> , 2023, 113, 109247.	1.9	2
6338	Effect of Chia (<i>Salvia hispanica</i> L.) Associated with High-Fat Diet on the Intestinal Health of Wistar Rats. <i>Nutrients</i> , 2022, 14, 4924.	1.7	7
6339	Organomineral fertilizer application enhances <i>Perilla frutescens</i> nutritional quality and rhizosphere microbial community stability in karst mountain soils. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6340	Integrative web cloud computing and analytics using MiPair for design-based comparative analysis with paired microbiome data. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
6342	Risk Factors Associated with Severe <i>Clostridioides difficile</i> Infection in Patients with Cancer. <i>Infectious Diseases and Therapy</i> , 2023, 12, 209-225.	1.8	2
6343	Severe Scalp Psoriasis Microbiome Has Increased Biodiversity and Relative Abundance of <i>Pseudomonas</i> Compared to Mild Scalp Psoriasis. <i>Journal of Clinical Medicine</i> , 2022, 11, 7133.	1.0	5
6344	Spatial and lineage-dependent processes underpin floristic assembly in the megadiverse Eastern South American mountains. <i>Journal of Biogeography</i> , 0, , .	1.4	4
6345	The association of hyperketonemia with fecal and rumen microbiota at time of diagnosis in a case-control cohort of early lactation cows. <i>BMC Veterinary Research</i> , 2022, 18, .	0.7	2
6346	Impact of Daily Consumption of Whole-Grain Quinoa-Enriched Bread on Gut Microbiome in Males. <i>Nutrients</i> , 2022, 14, 4888.	1.7	2
6347	A comparative study to determine the association of gut microbiome with schizophrenia in Zhejiang, China. <i>BMC Psychiatry</i> , 2022, 22, .	1.1	3
6348	Bioinformatic Approaches for Describing the Oral Microbiota. <i>Methods in Molecular Biology</i> , 2023, , 105-130.	0.4	0
6349	Biofilms as potential reservoirs of stony coral tissue loss disease. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	7
6352	Molecular characterization of gut microbiome in weaning pigs supplemented with multi-strain probiotics using metagenomic, culturomic, and metabolomic approaches. <i>Animal Microbiome</i> , 2022, 4, .	1.5	0
6353	Influence of Geochemistry in the Tropical Hot Springs on Microbial Community Structure and Function. <i>Current Microbiology</i> , 2023, 80, .	1.0	1
6354	Introducing sedum affects root-soil interface phytoremediation of heavy metals in bamboo forest and potential risks from edible bamboo shoots. <i>Land Degradation and Development</i> , 2023, 34, 1820-1829.	1.8	1
6355	Bacterial diversity across four drinking water distribution systems in Croatia: impacts of water management practices and disinfection by-products. <i>FEMS Microbiology Ecology</i> , 2022, 99, .	1.3	0

#	ARTICLE	IF	CITATIONS
6356	Effects of Tillage and Winter Cover Management in a Maize Soybean Rotation on Soil Bacterial and Fungal Community Composition. <i>Land</i> , 2022, 11, 2259.	1.2	3
6358	Hatchery tanks induce intense reduction in microbiota diversity associated with gills and guts of two endemic species of the São Francisco River. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
6359	Characterization of the gut microbiome and resistome of Galapagos marine iguanas (<i>Amblyrhynchus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	0
6360	Micronutrient Biosynthesis Potential of Spontaneous Grain Fermentation Microbiomes. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 16621.	1.2	1
6361	Communities of endophytic fungi in a Puerto Rican rainforest vary along a gradient of disturbance due to Hurricane Maria. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
6362	The correlation between dysfunctional intestinal flora and pathology feature of patients with pulmonary tuberculosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	6
6363	Sex Differences in Fecal Microbiome Composition and Function of Dromedary Camels in Saudi Arabia. <i>Animals</i> , 2022, 12, 3430.	1.0	2
6364	Elevated inflammatory fecal immune factors in men who have sex with men with HIV associate with microbiome composition and gut barrier function. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
6365	Changes in Phylogenetic and Functional Diversity of Ciliates along the Course of a Mediterranean Karstic River. <i>Microorganisms</i> , 2022, 10, 2493.	1.6	1
6366	Modeling and analysis of the dynamics of communities of microbial DNA sequences in environments. <i>Nonlinear Dynamics</i> , 2023, 111, 5767-5797.	2.7	0
6367	High Throughput Sequencing Reveals Distinct Bacterial Communities and Functional Diversity in Two Typical Coastal Bays. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1878.	1.2	1
6368	The community ecology perspective of omics data. <i>Microbiome</i> , 2022, 10, .	4.9	6
6369	Longitudinal analysis of the faecal microbiome in pigs fed <i>Cyberlindnera jadinii</i> yeast as a protein source during the weanling period followed by a rapeseed- and faba bean-based grower-finisher diet. <i>Animal Microbiome</i> , 2022, 4, .	1.5	2
6370	Exploring the mechanism of a novel recirculating aquaculture system based on water quality parameters and bacterial communities. <i>Environmental Science and Pollution Research</i> , 2023, 30, 34760-34774.	2.7	3
6371	Dietary supplementation with Mexican foods, <i>Opuntia ficus indica</i> , <i>Theobroma cacao</i> , and <i>Acheta domesticus</i> : Improving obesogenic and microbiota features in obese mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
6372	Chronic dust bronchitis: composition of the sputum bacterial microbiome and its association with chromosome damage in blood lymphocytes. <i>Ecological Genetics</i> , 2022, 20, 325-337.	0.1	0
6373	Comparison of bacterial community structure in PM2.5 during hazy and non-hazy periods in Guilin, South China. <i>Aerobiologia</i> , 2023, 39, 87-103.	0.7	3
6374	Marker gene analysis reveals novel viral genetic diversity in unsaturated soils. <i>Biology and Fertility of Soils</i> , 0, , .	2.3	0

#	ARTICLE	IF	CITATIONS
6375	Butyrate as a Potential Driver of a Dysbiotic Shift of the Tongue Microbiota. <i>MSphere</i> , 2023, 8, .	1.3	1
6376	Effect of proton pump inhibitors in infants with esophageal atresia on the gut microbiome: a pilot cohort. <i>Gut Pathogens</i> , 2022, 14, .	1.6	4
6377	Alterations in the cutaneous microbiome of patients with psoriasis and psoriatic arthritis reveal similarities between non-lesional and lesional skin. <i>Annals of the Rheumatic Diseases</i> , 2023, 82, 507-514.	0.5	6
6378	HPV-related cervical diseases: Alteration of vaginal microbiotas and promising potential for diagnosis. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	3
6379	Gut microbiota in dementia with Lewy bodies. <i>Npj Parkinson's Disease</i> , 2022, 8, .	2.5	7
6380	Gut microbiota modulates bleomycin-induced acute lung injury response in mice. <i>Respiratory Research</i> , 2022, 23, .	1.4	9
6381	Effect of Chemotherapy on the Gut Microbiome of Breast Cancer Patients During the First Year of Treatment. <i>Breast Cancer: Targets and Therapy</i> , 0, Volume 14, 433-451.	1.0	3
6382	A fast kernel independence test for cluster-correlated data. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
6385	Internal and external microbiota of home-caught <i>Anopheles coluzzii</i> (Diptera: Culicidae) from Côte d'Ivoire, Africa: Mosquitoes are filthy. <i>PLoS ONE</i> , 2022, 17, e0278912.	1.1	2
6386	Unveiling the Wheat Microbiome under Varied Agricultural Field Conditions. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
6387	Benchmarking Bioinformatic Tools for Amplicon-Based Sequencing of Norovirus. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	3
6388	The role of microbial ecology in improving the performance of anaerobic digestion of sewage sludge. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
6389	Gut microbiota of homing pigeons shows summer-winter variation under constant diet indicating a substantial effect of temperature. <i>Animal Microbiome</i> , 2022, 4, .	1.5	3
6390	High-fat diet and estrogen modulate the gut microbiota in a sex-dependent manner in mice. <i>Communications Biology</i> , 2023, 6, .	2.0	10
6391	Altered gut microbiota in individuals with episodic and chronic migraine. <i>Scientific Reports</i> , 2023, 13, .	1.6	7
6392	Diagnostic and prognostic potential of the microbiome in ovarian cancer treatment response. <i>Scientific Reports</i> , 2023, 13, .	1.6	17
6394	Allium-Derived Compound Propyl Propane Thiosulfonate (PTSO) Reduces <i>Vibrio</i> Populations and Increases Body Weight of European Seabass (<i>Dicentrarchus labrax</i>) Juveniles. <i>Antibiotics</i> , 2023, 12, 134.	1.5	1
6395	Type 1 diabetes, periodontal health, and a familial history of hyperlipidaemia is associated with oral microbiota in children: a cross-sectional study. <i>BMC Oral Health</i> , 2023, 23, .	0.8	3

#	ARTICLE	IF	CITATIONS
6396	Oropharyngeal, proximal colonic, and vaginal microbiomes of healthy Korean native black pig gilts. <i>BMC Microbiology</i> , 2023, 23, .	1.3	2
6397	Microbiome analysis of raw honey reveals important factors influencing the bacterial and fungal communities. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
6398	Screening and Characterization of <i>Pediococcus acidilactici</i> LC-9-1 toward Selection as a Potential Probiotic for Poultry with Antibacterial and Antioxidative Properties. <i>Antioxidants</i> , 2023, 12, 215.	2.2	7
6399	The gestational membrane microbiome in the presence or absence of intraamniotic infection. <i>American Journal of Obstetrics & Gynecology MFM</i> , 2023, 5, 100837.	1.3	1
6400	Interactions between perceived stress and microbial-host immune components: two demographically and geographically distinct pregnancy cohorts. <i>Translational Psychiatry</i> , 2023, 13, .	2.4	5
6401	Microbiome Data Analysis and Interpretation: Correlation Inference and Dynamic Pattern Discovery. <i>Translational Bioinformatics</i> , 2023, , 119-144.	0.0	0
6402	Exacerbation of allergic rhinitis by the commensal bacterium <i>Streptococcus salivarius</i> . <i>Nature Microbiology</i> , 2023, 8, 218-230.	5.9	10
6403	PhyloPlus: a Universal Tool for Phylogenetic Interrogation of Metagenomic Communities. <i>MBio</i> , 0, , .	1.8	0
6404	Solitary bee larvae modify bacterial diversity of pollen provisions in the stem-nesting bee, <i>Osmia cornifrons</i> (Megachilidae). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
6405	Distribution and diversity of anaerobic thermophiles and putative anaerobic nickel-dependent carbon monoxide-oxidizing thermophiles in mesothermal soils and sediments. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6408	Machine learning and network analysis of the gut microbiome from patients with schizophrenia and non-psychiatric subject controls reveal behavioral risk factors and bacterial interactions. <i>Schizophrenia Research</i> , 2023, 251, 49-58.	1.1	1
6409	Diarrhea-predominant Irritable Bowel Syndrome-like Symptoms in Patients With Quiescent Crohn's Disease: Comprehensive Analysis of Clinical Features and Intestinal Environment Including the Gut Microbiome, Organic Acids, and Intestinal Permeability. <i>Journal of Neurogastroenterology and Motility</i> , 2023, 29, 102-112.	0.8	3
6410	Altered gastrointestinal tract structure and microbiome following cerebral malaria infection. <i>Parasitology Research</i> , 0, , .	0.6	0
6411	Gut microbiota composition can reflect immune responses of latent tuberculosis infection in patients with poorly controlled diabetes. <i>Respiratory Research</i> , 2023, 24, .	1.4	4
6412	Potential of shrimp waste meal and insect exuviae as sustainable sources of chitin for fish feeds. <i>Aquaculture</i> , 2023, 567, 739256.	1.7	7
6413	Fructooligosaccharides (FOS) differentially modifies the in vitro gut microbiota in an age-dependent manner. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	4
6414	Impact of Nesting Mode, Diet, and Taxonomy in Structuring the Associated Microbial Communities of Amazonian Ants. <i>Diversity</i> , 2023, 15, 126.	0.7	0
6415	Geography and elevation as drivers of cloacal microbiome assemblages of a passerine bird distributed across Sulawesi, Indonesia. <i>Animal Microbiome</i> , 2023, 5, .	1.5	3

#	ARTICLE	IF	CITATIONS
6416	Prophylactic Effect of Bovine Colostrum on Intestinal Microbiota and Behavior in Wild-Type and Zonulin Transgenic Mice. <i>Biomedicines</i> , 2023, 11, 91.	1.4	5
6417	Gut microbiota mediates positive effects of liraglutide on dyslipidemia in mice fed a high-fat diet. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	4
6418	An exploration of mechanism of high quality and yield of <i>Gastrodia elata</i> Bl. f. <i>glauca</i> by the isolation, identification and evaluation of <i>Armillaria</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	8
6419	Modulating the Gut Microbiota with Alginate Oligosaccharides In Vitro. <i>Nutraceuticals</i> , 2023, 3, 26-38.	0.6	1
6420	KMCP: accurate metagenomic profiling of both prokaryotic and viral populations by pseudo-mapping. <i>Bioinformatics</i> , 2023, 39, .	1.8	15
6421	Reproductive Microbiomes in Domestic Livestock: Insights Utilizing 16S rRNA Gene Amplicon Community Sequencing. <i>Animals</i> , 2023, 13, 485.	1.0	9
6422	multiMIAT: an optimal microbiome-based association test for multicategory phenotypes. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	0
6423	A Machine Learning Approach Reveals a Microbiota Signature for Infection with <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in Cattle. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
6424	An in vitro analysis of how lactose modifies the gut microbiota structure and function of adults in a donor-independent manner. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	7
6425	Testing the passive sampling hypothesis: The role of dispersal in shaping microbial species-area relationship. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
6426	A convenient correspondence between k-mer-based metagenomic distances and phylogenetically-informed β -diversity measures. <i>PLoS Computational Biology</i> , 2023, 19, e1010821.	1.5	0
6428	The rhizosphere Microbiome of <i>Malus sieversii</i> (Ldb.) Roem. in the geographic and environmental gradients of China's Xinjiang. <i>BMC Microbiology</i> , 2023, 23, .	1.3	1
6429	Artisanal and farmer bread making practices differently shape fungal species community composition in French sourdoughs. , 0, 3, .		4
6430	The structure and diversity of microbial communities in <i>Paederus fuscipes</i> (Coleoptera: Staphylinidae): from ecological paradigm to pathobiome. <i>Microbiome</i> , 2023, 11, .	4.9	5
6431	Effect of feed restriction and refeeding on body condition, digestive functionality and intestinal microbiota in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Fish Physiology and Biochemistry</i> , 2023, 49, 169-189.	0.9	2
6432	Individuality and stability of the koala (<i>Phascolarctos cinereus</i>) faecal microbiota through time. <i>PeerJ</i> , 0, 11, e14598.	0.9	3
6433	Functional significance of microbial diversity in arid soils: biological soil crusts and nitrogen fixation as a model system. <i>FEMS Microbiology Ecology</i> , 0, , .	1.3	0
6434	The mediating roles of the oral microbiome in saliva and subgingival sites between e-cigarette smoking and gingival inflammation. <i>BMC Microbiology</i> , 2023, 23, .	1.3	6

#	ARTICLE	IF	CITATIONS
6435	Insights into the bacterial and archaeal population dynamics in the deep-sea hydrothermal sediments exposed to lights with different wavelengths. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2023, 195, 103996.	0.6	0
6436	Effects of weight loss and feeding specially formulated diets on the body composition, blood metabolite profiles, voluntary physical activity, and fecal metabolites and microbiota of obese dogs. <i>Journal of Animal Science</i> , 2023, 101, .	0.2	3
6437	Gallbladder microbiota in healthy dogs and dogs with mucocele formation. <i>PLoS ONE</i> , 2023, 18, e0281432.	1.1	1
6438	Best practice for wildlife gut microbiome research: A comprehensive review of methodology for 16S rRNA gene investigations. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
6439	Altered Faecal Microbiota Composition and Structure of Ghanaian Children with Acute Gastroenteritis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3607.	1.8	4
6441	THE ACTUAL CONDITION ELUCIDATION OF MICROBIOME IN A COOL OR HEAT PIT PART 2: COMPARISON OF FUNGAL FLORA BETWEEN INDOOR ENVIRONMENTS AND THE ENVIRONMENT IN A PIT. <i>Journal of Environmental Engineering (Japan)</i> , 2023, 88, 186-194.	0.1	0
6442	Intraperitoneal injection of β -glucan during the suckling period improved the intestinal health of newly weaned rabbits by enhancing immune responses. <i>Livestock Science</i> , 2023, , 105214.	0.6	0
6443	<i>Agaricus subrufescens</i> fermented rye affects the development of intestinal microbiota, local intestinal and innate immunity in suckling-to-nursery pigs. <i>Animal Microbiome</i> , 2023, 5, .	1.5	0
6444	Cecal Microbial Succession and Its Apparent Association with Nutrient Metabolism in Broiler Chickens. <i>MSphere</i> , 2023, 8, .	1.3	4
6445	Metabarcoding inventory of an arctic tundra soil ecosystem reveals highly heterogeneous communities at a small scale. <i>Polar Biology</i> , 2023, 46, 461-471.	0.5	2
6446	Fecal microbiota transplantation from <i>Suncus murinus</i> , an obesity-resistant animal, to C57BL/6NCR mice, and the antibiotic effects in the approach. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
6447	Effect of a Multispecies Synbiotic Supplementation on Body Composition, Antioxidant Status, and Gut Microbiomes in Overweight and Obese Subjects: A Randomized, Double-Blind, Placebo-Controlled Study. <i>Nutrients</i> , 2023, 15, 1863.	1.7	3
6448	Dysregulation of the microbiota-brain axis during long-term exposure to polystyrene nanoplastics in rats and the protective role of dihydrocaffeic acid. <i>Science of the Total Environment</i> , 2023, 874, 162101.	3.9	7
6449	An in vitro model of the chicken gastrointestinal tract with special emphasis to the cecal microbiota. <i>Poultry Science</i> , 2023, 102, 102654.	1.5	1
6450	Phylogenetic diversity of the mangrove crabs' communities in the Persian Gulf; its relationship with functional diversity highlights conservation priorities. <i>Marine Biodiversity</i> , 2023, 53, .	0.3	2
6451	Changes in soil bacterial and fungal community characteristics in response to long-term mulched drip irrigation in oasis agroecosystems. <i>Agricultural Water Management</i> , 2023, 279, 108178.	2.4	3
6452	Variation of sulfate reducing bacteria communities in ionic rare earth tailings and the potential of a single cadmium resistant strain in bioremediation. <i>Chemosphere</i> , 2023, 328, 138615.	4.2	1
6453	Application of bio-slow sand filters for drinking water production: Linking purification performance to bacterial community and metabolic functions. <i>Journal of Water Process Engineering</i> , 2023, 53, 103622.	2.6	7

#	ARTICLE	IF	CITATIONS
6456	Function of CAZymes encoded by highly abundant genes in rhizosphere microbiome of <i>Moringa oleifera</i> . <i>Saudi Journal of Biological Sciences</i> , 2023, 30, 103578.	1.8	1
6457	Lasting consequences on physiology and social behavior following cesarean delivery in prairie voles. <i>Hormones and Behavior</i> , 2023, 150, 105314.	1.0	2
6458	Cyprinid herpesvirus 2 infection changes microbiota and metabolites in the gibel carp (<i>Carassius</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	1.8	3
6459	Combination of <i>Aspergillus niger</i> MJ1 with <i>Pseudomonas stutzeri</i> DSM4166 or mutant <i>Pseudomonas fluorescens</i> CHAO-nif improved crop quality, soil properties, and microbial communities in barrier soil. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
6460	Short-term effects of Chlorhexidine mouthwash and Listerine on oral microbiome in hospitalized patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	4
6461	Autophagy controls mucus secretion from intestinal goblet cells by alleviating ER stress. <i>Cell Host and Microbe</i> , 2023, 31, 433-446.e4.	5.1	32
6462	Changes of gut microbiome and metabolome in the AOM/DSS mouse model of colorectal cancer with FLASH radiation. <i>Radiation Medicine and Protection</i> , 2023, 4, 1-10.	0.4	0
6463	Comparative Analyses of Soil Bacterial Colonies of Two Types of Chinese Ginger after a Major Flood Disaster. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
6464	Changes to Soil Microbiome Resulting from Synergetic Effects of Fungistatic Compounds Pyrimethanil and Fluopyram in Lowbush Blueberry Agriculture, with Nine Fungicide Products Tested. <i>Microorganisms</i> , 2023, 11, 410.	1.6	1
6465	The diarrheal mechanism of mice with a high-fat diet in a fatigued state is associated with intestinal mucosa microbiota. <i>3 Biotech</i> , 2023, 13, .	1.1	10
6466	<i>Limosilactobacillus reuteri</i> administration alters the gut-brain-behavior axis in a sex-dependent manner in socially monogamous prairie voles. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
6467	Sediment microbial community structure associated to different ecological types of mangroves in CelestÃn, a coastal lagoon in the Yucatan Peninsula, Mexico. <i>PeerJ</i> , 0, 11, e14587.	0.9	0
6468	The dynamics of the microbiome in Ixodidae are shaped by tick ontogeny and pathogens in Sarawak, Malaysian Borneo. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
6469	Diverse Microbial Hot Spring Mat Communities at Black Canyon of the Colorado River. <i>Microbial Ecology</i> , 0, , .	1.4	1
6470	Dissecting the microbial community structure of internal organs during the early postmortem period in a murine corpse model. <i>BMC Microbiology</i> , 2023, 23, .	1.3	2
6471	Improvement in bioconversion efficiency and reduction of ammonia emission by introduction of fruit fermentation broth in a black soldier fly larvae and kitchen waste conversion system. <i>Insect Science</i> , 2023, 30, 975-990.	1.5	2
6472	Cloacal microbiota are biogeographically structured in larks from desert, tropical and temperate areas. <i>BMC Microbiology</i> , 2023, 23, .	1.3	0
6473	Sparse tree-based clustering of microbiome data to characterize microbiome heterogeneity in pancreatic cancer. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2023, 72, 20-36.	0.5	0

#	ARTICLE	IF	CITATIONS
6474	Microbiome Composition and Microbial Community Structure in Mosquito Vectors <i>Aedes aegypti</i> and <i>Aedes albopictus</i> in Northeastern Thailand, a Dengue-Endemic Area. <i>Insects</i> , 2023, 14, 184.	1.0	2
6475	A bacteriocyte symbiont determines whitefly sex ratio by regulating mitochondrial function. <i>Cell Reports</i> , 2023, 42, 112102.	2.9	3
6476	Functional and Compositional Changes in the Fecal Microbiome of a Shorebird during Migratory Stopover. <i>MSystems</i> , 2023, 8, .	1.7	3
6477	Geraniol-a potential alternative to antibiotics for bovine mastitis treatment without disturbing the host microbial community or causing drug residues and resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	5
6478	Subgingival microbiome in periodontal health, gingivitis and different stages of periodontitis. <i>Journal of Clinical Periodontology</i> , 2023, 50, 905-920.	2.3	8
6479	Disrupted diurnal oscillations of the gut microbiota in patients with alcohol dependence. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	2
6480	A Bacillaceae consortium positively impacts arbuscular mycorrhizal fungus colonisation, plant phosphate nutrition, and tuber yield in <i>Solanum tuberosum</i> cv. Jazzy. <i>Symbiosis</i> , 2023, 89, 235-250.	1.2	0
6481	A Healthy Vaginal Microbiota Remains Stable during Oral Probiotic Supplementation: A Randomised Controlled Trial. <i>Microorganisms</i> , 2023, 11, 499.	1.6	1
6482	Maximum summer temperatures predict the temperature adaptation of Arctic soil bacterial communities. <i>Biogeosciences</i> , 2023, 20, 767-780.	1.3	4
6483	Effects of field inoculation of potato tubers with the arbuscular mycorrhizal fungus <i>Rhizophagus irregularis</i> DAOM 197198 are cultivar dependent. <i>Symbiosis</i> , 2023, 89, 213-226.	1.2	0
6484	Extreme Niche Partitioning and Microbial Dark Matter in a Mauna Loa Lava Tube. <i>Journal of Geophysical Research E: Planets</i> , 2023, 128, .	1.5	3
6485	Effects of feeding <i>Saccharomyces cerevisiae</i> fermentation postbiotic on the fecal microbial community of Holstein dairy calves. <i>Animal Microbiome</i> , 2023, 5, .	1.5	0
6486	Microbiome response in an urban river system is dominated by seasonality over wastewater treatment upgrades. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	0
6487	Evaluation of high-protein diets differing in protein source in healthy adult dogs. <i>Journal of Animal Science</i> , 2023, 101, .	0.2	2
6488	Hazardous potential evaluation of biochar exposure on mice through analyses of gut-microbiome and fatty acids in brain. <i>Chemical Engineering Journal</i> , 2023, 461, 142006.	6.6	1
6489	Targeting the gut-lung axis by synbiotic feeding to infants in a randomized controlled trial. <i>BMC Biology</i> , 2023, 21, .	1.7	5
6490	Design of the Building Research in CRC prevention (BRIDGE-CRC) trial: a 6-month, parallel group Mediterranean diet and weight loss randomized controlled lifestyle intervention targeting the bile acid-gut microbiome axis to reduce colorectal cancer risk among African American/Black adults with obesity. <i>Trials</i> , 2023, 24, .	0.7	1
6491	The Pathogen <i>Aeromonas salmonicida</i> achromogenes Induces Fast Immune and Microbiota Modifications in Rainbow Trout. <i>Microorganisms</i> , 2023, 11, 539.	1.6	3

#	ARTICLE	IF	CITATIONS
6492	Fecal Microbiota, Forage Nutrients, and Metabolic Responses of Horses Grazing Warm- and Cool-Season Grass Pastures. <i>Animals</i> , 2023, 13, 790.	1.0	2
6493	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlan 4. <i>Nature Biotechnology</i> , 2023, 41, 1633-1644.	9.4	132
6494	Cover Crops Modulate the Response of Arbuscular Mycorrhizal Fungi to Water Supply: A Field Study in Corn. <i>Plants</i> , 2023, 12, 1015.	1.6	3
6495	Estuarine Sediment Microbiomes from a Chronosequence of Restored Urban Salt Marshes. <i>Microbial Ecology</i> , 0, , .	1.4	0
6496	Gut-Microbiota Dysbiosis in Stroke-Prone Spontaneously Hypertensive Rats with Diet-Induced Steatohepatitis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4603.	1.8	1
6497	Longitudinal Analysis of the Intestinal Microbiota among a Cohort of Children in Rural and Urban Areas of Pakistan. <i>Nutrients</i> , 2023, 15, 1213.	1.7	0
6498	Variable preterm oral microbiome stabilizes and reflects a full-term infant profile within three months. <i>Pediatric Research</i> , 0, , .	1.1	4
6499	Rationale, Design and Participants Baseline Characteristics of a Crossover Randomized Controlled Trial of the Effect of Replacing SSBs with NSBs versus Water on Glucose Tolerance, Gut Microbiome and Cardiometabolic Risk in Overweight or Obese Adult SSB Consumer: Strategies to Oppose SUGARS with Non-Nutritive Sweeteners or Water (STOP Sugars NOW) Trial and Ectopic Fat Sub-Study. <i>Nutrients</i> , 2023, 15, 1238.	1.7	2
6500	Changes in upper airways microbiota in ventilator-associated pneumonia. <i>Intensive Care Medicine Experimental</i> , 2023, 11, .	0.9	4
6501	Fine-scale spatial variation shape fecal microbiome diversity and composition in black-tailed prairie dogs (<i>Cynomys ludovicianus</i>). <i>BMC Microbiology</i> , 2023, 23, .	1.3	1
6502	The koala gut microbiome is largely unaffected by host translocation but rather influences host diet. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
6503	From defaults to databases: parameter and database choice dramatically impact the performance of metagenomic taxonomic classification tools. <i>Microbial Genomics</i> , 2023, 9, .	1.0	12
6504	First morphological and molecular investigation of the mycobiota associated with <i>Astragalus nebrodensis</i> in its natural environment (Madonie mountains, Sicily). <i>Plant Biosystems</i> , 2023, 157, 688-698.	0.8	1
6505	Cold Exposure-induced Alterations in the Brain Peptidome and Gut Microbiome Are Linked to Energy Homeostasis in Mice. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100525.	2.5	1
6506	Soil Inoculation and Blocker-Mediated Sequencing Show Effects of the Antibacterial T6SS on Agrobacterial Tumorigenesis and Gallobiome. <i>MBio</i> , 2023, 14, .	1.8	3
6507	Predicting Neurodegenerative Disease Using Prepathology Gut Microbiota Composition: a Longitudinal Study in Mice Modeling Alzheimer's Disease Pathologies. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	11
6508	Effects of grazing and fire management on rangeland soil and biocrust microbiomes. <i>Ecological Indicators</i> , 2023, 148, 110094.	2.6	2
6510	Microbiome and function alterations in the gastric mucosa of asymptomatic patients with <i>Helicobacter pylori</i> infection. <i>Helicobacter</i> , 0, , .	1.6	0

#	ARTICLE	IF	CITATIONS
6511	Association of aberrant brain network dynamics with gut microbial composition uncovers disrupted brain-gut-microbiome interactions in irritable bowel syndrome: Preliminary findings. <i>European Journal of Neurology</i> , 2023, 30, 3529-3539.	1.7	1
6512	The tropical cookbook: Termite diet and phylogenetics—Over geographical origin—Drive the microbiome and functional genetic structure of nests. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
6513	Effects of Consuming Fermented Fish (Surströmming) on the Fecal Microflora in Healthy Individuals. <i>Journal of Medicinal Food</i> , 2023, 26, 185-192.	0.8	0
6514	A phytobiotic extract, in an aqueous or in a cyclodextrin encapsulated form, added in diet affects meat oxidation, cellular responses and intestinal morphometry and microbiota of broilers. <i>Frontiers in Animal Science</i> , 0, 4, .	0.8	2
6515	Characterization of Oral Microbiota Following Chemotherapy in Patients With Hematopoietic Malignancies. <i>Integrative Cancer Therapies</i> , 2023, 22, 153473542311593.	0.8	0
6516	Distribution characteristics of oral microbiota and its relationship with intestinal microbiota in patients with type 2 diabetes mellitus. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	3
6517	Comparative Gut Microbiome Differences between High and Low Aortic Arch Calcification Score in Patients with Chronic Diseases. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5673.	1.8	4
6519	Dose-dependent impact of compost on rhizosphere bacterial community in heavy metal-contaminated paddy soil. <i>Transactions of Nonferrous Metals Society of China</i> , 2023, 33, 642-652.	1.7	0
6520	Seasonal variation in near-surface seasonally thawed active layer and permafrost soil microbial communities. <i>Environmental Research Letters</i> , 2023, 18, 055001.	2.2	4
6521	Effects of <i>Eimeria acervulina</i> infection on the luminal and mucosal microbiota of the duodenum and jejunum in broiler chickens. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
6522	Comprehensive characterization of maternal, fetal, and neonatal microbiomes supports prenatal colonization of the gastrointestinal tract. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
6523	Intestinal iron bio-accessibility changes by Lignin and the subsequent impact on cell metabolism and intestinal microbiome communities. <i>Food and Function</i> , 2023, 14, 3673-3685.	2.1	2
6524	Flex Meta-Storms elucidates the microbiome local beta-diversity under specific phenotypes. <i>Bioinformatics</i> , 2023, 39, .	1.8	2
6525	Revisiting Microbial Diversity in Hypersaline Microbial Mats from Guerrero Negro for a Better Understanding of Methanogenic Archaeal Communities. <i>Microorganisms</i> , 2023, 11, 812.	1.6	2
6526	The Impact of Mineral and Energy Supplementation and Phytogetic Compounds on Rumen Microbial Diversity and Nitrogen Utilization in Grazing Beef Cattle. <i>Microorganisms</i> , 2023, 11, 810.	1.6	2
6528	No evidence for associations between brood size, gut microbiome diversity and survival in great tit (<i>Parus major</i>) nestlings. <i>Animal Microbiome</i> , 2023, 5, .	1.5	1
6529	Apparent total tract macronutrient digestibility of mildly cooked human-grade vegan dog foods and their effects on the blood metabolites and fecal characteristics, microbiota, and metabolites of adult dogs. <i>Journal of Animal Science</i> , 2023, 101, .	0.2	0
6530	Emerging investigator series: differential effects of carbon nanotubes and graphene on the tomato rhizosphere microbiome. <i>Environmental Science: Nano</i> , 2023, 10, 1570-1584.	2.2	1

#	ARTICLE	IF	CITATIONS
6531	Comparison of the respiratory bacterial microbiome in cats with feline asthma and chronic bronchitis. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	0
6532	Biodiversity, biogeography, and connectivity of polychaetes in the world's largest marine minerals exploration frontier. <i>Diversity and Distributions</i> , 2023, 29, 727-747.	1.9	5
6533	Gut content microbiota dysbiosis and dysregulated lipid metabolism in diarrhea caused by high-fat diet in a fatigued state. <i>Food and Function</i> , 2023, 14, 3880-3892.	2.1	10
6535	Oral supplementation of nicotinamide riboside alters intestinal microbial composition in rats and mice, but not humans. , 2023, 9, .		5
6536	Occurrence of <i>Aeromonas</i> Species in the Cutaneous Mucus of Barbours' Seahorses (<i>Hippocampus</i>) Tj ETQq0 0,0 rgBT /Overlock 10	1.0	0
6537	Bacterial microbiome in tropical lichens and the effect of the isolation method on culturable lichen-derived actinobacteria. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
6538	Wildlife gut microbiomes of sympatric generalist species respond differently to anthropogenic landscape disturbances. <i>Animal Microbiome</i> , 2023, 5, .	1.5	2
6539	Bacillus- and Lactobacillus-Based Dietary Synbiotics Are Associated with Shifts in the Oropharyngeal, Proximal Colonic, and Vaginal Microbiomes of Korean Native Black Pigs. <i>Fermentation</i> , 2023, 9, 359.	1.4	0
6540	Gut Bacterial Communities in HIV-Infected Individuals with Metabolic Syndrome: Effects of the Therapy with Integrase Strand Transfer Inhibitor-Based and Protease Inhibitor-Based Regimens. <i>Microorganisms</i> , 2023, 11, 951.	1.6	3
6541	Methane emission, nutrient digestibility, and rumen microbiota in Holstein heifers fed 14 different grass or clover silages as the sole feed. <i>Journal of Dairy Science</i> , 2023, , .	1.4	1
6542	The mature phyllosphere microbiome of grapevine is associated with resistance against <i>Plasmopara viticola</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
6543	Body Size Poorly Predicts Host-Associated Microbial Diversity in Wild Birds. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
6544	MiSurv: an Integrative Web Cloud Platform for User-Friendly Microbiome Data Analysis with Survival Responses. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
6545	The Local Tumor Microbiome Is Associated with Survival in Late-Stage Colorectal Cancer Patients. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
6546	Research Note: Therapeutic effect of a <i>Salmonella</i> phage combination on chicks infected with <i>Salmonella</i> Typhimurium. <i>Poultry Science</i> , 2023, 102, 102715.	1.5	4
6549	Screening and characterization of <i>Bacillus velezensis</i> LB-Y-1 toward selection as a potential probiotic for poultry with multi-enzyme production property. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
6550	Impact of Wood Age on Termite Microbial Assemblages. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	1
6551	Evolink: A Phylogenetic Approach for Rapid Identification of Genotype-Phenotype Associations in Large-scale Microbial Multi-Species Data. <i>Bioinformatics</i> , 0, , .	1.8	0

#	ARTICLE	IF	CITATIONS
6553	Kernel-based genetic association analysis for microbiome phenotypes identifies host genetic drivers of beta-diversity. <i>Microbiome</i> , 2023, 11, .	4.9	1
6629	High-throughput sequencing reveals the dominance of <i>Shewanella</i> species in the intestinal microbiota of barbour's seahorses (<i>Hippocampus barbouri</i>). , 0, .		0
6632	Alpha Diversity. , 2023, , 289-333.		1
6633	Beta Diversity Metrics and Ordination. , 2023, , 335-395.		0
6634	Moving Beyond OTU Methods. , 2023, , 227-288.		0
6635	Assigning Taxonomy, Building Phylogenetic Tree. , 2023, , 123-146.		0
6647	Interactions of Pathogenic <i>Escherichia coli</i> with Gut Microbiota. , 2023, , 277-294.		0
6742	Measuring and Estimating Species Richness, Taxonomic and Phylogenetic Diversity, and Related Biotic (Dis)similarity Indices From Sampling Data. , 2024, , 314-339.		0
6773	Exploring the Impact of Microbial Invasion on the Diseases Involving Gut-Brain Axis in Animals. <i>Livestock Diseases and Management</i> , 2023, , 203-213.	0.5	0
6931	Metagenomics approaches for microbiome analysis. , 2024, , 191-204.		0
6953	Stratification of Prokaryotic Communities in the White Sea Bottom Sediments. <i>Microbiology</i> , 2023, 92, S83-S87.	0.5	0