PyNAST: a flexible tool for aligning sequences to a temp

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Citation Report

#	ARTICLE	IF	CITATIONS
6	arrayQualityMetricsâ€”a bioconductor package for quality assessment of microarray data. Bioinformatics, 2009, 25, 415-416.	1.8	885
7	Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. BMC Microbiology, 2010, 10, 206.	1.3	335
8	Postprandial remodeling of the gut microbiota in Burmese pythons. ISME Journal, 2010, 4, 1375-1385.	4.4	229
9	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. Nature Methods, 2010, 7, 668-669.	9.0	647
10	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. Environmental Microbiology, 2010, 12, 2998-3006.	1.8	551
11	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. Genome Research, 2010, 20, 1411-1419.	2.4	284
12	The Effects of Alignment Quality, Distance Calculation Method, Sequence Filtering, and Region on the Analysis of 16S rRNA Gene-Based Studies. PLoS Computational Biology, 2010, 6, e1000844.	1.5	315
13	Metabolite-based mutualism between Pseudomonas aeruginosa PA14 and Enterobacter aerogenes enhances current generation in bioelectrochemical systems. Energy and Environmental Science, 2011, 4, 4550.	15.6	109
14	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. Current Protocols in Bioinformatics, 2011, 36, Unit 10.7..	25.8	507
15	Topographical Continuity of Bacterial Populations in the Healthy Human Respiratory Tract. American Journal of Respiratory and Critical Care Medicine, 2011, 184, 957-963.	2.5	912
16	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€“ standard operating procedure, version1.0. Nature Precedings, 2011, , .	0.1	5
17	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€“ standard operating procedure, version 1.0. Nature Precedings, 2011, , .	0.1	0
18	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€“ standard operating procedure, version 1.0. Nature Precedings, 2011, , .	0.1	3
19	CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing â€“ standard operating procedure, version 1.1. Nature Precedings, 0, , .	0.1	2
20	Spatial variability in airborne bacterial communities across land-use types and their relationship to the bacterial communities of potential source environments. ISME Journal, 2011, 5, 601-612.	4.4	385
21	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
22	Enteral Tube Feeding Alters the Oral Indigenous Microbiota in Elderly Adults. Applied and Environmental Microbiology, 2011, 77, 6739-6745.	1.4	37
23	Sources of Bacteria in Outdoor Air across Cities in the Midwestern United States. Applied and Environmental Microbiology, 2011, 77, 6350-6356.	1.4	237

#	ARTICLE	IF	CITATIONS
24	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
25	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
26	Incorporating 16S Gene Copy Number Information Improves Estimates of Microbial Diversity and Abundance. PLoS Computational Biology, 2012, 8, e1002743.	1.5	400
27	Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. Genome Research, 2012, 22, 2146-2152.	2.4	167
28	Interleukin-1Î² (IL-1Î²) promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. Gut, 2012, 61, 373-384.	6.1	68
29	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. ISME Journal, 2012, 6, 94-103.	4.4	537
30	Stimulated bacterioplankton growth and selection for certain bacterial taxa in the vicinity of the ctenophore Mnemiopsis leidyi. Frontiers in Microbiology, 2012, 3, 302.	1.5	32
31	Discrimination of the oral microbiota associated with high hydrogen sulfide and methyl mercaptan production. Scientific Reports, 2012, 2, 215.	1.6	68
32	Geographical and ecological stability of the symbiotic midâ€gut microbiota in <scp>E</scp>uropean firebugs, <i><scp>P</scp>yrrhocoris apterus</i> (<scp>H</scp>emiptera, <scp>P</scp>yrrhocoridae). Molecular Ecology, 2012, 21, 6134-6151.	2.0	121
33	Deep sequencing reveals extensive variation in the gut microbiota of wild mosquitoes from <scp>K</scp>enya. Molecular Ecology, 2012, 21, 5138-5150.	2.0	256
34	Intestinal microbiota associated with differential feed conversion efficiency in chickens. Applied Microbiology and Biotechnology, 2012, 96, 1361-1369.	1.7	229
35	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. Cell, 2012, 150, 470-480.	13.5	1,603
36	Advances in the methods for studying gut microbiota and their relevance to the research of dietary fiber functions. Food Research International, 2012, 48, 916-929.	2.9	49
37	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. Journal of Biotechnology, 2012, 158, 248-258.	1.9	198
38	â€œRemakeâ€• by High-Throughput Sequencing of the Microbiota Involved in the Production of Water Buffalo Mozzarella Cheese. Applied and Environmental Microbiology, 2012, 78, 8142-8145.	1.4	165
39	SINA: Accurate high-throughput multiple sequence alignment of ribosomal RNA genes. Bioinformatics, 2012, 28, 1823-1829.	1.8	2,826
40	Spatial and Species Variations in Bacterial Communities Associated with Corals from the Red Sea as Revealed by Pyrosequencing. Applied and Environmental Microbiology, 2012, 78, 7173-7184.	1.4	97
41	Saliva microbiomes distinguish caries-active from healthy human populations. ISME Journal, 2012, 6, 1-10.	4.4	320

#	ARTICLE	IF	CITATIONS
42	Antibiotics in early life alter the murine colonic microbiome and adiposity. Nature, 2012, 488, 621-626.	13.7	1,358
43	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. ISME Journal, 2012, 6, 1715-1727.	4.4	547
44	Pyrosequencing of 16S rRNA genes in fecal samples reveals high diversity of hindgut microflora in horses and potential links to chronic laminitis. BMC Veterinary Research, 2012, 8, 231.	0.7	143
45	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. Current Protocols in Microbiology, 2012, 27, Unit 1E.5..	6.5	486
46	Millimeter-scale patterns of phylogenetic and trait diversity in a salt marsh microbial mat. Frontiers in Microbiology, 2012, 3, 293.	1.5	52
47	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. ISME Journal, 2012, 6, 610-618.	4.4	4,581
48	Comparison of Storage Conditions for Human Vaginal Microbiome Studies. PLoS ONE, 2012, 7, e36934.	1.1	59
49	Bacterial Communities in the Sediments of Dianchi Lake, a Partitioned Eutrophic Waterbody in China. PLoS ONE, 2012, 7, e37796.	1.1	131
50	The Relation between Oral Candida Load and Bacterial Microbiome Profiles in Dutch Older Adults. PLoS ONE, 2012, 7, e42770.	1.1	94
51	A Direct PCR Approach to Accelerate Analyses of Human-Associated Microbial Communities. PLoS ONE, 2012, 7, e44563.	1.1	60
52	Diversity and Succession of Bacterial Communities in the Uterine Fluid of Postpartum Metritic, Endometritic and Healthy Dairy Cows. PLoS ONE, 2012, 7, e53048.	1.1	121
53	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
54	Microbial communities associated with wet flue gas desulfurization systems. Frontiers in Microbiology, 2012, 3, 412.	1.5	10
55	Gut microbiota composition correlates with diet and health in the elderly. Nature, 2012, 488, 178-184.	13.7	2,618
56	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
57	Colonic microbiome is altered in alcoholism. American Journal of Physiology - Renal Physiology, 2012, 302, G966-G978.	1.6	600
58	Soil microbial community response to drying and rewetting stress: does historical precipitation regime matter?. Biogeochemistry, 2012, 109, 101-116.	1.7	360
59	Experimental and analytical tools for studying the human microbiome. Nature Reviews Genetics, 2012, 13, 47-58.	7.7	601

#	Article	IF	Citations
60	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. Obesity, 2012, 20, 738-747.	1.5	352
61	Seasonal variability in airborne bacterial communities at a high-elevation site. Atmospheric Environment, 2012, 50, 41-49.	1.9	226
62	Phylogenetic clustering increases with elevation for microbes. Environmental Microbiology Reports, 2012, 4, 217-226.	1.0	144
63	Microbiome analysis among bats describes influences of host phylogeny, life history, physiology and geography. Molecular Ecology, 2012, 21, 2617-2627.	2.0	195
64	Alterations in composition and diversity of the intestinal microbiota in patients with diarrheaâ€predominant irritable bowel syndrome. Neurogastroenterology and Motility, 2012, 24, 521.	1.6	350
65	Experience matters: prior exposure to plant toxins enhances diversity of gut microbes in herbivores. Ecology Letters, 2012, 15, 1008-1015.	3.0	92
66	Deepâ€sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. Environmental Microbiology, 2012, 14, 2405-2416.	1.8	275
67	Biodiversity soup: metabarcoding of arthropods for rapid biodiversity assessment and biomonitoring. Methods in Ecology and Evolution, 2012, 3, 613-623.	2.2	543
68	Large-Scale Survey of Gut Microbiota Associated With MHE Via 16S rRNA-Based Pyrosequencing. American Journal of Gastroenterology, 2013, 108, 1601-1611.	0.2	149
69	Prokaryotic Communities Differ Along a Geothermal Soil Photic Gradient. Microbial Ecology, 2013, 65, 171-179.	1.4	0
70	Functional and compositional succession of bacterioplankton in response to a gradient in bioavailable dissolved organic carbon. Environmental Microbiology, 2013, 15, 2616-2628.	1.8	54
71	Accurate and universal delineation of prokaryotic species. Nature Methods, 2013, 10, 881-884.	9.0	311
72	Survival in hostile territory: the microbiota of the stomach. FEMS Microbiology Reviews, 2013, 37, 736-761.	3.9	126
74	Secondary structure improves OTU assignments of 16S rRNA gene sequences. ISME Journal, 2013, 7, 457-460.	4.4	63
75	Characterization of bacterial and archaeal communities in air-cathode microbial fuel cells, open circuit and sealed-off reactors. Applied Microbiology and Biotechnology, 2013, 97, 9885-9895.	1.7	84
76	Investigating the Diversity of Pseudomonas spp. in Soil Using Culture Dependent and Independent Techniques. Current Microbiology, 2013, 67, 423-430.	1.0	20
77	Enrichment of lung microbiome with supraglottic taxa is associated with increased pulmonary inflammation. Microbiome, 2013, 1, 19.	4.9	355
78	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. Letters in Applied Microbiology, 2013, 57, 492-501.	1.0	90

#	ARTICLE	IF	CITATIONS
79	Diverse populations of lake water bacteria exhibit chemotaxis towards inorganic nutrients. ISME Journal, 2013, 7, 1661-1664.	4.4	44
80	Systems biological approaches to measure and understand vaccine immunity in humans. Seminars in Immunology, 2013, 25, 209-218.	2.7	58
81	Cell Size Distributions of Soil Bacterial and Archaeal Taxa. Applied and Environmental Microbiology, 2013, 79, 7610-7617.	1.4	98
82	Microbiota Modulate Behavioral and Physiological Abnormalities Associated with Neurodevelopmental Disorders. Cell, 2013, 155, 1451-1463.	13.5	2,596
83	Gut Microbiota from Twins Discordant for Obesity Modulate Metabolism in Mice. Science, 2013, 341, 1241214.	6.0	3,006
84	Microbial communities associated with the degradation of oak wood in the Blanes submarine canyon and its adjacent open slope (NW Mediterranean). Progress in Oceanography, 2013, 118, 137-143.	1.5	26
85	Use of bifidobacterial specific terminal restriction fragment length polymorphisms to complement next generation sequence profiling of infant gut communities. Anaerobe, 2013, 19, 62-69.	1.0	20
86	Analysis of bacterial diversity in sponges collected off Chujado, an Island in Korea, using barcoded 454 pyrosequencing: Analysis of a distinctive sponge group containing Chloroflexi. Journal of Microbiology, 2013, 51, 570-577.	1.3	13
87	Genome resolved analysis of a premature infant gut microbial community reveals a Varibaculum cambriense genome and a shift towards fermentation-based metabolism during the third week of life. Microbiome, 2013, 1, 30.	4.9	50
88	Community differentiation of the cutaneous microbiota in psoriasis. Microbiome, 2013, 1, 31.	4.9	353
89	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	0.4	553
90	Reactor performance in terms of COD and nitrogen removal and bacterial community structure of a three-stage rotating bioelectrochemical contactor. Water Research, 2013, 47, 881-894.	5.3	82
91	Surveying the Microbiome of Ants: Comparing 454 Pyrosequencing with Traditional Methods To Uncover Bacterial Diversity. Applied and Environmental Microbiology, 2013, 79, 525-534.	1.4	122
92	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nature Methods, 2013, 10, 57-59.	9.0	3,402
93	Distinct cutaneous bacterial assemblages in a sampling of South American Amerindians and US residents. ISME Journal, 2013, 7, 85-95.	4.4	101
94	Influence of hydraulic regimes on bacterial community structure and composition in an experimental drinking water distribution system. Water Research, 2013, 47, 503-516.	5.3	240
95	16<scp>S rRNA</scp> survey revealed complex bacterial communities and evidence of bacterial interference on human adenoids. Environmental Microbiology, 2013, 15, 535-547.	1.8	39
96	Bacteria and diatom coâ€occurrence patterns in microbial mats from polar desert streams. Environmental Microbiology, 2013, 15, 1115-1131.	1.8	44

#	ARTICLE	IF	CITATIONS
97	The intestinal microbiota in aged mice is modulated by dietary resistant starch and correlated with improvements in host responses. FEMS Microbiology Ecology, 2013, 83, 299-309.	1.3	166
98	Characterization of cecal microbiota of the emu (Dromaius novaehollandiae). Veterinary Microbiology, 2013, 166, 304-310.	0.8	35
99	Leaf litter is the main driver for changes in bacterial community structures in the rhizosphere of ash and beech. Applied Soil Ecology, 2013, 72, 150-160.	2.1	45
100	Establishing a relationship between bacteria in the human gut and Complex Regional Pain Syndrome. Brain, Behavior, and Immunity, 2013, 29, 62-69.	2.0	18
101	Investigation of the koala (Phascolarctos cinereus) hindgut microbiome via 16S pyrosequencing. Veterinary Microbiology, 2013, 167, 554-564.	0.8	51
102	Chronic N-amended soils exhibit an altered bacterial community structure in Harvard Forest, MA, USA. FEMS Microbiology Ecology, 2013, 83, 478-493.	1.3	85
103	Propionibacterium acnes Strain Populations in the Human Skin Microbiome Associated with Acne. Journal of Investigative Dermatology, 2013, 133, 2152-2160.	0.3	557
104	Temporal variability in soil microbial communities across land-use types. ISME Journal, 2013, 7, 1641-1650.	4.4	408
105	Testing three pipelines for 18S rDNA-based metabarcoding of soil faunal diversity. Science China Life Sciences, 2013, 56, 73-81.	2.3	24
106	Phylogenetic analysis of nitrate- and sulfate-reducing bacteria in a hydrogen-fed biofilm. FEMS Microbiology Ecology, 2013, 85, 158-167.	1.3	43
107	Effects of Multiple Electron Acceptors on Microbial Interactions in a Hydrogen-Based Biofilm. Environmental Science & Technology, 2013, 47, 7396-7403.	4.6	48
108	Impact of Organosulfur Content on Diesel Fuel Stability and Implications for Carbon Steel Corrosion. Environmental Science & Technology, 2013, 47, 6052-6062.	4.6	36
109	<i>In situ</i> chemistry and microbial community compositions in five deepâ€sea hydrothermal fluid samples from <scp>I</scp>rina <scp>II</scp> in the <scp>L</scp>ogatchev field. Environmental Microbiology, 2013, 15, 1551-1560.	1.8	47
110	Bacterial abundance and composition in marine sediments beneath the <scp>R</scp>oss <scp>I</scp>ce <scp>S</scp>helf, <scp>A</scp>ntarctica. Geobiology, 2013, 11, 377-395.	1.1	36
112	Relative impacts of tillage, residue management and crop-rotation on soil bacterial communities in a semi-arid agroecosystem. Soil Biology and Biochemistry, 2013, 65, 86-95.	4.2	251
113	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. ISME Journal, 2013, 7, 50-60.	4.4	198
114	Early Diet Impacts Infant Rhesus Gut Microbiome, Immunity, and Metabolism. Journal of Proteome Research, 2013, 12, 2833-2845.	1.8	90
115	Reliable, verifiable and efficient monitoring of biodiversity via metabarcoding. Ecology Letters, 2013, 16, 1245-1257.	3.0	514

#	ARTICLE	IF	CITATIONS
116	Association of gut microbiota with post-operative clinical course in Crohnâ€™s disease. BMC Gastroenterology, 2013, 13, 131.	0.8	95
117	Probiotic Dosing of Ruminococcus flavefaciens Affects Rumen Microbiome Structure and Function in Reindeer. Microbial Ecology, 2013, 66, 840-849.	1.4	15
118	Outgrowth of the Bacterial Airway Microbiome after Rhinovirus Exacerbation of Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2013, 188, 1224-1231.	2.5	329
119	Using a Two-Stage Hydrogen-Based Membrane Biofilm Reactor (MBfR) to Achieve Complete Perchlorate Reduction in the Presence of Nitrate and Sulfate. Environmental Science & Technology, 2013, 47, 1565-1572.	4.6	78
120	High-performance computing and the cloud. Xrds, 2013, 19, 52-57.	0.2	3
121	Standard methods for research on<i>Apis mellifera</i>gut symbionts. Journal of Apicultural Research, 2013, 52, 1-24.	0.7	98
122	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
123	FunFrame: functional gene ecological analysis pipeline. Bioinformatics, 2013, 29, 1212-1214.	1.8	12
124	Surface Microbes in the Neonatal Intensive Care Unit: Changes with Routine Cleaning and over Time. Journal of Clinical Microbiology, 2013, 51, 2617-2624.	1.8	73
125	Quantitation and Composition of Cutaneous Microbiota in Diabetic and Nondiabetic Men. Journal of Infectious Diseases, 2013, 207, 1105-1114.	1.9	90
126	Microbial Diversity and Structure Are Drivers of the Biological Barrier Effect against Listeria monocytogenes in Soil. PLoS ONE, 2013, 8, e76991.	1.1	94
127	Distinct Distal Gut Microbiome Diversity and Composition in Healthy Children from Bangladesh and the United States. PLoS ONE, 2013, 8, e53838.	1.1	278
128	Facility-Specific â€œHouseâ€•Microbiome Drives Microbial Landscapes of Artisan Cheesemaking Plants. Applied and Environmental Microbiology, 2013, 79, 5214-5223.	1.4	232
129	Utilization of Heme as an Iron Source by Marine Alphaproteobacteria in the Roseobacter Clade. Applied and Environmental Microbiology, 2013, 79, 5753-5762.	1.4	31
130	IL-22 Deficiency Alters Colonic Microbiota To Be Transmissible and Colitogenic. Journal of Immunology, 2013, 190, 5306-5312.	0.4	224
131	Unique Vaginal Microbiota That Includes an Unknown Mycoplasma-Like Organism Is Associated With Trichomonas vaginalis Infection. Journal of Infectious Diseases, 2013, 207, 1922-1931.	1.9	81
132	Analysis of the bacterial communities associated with two antâ€“plant symbioses. MicrobiologyOpen, 2013, 2, 276-283.	1.2	35
133	Uranium redox transition pathways in acetate-amended sediments. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4506-4511.	3.3	161

#	Article	IF	Citations
134	Streptomycin Application Has No Detectable Effect on Bacterial Community Structure in Apple Orchard Soil. Applied and Environmental Microbiology, 2013, 79, 6617-6625.	1.4	38
135	<scp>A</scp>ctinobacteria as essential symbionts in firebugs and cotton stainers (<scp>H</scp>emiptera, <scp>P</scp>yrrhocoridae). Environmental Microbiology, 2013, 15, 1956-1968.	1.8	110
136	Oligotyping: differentiating between closely related microbial taxa using 16S <scp>rRNA</scp> gene data. Methods in Ecology and Evolution, 2013, 4, 1111-1119.	2.2	652
137	Distinctive Microbial Community Structure in Highly Stratified Deep-Sea Brine Water Columns. Applied and Environmental Microbiology, 2013, 79, 3425-3437.	1.4	57
138	Evidence for a persistent microbial seed bank throughout the global ocean. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4651-4655.	3.3	200
139	Microbiome Assembly across Multiple Body Sites in Low-Birthweight Infants. MBio, 2013, 4, e00782-13.	1.8	147
140	Aquacultured Rainbow Trout (Oncorhynchus mykiss) Possess a Large Core Intestinal Microbiota That Is Resistant to Variation in Diet and Rearing Density. Applied and Environmental Microbiology, 2013, 79, 4974-4984.	1.4	191
141	Identification of Norovirus in Sewage by Using Pyrosequencing. Journal of Japan Society of Civil Engineers Ser G (Environmental Research), 2013, 69, III_639-III_646.	0.1	0
142	Histamineâ€2 Receptor Blockers Alter the Fecal Microbiota in Premature Infants. Journal of Pediatric Gastroenterology and Nutrition, 2013, 56, 397-400.	0.9	94
143	Metabolomic Phenotyping Validates the Infant Rhesus Monkey as a Model of Human Infant Metabolism. Journal of Pediatric Gastroenterology and Nutrition, 2013, 56, 355-363.	0.9	54
144	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. ELife, 2013, 2, e01104.	2.8	270
145	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature Populus deltoides Trees. PLoS ONE, 2013, 8, e76382.	1.1	315
146	Identification of differential duodenal gene expression levels and microbiota abundance correlated with differences in energy utilisation in chickens. Animal Production Science, 2013, 53, 1269.	0.6	18
147	Colonization patterns of soil microbial communities in the Atacama Desert. Microbiome, 2013, 1, 28.	4.9	215
148	Spatial variability of particle-attached and free-living bacterial diversity in surface waters from the Mackenzie River to the Beaufort Sea (Canadian Arctic). Biogeosciences, 2013, 10, 2747-2759.	1.3	110
149	A Comprehensive Census of Microbial Diversity in Hot Springs of Tengchong, Yunnan Province China Using 16S rRNA Gene Pyrosequencing. PLoS ONE, 2013, 8, e53350.	1.1	216
150	Comparison of the Distal Gut Microbiota from People and Animals in Africa. PLoS ONE, 2013, 8, e54783.	1.1	63
151	The Poultry-Associated Microbiome: Network Analysis and Farm-to-Fork Characterizations. PLoS ONE, 2013, 8, e57190.	1.1	104

#	Article	IF	Citations
152	Assessing the Consequences of Denoising Marker-Based Metagenomic Data. PLoS ONE, 2013, 8, e60458.	1.1	51
153	CLUSTOM: A Novel Method for Clustering 16S rRNA Next Generation Sequences by Overlap Minimization. PLoS ONE, 2013, 8, e62623.	1.1	18
154	Factors Controlling Soil Microbial Biomass and Bacterial Diversity and Community Composition in a Cold Desert Ecosystem: Role of Geographic Scale. PLoS ONE, 2013, 8, e66103.	1.1	98
155	Monitoring Seasonal Changes in Winery-Resident Microbiota. PLoS ONE, 2013, 8, e66437.	1.1	167
156	Season, Irrigation, Leaf Age, and Escherichia coli Inoculation Influence the Bacterial Diversity in the Lettuce Phyllosphere. PLoS ONE, 2013, 8, e68642.	1.1	121
157	Prospecting Environmental Mycobacteria: Combined Molecular Approaches Reveal Unprecedented Diversity. PLoS ONE, 2013, 8, e68648.	1.1	34
158	Light Structures Phototroph, Bacterial and Fungal Communities at the Soil Surface. PLoS ONE, 2013, 8, e69048.	1.1	24
159	Comprehensive Genomic Characterization of Campylobacter Genus Reveals Some Underlying Mechanisms for its Genomic Diversification. PLoS ONE, 2013, 8, e70241.	1.1	16
160	Impact of Ileocecal Resection and Concomitant Antibiotics on the Microbiome of the Murine Jejunum and Colon. PLoS ONE, 2013, 8, e73140.	1.1	54
161	Development of the Preterm Gut Microbiome in Twins at Risk of Necrotising Enterocolitis and Sepsis. PLoS ONE, 2013, 8, e73465.	1.1	114
162	An In Vitro Model of the Horse Gut Microbiome Enables Identification of Lactate-Utilizing Bacteria That Differentially Respond to Starch Induction. PLoS ONE, 2013, 8, e77599.	1.1	70
163	Distinct Phyllosphere Bacterial Communities on Arabidopsis Wax Mutant Leaves. PLoS ONE, 2013, 8, e78613.	1.1	81
164	Functional gene pyrosequencing and network analysis: an approach to examine the response of denitrifying bacteria to increased nitrogen supply in salt marsh sediments. Frontiers in Microbiology, 2013, 4, 342.	1.5	52
165	Microbial diversity and methanogenic activity of Antrim Shale formation waters from recently fractured wells. Frontiers in Microbiology, 2013, 4, 367.	1.5	79
166	Structure, Composition and Metagenomic Profile of Soil Microbiomes Associated to Agricultural Land Use and Tillage Systems in Argentine Pampas. PLoS ONE, 2014, 9, e99949.	1.1	191
167	The Personal Human Oral Microbiome Obscures the Effects of Treatment on Periodontal Disease. PLoS ONE, 2014, 9, e86708.	1.1	79
168	Relationship between the Rumen Microbiome and Residual Feed Intake-Efficiency of Brahman Bulls Stocked on Bermudagrass Pastures. PLoS ONE, 2014, 9, e91864.	1.1	90
169	Toward Understanding the Dynamics of Microbial Communities in an Estuarine System. PLoS ONE, 2014, 9, e94449.	1.1	24

#	ARTICLE	IF	CITATIONS
170	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. PLoS ONE, 2014, 9, e94710.	1.1	43
171	Improved Yield of High Molecular Weight DNA Coincides with Increased Microbial Diversity Access from Iron Oxide Cemented Sub-Surface Clay Environments. PLoS ONE, 2014, 9, e102826.	1.1	25
172	Identification of the Microbiota in Carious Dentin Lesions Using 16S rRNA Gene Sequencing. PLoS ONE, 2014, 9, e103712.	1.1	75
173	Microbial Community Structure of Relict Niter-Beds Previously Used for Saltpeter Production. PLoS ONE, 2014, 9, e104752.	1.1	4
174	Relationships between Bacterial Community Composition, Functional Trait Composition and Functioning Are Context Dependent â€" but What Is the Context?. PLoS ONE, 2014, 9, e112409.	1.1	2
175	Maternal Obesity Is Associated with Alterations in the Gut Microbiome in Toddlers. PLoS ONE, 2014, 9, e113026.	1.1	149
176	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. PLoS ONE, 2014, 9, e114804.	1.1	110
177	The Antipsychotic Olanzapine Interacts with the Gut Microbiome to Cause Weight Gain in Mouse. PLoS ONE, 2014, 9, e115225.	1.1	147
178	Investigation of bacterial diversity in the feces of cattle fed different diets1. Journal of Animal Science, 2014, 92, 683-694.	0.2	134
179	Temporal dynamics in the ruminal microbiome of dairy cows during the transition period. Journal of Animal Science, 2014, 92, 4014-4022.	0.2	101
180	Zooplankton diversity across three Red Sea reefs using pyrosequencing. Frontiers in Marine Science, 2014, 1, .	1.2	37
181	Pinus flexilis and Piceae engelmannii share a simple and consistent needle endophyte microbiota with a potential role in nitrogen fixation. Frontiers in Microbiology, 2014, 5, 333.	1.5	81
182	Two distinct microbial communities revealed in the sponge Cinachyrella. Frontiers in Microbiology, 2014, 5, 581.	1.5	42
183	Oligotyping analysis of the human oral microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2875-84.	3.3	295
184	A Phylogenomic View of Ecological Specialization in the Lachnospiraceae, a Family of Digestive Tract-Associated Bacteria. Genome Biology and Evolution, 2014, 6, 703-713.	1.1	601
185	Metagenomic analyses of bacteria on human hairs: a qualitative assessment for applications in forensic science. Investigative Genetics, 2014, 5, 16.	3.3	69
186	Effects of straw amendment and moisture on microbial communities in Chinese fluvo-aquic soil. Journal of Soils and Sediments, 2014, 14, 1829-1840.	1.5	91
187	The gut microbiota of Colombians differs from that of Americans, Europeans and Asians. BMC Microbiology, 2014, 14, 311.	1.3	178

#	ARTICLE	IF	CITATIONS
188	Indoor-Air Microbiome in an Urban Subway Network: Diversity and Dynamics. Applied and Environmental Microbiology, 2014, 80, 6760-6770.	1.4	141
189	Dietary supplementation with lactose or artificial sweetener enhances swine gut<i>Lactobacillus</i>population abundance. British Journal of Nutrition, 2014, 111, S30-S35.	1.2	77
190	Microbial cargo: do bacteria on symbiotic propagules reinforce the microbiome of lichens?. Environmental Microbiology, 2014, 16, 3743-3752.	1.8	78
191	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. Frontiers in Microbiology, 2014, 5, 298.	1.5	130
192	The Tandem Repeats Enabling Reversible Switching between the Two Phases of Î²-Lactamase Substrate Spectrum. PLoS Genetics, 2014, 10, e1004640.	1.5	11
193	Helminth Colonization Is Associated with Increased Diversity of the Gut Microbiota. PLoS Neglected Tropical Diseases, 2014, 8, e2880.	1.3	353
194	Captivity results in disparate loss of gut microbial diversity in closely related hosts. , 2014, 2, cou009-cou009.		132
195	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
196	Changes in the deep subsurface microbial biosphere resulting from a field-scale CO2 geosequestration experiment. Frontiers in Microbiology, 2014, 5, 209.	1.5	44
197	A Compositional Look at the Human Gastrointestinal Microbiome and Immune Activation Parameters in HIV Infected Subjects. PLoS Pathogens, 2014, 10, e1003829.	2.1	343
198	Late winter under ice pelagic microbial communities in the high Arctic Ocean and the impact of short-term exposure to elevated CO₂levels. Frontiers in Microbiology, 2014, 5, 490.	1.5	21
199	Metagenome Sequencing of the Prokaryotic Microbiota of the Hypersaline and Meromictic Soap Lake, Washington. Genome Announcements, 2014, 2, .	0.8	4
200	Effect of Copper Treatment on the Composition and Function of the Bacterial Community in the Sponge <i>Haliclona cymaeformis</i>. MBio, 2014, 5, e01980.	1.8	39
201	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. BMC Microbiology, 2014, 14, 189.	1.3	292
202	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. MicrobiologyOpen, 2014, 3, 910-921.	1.2	89
203	Altered Oral Viral Ecology in Association with Periodontal Disease. MBio, 2014, 5, e01133-14.	1.8	171
204	Metagenomic Sequencing of Two Salton Sea Microbiomes. Genome Announcements, 2014, 2, .	0.8	9
205	Bacterial Communities of Traditional Salted and Fermented Seafoods from Jeju Island of Korea Using 16S rRNA Gene Clone Library Analysis. Journal of Food Science, 2014, 79, M927-34.	1.5	37

#	ARTICLE	IF	CITATIONS
206	Shotgun microbial profiling of fossil remains. Molecular Ecology, 2014, 23, 1780-1798.	2.0	55
207	Shifts in microbial community structure and function in lightâ€•and darkâ€grown biofilms driven by warming. Environmental Microbiology, 2014, 16, 2550-2567.	1.8	38
208	Deodorization of pig slurry and characterization of bacterial diversity using 16S rDNA sequence analysis. Journal of Microbiology, 2014, 52, 918-929.	1.3	8
209	Bacterial community structure and soil properties of a subarctic tundra soil in Council, Alaska. FEMS Microbiology Ecology, 2014, 89, 465-475.	1.3	121
210	Spatial distribution of microbial communities associated with dune landform in the Gurbantunggut Desert, China. Journal of Microbiology, 2014, 52, 898-907.	1.3	16
211	Contrasting soil fungal community responses to experimental nitrogen addition using the large subunit <scp>rRNA</scp> taxonomic marker and cellobiohydrolase I functional marker. Molecular Ecology, 2014, 23, 4406-4417.	2.0	36
212	Comparative analysis of bacterial community-metagenomics in coastal Gulf of Mexico sediment microcosms following exposure to Macondo oil (MC252). Antonie Van Leeuwenhoek, 2014, 106, 993-1009.	0.7	21
213	First Evidence of Amoebaeâ€"Mycobacteria Association in Drinking Water Network. Environmental Science & Technology, 2014, 48, 11872-11882.	4.6	99
214	Oxygen Suppresses Light-Driven Anodic Current Generation by a Mixed Phototrophic Culture. Environmental Science & Technology, 2014, 48, 14000-14006.	4.6	17
215	Co-inoculating ruminal content neither provides active hydrolytic microbes nor improves methanization of¹³C-cellulose in batch digesters. FEMS Microbiology Ecology, 2014, 87, 616-629.	1.3	41
216	Dietary Î±-mangostin, a xanthone from mangosteen fruit, exacerbates experimental colitis and promotes dysbiosis in mice. Molecular Nutrition and Food Research, 2014, 58, 1226-1238.	1.5	37
217	Unique and shared responses of the gut microbiota to prolonged fasting: a comparative study across five classes of vertebrate hosts. FEMS Microbiology Ecology, 2014, 90, 883-894.	1.3	183
218	Anaerobic codigestion of sewage sludge and glycerol, focusing on process kinetics, microbial dynamics and sludge dewaterability. Water Research, 2014, 67, 355-366.	5.3	92
219	Herbivorous rodents (<scp><i>N</i></scp><i>eotoma spp.</i>) harbour abundant and active foregut microbiota. Environmental Microbiology, 2014, 16, 2869-2878.	1.8	78
220	Marek's disease virus influences the core gut microbiome of the chicken during the early and late phases of viral replication. FEMS Microbiology Ecology, 2014, 90, 300-312.	1.3	38
221	Exercise Prevents Weight Gain and Alters the Gut Microbiota in a Mouse Model of High Fat Diet-Induced Obesity. PLoS ONE, 2014, 9, e92193.	1.1	451
222	Changes in the Bacterial Community Structure in Stored Wormbed Leachate. Journal of Molecular Microbiology and Biotechnology, 2014, 24, 105-113.	1.0	10
223	Soluble maize fibre affects short-term calcium absorption in adolescent boys and girls: a randomised controlled trial using dual stable isotopic tracers. British Journal of Nutrition, 2014, 112, 446-456.	1.2	95

#	Article	IF	Citations
224	Comparison of environmental and isolate Sulfobacillus genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. BMC Genomics, 2014, 15, 1107.	1.2	65
225	Bacterial community composition of chronic periodontitis and novel oral sampling sites for detecting disease indicators. Microbiome, 2014, 2, 32.	4.9	77
226	Improved characterization of medically relevant fungi in the human respiratory tract using next-generation sequencing. Genome Biology, 2014, 15, 487.	3.8	127
227	Altered microbiota associated with abnormal humoral immune responses to commensal organisms in enthesitis-related arthritis. Arthritis Research and Therapy, 2014, 16, 486.	1.6	176
228	Broad scope method for creating humanized animal models for animal health and disease research through antibiotic treatment and human fecal transfer. Gut Microbes, 2014, 5, 183-191.	4.3	90
229	Human and Environmental Impacts on River Sediment Microbial Communities. PLoS ONE, 2014, 9, e97435.	1.1	115
230	Soil bacterial community composition altered by increased nutrient availability in Arctic tundra soils. Frontiers in Microbiology, 2014, 5, 516.	1.5	188
231	The structures of the colonic mucosa-associated and luminal microbial communities are distinct and differentially affected by a prolonged murine stressor. Gut Microbes, 2014, 5, 748-760.	4.3	91
232	Early life establishment of site-specific microbial communities in the gut. Gut Microbes, 2014, 5, 192-201.	4.3	55
233	Validation of IMP Dehydrogenase Inhibitors in a Mouse Model of Cryptosporidiosis. Antimicrobial Agents and Chemotherapy, 2014, 58, 1603-1614.	1.4	56
234	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. Microbiome, 2014, 2, 1.	4.9	437
235	Indoor-Biofilter Growth and Exposure to Airborne Chemicals Drive Similar Changes in Plant Root Bacterial Communities. Applied and Environmental Microbiology, 2014, 80, 4805-4813.	1.4	28
236	Bacterial Communities in Soil Under Moss and Lichen-Moss Crusts. Geomicrobiology Journal, 2014, 31, 152-160.	1.0	28
237	Host-specific adaptation governs the interaction of the marine diatom, <i>Pseudo-nitzschia</i> and their microbiota. ISME Journal, 2014, 8, 63-76.	4.4	137
238	Using high-throughput sequencing to assess the impacts of treated and untreated wastewater discharge on prokaryotic communities in an urban river. Applied Microbiology and Biotechnology, 2014, 98, 1841-1851.	1.7	63
239	Analysis of bacterial diversity in sponges collected from chuuk and kosrae islands in micronesia. Journal of Microbiology, 2014, 52, 20-26.	1.3	4
240	Composition and activity of rhizosphere microbial communities associated with healthy and diseased greenhouse tomatoes. Plant and Soil, 2014, 380, 337-347.	1.8	62
241	Convergence of gut microbiomes in myrmecophagous mammals. Molecular Ecology, 2014, 23, 1301-1317.	2.0	311

#	ARTICLE	IF	CITATIONS
242	The bacteriological composition of biomass recovered by flushing an operational drinking water distribution system. Water Research, 2014, 54, 100-114.	5.3	95
243	Divergent Responses of Soil Fungi Functional Groups to Short-term Warming. Microbial Ecology, 2014, 68, 708-715.	1.4	85
244	Multiple ITS Haplotypes in the Genome of the Lichenized Basidiomycete Cora inversa (Hygrophoraceae): Fact or Artifact?. Journal of Molecular Evolution, 2014, 78, 148-162.	0.8	31
245	Mutualistic ants as an indirect defence against leaf pathogens. New Phytologist, 2014, 202, 640-650.	3.5	42
246	FXR is a molecular target for the effects of vertical sleeve gastrectomy. Nature, 2014, 509, 183-188.	13.7	810
247	Why are some microbes more ubiquitous than others? Predicting the habitat breadth of soil bacteria. Ecology Letters, 2014, 17, 794-802.	3.0	243
248	Mosquitoes rely on their gut microbiota for development. Molecular Ecology, 2014, 23, 2727-2739.	2.0	429
249	Microbial Community Dynamics and Stability during an Ammonia-Induced Shift to Syntrophic Acetate Oxidation. Applied and Environmental Microbiology, 2014, 80, 3375-3383.	1.4	118
250	Characterizing changes in soil bacterial community structure in response to short-term warming. FEMS Microbiology Ecology, 2014, 89, 281-292.	1.3	107
251	Spatial and temporal variations of microbial community in a mixed plugâ€flow loop reactor fed with dairy manure. Microbial Biotechnology, 2014, 7, 332-346.	2.0	60
252	Humboldtâ€™s spa: microbial diversity is controlled by temperature in geothermal environments. ISME Journal, 2014, 8, 1166-1174.	4.4	186
253	AIEC pathobiont instigates chronic colitis in susceptible hosts by altering microbiota composition. Gut, 2014, 63, 1069-1080.	6.1	182
254	Specificity and transcriptional activity of microbiota associated with low and high microbial abundance sponges from the Red Sea. Molecular Ecology, 2014, 23, 1348-1363.	2.0	139
255	Exploring links between pH and bacterial community composition in soils from the Craibstone Experimental Farm. FEMS Microbiology Ecology, 2014, 87, 403-415.	1.3	154
256	Metaproteomics Analysis Reveals the Adaptation Process for the Chicken Gut Microbiota. Applied and Environmental Microbiology, 2014, 80, 478-485.	1.4	65
257	Biogeography of the Sediment Bacterial Community Responds to a Nitrogen Pollution Gradient in the East China Sea. Applied and Environmental Microbiology, 2014, 80, 1919-1925.	1.4	98
258	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders (<i>Plethodon cinereus</i>). ISME Journal, 2014, 8, 830-840.	4.4	316
259	Soil extracellular enzyme activities correspond with abiotic factors more than fungal community composition. Biogeochemistry, 2014, 117, 23-37.	1.7	112

#	Article	IF	Citations
260	Phylogeny-based classification of microbial communities. Bioinformatics, 2014, 30, 449-456.	1.8	29
261	Phyllosphere Microbiota Composition and Microbial Community Transplantation on Lettuce Plants Grown Indoors. MBio, 2014, 5, .	1.8	84
262	Microbial heterotrophic production in an oligotrophic acidic geothermal lake: responses to organic amendments and terrestrial plant litter. FEMS Microbiology Ecology, 2014, 89, 606-624.	1.3	8
263	Enrichment of anodophilic nitrogen fixing bacteria in a bioelectrochemical system. Water Research, 2014, 64, 73-81.	5.3	23
264	Response of phyllosphere bacterial communities to elevated CO2 during rice growing season. Applied Microbiology and Biotechnology, 2014, 98, 9459-9471.	1.7	59
265	Changes in free-living bacterial community diversity reflect the magnitude of environmental variability. FEMS Microbiology Ecology, 2014, 87, 291-301.	1.3	40
266	Urea Uptake and Carbon Fixation by Marine Pelagic Bacteria and Archaea during the Arctic Summer and Winter Seasons. Applied and Environmental Microbiology, 2014, 80, 6013-6022.	1.4	71
267	Biofouling and Microbial Communities in Membrane Distillation and Reverse Osmosis. Environmental Science & Technology, 2014, 48, 13155-13164.	4.6	75
268	Internal Porosity of Mineral Coating Supports Microbial Activity in Rapid Sand Filters for Groundwater Treatment. Applied and Environmental Microbiology, 2014, 80, 7010-7020.	1.4	40
269	Comparative survey of bacterial and archaeal communities in high arsenic shallow aquifers using 454 pyrosequencing and traditional methods. Ecotoxicology, 2014, 23, 1878-1889.	1.1	12
270	Soil Microbial Responses to Increased Moisture and Organic Resources along a Salinity Gradient in a Polar Desert. Applied and Environmental Microbiology, 2014, 80, 3034-3043.	1.4	171
271	Variation in gut microbial communities and its association with pathogen infection in wild bumble bees (<i>Bombus</i>). ISME Journal, 2014, 8, 2369-2379.	4.4	193
272	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E139-48.	3.3	791
273	Gastric microbiota is altered in oesophagitis and <scp>B</scp>arrett's oesophagus and further modified by proton pump inhibitors. Environmental Microbiology, 2014, 16, 2905-2914.	1.8	150
274	Structural changes in the gut microbiome of constipated patients. Physiological Genomics, 2014, 46, 679-686.	1.0	271
275	Vertebrate Decomposition Is Accelerated by Soil Microbes. Applied and Environmental Microbiology, 2014, 80, 4920-4929.	1.4	84
276	Effect of postextraction algal residue supplementation on the ruminal microbiome of steers consuming low-quality forage1. Journal of Animal Science, 2014, 92, 5063-5075.	0.2	20
277	Investigation of bacterial and fungal diversity in tarag using high-throughput sequencing. Journal of Dairy Science, 2014, 97, 6085-6096.	1.4	61

#	ARTICLE	IF	CITATIONS
278	Responsiveness of cardiometabolic-related microbiota to diet is influenced by host genetics. Mammalian Genome, 2014, 25, 583-599.	1.0	66
279	Nitrate Shaped the Selenate-Reducing Microbial Community in a Hydrogen-Based Biofilm Reactor. Environmental Science & Technology, 2014, 48, 3395-3402.	4.6	106
280	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141988.	1.2	295
281	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. ISME Journal, 2014, 8, 1464-1475.	4.4	325
282	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. Nature, 2014, 514, 508-512.	13.7	366
283	Temporal Dynamics of the Cecal Gut Microbiota of Juvenile Arctic Ground Squirrels: a Strong Litter Effect across the First Active Season. Applied and Environmental Microbiology, 2014, 80, 4260-4268.	1.4	15
284	Stratified Microbial Structure and Activity in Sulfide- and Methane-Producing Anaerobic Sewer Biofilms. Applied and Environmental Microbiology, 2014, 80, 7042-7052.	1.4	95
285	Sequentially aerated membrane biofilm reactors for autotrophic nitrogen removal: microbial community composition and dynamics. Microbial Biotechnology, 2014, 7, 32-43.	2.0	50
286	Paenibacillus lentus sp. nov., a Î²-mannanolytic bacterium isolated from mixed soil samples in a selective enrichment using guar gum as the sole carbon source. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 1166-1172.	0.8	22
287	Molecular Analysis for Screening Human Bacterial Pathogens in Municipal Wastewater Treatment and Reuse. Environmental Science & Technology, 2014, 48, 11610-11619.	4.6	71
288	Contrasting Response Patterns of Rice Phyllosphere Bacterial Taxa to Elevated CO2. Pedosphere, 2014, 24, 544-552.	2.1	8
289	Virus-helminth coinfection reveals a microbiota-independent mechanism of immunomodulation. Science, 2014, 345, 578-582.	6.0	238
290	Conducting a Microbiome Study. Cell, 2014, 158, 250-262.	13.5	625
291	Using metabarcoding to ask if easily collected soil and leaf-litter samples can be used as a general biodiversity indicator. Ecological Indicators, 2014, 46, 379-389.	2.6	74
292	Lactivibrio alcoholicus gen. nov., sp. nov., an anaerobic, mesophilic, lactate-, alcohol-, carbohydrate- and amino-acid-degrading bacterium in the phylum Synergistetes. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2137-2145.	0.8	41
293	Improved resolution of bacteria by high throughput sequence analysis of the rRNA internal transcribed spacer. Journal of Microbiological Methods, 2014, 105, 82-87.	0.7	30
294	The Role of Bacteria in the Pathogenesis and Progression of Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 906-913.	2.5	453
295	Getting Started with Microbiome Analysis: Sample Acquisition to Bioinformatics. Current Protocols in Human Genetics, 2014, 82, 18.8.1-29.	3.5	111

#	ARTICLE	IF	CITATIONS
296	Gastrointestinal microbiota of wild and inbred individuals of two house mouse subspecies assessed using highâ€throughput parallel pyrosequencing. Molecular Ecology, 2014, 23, 5048-5060.	2.0	66
297	Conservation of streptococcal CRISPRs on human skin and saliva. BMC Microbiology, 2014, 14, 146.	1.3	44
298	Comparative assessment of the bacterial communities associated with Aedes aegypti larvae and water from domestic water storage containers. Parasites and Vectors, 2014, 7, 391.	1.0	71
299	Characterization of the nasopharyngeal microbiota in health and during rhinovirus challenge. Microbiome, 2014, 2, 22.	4.9	107
300	Human oral viruses are personal, persistent and gender-consistent. ISME Journal, 2014, 8, 1753-1767.	4.4	159
301	A Hidden Pitfall in the Preparation of Agar Media Undermines Microorganism Cultivability. Applied and Environmental Microbiology, 2014, 80, 7659-7666.	1.4	192
302	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
303	Pyrosequencing Reveals the Microbial Communities in the Red Sea Sponge Carteriospongia foliascens and Their Impressive Shifts in Abnormal Tissues. Microbial Ecology, 2014, 68, 621-632.	1.4	37
304	Bacterial colonization of a fumigated alkaline saline soil. Extremophiles, 2014, 18, 733-743.	0.9	4
305	Bacterial community structure in fumigated soil. Soil Biology and Biochemistry, 2014, 73, 122-129.	4.2	26
306	Recovering glycoside hydrolase genes from active tundra cellulolytic bacteria. Canadian Journal of Microbiology, 2014, 60, 469-476.	0.8	29
307	Effects of Season and Host Physiological State on the Diversity, Density, and Activity of the Arctic Ground Squirrel Cecal Microbiota. Applied and Environmental Microbiology, 2014, 80, 5611-5622.	1.4	87
308	Polymicrobial airway bacterial communities in adult bronchiectasis patients. BMC Microbiology, 2014, 14, 130.	1.3	50
309	Amphibian skin may select for rare environmental microbes. ISME Journal, 2014, 8, 2207-2217.	4.4	255
310	454 pyrosequencing reveals changes in the faecal microbiota of adults consuming<i>Lactobacillus casei</i>Zhang. FEMS Microbiology Ecology, 2014, 88, 612-622.	1.3	64
311	Communities of sediment ammonia-oxidizing bacteria along a coastal pollution gradient in the East China Sea. Marine Pollution Bulletin, 2014, 86, 147-153.	2.3	15
312	Bifidobacterium longum subsp. infantis in experimental necrotizing enterocolitis: alterations in inflammation, innate immune response, and the microbiota. Pediatric Research, 2014, 76, 326-333.	1.1	95
313	Wastewater Irrigation Increases the Abundance of Potentially Harmful Gammaproteobacteria in Soils in Mezquital Valley, Mexico. Applied and Environmental Microbiology, 2014, 80, 5282-5291.	1.4	80

#	ARTICLE	IF	CITATIONS
314	Pyrosequencing Analysis Yields Comprehensive Assessment of Microbial Communities in Pilot-Scale Two-Stage Membrane Biofilm Reactors. Environmental Science & Technology, 2014, 48, 7511-7518.	4.6	37
315	Response of Soil-Associated Microbial Communities to Intrusion of Coal Mine-Derived Acid Mine Drainage. Environmental Science & Technology, 2014, 48, 8556-8563.	4.6	51
316	Variation in the hindgut microbial communities of the Florida manatee,<i>Trichechus manatus latirostris</i>over winter in Crystal River, Florida. FEMS Microbiology Ecology, 2014, 87, 601-615.	1.3	26
317	The bacterial communities of bioelectrochemical systems associated with the sulfate removal under different pHs. Process Biochemistry, 2014, 49, 1345-1351.	1.8	52
318	Impact of sampler selection on the characterization of the indoor microbiome via high-throughput sequencing. Building and Environment, 2014, 80, 274-282.	3.0	45
319	Effects of dissimilatory sulfate reduction on FeIII (hydr)oxide reduction and microbial community development. Geochimica Et Cosmochimica Acta, 2014, 129, 177-190.	1.6	68
320	Managing the interactions between sulfate- and perchlorate-reducing bacteria when using hydrogen-fed biofilms to treat a groundwater with a high perchlorate concentration. Water Research, 2014, 55, 215-224.	5.3	57
321	Bacterioplankton assemblages as biological indicators of shrimp health status. Ecological Indicators, 2014, 38, 218-224.	2.6	99
322	Characterization of the gut microbiota in leptin deficient obese mice â€" Correlation to inflammatory and diabetic parameters. Research in Veterinary Science, 2014, 96, 241-250.	0.9	75
323	A large column analog experiment of stable isotope variations during reactive transport: II. Carbon mass balance, microbial community structure and predation. Geochimica Et Cosmochimica Acta, 2014, 124, 394-409.	1.6	17
324	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. ISME Journal, 2014, 8, 1989-2001.	4.4	221
325	Is bacterial moisture niche a good predictor of shifts in community composition under longâ€term drought?. Ecology, 2014, 95, 110-122.	1.5	97
326	Effects of light and prey availability on Arctic freshwater protist communities examined by high-throughput DNA and RNA sequencing. FEMS Microbiology Ecology, 2014, 88, 550-564.	1.3	62
327	Soil properties and tree species drive ÃŸ-diversity of soil bacterial communities. Soil Biology and Biochemistry, 2014, 76, 201-209.	4.2	92
328	Diversity and distribution of eukaryotic microbes in and around a brine pool adjacent to the Thuwal cold seeps in the Red Sea. Frontiers in Microbiology, 2014, 5, 37.	1.5	30
329	Nitrogen cycling processes and microbial community composition in bed sediments in the Yukon River at Pilot Station. Journal of Geophysical Research G: Biogeosciences, 2014, 119, 2328-2344.	1.3	42
330	Time-Resolved DNA Stable Isotope Probing Links <i>Desulfobacterales</i>- and <i>Coriobacteriaceae</i>-Related Bacteria to Anaerobic Degradation of Benzene under Methanogenic Conditions. Microbes and Environments, 2014, 29, 191-199.	0.7	40
331	High-Throughput Sequencing Characterizes Intertidal Meiofaunal Communities in Northern Gulf of Mexico (Dauphin Island and Mobile Bay, Alabama). Biological Bulletin, 2014, 227, 161-174.	0.7	32

#	ARTICLE	IF	CITATIONS
332	EXHAUSTIVE GENETIC ANALYSIS FOR <i>NOROVIRUS</i> GII ACCUMULATED IN CULTURED OYSTES BY USING PYROSEQUENCING. Journal of Japan Society of Civil Engineers Ser G (Environmental Research), 2014, 70, III_305-III_311.	0.1	0
333	The dynamics of biofilm bacterial communities is driven by flow wax and wane in a temporary stream. Limnology and Oceanography, 2014, 59, 2057-2067.	1.6	30
334	Characterization and quantification of the fungal microbiome in serial samples from individuals with cystic fibrosis. Microbiome, 2014, 2, 40.	4.9	128
335	Bacterial symbiont sharing in <i><scp>M</scp>egalomyrmex</i> social parasites and their fungusâ€growing ant hosts. Molecular Ecology, 2015, 24, 3151-3169.	2.0	43
336	Vancomycin treatment and butyrate supplementation modulate gut microbe composition and severity of neointimal hyperplasia after arterial injury. Physiological Reports, 2015, 3, e12627.	0.7	22
337	Archaeal enrichment in the hypoxic zone in the northern <scp>G</scp>ulf of <scp>M</scp>exico. Environmental Microbiology, 2015, 17, 3847-3856.	1.8	51
338	Dynamics of marine bacterial community diversity of the coastal waters of the reefs, inlets, and wastewater outfalls of southeast <scp>F</scp>lorida. MicrobiologyOpen, 2015, 4, 390-408.	1.2	81
339	Microbial ecology and geoelectric responses across a groundwater plume. Interpretation, 2015, 3, SAB9-SAB21.	0.5	3
340	The nasopharyngeal microbiota of feedlot cattle. Scientific Reports, 2015, 5, 15557.	1.6	64
341	Habitat fragmentation is associated to gut microbiota diversity of an endangered primate: implications for conservation. Scientific Reports, 2015, 5, 14862.	1.6	170
342	Transgenic banana plants expressing Xanthomonas wilt resistance genes revealed a stable non-target bacterial colonization structure. Scientific Reports, 2015, 5, 18078.	1.6	31
343	Insights into the distribution and abundance of the ubiquitous Candidatus Saccharibacteria phylum following tag pyrosequencing. Scientific Reports, 2014, 4, 3957.	1.6	66
344	Annual periodicity in planktonic bacterial and archaeal community composition of eutrophic Lake Taihu. Scientific Reports, 2015, 5, 15488.	1.6	74
345	Increased diversity of egg-associated bacteria on brown trout (Salmo trutta) at elevated temperatures. Scientific Reports, 2015, 5, 17084.	1.6	29
346	Bacterial diversity is strongly associated with historical penguin activity in an Antarctic lake sediment profile. Scientific Reports, 2015, 5, 17231.	1.6	23
347	MICCA: a complete and accurate software for taxonomic profiling of metagenomic data. Scientific Reports, 2015, 5, 9743.	1.6	228
348	Microbial Community Analysis Using High-Throughput Amplicon Sequencing. , 2015, , 2.4.2-1-2.4.2-26.		4
349	454 pyrosequencing-based characterization of the bacterial consortia in a well established nitrifying reactor. Water Science and Technology, 2015, 72, 990-997.	1.2	33

#	Article	IF	Citations
350	Characterising the bacterial microbiota across the gastrointestinal tracts of dairy cattle: membership and potential function. Scientific Reports, 2015, 5, 16116.	1.6	495
351	In situ environment rather than substrate type dictates microbial community structure of biofilms in a cold seep system. Scientific Reports, 2014, 4, 3587.	1.6	49
352	Distinct composition of the oral indigenous microbiota in South Korean and Japanese adults. Scientific Reports, 2014, 4, 6990.	1.6	58
353	In vitro characterisation of the fermentation profile and prebiotic capacity of gold-fleshed kiwifruit. Beneficial Microbes, 2015, 6, 829-839.	1.0	10
354	Species sorting during biofilm assembly by artificial substrates deployed in a cold seep system. Scientific Reports, 2015, 4, 6647.	1.6	43
355	Evidence of bacterioplankton community adaptation in response to long-term mariculture disturbance. Scientific Reports, 2015, 5, 15274.	1.6	45
356	Modulation of gut microbiota in rats fed highâ€fat diets by processing wholeâ€grain barley to barley malt. Molecular Nutrition and Food Research, 2015, 59, 2066-2076.	1.5	181
357	Maternal fucosyltransferase 2 status affects the gut bifidobacterial communities of breastfed infants. Microbiome, 2015, 3, 13.	4.9	319
358	An accurate and efficient experimental approach for characterization of the complex oral microbiota. Microbiome, 2015, 3, 48.	4.9	95
359	Chemostat culture systems support diverse bacteriophage communities from human feces. Microbiome, 2015, 3, 58.	4.9	50
360	Relative and contextual contribution of different sources to the composition and abundance of indoor air bacteria in residences. Microbiome, 2015, 3, 61.	4.9	84
361	Resistivity and induced polarization monitoring of biogas combined with microbial ecology at a brownfield site. Interpretation, 2015, 3, SAB43-SAB56.	0.5	4
362	Characterisation of the faecal metabolome and microbiome of Thoroughbred racehorses. Equine Veterinary Journal, 2015, 47, 580-586.	0.9	51
363	Microbial diversity in shallowâ€water hydrothermal sediments of Kueishan Island, Taiwan as revealed by pyrosequencing. Journal of Basic Microbiology, 2015, 55, 1308-1318.	1.8	34
364	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
365	Microbial ecosystems are dominated by specialist taxa. Ecology Letters, 2015, 18, 974-982.	3.0	74
366	Metagenomic Analysis of CrohnÊ¼s Disease Patients Identifies Changes in the Virome and Microbiome Related to Disease Status and Therapy, and Detects Potential Interactions and Biomarkers. Inflammatory Bowel Diseases, 2015, 21, 2515-2532.	0.9	79
367	The Role of Curcumin in Modulating Colonic Microbiota During Colitis and Colon Cancer Prevention. Inflammatory Bowel Diseases, 2015, 21, 2483-2494.	0.9	166

#	Article	IF	Citations
368	Bacterial biogeography in the coastal waters of northern <scp>Z</scp>hejiang, <scp>E</scp>ast <scp>C</scp>hina <scp>S</scp>ea is highly controlled by spatially structured environmental gradients. Environmental Microbiology, 2015, 17, 3898-3913.	1.8	93
369	Enhanced salinities, as a proxy of seawater desalination discharges, impact coastal microbial communities of the eastern <scp>M</scp>editerranean <scp>S</scp>ea. Environmental Microbiology, 2015, 17, 4105-4120.	1.8	33
370	Archaeal Communities in a Heterogeneous Hypersaline-Alkaline Soil. Archaea, 2015, 2015, 1-11.	2.3	24
371	Intestinal Microbial Dysbiosis and Colonic Epithelial Cell Hyperproliferation by Dietary Î±-Mangostin is Independent of Mouse Strain. Nutrients, 2015, 7, 764-784.	1.7	19
372	Methane and microbial dynamics in the Gulf of Mexico water column. Frontiers in Marine Science, 2015, 2, .	1.2	25
373	Microbial responses to changes in flow status in temporary headwater streams: a cross-system comparison. Frontiers in Microbiology, 2015, 6, 522.	1.5	41
374	Microbial community changes along the active seepage site of one cold seep in the Red Sea. Frontiers in Microbiology, 2015, 6, 739.	1.5	12
375	Associative patterns among anaerobic fungi, methanogenic archaea, and bacterial communities in response to changes in diet and age in the rumen of dairy cows. Frontiers in Microbiology, 2015, 6, 781.	1.5	112
376	Insights into the bacterial community and its temporal succession during the fermentation of wine grapes. Frontiers in Microbiology, 2015, 6, 809.	1.5	69
377	Soil bacterial and fungal community responses to nitrogen addition across soil depth and microhabitat in an arid shrubland. Frontiers in Microbiology, 2015, 6, 891.	1.5	127
378	The diversity of the N2O reducers matters for the N2O:N2 denitrification end-product ratio across an annual and a perennial cropping system. Frontiers in Microbiology, 2015, 6, 971.	1.5	114
379	Bacterial endophyte communities in the foliage of coast redwood and giant sequoia. Frontiers in Microbiology, 2015, 6, 1008.	1.5	49
380	An abundance of Epsilonproteobacteria revealed in the gut microbiome of the laboratory cultured sea urchin, Lytechinus variegatus. Frontiers in Microbiology, 2015, 6, 1047.	1.5	82
381	Rumen microbial communities influence metabolic phenotypes in lambs. Frontiers in Microbiology, 2015, 6, 1060.	1.5	98
382	The effect of diet and host genotype on ceca microbiota of Japanese quail fed a cholesterol enriched diet. Frontiers in Microbiology, 2015, 6, 1092.	1.5	20
383	Effects of sludge inoculum and organic feedstock on active microbial communities and methane yield during anaerobic digestion. Frontiers in Microbiology, 2015, 6, 1114.	1.5	40
384	Pyrosequencing of the bacteria associated with Platygyra carnosus corals with skeletal growth anomalies reveals differences in bacterial community composition in apparently healthy and diseased tissues. Frontiers in Microbiology, 2015, 6, 1142.	1.5	35
385	Responses of soil microeukaryotic communities to short-term fumigation-incubation revealed by MiSeq amplicon sequencing. Frontiers in Microbiology, 2015, 6, 1149.	1.5	23

#	ARTICLE	IF	CITATIONS
386	Panamanian frog species host unique skin bacterial communities. Frontiers in Microbiology, 2015, 6, 1171.	1.5	144
387	Resistance of Undisturbed Soil Microbiomes to Ceftriaxone Indicates Extended Spectrum Î²-Lactamase Activity. Frontiers in Microbiology, 2015, 6, 1233.	1.5	14
388	Comparative Gut Microbiota of 59 Neotropical Bird Species. Frontiers in Microbiology, 2015, 6, 1403.	1.5	216
389	High-Up: A Remote Reservoir of Microbial Extremophiles in Central Andean Wetlands. Frontiers in Microbiology, 2015, 6, 1404.	1.5	80
390	Pyrosequencing Reveals a Core Community of Anodic Bacterial Biofilms in Bioelectrochemical Systems from China. Frontiers in Microbiology, 2015, 6, 1410.	1.5	40
391	Bacterial Composition and Survival on Sahara Dust Particles Transported to the European Alps. Frontiers in Microbiology, 2015, 6, 1454.	1.5	77
392	Microbial Community Analysis of Anaerobic Reactors Treating Soft Drink Wastewater. PLoS ONE, 2015, 10, e0119131.	1.1	27
393	The Unique Chemistry of Eastern Mediterranean Water Masses Selects for Distinct Microbial Communities by Depth. PLoS ONE, 2015, 10, e0120605.	1.1	65
394	The Gut Microbiota Composition in Dichorionic Triplet Sets Suggests a Role for Host Genetic Factors. PLoS ONE, 2015, 10, e0122561.	1.1	35
395	Cultivation-Based and Molecular Assessment of Bacterial Diversity in the Rhizosheath of Wheat under Different Crop Rotations. PLoS ONE, 2015, 10, e0130030.	1.1	47
396	Bioinformatic Amplicon Read Processing Strategies Strongly Affect Eukaryotic Diversity and the Taxonomic Composition of Communities. PLoS ONE, 2015, 10, e0130035.	1.1	67
397	Litter Breakdown and Microbial Succession on Two Submerged Leaf Species in a Small Forested Stream. PLoS ONE, 2015, 10, e0130801.	1.1	21
398	Deep Characterization of the Microbiomes of Calophya spp. (Hemiptera: Calophyidae) Gall-Inducing Psyllids Reveals the Absence of Plant Pathogenic Bacteria and Three Dominant Endosymbionts. PLoS ONE, 2015, 10, e0132248.	1.1	22
399	Rescue of Fructose-Induced Metabolic Syndrome by Antibiotics or Faecal Transplantation in a Rat Model of Obesity. PLoS ONE, 2015, 10, e0134893.	1.1	135
400	A Pyrosequencing Investigation of Differences in the Feline Subgingival Microbiota in Health, Gingivitis and Mild Periodontitis. PLoS ONE, 2015, 10, e0136986.	1.1	41
401	Community Structure and Function of Amphibian Skin Microbes: An Experiment with Bullfrogs Exposed to a Chytrid Fungus. PLoS ONE, 2015, 10, e0139848.	1.1	120
402	Flea-Associated Bacterial Communities across an Environmental Transect in a Plague-Endemic Region of Uganda. PLoS ONE, 2015, 10, e0141057.	1.1	16
403	Lactobacillus casei Shirota Supplementation Does Not Restore Gut Microbiota Composition and Gut Barrier in Metabolic Syndrome: A Randomized Pilot Study. PLoS ONE, 2015, 10, e0141399.	1.1	45

#	Article	IF	Citations
404	The Influence of Age and Gender on Skin-Associated Microbial Communities in Urban and Rural Human Populations. PLoS ONE, 2015, 10, e0141842.	1.1	181
405	Antepartum Antibiotic Treatment Increases Offspring Susceptibility to Experimental Colitis: A Role of the Gut Microbiota. PLoS ONE, 2015, 10, e0142536.	1.1	137
406	Evaluating DNA Extraction Methods for Community Profiling of Pig Hindgut Microbial Community. PLoS ONE, 2015, 10, e0142720.	1.1	8
407	Oral Microbiota and Risk for Esophageal Squamous Cell Carcinoma in a High-Risk Area of China. PLoS ONE, 2015, 10, e0143603.	1.1	146
408	Spatial Homogeneity of Bacterial Communities Associated with the Surface Mucus Layer of the Reef-Building Coral Acropora palmata. PLoS ONE, 2015, 10, e0143790.	1.1	20
409	Spatial Patterns in Biofilm Diversity across Hierarchical Levels of River-Floodplain Landscapes. PLoS ONE, 2015, 10, e0144303.	1.1	9
410	Comparative Analysis of Prokaryotic Communities Associated with Organic and Conventional Farming Systems. PLoS ONE, 2015, 10, e0145072.	1.1	83
411	Mapping microbial ecosystems and spoilage-gene flow in breweries highlights patterns of contamination and resistance. ELife, 2015, 4, .	2.8	71
412	The effect of copper sulfate addition on the performance of an anaerobic digester treating dairy manure. , 2015, , .		0
413	The effect of polydextrose and probiotic lactobacilli in a<i>Clostridium difficileâ€“</i>infected human colonic model. Microbial Ecology in Health and Disease, 2015, 26, 27988.	3.8	16
414	Antibiotic Resistome and Its Association with Bacterial Communities during Sewage Sludge Composting. Environmental Science & Technology, 2015, 49, 7356-7363.	4.6	736
415	Monitoring the dynamics of syntrophic Î²-oxidizing bacteria during anaerobic degradation of oleic acid by quantitative PCR. FEMS Microbiology Ecology, 2015, 91, .	1.3	41
416	Temperature sensitivity of soil bacterial community along contrasting warming gradient. Applied Soil Ecology, 2015, 94, 40-48.	2.1	77
417	Microbial biogeography of the transnational fermented milk matsoni. Food Microbiology, 2015, 50, 12-19.	2.1	47
418	Baiting of rhizosphere bacteria with hyphae of common soil fungi reveals a diverse group of potentially mycophagous secondary consumers. Soil Biology and Biochemistry, 2015, 88, 73-82.	4.2	58
419	Bacterial diversity in soils subjected to long-term chemical fertilization can be more stably maintained with the addition of livestock manure than wheat straw. Soil Biology and Biochemistry, 2015, 88, 9-18.	4.2	560
420	The Bamboo-Eating Giant Panda Harbors a Carnivore-Like Gut Microbiota, with Excessive Seasonal Variations. MBio, 2015, 6, e00022-15.	1.8	282
421	Early colonizers of unoccupied habitats represent a minority of the soil bacterial community. FEMS Microbiology Ecology, 2015, 91, .	1.3	11

#	ARTICLE	IF	CITATIONS
422	Shifts in Bacterial Communities of Eggshells and Antimicrobial Activities in Eggs during Incubation in a Ground-Nesting Passerine. PLoS ONE, 2015, 10, e0121716.	1.1	23
423	Analysis of Bacterial Diversity During Acetic Acid Fermentation of Tianjin Duliu Aged Vinegar by 454 Pyrosequencing. Current Microbiology, 2015, 71, 195-203.	1.0	25
424	Meiofaunal community analysis by high-throughput sequencing: Comparison of extraction, quality filtering, and clustering methods. Marine Genomics, 2015, 23, 67-75.	0.4	72
425	Evolutionary transition in symbiotic syndromes enabled diversification of phytophagous insects on an imbalanced diet. ISME Journal, 2015, 9, 2587-2604.	4.4	63
426	Bovine Colostrum Modulates Myeloablative Chemotherapyâ€“Induced Gut Toxicity in Piglets. Journal of Nutrition, 2015, 145, 1472-1480.	1.3	20
427	Microbial degradation of isosaccharinic acid at high pH. ISME Journal, 2015, 9, 310-320.	4.4	52
428	Application of a Bayesian nonparametric model to derive toxicity estimates based on the response of Antarctic microbial communities to fuelâ€contaminated soil. Ecology and Evolution, 2015, 5, 2633-2645.	0.8	9
429	Characterization of microbial community structure during continuous anaerobic digestion of straw and cow manure. Microbial Biotechnology, 2015, 8, 815-827.	2.0	197
430	A new fungal large subunit ribosomal RNA primer for high throughput sequencing surveys. FEMS Microbiology Ecology, 2016, 92, fiv153.	1.3	30
431	Rhythmicity of the intestinal microbiota is regulated by gender and the host circadian clock. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10479-10484.	3.3	410
432	Gravidas with class III obesity: evaluating the abdominal skin microbiota above and below the panniculus. Journal of Maternal-Fetal and Neonatal Medicine, 2016, 29, 1-5.	0.7	3
433	Metagenome Sequencing Reveals <i>Rhodococcus</i> Dominance in Farpuk Cave, Mizoram, India, an Eastern Himalayan Biodiversity Hot Spot Region. Genome Announcements, 2015, 3, .	0.8	19
434	Risperidone-induced weight gain is mediated through shifts in the gut microbiome and suppression of energy expenditure. EBioMedicine, 2015, 2, 1725-1734.	2.7	116
435	Interactions between multiple helminths and the gut microbiota in wild rodents. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140295.	1.8	139
436	Microbial biogeography of a university campus. Microbiome, 2015, 3, 66.	4.9	28
437	Novel Mass Bio System (MBS) and its potential application in advanced treatment of coal gasification wastewater. RSC Advances, 2015, 5, 88692-88702.	1.7	25
438	Gut microbiome composition is associated with temperament during early childhood. Brain, Behavior, and Immunity, 2015, 45, 118-127.	2.0	148
439	Initial community and environment determine the response of bacterial communities to dispersant and oil contamination. Marine Pollution Bulletin, 2015, 90, 106-114.	2.3	22

#	ARTICLE	IF	CITATIONS
440	Seasonal Community Succession of the Phyllosphere Microbiome. Molecular Plant-Microbe Interactions, 2015, 28, 274-285.	1.4	275
441	Gut microbial markers are associated with diabetes onset, regulatory imbalance, and IFN-Î³ level in NOD Mice. Gut Microbes, 2015, 6, 101-109.	4.3	122
442	Bacterial community structure in maize residue amended soil with contrasting management practices. Applied Soil Ecology, 2015, 90, 49-59.	2.1	83
443	Gut microbial and short-chain fatty acid profiles in adults with chronic constipation before and after treatment with lubiprostone. Anaerobe, 2015, 33, 33-41.	1.0	49
444	The nexus of syntrophyâ€associated microbiota in anaerobic digestion revealed by longâ€term enrichment and community survey. Environmental Microbiology, 2015, 17, 1707-1720.	1.8	149
445	Dental plaque development on a hydroxyapatite disk in young adults observed by using a barcoded pyrosequencing approach. Scientific Reports, 2015, 5, 8136.	1.6	52
446	Bacterial Community Structure of Autotrophic Denitrification Biocathode by 454 Pyrosequencing of the 16S rRNA Gene. Microbial Ecology, 2015, 69, 492-499.	1.4	83
447	Bacterial community shift in the coastal Gulf of Mexico salt-marsh sediment microcosm in vitro following exposure to the Mississippi Canyon Block 252 oil (MC252). 3 Biotech, 2015, 5, 379-392.	1.1	40
448	The composition of the gut microbiota shapes the colon mucus barrier. EMBO Reports, 2015, 16, 164-177.	2.0	519
449	Ammonia-oxidizing archaea respond positively to inorganic nitrogen addition in desert soils. FEMS Microbiology Ecology, 2015, 91, 1-11.	1.3	17
450	Depth shapes Î±â€•and Î²â€diversities of microbial eukaryotes in surficial sediments of coastal ecosystems. Environmental Microbiology, 2015, 17, 3722-3737.	1.8	98
451	Inferred metagenomic comparison of mucosal and fecal microbiota from individuals undergoing routine screening colonoscopy reveals similar differences observed during active inflammation. Gut Microbes, 2015, 6, 48-56.	4.3	55
452	Metagenomic Insights into the Effects of Fructo-oligosaccharides (FOS) on the Composition of Fecal Microbiota in Mice. Journal of Agricultural and Food Chemistry, 2015, 63, 856-863.	2.4	90
453	Temporal Stability of the Microbial Community in Sewage-Polluted Seawater Exposed to Natural Sunlight Cycles and Marine Microbiota. Applied and Environmental Microbiology, 2015, 81, 2107-2116.	1.4	25
454	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. Bioinformatics, 2015, 31, 1607-1613.	1.8	12
455	Hydrogen export from intertidal cyanobacterial mats: sources, fluxes and the influence of community composition. Environmental Microbiology, 2015, 17, 3738-3753.	1.8	20
456	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. Plant and Soil, 2015, 388, 175-186.	1.8	47
457	Intraindividual variation in core microbiota in peri-implantitis and periodontitis. Scientific Reports, 2014, 4, 6602.	1.6	139

#	ARTICLE	IF	CITATIONS
458	Effects of Light and Autochthonous Carbon Additions on Microbial Turnover of Allochthonous Organic Carbon and Community Composition. Microbial Ecology, 2015, 69, 361-371.	1.4	17
459	Soil pH determines the alpha diversity but not beta diversity of soil fungal community along altitude in a typical Tibetan forest ecosystem. Journal of Soils and Sediments, 2015, 15, 1224-1232.	1.5	112
460	Microbial Community Composition and Ultrastructure of Granules from a Full-Scale Anammox Reactor. Microbial Ecology, 2015, 70, 118-131.	1.4	115
461	Diversity and dynamics of dominant and rare bacterial taxa in replicate sequencing batch reactors operated under different solids retention time. Applied Microbiology and Biotechnology, 2015, 99, 2361-2370.	1.7	16
462	Long-term nickel exposure altered the bacterial community composition but not diversity in two contrasting agricultural soils. Environmental Science and Pollution Research, 2015, 22, 10496-10505.	2.7	24
463	Electron donors and co-contaminants affect microbial community composition and activity in perchlorate degradation. Environmental Science and Pollution Research, 2015, 22, 6057-6067.	2.7	20
464	The shared microbiota of humans and companion animals as evaluated from Staphylococcus carriage sites. Microbiome, 2015, 3, 2.	4.9	95
465	Larval exposure to polychlorinated biphenyl 126 (PCBâ€126) causes persistent alteration of the amphibian gut microbiota. Environmental Toxicology and Chemistry, 2015, 34, 1113-1118.	2.2	42
466	Field-based evidence for consistent responses of bacterial communities to copper contamination in two contrasting agricultural soils. Frontiers in Microbiology, 2015, 6, 31.	1.5	47
467	Agroforestry leads to shifts within the gammaproteobacterial microbiome of banana plants cultivated in Central America. Frontiers in Microbiology, 2015, 6, 91.	1.5	40
468	Stable microbial community composition on the Greenland Ice Sheet. Frontiers in Microbiology, 2015, 6, 193.	1.5	56
469	Polar front associated variation in prokaryotic community structure in Arctic shelf seafloor. Frontiers in Microbiology, 2015, 6, 17.	1.5	34
470	Oligotyping reveals stronger relationship of organic soil bacterial community structure with N-amendments and soil chemistry in comparison to that of mineral soil at Harvard Forest, MA, USA. Frontiers in Microbiology, 2015, 6, 49.	1.5	6
471	Evident bacterial community changes but only slight degradation when polluted with pyrene in a red soil. Frontiers in Microbiology, 2015, 6, 22.	1.5	85
472	Successive bioanode regenerations to maintain efficient current production from biowaste. Bioelectrochemistry, 2015, 106, 133-140.	2.4	20
473	Kiwifruit fermentation drives positive gut microbial and metabolic changes irrespective of initial microbiota composition. Bioactive Carbohydrates and Dietary Fibre, 2015, 6, 37-45.	1.5	18
474	Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. Nature Communications, 2015, 6, 7618.	5.8	361
475	Seagrass (Zostera marina) Colonization Promotes the Accumulation of Diazotrophic Bacteria and Alters the Relative Abundances of Specific Bacterial Lineages Involved in Benthic Carbon and Sulfur Cycling. Applied and Environmental Microbiology, 2015, 81, 6901-6914.	1.4	87

#	ARTICLE	IF	CITATIONS
476	Characterization of <i>para</i> -Nitrophenol-Degrading Bacterial Communities in River Water by Using Functional Markers and Stable Isotope Probing. Applied and Environmental Microbiology, 2015, 81, 6890-6900.	1.4	33
477	Dominance of rumen microorganisms during cheese whey acidification: acidogenesis can be governed by a rare Selenomonas lacticifex-type fermentation. Applied Microbiology and Biotechnology, 2015, 99, 9309-9318.	1.7	8
478	Bacterial Community Profiling of Plastic Litter in the Belgian Part of the North Sea. Environmental Science & Technology, 2015, 49, 9629-9638.	4.6	320
479	Most of the Dominant Members of Amphibian Skin Bacterial Communities Can Be Readily Cultured. Applied and Environmental Microbiology, 2015, 81, 6589-6600.	1.4	58
480	Effect of headspace carbon dioxide sequestration on microbial biohydrogen communities. International Journal of Hydrogen Energy, 2015, 40, 9966-9976.	3.8	18
481	Validating the use of trap-collected feces for studying the gut microbiota of a small mammal (<i>Neotoma lepida</i>). Journal of Mammalogy, 2015, 96, 90-93.	0.6	20
482	Microbial community composition and diversity in Caspian Sea sediments. FEMS Microbiology Ecology, 2015, 91, 1-11.	1.3	70
483	Modulation of the intestinal microbiota and morphology of tilapia, Oreochromis niloticus, following the application of a multi-species probiotic. Applied Microbiology and Biotechnology, 2015, 99, 8403-8417.	1.7	131
484	Lactobacillus rhamnosus lowers zebrafish lipid content by changing gut microbiota and host transcription of genes involved in lipid metabolism. Scientific Reports, 2015, 5, 9336.	1.6	194
485	Pyrosequencing revealed highly microbial phylogenetic diversity in ferromanganese nodules from farmland. Environmental Sciences: Processes and Impacts, 2015, 17, 213-224.	1.7	6
486	Marine sediments microbes capable of electrode oxidation as a surrogate for lithotrophic insoluble substrate metabolism. Frontiers in Microbiology, 2014, 5, 784.	1.5	86
487	Fine-scale analysis of 16S rRNA sequences reveals a high level of taxonomic diversity among vaginal Atopobium spp.. Pathogens and Disease, 2015, 73, .	0.8	16
488	Operational, design and microbial aspects related to power production with microbial fuel cells implemented in constructed wetlands. Water Research, 2015, 84, 232-242.	5.3	126
489	Insights into the pan-microbiome: skin microbial communities of Chinese individuals differ from other racial groups. Scientific Reports, 2015, 5, 11845.	1.6	112
490	Changing composition of microbial communities indicates seepage fluid difference of the Thuwal Seeps in the Red Sea. Antonie Van Leeuwenhoek, 2015, 108, 461-471.	0.7	2
491	Time-dependent effect of graphene on the structure, abundance, and function of the soil bacterial community. Journal of Hazardous Materials, 2015, 297, 286-294.	6.5	85
492	Out of the dark: transitional subsurface-to-surface microbial diversity in a terrestrial serpentinizing seep (Manleluag, Pangasinan, the Philippines). Frontiers in Microbiology, 2015, 6, 44.	1.5	79
493	The human urine virome in association with urinary tract infections. Frontiers in Microbiology, 2015, 6, 14.	1.5	173

#	ARTICLE	IF	CITATIONS
494	Effect of polybrominated diphenyl ether (PBDE) treatment on the composition and function of the bacterial community in the sponge Haliclona cymaeformis. Frontiers in Microbiology, 2014, 5, 799.	1.5	9
495	Structure, mineralogy, and microbial diversity of geothermal spring microbialites associated with a deep oil drilling in Romania. Frontiers in Microbiology, 2015, 6, 253.	1.5	24
496	Explaining Diversity in Metagenomic Datasets by Phylogenetic-Based Feature Weighting. PLoS Computational Biology, 2015, 11, e1004186.	1.5	24
497	Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. MBio, 2015, 6, .	1.8	126
498	Consistent increase in abundance and diversity but variable change in community composition of bacteria in topsoil of rice paddy under short term biochar treatment across three sites from South China. Applied Soil Ecology, 2015, 91, 68-79.	2.1	133
499	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. ISME Journal, 2015, 9, 2642-2656.	4.4	82
500	Grazing intensity in subarctic tundra affects the temperature adaptation of soil microbial communities. Soil Biology and Biochemistry, 2015, 84, 147-157.	4.2	51
501	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
502	Mesophilic versus thermophilic anaerobic digestion of cattle manure: methane productivity and microbial ecology. Microbial Biotechnology, 2015, 8, 787-800.	2.0	141
503	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
504	The Gut Microbiota of Workers of the Litter-Feeding Termite Syntermes wheeleri (Termitidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	1.4	26
505	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
506	Detection and analysis of elusive members of a novel and diverse archaeal community within a thermal spring streamer consortium. Extremophiles, 2015, 19, 307-313.	0.9	26
507	Dynamics of extracellular DNA decomposition and bacterial community composition in soil. Soil Biology and Biochemistry, 2015, 86, 42-49.	4.2	69
508	High-throughput sequencing for the detection of the bacterial and fungal diversity in Mongolian naturally fermented cowâ€™s milk in Russia. BMC Microbiology, 2015, 15, 45.	1.3	67
509	Bacterial diversity and Clostridia abundance decrease with increasing severity of necrotizing enterocolitis. Microbiome, 2015, 3, 11.	4.9	107
510	Xylo-oligosaccharides and virginiamycin differentially modulate gut microbial composition in chickens. Microbiome, 2015, 3, 15.	4.9	127
511	Comparison of synthetic medium and wastewater used as dilution medium to design scalable microbial anodes: Application to food waste treatment. Bioresource Technology, 2015, 185, 106-115.	4.8	51

#	ARTICLE	IF	CITATIONS
512	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
513	16S Classifier: A Tool for Fast and Accurate Taxonomic Classification of 16S rRNA Hypervariable Regions in Metagenomic Datasets. PLoS ONE, 2015, 10, e0116106.	1.1	71
514	Changes in intestinal bacterial communities are closely associated with shrimp disease severity. Applied Microbiology and Biotechnology, 2015, 99, 6911-6919.	1.7	221
515	Phylogenetic structure of soil bacterial communities predicts ecosystem functioning. FEMS Microbiology Ecology, 2015, 91, .	1.3	47
516	Resistant starch diet induces change in the swine microbiome and a predominance of beneficial bacterial populations. Microbiome, 2015, 3, 16.	4.9	132
517	Mongolians core gut microbiota and its correlation with seasonal dietary changes. Scientific Reports, 2014, 4, 5001.	1.6	126
518	Nitric Oxide Treatment for the Control of Reverse Osmosis Membrane Biofouling. Applied and Environmental Microbiology, 2015, 81, 2515-2524.	1.4	45
519	Impact of metagenomic DNA extraction procedures on the identifiable endophytic bacterial diversity in Sorghum bicolor (L. Moench). Journal of Microbiological Methods, 2015, 112, 104-117.	0.7	71
520	Parent Material and Vegetation Influence Soil Microbial Community Structure Following 30-Years of Rock Weathering and Pedogenesis. Microbial Ecology, 2015, 69, 383-394.	1.4	36
521	Rapid recovery of soil bacterial communities after wildfire in a Chinese boreal forest. Scientific Reports, 2014, 4, 3829.	1.6	121
522	Two decades of warming increases diversity of a potentially lignolytic bacterial community. Frontiers in Microbiology, 2015, 6, 480.	1.5	73
523	Selection in the host structures the microbiota associated with developing cod larvae (<scp><i>G</i></scp><i>adus morhua</i>). Environmental Microbiology, 2015, 17, 3914-3924.	1.8	100
524	The geomicrobiology of CO2 geosequestration: a focused review on prokaryotic community responses to field-scale CO2 injection. Frontiers in Microbiology, 2015, 6, 263.	1.5	17
525	Temporal and spatial constraints on community assembly during microbial colonization of wood in seawater. ISME Journal, 2015, 9, 2657-2670.	4.4	35
526	The Soil Microbiome Influences Grapevine-Associated Microbiota. MBio, 2015, 6, .	1.8	747
527	Effect of preservation method on spider monkey (Ateles geoffroyi) fecal microbiota over 8weeks. Journal of Microbiological Methods, 2015, 113, 16-26.	0.7	118
528	Declining diversity of egg-associated bacteria during development of naturally spawned whitefish embryos (Coregonus spp.). Aquatic Sciences, 2015, 77, 481-497.	0.6	17
529	16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. Applied Microbiology and Biotechnology, 2015, 99, 4119-4129.	1.7	79

#	Article	IF	Citations
530	Bacterial diversity of polluted surface sediments in the northern Adriatic Sea. Systematic and Applied Microbiology, 2015, 38, 189-197.	1.2	45
531	Localâ€"global overlap in diversity informs mechanisms of bacterial biogeography. ISME Journal, 2015, 9, 2413-2422.	4.4	23
532	Physicochemical control of bacterial and protist community composition and diversity in <scp>A</scp>ntarctic sea ice. Environmental Microbiology, 2015, 17, 3869-3881.	1.8	48
533	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
534	Binary combination of epsilon-poly-l-lysine and isoeugenol affect progression of spoilage microbiota in fresh turkey meat, and delay onset of spoilage in Pseudomonas putida challenged meat. International Journal of Food Microbiology, 2015, 215, 131-142.	2.1	22
535	Cilantro microbiome before and after nonselective pre-enrichment for Salmonella using 16S rRNA and metagenomic sequencing. BMC Microbiology, 2015, 15, 160.	1.3	53
536	Nitrogen recovery from pig slurry in a two-chambered bioelectrochemical system. Bioresource Technology, 2015, 194, 373-382.	4.8	62
537	Host genetic variation impacts microbiome composition across human body sites. Genome Biology, 2015, 16, 191.	3.8	612
538	Baleen whales host a unique gut microbiome with similarities to both carnivores and herbivores. Nature Communications, 2015, 6, 8285.	5.8	184
539	Seasonal patterns of bacterial communities in the coastal brackish sediments of the Gulf of Finland, Baltic Sea. Estuarine, Coastal and Shelf Science, 2015, 165, 86-96.	0.9	22
540	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
541	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
542	Commensal <i>Bifidobacterium</i> promotes antitumor immunity and facilitates antiâ€"PD-L1 efficacy. Science, 2015, 350, 1084-1089.	6.0	2,782
543	Athletic equipment microbiota are shaped by interactions with human skin. Microbiome, 2015, 3, 25.	4.9	36
544	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. Scientific Reports, 2015, 5, 9156.	1.6	52
545	Determinism of bacterial metacommunity dynamics in the southern East China Sea varies depending on hydrography. Ecography, 2015, 38, 198-212.	2.1	61
546	Meat Processing Plant Microbiome and Contamination Patterns of Cold-Tolerant Bacteria Causing Food Safety and Spoilage Risks in the Manufacture of Vacuum-Packaged Cooked Sausages. Applied and Environmental Microbiology, 2015, 81, 7088-7097.	1.4	111
547	Silencing a key gene of the common symbiosis pathway in <scp><i>N</i></scp><i>icotiana attenuata</i> specifically impairs arbuscular mycorrhizal infection without influencing the rootâ€associated microbiome or plant growth. Plant, Cell and Environment, 2015, 38, 2398-2416.	2.8	33

#	ARTICLE	IF	CITATIONS
548	Declined soil suppressiveness to Fusarium oxysporum by rhizosphere microflora of cotton in soil sickness. Biology and Fertility of Soils, 2015, 51, 935-946.	2.3	58
549	Phylogenetic approaches to microbial community classification. Microbiome, 2015, 3, 47.	4.9	39
550	Biostimulation of biogas producing microcosm for enhancing oil recovery in low-permeability oil reservoir. RSC Advances, 2015, 5, 91869-91877.	1.7	8
551	Oral and faecal microbiota in volunteers with hypertension in a double blind, randomised placebo controlled trial with probiotics and fermented bilberries. Journal of Functional Foods, 2015, 18, 275-288.	1.6	10
552	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. Applied and Environmental Microbiology, 2015, 81, 6200-6209.	1.4	167
553	Gut Microbial Dysbiosis Due toHelicobacterDrives an Increase in Marginal Zone B Cells in the Absence of IL-10 Signaling in Macrophages. Journal of Immunology, 2015, 195, 3071-3085.	0.4	21
554	Interactions between Gut Microbiota, Host Genetics and Diet Modulate the Predisposition to Obesity and Metabolic Syndrome. Cell Metabolism, 2015, 22, 516-530.	7.2	433
555	Response of the rumen archaeal and bacterial populations to anti-methanogenic organosulphur compounds in continuous-culture fermenters. FEMS Microbiology Ecology, 2015, 91, fiv079.	1.3	23
556	Landscape Position Influences Microbial Composition and Function via Redistribution of Soil Water across a Watershed. Applied and Environmental Microbiology, 2015, 81, 8457-8468.	1.4	22
557	Functional overlap of the Arabidopsis leaf and root microbiota. Nature, 2015, 528, 364-369.	13.7	1,062
558	The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. American Journal of Physiology - Endocrinology and Metabolism, 2015, 309, E840-E851.	1.8	57
559	Dysbiosis of Gut Microbiota With Reduced Trimethylamineâ€Nâ€Oxide Level in Patients With Largeâ€Artery Atherosclerotic Stroke or Transient Ischemic Attack. Journal of the American Heart Association, 2015, 4, .	1.6	486
560	An improved method to set significance thresholds for <i>Î²</i> diversity testing in microbial community comparisons. Environmental Microbiology, 2015, 17, 3154-3167.	1.8	6
561	Shifts of tundra bacterial and archaeal communities along a permafrost thaw gradient in <scp>A</scp>laska. Molecular Ecology, 2015, 24, 222-234.	2.0	127
562	Whole Grain Oats Improve Insulin Sensitivity and Plasma Cholesterol Profile and Modify Gut Microbiota Composition in C57BL/6J Mice. Journal of Nutrition, 2015, 145, 222-230.	1.3	56
563	Assessment of the bacterial and fungal diversity in homeâ€made yoghurts of Xinjiang, China by pyrosequencing. Journal of the Science of Food and Agriculture, 2015, 95, 2007-2015.	1.7	28
564	Sulfur Dioxide Treatment Alters Wine Microbial Diversity and Fermentation Progression in a Dose-Dependent Fashion. American Journal of Enology and Viticulture, 2015, 66, 73-79.	0.9	56
565	Comparison of Artemiaâ€"bacteria associations in brines, laboratory cultures and the gut environment: a study based on Chilean hypersaline environments. Extremophiles, 2015, 19, 135-147.	0.9	17

#	ARTICLE	IF	CITATIONS
566	The current provided by oxygen-reducing microbial cathodes is related to the composition of their bacterial community. Bioelectrochemistry, 2015, 102, 42-49.	2.4	40
567	Intestinal Microbiota, Microbial Translocation, and Systemic Inflammation in Chronic HIV Infection. Journal of Infectious Diseases, 2015, 211, 19-27.	1.9	406
568	Ecological Succession and Viability of Human-Associated Microbiota on Restroom Surfaces. Applied and Environmental Microbiology, 2015, 81, 765-773.	1.4	89
569	Oceanographic structure drives the assembly processes of microbial eukaryotic communities. ISME Journal, 2015, 9, 990-1002.	4.4	115
570	In-depth diversity analysis of the bacterial community resident in the camel rumen. Systematic and Applied Microbiology, 2015, 38, 67-76.	1.2	92
571	Bacterial Community Composition and Fermentation Patterns in the Rumen of Sika Deer (Cervus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	63
572	Selection on soil microbiomes reveals reproducible impacts on plant function. ISME Journal, 2015, 9, 980-989.	4.4	549
573	Pyrosequencing reveals the effect of mobilizing agents and lignocellulosic substrate amendment on microbial community composition in a real industrial PAH-polluted soil. Journal of Hazardous Materials, 2015, 283, 35-43.	6.5	62
574	Altitudinal Distribution Patterns of Soil Bacterial and Archaeal Communities Along Mt. Shegyla on the Tibetan Plateau. Microbial Ecology, 2015, 69, 135-145.	1.4	166
575	Diversity and potential sources of microbiota associated with snow on western portions of the <scp>G</scp>reenland <scp>I</scp>ce <scp>S</scp>heet. Environmental Microbiology, 2015, 17, 594-609.	1.8	55
576	Phylogenetics and the Human Microbiome. Systematic Biology, 2015, 64, e26-e41.	2.7	36
577	Bacterial community structure in maize stubble-amended soils with different moisture levels estimated by bar-coded pyrosequencing. Applied Soil Ecology, 2015, 86, 62-70.	2.1	28
578	Human Milk Glycomics and Gut Microbial Genomics in Infant Feces Show a Correlation between Human Milk Oligosaccharides and Gut Microbiota: A Proof-of-Concept Study. Journal of Proteome Research, 2015, 14, 491-502.	1.8	166
579	Species specificity of symbiosis and secondary metabolism in ascidians. ISME Journal, 2015, 9, 615-628.	4.4	85
580	Archaea and Bacteria Acclimate to High Total Ammonia in a Methanogenic Reactor Treating Swine Waste. Archaea, 2016, 2016, 1-10.	2.3	26
581	Co-occurrence patterns in aquatic bacterial communities across changing permafrost landscapes. Biogeosciences, 2016, 13, 175-190.	1.3	64
582	Tissue-Associated Bacterial Alterations in Rectal Carcinoma Patients Revealed by 16S rRNA Community Profiling. Frontiers in Cellular and Infection Microbiology, 2016, 6, 179.	1.8	125
583	Microbiome Analysis Across a Natural Copper Gradient at a Proposed Northern Canadian Mine Site. Frontiers in Environmental Science, 2016, 3, .	1.5	8

#	ARTICLE	IF	CITATIONS
584	Draft Genomes Shed Light on the Dual Bacterial Symbiosis that Dominates the Microbiome of the Coral Reef Sponge Amphimedon queenslandica. Frontiers in Marine Science, 2016, 3, .	1.2	60
585	Ontogenetic Changes in the Bacterial Symbiont Community of the Tropical Demosponge Amphimedon queenslandica: Metamorphosis Is a New Beginning. Frontiers in Marine Science, 2016, 3, .	1.2	49
586	Bacterioplankton Dynamics within a Large Anthropogenically Impacted Urban Estuary. Frontiers in Microbiology, 2015, 6, 1438.	1.5	98
587	A Lipid-Accumulating Alga Maintains Growth in Outdoor, Alkaliphilic Raceway Pond with Mixed Microbial Communities. Frontiers in Microbiology, 2015, 6, 1480.	1.5	30
588	Human Microbiota of the Argentine Population- A Pilot Study. Frontiers in Microbiology, 2016, 7, 51.	1.5	14
589	High Molecular Weight Barley Î²-Glucan Alters Gut Microbiota Toward Reduced Cardiovascular Disease Risk. Frontiers in Microbiology, 2016, 7, 129.	1.5	133
590	Fate of Viable but Non-culturable Listeria monocytogenes in Pig Manure Microcosms. Frontiers in Microbiology, 2016, 7, 245.	1.5	18
591	Novel, Deep-Branching Heterotrophic Bacterial Populations Recovered from Thermal Spring Metagenomes. Frontiers in Microbiology, 2016, 7, 304.	1.5	48
592	Vertebrate Hosts as Islands: Dynamics of Selection, Immigration, Loss, Persistence, and Potential Function of Bacteria on Salamander Skin. Frontiers in Microbiology, 2016, 7, 333.	1.5	65
593	Comparison of Fermentation and Wines Produced by Inoculation of Hanseniaspora vineae and Saccharomyces cerevisiae. Frontiers in Microbiology, 2016, 7, 338.	1.5	91
594	Diversity and Metabolic Potentials of Subsurface Crustal Microorganisms from the Western Flank of the Mid-Atlantic Ridge. Frontiers in Microbiology, 2016, 7, 363.	1.5	37
595	Associations between Ectomycorrhizal Fungi and Bacterial Needle Endophytes in Pinus radiata: Implications for Biotic Selection of Microbial Communities. Frontiers in Microbiology, 2016, 7, 399.	1.5	21
596	The Features of Fecal and Ileal Mucosa-Associated Microbiota in Dairy Calves during Early Infection with Mycobacterium avium Subspecies paratuberculosis. Frontiers in Microbiology, 2016, 7, 426.	1.5	44
597	Rhizosphere Microbiomes of European + Seagrasses Are Selected by the Plant, But Are Not Species Specific. Frontiers in Microbiology, 2016, 7, 440.	1.5	153
598	Mycobacterium avium Subspecies paratuberculosis Infection Modifies Gut Microbiota under Different Dietary Conditions in a Rabbit Model. Frontiers in Microbiology, 2016, 7, 446.	1.5	56
599	Carrageenan Gum and Adherent Invasive Escherichia coli in a Piglet Model of Inflammatory Bowel Disease: Impact on Intestinal Mucosa-associated Microbiota. Frontiers in Microbiology, 2016, 7, 462.	1.5	48
600	Municipal Solid Waste Landfills Harbor Distinct Microbiomes. Frontiers in Microbiology, 2016, 7, 534.	1.5	107
601	Individuality, Stability, and Variability of the Plaque Microbiome. Frontiers in Microbiology, 2016, 7, 564.	1.5	75

#	ARTICLE	IF	CITATIONS
602	Chitin Mixed in Potting Soil Alters Lettuce Growth, the Survival of Zoonotic Bacteria on the Leaves and Associated Rhizosphere Microbiology. Frontiers in Microbiology, 2016, 7, 565.	1.5	76
603	Development of Ruminal and Fecal Microbiomes Are Affected by Weaning But Not Weaning Strategy in Dairy Calves. Frontiers in Microbiology, 2016, 7, 582.	1.5	148
604	Nitrogen Stimulates the Growth of Subsurface Basalt-associated Microorganisms at the Western Flank of the Mid-Atlantic Ridge. Frontiers in Microbiology, 2016, 7, 633.	1.5	19
605	Experimental Evolution on a Wild Mammal Species Results in Modifications of Gut Microbial Communities. Frontiers in Microbiology, 2016, 7, 634.	1.5	27
606	Comparison of Microbial Communities Isolated from Feces of Asymptomatic Salmonella-Shedding and Non-Salmonella Shedding Dairy Cows. Frontiers in Microbiology, 2016, 7, 691.	1.5	7
607	Induction of Subacute Ruminal Acidosis Affects the Ruminal Microbiome and Epithelium. Frontiers in Microbiology, 2016, 7, 701.	1.5	131
608	Ecotoxicological Impact of the Bioherbicide Leptospermone on the Microbial Community of Two Arable Soils. Frontiers in Microbiology, 2016, 7, 775.	1.5	31
609	Capturing One of the Human Gut Microbiomeâ€™s Most Wanted: Reconstructing the Genome of a Novel Butyrate-Producing, Clostridial Scavenger from Metagenomic Sequence Data. Frontiers in Microbiology, 2016, 7, 783.	1.5	24
610	The Dark Side of the Mushroom Spring Microbial Mat: Life in the Shadow of Chlorophototrophs. I. Microbial Diversity Based on 16S rRNA Gene Amplicons and Metagenomic Sequencing. Frontiers in Microbiology, 2016, 7, 919.	1.5	123
611	Diversity and Distribution of Prokaryotes within a Shallow-Water Pockmark Field. Frontiers in Microbiology, 2016, 7, 941.	1.5	27
612	Diversity, Biogeography, and Biodegradation Potential of Actinobacteria in the Deep-Sea Sediments along the Southwest Indian Ridge. Frontiers in Microbiology, 2016, 7, 1340.	1.5	76
613	Phytoplankton-Associated Bacterial Community Composition and Succession during Toxic Diatom Bloom and Non-Bloom Events. Frontiers in Microbiology, 2016, 7, 1433.	1.5	60
614	From Mouth to Model: Combining in vivo and in vitro Oral Biofilm Growth. Frontiers in Microbiology, 2016, 7, 1448.	1.5	25
615	Upstream Freshwater and Terrestrial Sources Are Differentially Reflected in the Bacterial Community Structure along a Small Arctic River and Its Estuary. Frontiers in Microbiology, 2016, 7, 1474.	1.5	38
616	Alteration of Fecal Microbiota Profiles in Juvenile Idiopathic Arthritis. Associations with HLA-B27 Allele and Disease Status. Frontiers in Microbiology, 2016, 7, 1703.	1.5	65
617	The Microbiota of Recreational Freshwaters and the Implications for Environmental and Public Health. Frontiers in Microbiology, 2016, 7, 1826.	1.5	70
618	Microbial Communities of Lycaenid Butterflies Do Not Correlate with Larval Diet. Frontiers in Microbiology, 2016, 7, 1920.	1.5	75
619	Local and Regional Diversity Reveals Dispersal Limitation and Drift as Drivers for Groundwater Bacterial Communities from a Fractured Granite Formation. Frontiers in Microbiology, 2016, 7, 1933.	1.5	19

#	ARTICLE	IF	CITATIONS
620	Dynamics in the Strawberry Rhizosphere Microbiome in Response to Biochar and Botrytis cinerea Leaf Infection. Frontiers in Microbiology, 2016, 7, 2062.	1.5	59
621	Early Recovery of Salmonella from Food Using a 6-Hour Non-selective Pre-enrichment and Reformulation of Tetrathionate Broth. Frontiers in Microbiology, 2016, 7, 2103.	1.5	38
622	Metabarcoding of Bacteria Associated with the Acute Oak Decline Syndrome in England. Forests, 2016, 7, 95.	0.9	32
623	Reduced Diversity in the Bacteriome of the Phytophagous Mite Brevipalpus yothersi (Acari:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.0	3
624	The Potential of Class II Bacteriocins to Modify Gut Microbiota to Improve Host Health. PLoS ONE, 2016, 11, e0164036.	1.1	102
625	Impact of Organic Carbon Electron Donors on Microbial Community Development under Iron- and Sulfate-Reducing Conditions. PLoS ONE, 2016, 11, e0146689.	1.1	40
626	Cervical Microbiome and Cytokine Profile at Various Stages of Cervical Cancer: A Pilot Study. PLoS ONE, 2016, 11, e0153274.	1.1	275
627	Chronic Psychological Stress Disrupted the Composition of the Murine Colonic Microbiota and Accelerated a Murine Model of Inflammatory Bowel Disease. PLoS ONE, 2016, 11, e0150559.	1.1	25
628	Safety Evaluation of Neo Transgenic Pigs by Studying Changes in Gut Microbiota Using High-Throughput Sequencing Technology. PLoS ONE, 2016, 11, e0150937.	1.1	7
629	Helicobacter pylori Eradication Causes Perturbation of the Human Gut Microbiome in Young Adults. PLoS ONE, 2016, 11, e0151893.	1.1	109
630	Impact of the Chromatin Remodeling Factor CHD1 on Gut Microbiome Composition of Drosophila melanogaster. PLoS ONE, 2016, 11, e0153476.	1.1	11
631	A Novel Analysis Method for Paired-Sample Microbial Ecology Experiments. PLoS ONE, 2016, 11, e0154804.	1.1	9
632	Molecular Properties of Guar Gum and Pectin Modify Cecal Bile Acids, Microbiota, and Plasma Lipopolysaccharide-Binding Protein in Rats. PLoS ONE, 2016, 11, e0157427.	1.1	30
633	Effect of Co-Composting Cattle Manure with Construction and Demolition Waste on the Archaeal, Bacterial, and Fungal Microbiota, and on Antimicrobial Resistance Determinants. PLoS ONE, 2016, 11, e0157539.	1.1	54
634	Key Microbiota Identification Using Functional Gene Analysis during Pepper (Piper nigrum L.) Peeling. PLoS ONE, 2016, 11, e0165206.	1.1	0
635	Distribution of Root-Associated Bacterial Communities Along a Salt-Marsh Primary Succession. Frontiers in Plant Science, 2015, 6, 1188.	1.7	27
636	Rhizospheric Bacterial Community of Endemic Rhododendron arboreum Sm. Ssp. delavayi along Eastern Himalayan Slope in Tawang. Frontiers in Plant Science, 2016, 07, 1345.	1.7	14
637	Development of the Chick Microbiome: How Early Exposure Influences Future Microbial Diversity. Frontiers in Veterinary Science, 2016, 3, 2.	0.9	246

#	Article	IF	Citations
638	Microbial ecology of the salmon necrobiome: evidence salmon carrion decomposition influences aquatic and terrestrial insect microbiomes. Environmental Microbiology, 2016, 18, 1511-1522.	1.8	86
639	Fieldâ€based evidence for copper contamination induced changes of antibiotic resistance in agricultural soils. Environmental Microbiology, 2016, 18, 3896-3909.	1.8	216
640	Microbial biogeography of permafrost thaw ponds across the changing northern landscape. Ecography, 2016, 39, 609-618.	2.1	55
641	MAIT, MR1, microbes and riboflavin: a paradigm for the co-evolution of invariant TCRs and restricting MHCI-like molecules?. Immunogenetics, 2016, 68, 537-548.	1.2	45
642	Spatial and temporal investigation of the microbiome of the Caribbean octocoral<i>Erythropodium caribaeorum</i>. FEMS Microbiology Ecology, 2016, 92, fiw147.	1.3	25
643	Metabarcoding reveals environmental factors influencing spatioâ€temporal variation in pelagic microâ€eukaryotes. Molecular Ecology, 2016, 25, 3593-3604.	2.0	37
644	Growth of high-elevation Cryptococcus sp. during extreme freezeâ€“thaw cycles. Extremophiles, 2016, 20, 579-588.	0.9	17
645	Spatial scale drives patterns in soil bacterial diversity. Environmental Microbiology, 2016, 18, 2039-2051.	1.8	194
646	Field degradation of aminopyralid and clopyralid and microbial community response to application in Alaskan soils. Environmental Toxicology and Chemistry, 2016, 35, 485-493.	2.2	13
647	Reconstruction of metabolic networks in a fluoranthene-degrading enrichments from polycyclic aromatic hydrocarbon polluted soil. Journal of Hazardous Materials, 2016, 318, 90-98.	6.5	44
648	Methanogenic paraffin degradation proceeds via alkane addition to fumarate by <i>â€˜Smithellaâ€™</i> spp. mediated by a syntrophic coupling with hydrogenotrophic methanogens. Environmental Microbiology, 2016, 18, 2604-2619.	1.8	71
649	Characterizing the bacterial communities in retail stores in the United States. Indoor Air, 2016, 26, 857-868.	2.0	26
650	Microbial <scp>F</scp>e(<scp>III</scp>) oxide reduction potential in <scp>C</scp>hocolate <scp>P</scp>ots hot spring, <scp>Y</scp>ellowstone <scp>N</scp>ational <scp>P</scp>ark. Geobiology, 2016, 14, 255-275.	1.1	59
651	Acute dextran sulfate sodium (DSS)â€induced colitis promotes gut microbial dysbiosis in mice. Journal of Basic Microbiology, 2016, 56, 986-998.	1.8	208
652	Effects of Specimen Collection Methodologies and Storage Conditions on the Short-Term Stability of Oral Microbiome Taxonomy. Applied and Environmental Microbiology, 2016, 82, 5519-5529.	1.4	30
653	Lignocellulose-derived thin stillage composition and efficient biological treatment with a high-rate hybrid anaerobic bioreactor system. Biotechnology for Biofuels, 2016, 9, 120.	6.2	25
654	Subalpine conifers in different geographical locations host highly similar foliar bacterial endophyte communities. FEMS Microbiology Ecology, 2016, 92, fiw124.	1.3	23
655	Geological connectivity drives microbial community structure and connectivity in polar, terrestrial ecosystems. Environmental Microbiology, 2016, 18, 1834-1849.	1.8	51

#	ARTICLE	IF	CITATIONS
656	Bacterial indicator taxa in soils under different long-term agricultural management. Journal of Applied Microbiology, 2016, 120, 921-933.	1.4	56
657	Diversity of ribosomal 16S DNA- and RNA-based bacterial community in an office building drinking water system. Journal of Applied Microbiology, 2016, 120, 1723-1738.	1.4	47
658	Characterization of pollen and bacterial community composition in brood provisions of a small carpenter bee. Molecular Ecology, 2016, 25, 2302-2311.	2.0	97
659	Investigation of Microbial Diversity in Geothermal Hot Springs in Unkeshwar, India, Based on 16S rRNA Amplicon Metagenome Sequencing. Genome Announcements, 2016, 4, .	0.8	11
660	Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. Scientific Reports, 2016, 6, 33430.	1.6	25
661	New multi-scale perspectives on the stromatolites of Shark Bay, Western Australia. Scientific Reports, 2016, 6, 20557.	1.6	115
662	Functional analysis for gut microbes of the brown tree frog (Polypedates megacephalus) in artificial hibernation. BMC Genomics, 2016, 17, 1024.	1.2	68
663	Lingonberries alter the gut microbiota and prevent low-grade inflammation in high-fat diet fed mice. Food and Nutrition Research, 2016, 60, 29993.	1.2	64
664	Urban-development-induced Changes in the Diversity and Composition of the Soil Bacterial Community in Beijing. Scientific Reports, 2016, 6, 38811.	1.6	73
665	Effects of changes in straw chemical properties and alkaline soils on bacterial communities engaged in straw decomposition at different temperatures. Scientific Reports, 2016, 6, 22186.	1.6	34
666	Surfactant-associated bacteria in the near-surface layer of the ocean. Scientific Reports, 2016, 6, 19123.	1.6	53
667	Disturbance Regimes Predictably Alter Diversity in an Ecologically Complex Bacterial System. MBio, 2016, 7, .	1.8	47
668	Probiotic treatment reduces appetite and glucose level in the zebrafish model. Scientific Reports, 2016, 6, 18061.	1.6	85
669	Atmospheric Deposition-Carried Zn and Cd from a Zinc Smelter and Their Effects on Soil Microflora as Revealed by 16S rDNA. Scientific Reports, 2016, 6, 39148.	1.6	19
670	Regional variations in the diversity and predicted metabolic potential of benthic prokaryotes in coastal northern Zhejiang, East China Sea. Scientific Reports, 2016, 6, 38709.	1.6	35
671	Exploring the methanogen and bacterial communities of rumen environments: solid adherent, fluid and epimural. FEMS Microbiology Ecology, 2017, 93, fiw251.	1.3	83
672	The human milk oligosaccharide 2â€²-fucosyllactose attenuates the severity of experimental necrotising enterocolitis by enhancing mesenteric perfusion in the neonatal intestine. British Journal of Nutrition, 2016, 116, 1175-1187.	1.2	145
673	Amphibian gut microbiota shifts differentially in community structure but converges on habitat-specific predicted functions. Nature Communications, 2016, 7, 13699.	5.8	145

#	ARTICLE	IF	CITATIONS
674	Anode potential influences the structure and function of anodic electrode and electrolyte-associated microbiomes. Scientific Reports, 2016, 6, 39114.	1.6	57
675	A novel open-type biosensor for the in-situ monitoring of biochemical oxygen demand in an aerobic environment. Scientific Reports, 2016, 6, 38552.	1.6	41
676	Gut Microbiota and Metabolic Phenotype of Portunus Trituberculatus. Chinese Journal of Analytical Chemistry, 2016, 44, 1867-1873.	0.9	10
677	The developing hypopharyngeal microbiota in early life. Microbiome, 2016, 4, 70.	4.9	46
678	Influence of maternal breast milk ingestion on acquisition of the intestinal microbiome in preterm infants. Microbiome, 2016, 4, 68.	4.9	155
679	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. Biotechnology for Biofuels, 2016, 9, 156.	6.2	120
680	MetaDP: a comprehensive web server for disease prediction of 16S rRNA metagenomic datasets. Biophysics Reports, 2016, 2, 106-115.	0.2	9
681	Changes in fecal microbiota and metabolomics in a child with juvenile idiopathic arthritis (JIA) responding to two treatment periods with exclusive enteral nutrition (EEN). Clinical Rheumatology, 2016, 35, 1501-1506.	1.0	22
682	Enhancing tetrabromobisphenol A biodegradation in river sediment microcosms and understanding the corresponding microbial community. Environmental Pollution, 2016, 208, 796-802.	3.7	65
683	Metabolic Model-Based Integration of Microbiome Taxonomic and Metabolomic Profiles Elucidates Mechanistic Links between Ecological and Metabolic Variation. MSystems, 2016, 1, .	1.7	167
684	Host genetics is associated with the gut microbial community membership rather than the structure. Molecular BioSystems, 2016, 12, 1676-1686.	2.9	11
685	Comparative studies of the composition of bacterial microbiota associated with the ruminal content, ruminal epithelium and in the faeces of lactating dairy cows. Microbial Biotechnology, 2016, 9, 257-268.	2.0	150
686	Biological, physicochemical and plant health responses in lettuce and strawberry in soil or peat amended with biochar. Applied Soil Ecology, 2016, 107, 1-12.	2.1	122
687	Combined effects of exogenous enzymes and probiotic on Nile tilapia (Oreochromis niloticus) growth, intestinal morphology and microbiome. Aquaculture, 2016, 463, 61-70.	1.7	102
688	Detection of Antibiotic Resistance Genes in Source and Drinking Water Samples from a First Nations Community in Canada. Applied and Environmental Microbiology, 2016, 82, 4767-4775.	1.4	103
689	Evolution of the nasopharyngeal microbiota of beef cattle from weaning to 40 days after arrival at a feedlot. Veterinary Microbiology, 2016, 187, 75-81.	0.8	70
690	Characterization of Biofilm Bacterial Communities in a Vertical Unsaturated-Flow Bioreactor Treating Domestic Greywater. Environmental Processes, 2016, 3, 325-340.	1.7	12
691	Immunization with a heat-killed preparation of the environmental bacterium <i>Mycobacterium vaccae</i> promotes stress resilience in mice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3130-9.	3.3	186

#	Article	IF	Citations
692	Bacterial and eukaryal diversity in soils forming from acid mine drainage precipitates under reclaimed vegetation and biological crusts. Applied Soil Ecology, 2016, 105, 57-66.	2.1	32
693	rRNA Gene Expression of Abundant and Rare Activated-Sludge Microorganisms and Growth Rate Induced Micropollutant Removal. Environmental Science & Technology, 2016, 50, 6299-6309.	4.6	46
694	Multiple paths of electron flow to current in microbial electrolysis cells fed with low and high concentrations of propionate. Applied Microbiology and Biotechnology, 2016, 100, 5999-6011.	1.7	56
695	Nutrient treatments alter microbial mat colonization in two glacial meltwater streams from the McMurdo Dry Valleys, Antarctica. FEMS Microbiology Ecology, 2016, 92, fiw049.	1.3	32
696	Gut microbiota analysis reveals a marked shift to bifidobacteria by a starter infant formula containing a synbiotic of bovine milkâ€•derived oligosaccharides and <scp><i>B</i></scp><i>ifidobacterium animalis</i> subsp. <i>lactis</i>â€...<scp>CNCM I</scp>â€•3446. Environmental Microbiology, 2016, 18, 2185-2195.	1.8	68
697	Evaluation of the effects of intrapartum antibiotic prophylaxis on newborn intestinal microbiota using a sequencing approach targeted to multi hypervariable 16S rDNA regions. Applied Microbiology and Biotechnology, 2016, 100, 5537-5546.	1.7	84
698	The effects of family, dentition, and dental caries on the salivary microbiome. Annals of Epidemiology, 2016, 26, 348-354.	0.9	19
699	Gut microbiome remodeling induces depressive-like behaviors through a pathway mediated by the hostâ€™s metabolism. Molecular Psychiatry, 2016, 21, 786-796.	4.1	1,397
700	Asymmetrical response of anaerobic digestion microbiota to temperature changes. Applied Microbiology and Biotechnology, 2016, 100, 1445-1457.	1.7	23
701	Short-Term Exposure to Coal Combustion Waste Has Little Impact on the Skin Microbiome of Adult Spring Peepers (Pseudacris crucifer). Applied and Environmental Microbiology, 2016, 82, 3493-3502.	1.4	21
702	Assessment of Bacterial Communities and Predictive Functional Profiling in Soils Subjected to Short-Term Fumigation-Incubation. Microbial Ecology, 2016, 72, 240-251.	1.4	22
703	Structural and functional differentiation of the root-associated bacterial microbiomes of perennial ryegrass. Soil Biology and Biochemistry, 2016, 98, 1-10.	4.2	99
704	The Chthonomonas calidirosea Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's TaupÅ•Volcanic Zone. Applied and Environmental Microbiology, 2016, 82, 3572-3581.	1.4	9
705	Microbial community dynamics in continuous microbial fuel cells fed with synthetic wastewater and pig slurry. Bioelectrochemistry, 2016, 111, 70-82.	2.4	42
706	Multidrug resistance phenotypes are widespread over different bacterial taxonomic groups thriving in surface water. Science of the Total Environment, 2016, 563-564, 1-9.	3.9	56
707	Natural decay process affects the abundance and community structure of Bacteria and Archaea in<i>Picea abies</i>logs. FEMS Microbiology Ecology, 2016, 92, fiw087.	1.3	46
708	Genetic assessment of meiobenthic community composition and spatial distribution in coastal sediments along northern Gulf of Mexico. Marine Environmental Research, 2016, 119, 166-175.	1.1	15
709	Effect of long-term application of agrotechnical techniques and crops on soil microbial communities. Microbiology, 2016, 85, 231-242.	0.5	5

#	ARTICLE	IF	CITATIONS
710	Assessing the microbiomes of scalder and chiller tank waters throughout a typical commercial poultry processing day. Poultry Science, 2016, 95, 2372-2382.	1.5	26
711	Microbiome changes through ontogeny of a tick pathogen vector. Molecular Ecology, 2016, 25, 4963-4977.	2.0	140
712	Effects of Proton Pump Inhibitors on the Gastric Mucosa-Associated Microbiota in Dyspeptic Patients. Applied and Environmental Microbiology, 2016, 82, 6633-6644.	1.4	85
713	Distinctive gut microbial community structure in both the wild and farmed Swan goose (<i>Anser) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	36
714	A chronic rhinosinusitisâ€“derived isolate of <i>Pseudomonas aeruginosa</i> induces acute and pervasive effects on the murine upper airway microbiome and host immune response. International Forum of Allergy and Rhinology, 2016, 6, 1229-1237.	1.5	15
715	Excess phosphate loading shifts bacterioplankton community composition in oligotrophic coastal water microcosms over time. Journal of Experimental Marine Biology and Ecology, 2016, 483, 139-146.	0.7	16
716	Bacterial diversity of the American sand fly Lutzomyia intermedia using high-throughput metagenomic sequencing. Parasites and Vectors, 2016, 9, 480.	1.0	41
717	Bacterial microbiota associated with flower pollen is influenced by pollination type, and shows a high degree of diversity and speciesâ€specificity. Environmental Microbiology, 2016, 18, 5161-5174.	1.8	132
718	16S rRNA gene-based comprehensive analysis of microbial community compositions in a full-scale leachate treatment system. Journal of Bioscience and Bioengineering, 2016, 122, 708-715.	1.1	15
719	Identification of growing bacteria during litter decomposition in freshwater through quantitative stable isotope probing. Environmental Microbiology Reports, 2016, 8, 975-982.	1.0	20
720	Vineyard soil bacterial diversity and composition revealed by 16S rRNA genes: Differentiation by vineyard management. Soil Biology and Biochemistry, 2016, 103, 337-348.	4.2	95
721	Response of Germfree Mice to Colonization by Oxalobacter formigenes and Altered Schaedler Flora. Applied and Environmental Microbiology, 2016, 82, 6952-6960.	1.4	20
722	Effects of field conditions on fecal microbiota. Journal of Microbiological Methods, 2016, 130, 180-188.	0.7	28
723	Effect of dietary interventions on the intestinal microbiota of Mongolian hosts. Science Bulletin, 2016, 61, 1605-1614.	4.3	16
724	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. Contemporary Clinical Trials, 2016, 50, 201-212.	0.8	22
725	Characterization and comparison of the temporal dynamics of ruminal bacterial microbiota colonizing rice straw and alfalfa hay within ruminants. Journal of Dairy Science, 2016, 99, 9668-9681.	1.4	100
726	Highlighting the microbial diversity of 12 French cheese varieties. International Journal of Food Microbiology, 2016, 238, 265-273.	2.1	108
727	Resolving colocalization of bacteria and metal(loid)s on plant root surfaces by combining fluorescence in situ hybridization (FISH) with multiple-energy micro-focused X-ray fluorescence (ME) Tj ETQq1 1 0.784314 rgBT /Overlo	6.7	3

#	ARTICLE	IF	CITATIONS
728	Diet may influence the oral microbiome composition in cats. Microbiome, 2016, 4, 23.	4.9	43
729	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. Talanta, 2016, 160, 148-156.	2.9	0
730	Purified rutin and rutinâ€rich asparagus attenuates disease severity and tissue damage following dextran sodium sulfateâ€induced colitis. Molecular Nutrition and Food Research, 2016, 60, 2396-2412.	1.5	27
731	Multiple synergistic benefits of selective fermentation of Scenedesmus biomass for fuel recovery via wet-biomass extraction. Algal Research, 2016, 17, 253-260.	2.4	14
732	Preparation of a standardised faecal slurry for ex-vivo microbiota studies which reduces inter-individual donor bias. Journal of Microbiological Methods, 2016, 129, 109-116.	0.7	29
733	Bacterial community composition is shaped by soil secondary salinization and acidification brought on by high nitrogen fertilization rates. Applied Soil Ecology, 2016, 108, 76-83.	2.1	81
734	Using PacBio Long-Read High-Throughput Microbial Gene Amplicon Sequencing To Evaluate Infant Formula Safety. Journal of Agricultural and Food Chemistry, 2016, 64, 6993-7001.	2.4	24
735	Patterns of bacterial biodiversity in the glacial meltwater streams of the McMurdo Dry Valleys, Antarctica. FEMS Microbiology Ecology, 2016, 92, fiw148.	1.3	41
736	Effects of host genetics and environment on eggâ€associated microbiotas in brown trout (<i>Salmo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.0	28
737	Using the gut microbiota as a novel tool for examining colobine primate GI health. Global Ecology and Conservation, 2016, 7, 225-237.	1.0	76
738	Lactulose Differently Modulates the Composition of Luminal and Mucosal Microbiota in C57BL/6J Mice. Journal of Agricultural and Food Chemistry, 2016, 64, 6240-6247.	2.4	98
739	Plant diversity accurately predicts insect diversity in two tropical landscapes. Molecular Ecology, 2016, 25, 4407-4419.	2.0	71
740	High-Level Culturability of Epiphytic Bacteria and Frequency of Biosurfactant Producers on Leaves. Applied and Environmental Microbiology, 2016, 82, 5997-6009.	1.4	32
741	The Core and Seasonal Microbiota of Raw Bovine Milk in Tanker Trucks and the Impact of Transfer to a Milk Processing Facility. MBio, 2016, 7, .	1.8	105
742	Proteobacteria become predominant during regrowth after water disinfection. Science of the Total Environment, 2016, 573, 313-323.	3.9	77
743	Molecular Microbiological Profile of Chronic Suppurative Otitis Media. Journal of Clinical Microbiology, 2016, 54, 2538-2546.	1.8	48
744	Solanum lycopersicum (tomato) hosts robust phyllosphere and rhizosphere bacterial communities when grown in soil amended with various organic and synthetic fertilizers. Science of the Total Environment, 2016, 573, 555-563.	3.9	51
745	Identification of Oligosaccharides in Feces of Breast-fed Infants and Their Correlation with the Gut Microbial Community. Molecular and Cellular Proteomics, 2016, 15, 2987-3002.	2.5	77

#	ARTICLE	IF	CITATIONS
746	Contrasting Ecological Processes and Functional Compositions Between Intestinal Bacterial Community in Healthy and Diseased Shrimp. Microbial Ecology, 2016, 72, 975-985.	1.4	142
747	Cutaneous microbiome effects of fluticasone propionate cream and adjunctive bleach baths in childhood atopic dermatitis. Journal of the American Academy of Dermatology, 2016, 75, 481-493.e8.	0.6	127
748	Dense water plumes modulate richness and productivity of deep sea microbes. Environmental Microbiology, 2016, 18, 4537-4548.	1.8	17
749	Pyrene dissipation potential varies with soil type and associated bacterial community changes. Soil Biology and Biochemistry, 2016, 103, 71-85.	4.2	43
750	Coping with copper: legacy effect of copper on potential activity of soil bacteria following a century of exposure. FEMS Microbiology Ecology, 2016, 92, fiw175.	1.3	126
751	Bacterial Communities Associated with Different <i>Anthurium andraeanum</i> L. Plant Tissues. Microbes and Environments, 2016, 31, 321-328.	0.7	28
752	Common methods for fecal sample storage in field studies yield consistent signatures of individual identity in microbiome sequencing data. Scientific Reports, 2016, 6, 31519.	1.6	63
753	Characterising the interspecific variations and convergence of gut microbiota in Anseriformes herbivores at wintering areas. Scientific Reports, 2016, 6, 32655.	1.6	46
754	Diet-Microbiota Interactions Mediate Global Epigenetic Programming in Multiple Host Tissues. Molecular Cell, 2016, 64, 982-992.	4.5	405
755	Temperature mediates continental-scale diversity of microbes in forest soils. Nature Communications, 2016, 7, 12083.	5.8	419
756	Intestinal Microbiota Distinguish Gout Patients from Healthy Humans. Scientific Reports, 2016, 6, 20602.	1.6	238
757	Biodiversity and Activity of the Gut Microbiota across the Life History of the Insect Herbivore Spodoptera littoralis. Scientific Reports, 2016, 6, 29505.	1.6	277
758	Multi-marker metabarcoding of coral skeletons reveals a rich microbiome and diverse evolutionary origins of endolithic algae. Scientific Reports, 2016, 6, 31508.	1.6	103
759	Nutrient enrichment induces dormancy and decreases diversity of active bacteria in salt marsh sediments. Nature Communications, 2016, 7, 12881.	5.8	119
760	Bacterial Community Structures in Freshwater Polar Environments of Svalbard. Microbes and Environments, 2016, 31, 401-409.	0.7	44
761	Thermal discharge-created increasing temperatures alter the bacterioplankton composition and functional redundancy. AMB Express, 2016, 6, 68.	1.4	22
762	Contrasting elevational diversity patterns for soil bacteria between two ecosystems divided by the treeline. Science China Life Sciences, 2016, 59, 1177-1186.	2.3	25
763	Differences in CD8Î±Î± and cecal microbiome community during proliferation and late cytolytic phases of Marek's disease virus infection are associated with genetic resistance to Marek's disease. FEMS Microbiology Ecology, 2016, 92, fiw188.	1.3	17

#	ARTICLE	IF	CITATIONS
764	High-fat diet modifies the PPAR-Î³ pathway leading to disruption of microbial and physiological ecosystem in murine small intestine. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5934-E5943.	3.3	180
765	Neonatal gut microbiota associates with childhood multisensitized atopy and T cell differentiation. Nature Medicine, 2016, 22, 1187-1191.	15.2	844
766	Longitudinal Survey of Microbiota in Hospitalized Preterm Veryâ€Łowâ€Birthâ€Weight Infants. Journal of Pediatric Gastroenterology and Nutrition, 2016, 62, 292-303.	0.9	58
767	Death Becomes Them: Bacterial Community Dynamics and Stilbene Antibiotic Production in Cadavers of Galleria mellonella Killed by Heterorhabditis and Photorhabdus spp. Applied and Environmental Microbiology, 2016, 82, 5824-5837.	1.4	17
768	Antibiotics, birth mode, and diet shape microbiome maturation during early life. Science Translational Medicine, 2016, 8, 343ra82.	5.8	1,012
769	Effects of multiple dimensions of bacterial diversity on functioning, stability and multifunctionality. Ecology, 2016, 97, 2716-2728.	1.5	64
770	Midtrimester Cervicovaginal Microbiota: Identification of Microbial Variations Associated with Puerperal Infection at Term. American Journal of Perinatology, 2016, 33, 1165-1175.	0.6	8
771	Successional trajectories of bacterioplankton community over the complete cycle of a sudden phytoplankton bloom in the Xiangshan Bay, East China Sea. Environmental Pollution, 2016, 219, 750-759.	3.7	20
772	Glial-cell-derived neuroregulators control type 3 innate lymphoid cells and gut defence. Nature, 2016, 535, 440-443.	13.7	272
773	Characterization of three plant biomass-degrading microbial consortia by metagenomics- and metasecretomics-based approaches. Applied Microbiology and Biotechnology, 2016, 100, 10463-10477.	1.7	73
774	Mosquitoes host communities of bacteria that are essential for development but vary greatly between local habitats. Molecular Ecology, 2016, 25, 5806-5826.	2.0	250
775	A high-resolution map of the gut microbiota in Atlantic salmon (Salmo salar): A basis for comparative gut microbial research. Scientific Reports, 2016, 6, 30893.	1.6	246
776	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. MSphere, 2016, 1, .	1.3	28
777	Evolution of the microbial community of the biofilm in a methane-based membrane biofilm reactor reducing multiple electron acceptors. Environmental Science and Pollution Research, 2016, 23, 9540-9548.	2.7	38
778	Individual Apostichopus japonicus fecal microbiome reveals a link with polyhydroxybutyrate producers in host growth gaps. Scientific Reports, 2016, 6, 21631.	1.6	81
779	Joint effects of pregnancy, sociocultural, and environmental factors on early life gut microbiome structure and diversity. Scientific Reports, 2016, 6, 31775.	1.6	122
780	Endemic hydrothermal vent species identified in the open ocean seed bank. Nature Microbiology, 2016, 1, 16086.	5.9	55
781	Soil bacterial and fungal community dynamics in relation to Panax notoginseng death rate in a continuous cropping system. Scientific Reports, 2016, 6, 31802.	1.6	155

#	ARTICLE	IF	CITATIONS
782	Gut microbiota of dung beetles correspond to dietary specializations of adults and larvae. Molecular Ecology, 2016, 25, 6092-6106.	2.0	79
783	Evaluating digestion efficiency in full-scale anaerobic digesters by identifying active microbial populations through the lens of microbial activity. Scientific Reports, 2016, 6, 34090.	1.6	87
784	NKT Cellâ€"Deficient Mice Harbor an Altered Microbiota That Fuels Intestinal Inflammation during Chemically Induced Colitis. Journal of Immunology, 2016, 197, 4464-4472.	0.4	92
785	Birth mode-dependent association between pre-pregnancy maternal weight status and the neonatal intestinal microbiome. Scientific Reports, 2016, 6, 23133.	1.6	120
786	Chronic warming stimulates growth of marsh grasses more than mangroves in a coastal wetland ecotone. Ecology, 2016, 97, 3167-3175.	1.5	24
787	Enrichment of the lung microbiome with oral taxa is associated with lung inflammation of a Th17 phenotype. Nature Microbiology, 2016, 1, 16031.	5.9	436
788	Assessing quality of Medicago sativa silage by monitoring bacterial composition with single molecule, real-time sequencing technology and various physiological parameters. Scientific Reports, 2016, 6, 28358.	1.6	75
789	Metagenomic approach reveals microbial diversity and predictive microbial metabolic pathways in Yucha, a traditional Li fermented food. Scientific Reports, 2016, 6, 32524.	1.6	74
790	Colonic transit time is related to bacterial metabolism and mucosal turnover in the gut. Nature Microbiology, 2016, 1, 16093.	5.9	321
791	The microenvironment of injured murine gut elicits a local pro-restitutive microbiota. Nature Microbiology, 2016, 1, 15021.	5.9	182
792	Antibiotic-induced perturbations in gut microbial diversity influences neuro-inflammation and amyloidosis in a murine model of Alzheimerâ€™s disease. Scientific Reports, 2016, 6, 30028.	1.6	469
793	Construction of a Species-Level Tree of Life for the Insects and Utility in Taxonomic Profiling. Systematic Biology, 2016, 66, syw099.	2.7	29
794	Potential use of bacterial community succession for estimating post-mortem interval as revealed by high-throughput sequencing. Scientific Reports, 2016, 6, 24197.	1.6	77
795	Vertical distribution of bacterial community is associated with the degree of soil organic matter decomposition in the active layer of moist acidic tundra. Journal of Microbiology, 2016, 54, 713-723.	1.3	48
796	Altered gut microbiota in Rett syndrome. Microbiome, 2016, 4, 41.	4.9	120
797	Comparison of placenta samples with contamination controls does not provide evidence for a distinct placenta microbiota. Microbiome, 2016, 4, 29.	4.9	447
798	Impacts of resistant starch and wheat bran consumption on enteric inflammation in relation to colonic bacterial community structures and short-chain fatty acid concentrations in mice. Gut Pathogens, 2016, 8, 67.	1.6	53
799	Unusual sub-genus associations of faecal Prevotella and Bacteroides with specific dietary patterns. Microbiome, 2016, 4, 57.	4.9	101

#	ARTICLE	IF	CITATIONS
800	Influence of GABA and GABA-producing Lactobacillus brevis DPC 6108 on the development of diabetes in a streptozotocin rat model. Beneficial Microbes, 2016, 7, 409-420.	1.0	46
801	Effect of Formula Containing <i>Lactobacillus reuteri</i> DSM 17938 on Fecal Microbiota of Infants Born by Cesareanâ€Section. Journal of Pediatric Gastroenterology and Nutrition, 2016, 63, 681-687.	0.9	49
802	Geography and Location Are the Primary Drivers of Office Microbiome Composition. MSystems, 2016, 1, .	1.7	110
803	Soluble Corn Fiber Increases Calcium Absorption Associated with Shifts in the Gut Microbiome: A Randomized Dose-Response Trial in Free-Living Pubertal Females. Journal of Nutrition, 2016, 146, 1298-1306.	1.3	117
804	Environmental Filtering Process Has More Important Roles than Dispersal Limitation in Shaping Large-Scale Prokaryotic Beta Diversity Patterns of Grassland Soils. Microbial Ecology, 2016, 72, 221-230.	1.4	28
805	Short-term waterlogging increases arbuscular mycorrhizal fungal species richness and shifts community composition. Plant and Soil, 2016, 404, 373-384.	1.8	28
806	<i>Caenorhabditis elegans</i> responses to bacteria from its natural habitats. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3941-9.	3.3	317
807	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. MBio, 2016, 7, .	1.8	325
808	A watering manipulation in a semiarid grassland induced changes in fungal but not bacterial community composition. Pedobiologia, 2016, 59, 121-127.	0.5	24
809	Biogeochemical gradients above a coal tar DNAPL. Science of the Total Environment, 2016, 563-564, 741-754.	3.9	6
810	Metagenomic analysis of rumen microbial population in dairy heifers fed a high grain diet supplemented with dicarboxylic acids or polyphenols. BMC Veterinary Research, 2016, 12, 29.	0.7	55
811	Bacterial community composition and fhs profiles of low- and high-ammonia biogas digesters reveal novel syntrophic acetate-oxidising bacteria. Biotechnology for Biofuels, 2016, 9, 48.	6.2	190
812	Physiological and microbial adjustments to diet quality permit facultative herbivory in an omnivorous lizard. Journal of Experimental Biology, 2016, 219, 1903-1912.	0.8	38
813	Immunogenicity and protective efficacy of recombinant <i>Clostridium difficile</i> flagellar protein FliC. Emerging Microbes and Infections, 2016, 5, 1-10.	3.0	44
814	Relationship of Bacterial Richness to Organic Degradation Rate and Sediment Age in Subseafloor Sediment. Applied and Environmental Microbiology, 2016, 82, 4994-4999.	1.4	47
815	Composition of the Cutaneous Bacterial Community in Japanese Amphibians: Effects of Captivity, Host Species, and Body Region. Microbial Ecology, 2016, 72, 460-469.	1.4	70
816	Colonization potential to reconstitute a microbe community in patients detected early after fecal microbe transplant for recurrent C. difficile. BMC Microbiology, 2016, 16, 5.	1.3	19
817	Large differences in potential denitrification and sediment microbial communities across the Laurentian great lakes. Biogeochemistry, 2016, 128, 353-368.	1.7	34

#	Article	IF	Citations
818	An extended singleâ€index multiplexed 16S rRNA sequencing for microbial community analysis on MiSeq illumina platforms. Journal of Basic Microbiology, 2016, 56, 321-326.	1.8	93
819	Evidence for foliar endophytic nitrogen fixation in a widely distributed subalpine conifer. New Phytologist, 2016, 210, 657-668.	3.5	135
820	Predominance of<i>Lactobacillus</i>spp. Among Patients Who Do Not Acquire Multidrug-Resistant Organisms. Clinical Infectious Diseases, 2016, 63, 937-943.	2.9	28
821	Indoor air bacterial communities in <scp>H</scp>ong <scp>K</scp>ong households assemble independently of occupant skin microbiomes. Environmental Microbiology, 2016, 18, 1754-1763.	1.8	47
822	Microbiome change by symbiotic invasion in lichens. Environmental Microbiology, 2016, 18, 1428-1439.	1.8	41
823	Environmental filtering decreases with fish development for the assembly of gut microbiota. Environmental Microbiology, 2016, 18, 4739-4754.	1.8	267
824	Microbiomeâ€“metabolome analysis reveals unhealthy alterations in the composition and metabolism of ruminal microbiota with increasing dietary grain in a goat model. Environmental Microbiology, 2016, 18, 525-541.	1.8	217
825	Arbuscular mycorrhizal fungal communities and Rhizophagus irregularis populations shift in response to short-term ploughing and fertilisation in a buffer strip. Mycorrhiza, 2016, 26, 33-46.	1.3	34
826	Ice cover extent drives phytoplankton and bacterial community structure in a large northâ€temperate lake: implications for a warming climate. Environmental Microbiology, 2016, 18, 1704-1719.	1.8	68
827	Copper pollution decreases the resistance of soil microbial community to subsequent dryâ€“rewetting disturbance. Journal of Environmental Sciences, 2016, 39, 155-164.	3.2	21
828	Vaginal Microbiota in Pregnancy: Evaluation Based on Vaginal Flora, Birth Outcome, and Race. American Journal of Perinatology, 2016, 33, 401-408.	0.6	34
829	Bacterial microbiome of breast milk and child saliva from low-income Mexican-American women and children. Pediatric Research, 2016, 79, 846-854.	1.1	62
830	Microbiota formed on attached stainless steel coupons correlates with the natural biofilm of the sink surface in domestic kitchens. Canadian Journal of Microbiology, 2016, 62, 148-160.	0.8	28
831	Intestinal microbiota in neonates requiring urgent surgery: assessing the role of probiotics using fecal DNA sequencing. Pediatric Surgery International, 2016, 32, 37-43.	0.6	6
832	Diversity and distribution patterns of acidobacterial communities in the black soil zone of northeast China. Soil Biology and Biochemistry, 2016, 95, 212-222.	4.2	113
833	Supraglacial bacterial community structures vary across the Greenland ice sheet. FEMS Microbiology Ecology, 2016, 92, fiv164.	1.3	48
834	Perfluoroalkyl Acids Inhibit Reductive Dechlorination of Trichloroethene by Repressing <i>Dehalococcoides</i>. Environmental Science & Technology, 2016, 50, 240-248.	4.6	42
835	Microbial community assembly and metabolic function during mammalian corpse decomposition. Science, 2016, 351, 158-162.	6.0	381

#	ARTICLE	IF	CITATIONS
836	Effects of organicâ€“inorganic compound fertilizer with reduced chemical fertilizer application on crop yields, soil biological activity and bacterial community structure in a riceâ€“wheat cropping system. Applied Soil Ecology, 2016, 99, 1-12.	2.1	286
837	Cooperative Mn(II) oxidation between two bacterial strains in an aquatic environment. Water Research, 2016, 89, 252-260.	5.3	40
838	Spatial variability of microbial richness and diversity and relationships with soil organic carbon, texture and structure across an agricultural field. Applied Soil Ecology, 2016, 103, 44-55.	2.1	83
839	The human milk oligosaccharide 2â€²-fucosyllactose augments the adaptive response to extensive intestinal. American Journal of Physiology - Renal Physiology, 2016, 310, G427-G438.	1.6	35
840	Effect of Dust Storms on the Atmospheric Microbiome in the Eastern Mediterranean. Environmental Science & Technology, 2016, 50, 4194-4202.	4.6	90
841	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
842	Bacterioplankton community resilience to ocean acidification: evidence from microbial network analysis. ICES Journal of Marine Science, 2016, 73, 865-875.	1.2	67
843	Highâ€throughput sequencing reveals the core gut microbiome of Barâ€headed goose (<i>Anser) Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	38
844	Do shifts in life strategies explain microbial community responses to increasing nitrogen in tundra soil?. Soil Biology and Biochemistry, 2016, 96, 216-228.	4.2	62
845	Soil bacterial community dynamics reflect changes in plant community and soil properties during the secondary succession of abandoned farmland in the Loess Plateau. Soil Biology and Biochemistry, 2016, 97, 40-49.	4.2	438
846	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
847	Direct and Indirect Horizontal Transmission of the Antifungal Probiotic Bacterium Janthinobacterium lividum on Green Frog (Lithobates clamitans) Tadpoles. Applied and Environmental Microbiology, 2016, 82, 2457-2466.	1.4	45
848	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
849	Antarctic eukaryotic soil diversity of the Prince Charles Mountains revealed by high-throughput sequencing. Soil Biology and Biochemistry, 2016, 95, 112-121.	4.2	66
850	Cheatgrass invasion alters the abundance and composition of dark septate fungal communities in sagebrush steppe. Botany, 2016, 94, 481-491.	0.5	11
851	Hydrolysed wheat gluten as part of a diet based on animal and plant proteins supports good growth performance of Asian seabass (Lates calcarifer), without impairing intestinal morphology or microbiota. Aquaculture, 2016, 453, 40-48.	1.7	73
852	Bacterial community dynamics in an anoxic-aerobic membrane bioreactor â€“ Impact on nutrient and trace organic contaminant removal. International Biodeterioration and Biodegradation, 2016, 109, 61-72.	1.9	63
853	Impacts of Pristine and Transformed Ag and Cu Engineered Nanomaterials on Surficial Sediment Microbial Communities Appear Short-Lived. Environmental Science & Technology, 2016, 50, 2641-2651.	4.6	63

#	ARTICLE	IF	CITATIONS
854	Responses of Soil Bacterial Communities to Nitrogen Deposition and Precipitation Increment Are Closely Linked with Aboveground Community Variation. Microbial Ecology, 2016, 71, 974-989.	1.4	86
855	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. Poultry Science, 2016, 95, 736-748.	1.5	15
856	MiSeq HV4 16S rRNA gene analysis of bacterial community composition among the cave sediments of Indo-Burma biodiversity hotspot. Environmental Science and Pollution Research, 2016, 23, 12216-12226.	2.7	23
857	Aflatoxin B₁Induced Compositional Changes in Gut Microbial Communities of Male F344 Rats. Toxicological Sciences, 2016, 150, 54-63.	1.4	78
858	Cervical Microbiota Associated with Higher Grade Cervical Intraepithelial Neoplasia in Women Infected with High-Risk Human Papillomaviruses. Cancer Prevention Research, 2016, 9, 357-366.	0.7	112
859	Wind and sunlight shape microbial diversity in surface waters of the North Pacific Subtropical Gyre. ISME Journal, 2016, 10, 1308-1322.	4.4	73
860	The microbiome of coral surface mucus has a key role in mediating holobiont health and survival upon disturbance. ISME Journal, 2016, 10, 2280-2292.	4.4	280
861	Impact of the [<i>GAR⁺</i>] Prion on Fermentation and Bacterial Community Composition with<i>Saccharomyces cerevisiae</i>UCD932. American Journal of Enology and Viticulture, 2016, 67, 296-307.	0.9	22
862	A high-throughput belowground plant diversity assay using next-generation sequencing of the trnL intron. Plant and Soil, 2016, 404, 361-372.	1.8	22
863	Changes in the composition and diversity of microbial communities during anaerobic nitrate reduction and Fe(II) oxidation at circumneutral pH in paddy soil. Soil Biology and Biochemistry, 2016, 94, 70-79.	4.2	134
864	Community shift of biofilms developed in a full-scale drinking water distribution system switching from different water sources. Science of the Total Environment, 2016, 544, 499-506.	3.9	37
865	Skin bacterial diversity of Panamanian frogs is associated with host susceptibility and presence of <i>Batrachochytrium dendrobatidis</i>. ISME Journal, 2016, 10, 1682-1695.	4.4	194
866	Bacterial diversity of Grenache and Carignan grape surface from different vineyards at Priorat wine region (Catalonia, Spain). International Journal of Food Microbiology, 2016, 219, 56-63.	2.1	108
867	Dietary flaxseed modulates the colonic microenvironment in healthy C57Bl/6 male mice which may alter susceptibility to gut-associated diseases. Journal of Nutritional Biochemistry, 2016, 28, 61-69.	1.9	58
868	Effects of salinity build-up on the performance and bacterial community structure of a membrane bioreactor. Bioresource Technology, 2016, 200, 305-310.	4.8	81
869	Roles of Sphincter of Oddi Laxity in Bile Duct Microenvironment in Patients with Cholangiolithiasis: From the Perspective of the Microbiome and Metabolome. Journal of the American College of Surgeons, 2016, 222, 269-280e10.	0.2	31
870	Assessment throughout a whole fishing year of the dominant microbiota of peeled brown shrimp (Crangon crangon) stored for 7 days under modified atmosphere packaging at 4ÂÂ°C without preservatives. Food Microbiology, 2016, 54, 60-71.	2.1	21
871	Microbial and Functional Diversity within the Phyllosphere of Espeletia Species in an Andean High-Mountain Ecosystem. Applied and Environmental Microbiology, 2016, 82, 1807-1817.	1.4	55

#	Article	IF	Citations
872	Carriage of Enterobacteria Producing Extended-Spectrum Î²-Lactamases and Composition of the Gut Microbiota in an Amerindian Community. Antimicrobial Agents and Chemotherapy, 2016, 60, 507-514.	1.4	37
873	Glyphosate effects on soil rhizosphere-associated bacterial communities. Science of the Total Environment, 2016, 543, 155-160.	3.9	171
874	Organoheterotrophic Bacterial Abundance Associates with Zinc Removal in Lignocellulose-Based Sulfate-Reducing Systems. Environmental Science & Technology, 2016, 50, 378-387.	4.6	28
875	From Rare to Dominant: a Fine-Tuned Soil Bacterial Bloom during Petroleum Hydrocarbon Bioremediation. Applied and Environmental Microbiology, 2016, 82, 888-896.	1.4	119
876	Microbial Mat Communities along an Oxygen Gradient in a Perennially Ice-Covered Antarctic Lake. Applied and Environmental Microbiology, 2016, 82, 620-630.	1.4	69
877	Bacterial communities estimated by pyrosequencing in the soils of chinampa, a traditional sustainable agro-ecosystem in Mexico. Journal of Soils and Sediments, 2016, 16, 1001-1011.	1.5	20
878	Diets enriched with cranberry beans alter the microbiota and mitigate colitis severity and associated inflammation. Journal of Nutritional Biochemistry, 2016, 28, 129-139.	1.9	90
879	Bacterial diversity indicates dietary overlap among bats of different feeding habits. Microbiological Research, 2016, 182, 99-108.	2.5	42
880	Comparative analysis of the gastrointestinal microbial communities of bar-headed goose (Anser) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 2016, 182, 59-67.	2.5	65
881	Composition of human faecal microbiota in resistance to Campylobacter infection. Clinical Microbiology and Infection, 2016, 22, 61.e1-61.e8.	2.8	74
882	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. Applied and Environmental Microbiology, 2016, 82, 157-166.	1.4	73
883	Inoculation of tanninâ€degrading bacteria into novel hosts increases performance on tanninâ€rich diets. Environmental Microbiology, 2016, 18, 1720-1729.	1.8	67
884	The Succession of Bacterial Community Structure in Groundwater from a 250-m Gallery in the Horonobe Underground Research Laboratory. Geomicrobiology Journal, 2017, 34, 489-499.	1.0	5
885	Effectiveness of ecological rescue for altered soil microbial communities and functions. ISME Journal, 2017, 11, 272-283.	4.4	135
886	Regional and global elevational patterns of microbial species richness and evenness. Ecography, 2017, 40, 393-402.	2.1	79
887	Reference Tree and Environmental Sequence Diversity of Labyrinthulomycetes. Journal of Eukaryotic Microbiology, 2017, 64, 88-96.	0.8	40
888	Identification of oral bacteria on titanium implant surfaces by 16S rDNA sequencing. Clinical Oral Implants Research, 2017, 28, 697-703.	1.9	22
889	Biochar alters the soil microbiome and soil function: results of nextâ€generation amplicon sequencing across Europe. GCB Bioenergy, 2017, 9, 591-612.	2.5	126

#	Article	IF	Citations
890	<i>In vitro</i> effects of sodium bicarbonate buffer on rumen fermentation, levels of lipopolysaccharide and biogenic amine, and composition of rumen microbiota. Journal of the Science of Food and Agriculture, 2017, 97, 1276-1285.	1.7	21
891	Testosterone levels are positively correlated with cloacal bacterial diversity and the relative abundance of Chlamydiae in breeding male rufousâ€collared sparrows. Functional Ecology, 2017, 31, 192-203.	1.7	24
892	The Composition of Human Milk and Infant Faecal Microbiota Over the First Three Months of Life: A Pilot Study. Scientific Reports, 2017, 7, 40597.	1.6	279
893	Variation in Metabolite Profiles of Amphibian Skin Bacterial Communities Across Elevations in the Neotropics. Microbial Ecology, 2017, 74, 227-238.	1.4	34
894	Alteration in successional trajectories of bacterioplankton communities in response to co-exposure of cadmium and phenanthrene in coastal water microcosms. Environmental Pollution, 2017, 221, 480-490.	3.7	10
895	Distinct bacterial communities across a gradient of vegetation from a preserved Brazilian Cerrado. Antonie Van Leeuwenhoek, 2017, 110, 457-469.	0.7	30
896	The Gut Microbiome of the Vector <i>Lutzomyia longipalpis</i> Is Essential for Survival of <i>Leishmania infantum</i>. MBio, 2017, 8, .	1.8	115
897	Composition of Gut Microbiota in the Gibel Carp (Carassius auratus gibelio) Varies with Host Development. Microbial Ecology, 2017, 74, 239-249.	1.4	115
898	Microbial changes linked to the accelerated degradation of the herbicide atrazine in a range of temperate soils. Environmental Science and Pollution Research, 2017, 24, 7359-7374.	2.7	33
899	Variation of the microbiota and metabolome along the canine gastrointestinal tract. Metabolomics, 2017, 13, 1.	1.4	51
900	Growth and Morbidity of Gambian Infants are Influenced by Maternal Milk Oligosaccharides and Infant Gut Microbiota. Scientific Reports, 2017, 7, 40466.	1.6	152
901	Polymetallic nodules, sediments, and deep waters in the equatorial North Pacific exhibit highly diverse and distinct bacterial, archaeal, and microeukaryotic communities. MicrobiologyOpen, 2017, 6, e00428.	1.2	93
902	Microbiome variation in corals with distinct depth distribution ranges across a shallowâ€“mesophotic gradient (15â€“85Âm). Coral Reefs, 2017, 36, 447-452.	0.9	34
903	Symbiotic bacterial communities in ants are modified by invasion pathway bottlenecks and alter host behavior. Ecology, 2017, 98, 861-874.	1.5	16
904	Helicobacter pylori infection is associated with an altered gastric microbiota in children. Mucosal Immunology, 2017, 10, 1169-1177.	2.7	80
905	Formulation of Biocides Increases Antimicrobial Potency and Mitigates the Enrichment of Nonsusceptible Bacteria in Multispecies Biofilms. Applied and Environmental Microbiology, 2017, 83, .	1.4	23
906	Frozen: Thawing and Its Effect on the Postmortem Microbiome in Two Pediatric Cases[,]. Journal of Forensic Sciences, 2017, 62, 1399-1405.	0.9	27
907	Characterization of bacterial communities from Masseiras, a unique Portuguese greenhouse agricultural system. Antonie Van Leeuwenhoek, 2017, 110, 665-676.	0.7	3

#	ARTICLE	IF	CITATIONS
908	New evidences on the altered gut microbiota in autism spectrum disorders. Microbiome, 2017, 5, 24.	4.9	668
909	Denitrification synergized with ANAMMOX for the anaerobic degradation of benzene: performance and microbial community structure. Applied Microbiology and Biotechnology, 2017, 101, 4315-4325.	1.7	18
910	Detection of genetic incompatibilities in non-model systems using simple genetic markers: hybrid breakdown in the haplodiploid spider mite Tetranychus evansi. Heredity, 2017, 118, 311-321.	1.2	24
911	The choice of the DNA extraction method may influence the outcome of the soil microbial community structure analysis. MicrobiologyOpen, 2017, 6, e00453.	1.2	50
912	Spatial impacts of inorganic ligand availability and localized microbial community structure on mitigation of zinc laden mine water in sulfate-reducing bioreactors. Water Research, 2017, 115, 50-59.	5.3	14
913	Simplified and representative bacterial community of maize roots. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2450-E2459.	3.3	487
914	Divergent extremes but convergent recovery of bacterial and archaeal soil communities to an ongoing subterranean coal mine fire. ISME Journal, 2017, 11, 1447-1459.	4.4	108
915	Effects of shearing on biogas production and microbial community structure during anaerobic digestion with recuperative thickening. Bioresource Technology, 2017, 234, 439-447.	4.8	32
916	Corexit 9500 Enhances Oil Biodegradation and Changes Active Bacterial Community Structure of Oil-Enriched Microcosms. Applied and Environmental Microbiology, 2017, 83, .	1.4	94
917	Unexplored Archaeal Diversity in the Great Ape Gut Microbiome. MSphere, 2017, 2, .	1.3	76
918	Fungal diversity in soils across a gradient of preserved Brazilian Cerrado. Journal of Microbiology, 2017, 55, 273-279.	1.3	21
919	Transplantation of fecal microbiota from patients with irritable bowel syndrome alters gut function and behavior in recipient mice. Science Translational Medicine, 2017, 9, .	5.8	366
920	The Fecal Microbial Community of Breast-fed Infants from Armenia and Georgia. Scientific Reports, 2017, 7, 40932.	1.6	28
921	Metagenomics approach to the study of the gut microbiome structure and function in zebrafish Danio rerio fed with gluten formulated diet. Journal of Microbiological Methods, 2017, 135, 69-76.	0.7	34
922	Unraveling the active microbial populations involved in nitrogen utilization in a vertical subsurface flow constructed wetland treating urban wastewater. Science of the Total Environment, 2017, 584-585, 642-650.	3.9	38
923	Cow, yak, and camel milk diets differentially modulated the systemic immunity and fecal microbiota of rats. Science Bulletin, 2017, 62, 405-414.	4.3	20
924	Changes in Microbiota in Rumen Digesta and Feces Due to a Grain-Based Subacute Ruminal Acidosis (SARA) Challenge. Microbial Ecology, 2017, 74, 485-495.	1.4	122
925	Examining the potential use and long-term stability of guaiac faecal occult blood test cards for microbial DNA 16S rRNA sequencing. Journal of Clinical Pathology, 2017, 70, 600-606.	1.0	16

#	Article	IF	Citations
926	Bacterial community diversity associated with different levels of dietary nutrition in the rumen of sheep. Applied Microbiology and Biotechnology, 2017, 101, 3717-3728.	1.7	55
927	Biodegradation of Phenanthrene in Polycyclic Aromatic Hydrocarbon-Contaminated Wastewater Revealed by Coupling Cultivation-Dependent and -Independent Approaches. Environmental Science & Technology, 2017, 51, 3391-3401.	4.6	93
928	A new perspective on studying burial environment before archaeological excavation: analyzing bacterial community distribution by high-throughput sequencing. Scientific Reports, 2017, 7, 41691.	1.6	16
929	Comparative study of the gut microbiome potentially related to milk protein in Murrah buffaloes (Bubalus bubalis) and Chinese Holstein cattle. Scientific Reports, 2017, 7, 42189.	1.6	33
930	Human and rat gut microbiome composition is maintained following sleep restriction. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1564-E1571.	3.3	106
931	Microbiomic differences in tumor and paired-normal tissue in head and neck squamous cell carcinomas. Genome Medicine, 2017, 9, 14.	3.6	97
932	Nitrate effects on chromate reduction in a methane-based biofilm. Water Research, 2017, 115, 130-137.	5.3	69
933	Seasonal patterns in Arctic prasinophytes and inferred ecology of <i>Bathycoccus</i> unveiled in an Arctic winter metagenome. ISME Journal, 2017, 11, 1372-1385.	4.4	54
934	Specificity of root microbiomes in nativeâ€grown <i>Nicotiana attenuata</i> and plant responses to <scp>UVB</scp> increase <i>Deinococcus</i> colonization. Molecular Ecology, 2017, 26, 2543-2562.	2.0	23
935	Bacterial microbiota of Kazakhstan cheese revealed by single molecule real time (SMRT) sequencing and its comparison with Belgian, Kalmykian and Italian artisanal cheeses. BMC Microbiology, 2017, 17, 13.	1.3	22
936	Use of Endophytic and Rhizosphere Bacteria To Improve Phytoremediation of Arsenic-Contaminated Industrial Soils by Autochthonous Betula celtiberica. Applied and Environmental Microbiology, 2017, 83, .	1.4	105
937	Microbiota fingerprints lose individually identifying features over time. Microbiome, 2017, 5, 1.	4.9	300
938	Effect of anaerobic soil disinfestation on the bacterial community and key soilborne phytopathogenic agents under walnut tree-crop nursery conditions. Plant and Soil, 2017, 415, 493-506.	1.8	25
939	Assessment of bacterial profiles in aged, home-made Sichuan paocai brine with varying titratable acidity by PacBio SMRT sequencing technology. Food Control, 2017, 78, 14-23.	2.8	143
940	Host genetic variation in mucosal immunity pathways influences the upper airway microbiome. Microbiome, 2017, 5, 16.	4.9	61
941	Ovarian cycling and reproductive state shape the vaginal microbiota in wild baboons. Microbiome, 2017, 5, 8.	4.9	41
942	Fumigation with dazomet modifies soil microbiota in apple orchards affected by replant disease. Applied Soil Ecology, 2017, 113, 71-79.	2.1	62
943	Effects of nasal instillation of a nitric oxide-releasing solution or parenteral administration of tilmicosin on the nasopharyngeal microbiota of beef feedlot cattle at high-risk of developing respiratory tract disease. Research in Veterinary Science, 2017, 115, 117-124.	0.9	23

#	ARTICLE	IF	CITATIONS
945	Safety of <i>Bifidobacterium animalis</i> Subsp. <i>Lactis</i> (<i>B. lactis</i>) Strain BBâ€12â€Supplemented Yogurt in Healthy Children. Journal of Pediatric Gastroenterology and Nutrition, 2017, 64, 302-309.	0.9	15
946	Microbial Community Structure in a Serpentine-Hosted Abiotic Gas Seepage at the Chimaera Ophiolite, Turkey. Applied and Environmental Microbiology, 2017, 83, .	1.4	37
947	Rice husk biochar impacts soil phosphorous availability, phosphatase activities and bacterial community characteristics in three different soil types. Applied Soil Ecology, 2017, 116, 12-22.	2.1	151
948	Influences of dissolved oxygen concentration on biocathodic microbial communities in microbial fuel cells. Bioelectrochemistry, 2017, 116, 39-51.	2.4	101
949	Distinct Soil Microbial Communities in habitats of differing soil water balance on the Tibetan Plateau. Scientific Reports, 2017, 7, 46407.	1.6	38
950	Mixing of water masses caused by a drifting iceberg affects bacterial activity, community composition and substrate utilization capability in the Southern Ocean. Environmental Microbiology, 2017, 19, 2453-2467.	1.8	21
951	Short Term High Fat Diet Induces Obesityâ€Enhancing Changes in Mouse Gut Microbiota That are Partially Reversed by Cessation of the High Fat Diet. Lipids, 2017, 52, 499-511.	0.7	66
952	Dominance of candidate Saccharibacteria in a membrane bioreactor treating medium age landfill leachate: Effects of organic load on microbial communities, hydrolytic potential and extracellular polymeric substances. Bioresource Technology, 2017, 238, 48-56.	4.8	64
953	Smokeless tobacco products harbor diverse bacterial microbiota that differ across products and brands. Applied Microbiology and Biotechnology, 2017, 101, 5391-5403.	1.7	40
954	Codiversification of gastrointestinal microbiota and phylogeny in passerines is not explained by ecological divergence. Molecular Ecology, 2017, 26, 5292-5304.	2.0	63
955	Nod2 and Nod2-regulated microbiota protect BALB/c mice from diet-induced obesity and metabolic dysfunction. Scientific Reports, 2017, 7, 548.	1.6	48
956	Temporal changes in cutaneous bacterial communities of terrestrialâ€•and aquaticâ€phase newts (Amphibia). Environmental Microbiology, 2017, 19, 3025-3038.	1.8	42
957	Do fecal and litter microbiomes vary within the major areas of a commercial poultry house, and does this affect sampling strategies for whole-house microbiomic studies?. Journal of Applied Poultry Research, 2017, 26, 325-336.	0.6	15
958	Mapping and comparing bacterial microbiota in the sinonasal cavity of healthy, allergic rhinitis, and chronic rhinosinusitis subjects. International Forum of Allergy and Rhinology, 2017, 7, 561-569.	1.5	86
959	pH-Mediated Microbial and Metabolic Interactions in Fecal Enrichment Cultures. MSphere, 2017, 2, .	1.3	105
960	Effectiveness of a full-scale horizontal slow sand filter for controlling phytopathogens in recirculating hydroponics: From microbial isolation to full microbiome assessment. Science of the Total Environment, 2017, 599-600, 780-788.	3.9	13
961	Spatial variation of microbial communities in sediments along the environmental gradients from Xiaoqing River to Laizhou Bay. Marine Pollution Bulletin, 2017, 120, 90-98.	2.3	33
962	Skin microbiota differs drastically between co-occurring frogs and newts. Royal Society Open Science, 2017, 4, 170107.	1.1	43

#	ARTICLE	IF	CITATIONS
963	Copper Pollution Increases the Resistance of Soil Archaeal Community to Changes in Water Regime. Microbial Ecology, 2017, 74, 877-887.	1.4	8
964	H₂O₂ Production in Microbial Electrochemical Cells Fed with Primary Sludge. Environmental Science & Technology, 2017, 51, 6139-6145.	4.6	44
965	Reduction in fecal microbiota diversity and short-chain fatty acid producers in Methicillin-resistant Staphylococcus aureus infected individuals as revealed by PacBio single molecule, real-time sequencing technology. European Journal of Clinical Microbiology and Infectious Diseases, 2017, 36, 1463-1472.	1.3	20
966	New insight with the effects of biochar amendment on bacterial diversity as indicators of biomarkers support the thermophilic phase during sewage sludge composting. Bioresource Technology, 2017, 238, 589-601.	4.8	159
967	Remediation of PAH polluted soils using a soil microbial fuel cell: Influence of electrode interval and role of microbial community. Journal of Hazardous Materials, 2017, 336, 110-118.	6.5	114
968	Cutting through the smoke: the diversity of microorganisms in deep-sea hydrothermal plumes. Royal Society Open Science, 2017, 4, 160829.	1.1	20
969	Impaired renal function and dysbiosis of gut microbiota contribute to increased trimethylamine-N-oxide in chronic kidney disease patients. Scientific Reports, 2017, 7, 1445.	1.6	201
970	Tolerability and safety of the intake of bovine milk oligosaccharides extracted from cheese whey in healthy human adults. Journal of Nutritional Science, 2017, 6, e6.	0.7	17
971	Nearly a decadeâ€long repeatable seasonal diversity patterns of bacterioplankton communities in the eutrophic Lake Donghu (Wuhan, China). Molecular Ecology, 2017, 26, 3839-3850.	2.0	76
972	Perinatal Bacterial Exposure Contributes to IL-13 Aeroallergen Response. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 419-427.	1.4	13
973	11Î²-hydroxysteroid dehydrogenase-1 deficiency alters the gut microbiome response to Western diet. Journal of Endocrinology, 2017, 232, 273-283.	1.2	11
974	Local and geographical factors jointly drive elevational patterns in three microbial groups across subarctic ponds. Global Ecology and Biogeography, 2017, 26, 973-982.	2.7	34
975	A niche for cyanobacteria producing chlorophyll <i>f</i> within a microbial mat. ISME Journal, 2017, 11, 2368-2378.	4.4	62
976	Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. Applied and Environmental Microbiology, 2017, 83, .	1.4	78
977	Illumina-Based Analysis of Bulk and Rhizosphere Soil Bacterial Communities in Paddy Fields Under Mixed Heavy Metal Contamination. Pedosphere, 2017, 27, 569-578.	2.1	82
978	Biogeography of cryoconite bacterial communities on glaciers of the Tibetan Plateau. FEMS Microbiology Ecology, 2017, 93, .	1.3	34
979	Application of Struvite Alters the Antibiotic Resistome in Soil, Rhizosphere, and Phyllosphere. Environmental Science & Technology, 2017, 51, 8149-8157.	4.6	196
980	Bacterial Diversity of Intestinal Microbiota in Patients with Substance Use Disorders Revealed by 16S rRNA Gene Deep Sequencing. Scientific Reports, 2017, 7, 3628.	1.6	97

#	Article	IF	Citations
981	Impact of drinking water treatment and distribution on the microbiome continuum: an ecological disturbance's perspective. Environmental Microbiology, 2017, 19, 3163-3174.	1.8	56
982	Effects of functional milk containing galactooligosaccharide, maltitol, and glucomannan on the production of hydrogen gas in the human intestine. Journal of Functional Foods, 2017, 35, 13-23.	1.6	10
983	Is the rate of mineralization of soil organic carbon under microbiological control?. Soil Biology and Biochemistry, 2017, 112, 127-139.	4.2	51
984	Diabetes-associated microbiota in fa/fa rats is modified by Roux-en-Y gastric bypass. ISME Journal, 2017, 11, 2035-2046.	4.4	52
985	Sulfide-Induced Dissimilatory Nitrate Reduction to Ammonium Supports Anaerobic Ammonium Oxidation (Anammox) in an Open-Water Unit Process Wetland. Applied and Environmental Microbiology, 2017, 83, .	1.4	49
986	Topical Antimicrobial Treatments Can Elicit Shifts to Resident Skin Bacterial Communities and Reduce Colonization by Staphylococcus aureus Competitors. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	48
987	Function of bacterial community dynamics in the formation of cadaveric semiochemicals during <i>in situ</i> carcass decomposition. Environmental Microbiology, 2017, 19, 3310-3322.	1.8	26
988	Membrane biofilm communities in full-scale membrane bioreactors are not randomly assembled and consist of a core microbiome. Water Research, 2017, 123, 124-133.	5.3	62
989	Soil prokaryotic communities in Chernobyl waste disposal trench T22 are modulated by organic matter and radionuclide contamination. FEMS Microbiology Ecology, 2017, 93, .	1.3	20
990	Microbial network, phylogenetic diversity and community membership in the active layer across a permafrost thaw gradient. Environmental Microbiology, 2017, 19, 3201-3218.	1.8	79
991	Bacterial Rhizoplane Colonization Patterns of Buchloe dactyloides Growing in Metalliferous Mine Tailings Reflect Plant Status and Biogeochemical Conditions. Microbial Ecology, 2017, 74, 853-867.	1.4	20
992	Design features of offshore oil production platforms influence their susceptibility to biocorrosion. Applied Microbiology and Biotechnology, 2017, 101, 6517-6529.	1.7	15
993	An 18S rRNA Workflow for Characterizing Protists in Sewage, with a Focus on Zoonotic Trichomonads. Microbial Ecology, 2017, 74, 923-936.	1.4	36
994	Bacterial colonization and succession in a newly opened hospital. Science Translational Medicine, 2017, 9, .	5.8	248
995	Relative roles of competition, environmental selection and spatial processes in structuring soil bacterial communities in the Qinghai-Tibetan Plateau. Applied Soil Ecology, 2017, 117-118, 223-232.	2.1	24
996	Temporal Dynamics of Bacterial and Fungal Colonization on Plastic Debris in the North Sea. Environmental Science & Technology, 2017, 51, 7350-7360.	4.6	239
997	Characterization of suspended bacteria from processing units in an advanced drinking water treatment plant of China. Environmental Science and Pollution Research, 2017, 24, 12176-12184.	2.7	7
998	Metagenomic analysis in Lake Onego (Russia) Synechococcus cyanobacteria. Journal of Great Lakes Research, 2017, 43, 43-54.	0.8	2

#	Article	IF	Citations
999	Identification of Microbial Profile of <i>Koji</i> Using Single Molecule, Realâ€Time Sequencing Technology. Journal of Food Science, 2017, 82, 1193-1199.	1.5	25
1000	Microbial Biogeography and Core Microbiota of the Rat Digestive Tract. Scientific Reports, 2017, 7, 45840.	1.6	127
1001	The Dynamic Microbiota Profile During Pepper (Piper nigrum L.) Peeling by Solid-State Fermentation. Current Microbiology, 2017, 74, 739-746.	1.0	10
1002	The role of a PSP-producing Alexandrium bloom in an unprecedented diamondback terrapin () Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	9
1003	Dynamic profile of the microbiota during coconut water pre-fermentation for nata de coco production. LWT - Food Science and Technology, 2017, 81, 87-93.	2.5	19
1004	Metagenomic analyses of bacterial endophytes associated with the phyllosphere of a Bt maize cultivar and its isogenic parental line from South Africa. World Journal of Microbiology and Biotechnology, 2017, 33, 80.	1.7	50
1005	Weaning age influences the severity of gastrointestinal microbiome shifts in dairy calves. Scientific Reports, 2017, 7, 198.	1.6	87
1006	Restoration of cefixime-induced gut microbiota changes by Lactobacillus cocktails and fructooligosaccharides in a mouse model. Microbiological Research, 2017, 200, 14-24.	2.5	54
1007	Changes in intestinal microbiota composition and metabolism coincide with increased intestinal permeability in young adults under prolonged physiological stress. American Journal of Physiology - Renal Physiology, 2017, 312, G559-G571.	1.6	239
1008	The nasopharyngeal microbiota of beef cattle before and after transport to a feedlot. BMC Microbiology, 2017, 17, 70.	1.3	69
1009	Members of Gammaproteobacteria as indicator species of healthy banana plants on Fusarium wilt-infested fields in Central America. Scientific Reports, 2017, 7, 45318.	1.6	89
1010	Community structure of the gut microbiota in sympatric species of wild <i>Drosophila</i>. Ecology Letters, 2017, 20, 629-639.	3.0	118
1011	Hunting for healthy microbiomes: determining the core microbiomes of Ceratina, Megalopta, and Apis bees and how they associate with microbes in bee collected pollen. Conservation Genetics, 2017, 18, 701-711.	0.8	68
1012	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. MSystems, 2017, 2, .	1.7	91
1013	Cutaneous microbiota of the Japanese giant salamander (Andrias japonicus), a representative of an ancient amphibian clade. Hydrobiologia, 2017, 795, 153-167.	1.0	12
1014	Effects of dietary inclusion of the yeasts Saccharomyces cerevisiae and Wickerhamomyces anomalus on gut microbiota of rainbow trout. Aquaculture, 2017, 473, 528-537.	1.7	66
1015	Enlightening discriminative network functional modules behind Principal Component Analysis separation in differential-omic science studies. Scientific Reports, 2017, 7, 43946.	1.6	45
1016	A Fast Small-Sample Kernel Independence Test for Microbiome Community-Level Association Analysis. Biometrics, 2017, 73, 1453-1463.	0.8	36

#	Article	IF	Citations
1017	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. Nature Chemical Biology, 2017, 13, 537-543.	3.9	141
1018	Microbial communities of aquatic environments on Heard Island characterized by pyrotag sequencing and environmental data. Scientific Reports, 2017, 7, 44480.	1.6	12
1020	Metagenomics of Hyperthermophilic Environments: Biodiversity and Biotechnology. , 2017, , 103-135.		7
1021	Contrasting patterns of diversity of abundant and rare bacterioplankton in freshwater lakes along an elevation gradient. Limnology and Oceanography, 2017, 62, 1570-1585.	1.6	49
1022	Distinct ecological niches of marine symbiotic N₂â€fixing cyanobacterium <i>Candidatus Atelocyanobacterium thalassa</i> sublineages. Journal of Phycology, 2017, 53, 451-461.	1.0	66
1023	Alternative Protein Sources in the Diet Modulate Microbiota and Functionality in the Distal Intestine of Atlantic Salmon (Salmo salar). Applied and Environmental Microbiology, 2017, 83, .	1.4	142
1024	Enhanced yields and soil quality in a wheatâ€“maize rotation using buried straw mulch. Journal of the Science of Food and Agriculture, 2017, 97, 3333-3341.	1.7	19
1025	Duodenal endoluminal barrier sleeve alters gut microbiota of ZDF rats. International Journal of Obesity, 2017, 41, 381-389.	1.6	17
1026	Environmental fluctuations and host skin bacteria shift survival advantage between frogs and their fungal pathogen. ISME Journal, 2017, 11, 349-361.	4.4	100
1027	High taxonomic variability despite stable functional structure across microbial communities. Nature Ecology and Evolution, 2017, 1, 15.	3.4	378
1028	Temporal dynamics of bacterioplankton communities in response to excessive nitrate loading in oligotrophic coastal water. Marine Pollution Bulletin, 2017, 114, 656-663.	2.3	8
1029	The effect of inoculum source and fluid shear force on the development of<i>inÂvitro</i>oral multispecies biofilms. Journal of Applied Microbiology, 2017, 122, 796-808.	1.4	19
1030	Regional synchrony in full-scale activated sludge bioreactors due to deterministic microbial community assembly. ISME Journal, 2017, 11, 500-511.	4.4	124
1031	Effects of Actinomycete Secondary Metabolites on Sediment Microbial Communities. Applied and Environmental Microbiology, 2017, 83, .	1.4	44
1032	Agricultural soil denitrifiers possess extensive nitrite reductase gene diversity. Environmental Microbiology, 2017, 19, 1189-1208.	1.8	61
1033	Clay-to-Carbon Ratio Controls the Effect of Herbicide Application on Soil Bacterial Richness and Diversity in a Loamy Field. Water, Air, and Soil Pollution, 2017, 228, 1.	1.1	3
1034	Long-Term Nickel Contamination Increases the Occurrence of Antibiotic Resistance Genes in Agricultural Soils. Environmental Science & Technology, 2017, 51, 790-800.	4.6	240
1035	Microbially Catalysed Selenate Removal in an Inverse Fluidised Bed Reactor. Solid State Phenomena, 0, 262, 677-681.	0.3	8

#	ARTICLE	IF	CITATIONS
1036	Adaptation to Chronic Nutritional Stress Leads to Reduced Dependence on Microbiota in <i>Drosophila melanogaster</i>. MBio, 2017, 8, .	1.8	39
1037	Contaminants of emerging concern affect <i>Trichoplusia ni</i> growth and development on artificial diets and a key host plant. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9923-E9931.	3.3	23
1038	Metagenomic insights into the effects of oligosaccharides on the microbial composition of cecal contents in constipated mice. Journal of Functional Foods, 2017, 38, 486-496.	1.6	33
1039	Revealing the gut bacteriome of Dendroctonus bark beetles (Curculionidae: Scolytinae): diversity, core members and co-evolutionary patterns. Scientific Reports, 2017, 7, 13864.	1.6	58
1040	Bridging spatially segregated redox zones with a microbial electrochemical snorkel triggers biogeochemical cycles in oil-contaminated River Tyne (UK) sediments. Water Research, 2017, 127, 11-21.	5.3	30
1041	Performance evaluation and microbial community analysis of the function and fate of ammonia in a sulfate-reducing EGSB reactor. Applied Microbiology and Biotechnology, 2017, 101, 7729-7739.	1.7	21
1042	Evaluation of the efficacy and safety of Ganoderma lucidum mycelium-fermented liquid on gut microbiota and its impact on cardiovascular risk factors in human. RSC Advances, 2017, 7, 45093-45100.	1.7	14
1043	A Distinctive and Host-Restricted Gut Microbiota in Populations of a Cactophilic Drosophila Species. Applied and Environmental Microbiology, 2017, 83, .	1.4	34
1044	Effects of contaminants of emerging concern on Megaselia scalaris (Lowe, Diptera: Phoridae) and its microbial community. Scientific Reports, 2017, 7, 8165.	1.6	18
1045	Natural polyreactive IgA antibodies coat the intestinal microbiota. Science, 2017, 358, .	6.0	344
1046	Development of a microbial test suite and data integration method for assessing microbial health of contaminated soil. Journal of Microbiological Methods, 2017, 143, 66-77.	0.7	9
1047	High reactivity of deep biota under anthropogenic CO2 injection into basalt. Nature Communications, 2017, 8, 1063.	5.8	55
1048	Prokaryotic Community Distribution along an Ecological Gradient of Salinity in Surface and Subsurface Saline Soils. Scientific Reports, 2017, 7, 13332.	1.6	33
1049	Hostâ€“microbiota interaction induces bi-phasic inflammation and glucose intolerance in mice. Molecular Metabolism, 2017, 6, 1371-1380.	3.0	30
1050	Core fecal microbiota of domesticated herbivorous ruminant, hindgut fermenters, and monogastric animals. MicrobiologyOpen, 2017, 6, e00509.	1.2	83
1051	Elevated precipitation modifies the relationship between plant diversity and soil bacterial diversity under nitrogen deposition in Stipa baicalensis steppe. Applied Soil Ecology, 2017, 119, 345-353.	2.1	24
1052	Emergence of <i>Leuconostoc mesenteroides</i> as a causative agent of oozing in carrots stored under nonâ€ventilated conditions. Microbial Biotechnology, 2017, 10, 1677-1689.	2.0	18
1053	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	1.9	84

#	ARTICLE	IF	CITATIONS
1054	Characterization of microbiota in<i>Arapaima gigas</i>intestine and isolation of potential probiotic bacteria. Journal of Applied Microbiology, 2017, 123, 1298-1311.	1.4	32
1055	Butyrate Supplementation at High Concentrations Alters Enteric Bacterial Communities and Reduces Intestinal Inflammation in Mice Infected with Citrobacter rodentium. MSphere, 2017, 2, .	1.3	87
1056	Intestinal microbiota is altered in patients with colon cancer and modified by probiotic intervention. BMJ Open Gastroenterology, 2017, 4, e000145.	1.1	266
1057	Coupling Bioflocculation of <i>Dehalococcoides mccartyi</i> to High-Rate Reductive Dehalogenation of Chlorinated Ethenes. Environmental Science & Technology, 2017, 51, 11297-11307.	4.6	18
1058	Hiding in Plain Sight: Mining Bacterial Species Records for Phenotypic Trait Information. MSphere, 2017, 2, .	1.3	69
1059	Fructooligosaccharide (FOS) and Galactooligosaccharide (GOS) Increase Bifidobacterium but Reduce Butyrate Producing Bacteria with Adverse Glycemic Metabolism in healthy young population. Scientific Reports, 2017, 7, 11789.	1.6	181
1060	Investigation on the anaerobic co-digestion of food waste with sewage sludge. Applied Microbiology and Biotechnology, 2017, 101, 7755-7766.	1.7	20
1061	Evaluation of Sedum as driver for plant microbial fuel cells in a semi-arid green roof ecosystem. Ecological Engineering, 2017, 108, 203-210.	1.6	49
1062	Identifying the Active Microbiome Associated with Roots and Rhizosphere Soil of Oilseed Rape. Applied and Environmental Microbiology, 2017, 83, .	1.4	141
1063	Low <i>Lactobacilli</i> abundance and polymicrobial diversity in the lower reproductive tract of female rhesus monkeys do not compromise their reproductive success. American Journal of Primatology, 2017, 79, e22691.	0.8	4
1064	Biodiversity and species competition regulate the resilience of microbial biofilm community. Molecular Ecology, 2017, 26, 6170-6182.	2.0	299
1065	Consumption of Two Healthy Dietary Patterns Restored Microbiota Dysbiosis in Obese Patients with Metabolic Dysfunction. Molecular Nutrition and Food Research, 2017, 61, 1700300.	1.5	107
1066	Antibiotic-induced perturbations in microbial diversity during post-natal development alters amyloid pathology in an aged APPSWE/PS1Î”E9 murine model of Alzheimerâ€™s disease. Scientific Reports, 2017, 7, 10411.	1.6	206
1067	Microbiome Alterations Are Correlated with Occurrence of Postharvest Stem-End Rot in Mango Fruit. Phytobiomes Journal, 2017, 1, 117-127.	1.4	72
1068	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>. MBio, 2017, 8, .	1.8	60
1069	Effects of biochar amendment on bacterial and fungal diversity for co-composting of gelatin industry sludge mixed with organic fraction of municipal solid waste. Bioresource Technology, 2017, 246, 214-223.	4.8	68
1070	Drought Stress Results in a Compartment-Specific Restructuring of the Rice Root-Associated Microbiomes. MBio, 2017, 8, .	1.8	336
1071	The dynamics of the bacterial communities developed in maize silage. Microbial Biotechnology, 2017, 10, 1663-1676.	2.0	77

#	ARTICLE	IF	CITATIONS
1072	Natural succession on abandoned cropland effectively decreases the soil erodibility and improves the fungal diversity. Ecological Applications, 2017, 27, 2142-2154.	1.8	44
1073	Silver nanoparticles deteriorate the mutual interaction between maize (Zea mays L.) and arbuscular mycorrhizal fungi: a soil microcosm study. Applied Soil Ecology, 2017, 119, 307-316.	2.1	40
1074	Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. Water Research, 2017, 124, 77-84.	5.3	82
1075	The impact of the bovine faecal microbiome on <i>Escherichia coli</i> O157:H7 prevalence and enumeration in naturally infected cattle. Journal of Applied Microbiology, 2017, 123, 1027-1042.	1.4	9
1076	A Method to Assess Bacteriocin Effects on the Gut Microbiota of Mice. Journal of Visualized Experiments, 2017, , .	0.2	3
1077	Relationships between gastrointestinal microbiota and blood group antigens. Physiological Genomics, 2017, 49, 473-483.	1.0	34
1078	Enhancing biodegradation of C16-alkyl quaternary ammonium compounds using an oxygen-based membrane biofilm reactor. Water Research, 2017, 123, 825-833.	5.3	57
1079	Bacterial community shift revealed Chromatiaceae and Alcaligenaceae as potential bioindicators in the receiving river due to palm oil mill effluent final discharge. Ecological Indicators, 2017, 82, 526-529.	2.6	18
1080	Diversity and stability of coral endolithic microbial communities at a naturally high <i>p</i>CO₂ reef. Molecular Ecology, 2017, 26, 5344-5357.	2.0	43
1081	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. MSystems, 2017, 2, .	1.7	47
1082	Investigation and manipulation of metabolically active methanogen community composition during rumen development in black goats. Scientific Reports, 2017, 7, 422.	1.6	51
1083	Identification of unique microbiomes associated with harmful algal blooms caused by Alexandrium fundyense and Dinophysis acuminata. Harmful Algae, 2017, 68, 17-30.	2.2	48
1084	Early-life disruption of amphibian microbiota decreases later-life resistance to parasites. Nature Communications, 2017, 8, 86.	5.8	146
1085	Comparison of DNA-, PMA-, and RNA-based 16S rRNA Illumina sequencing for detection of live bacteria in water. Scientific Reports, 2017, 7, 5752.	1.6	116
1086	Microbiota composition of the koala (Phascolarctos cinereus) ocular and urogenital sites, and their association with Chlamydia infection and disease. Scientific Reports, 2017, 7, 5239.	1.6	14
1087	Rapid Response of Eastern Mediterranean Deep Sea Microbial Communities to Oil. Scientific Reports, 2017, 7, 5762.	1.6	27
1088	Bottom-up effects on herbivore-induced plant defences: a case study based on compositional patterns of rhizosphere microbial communities. Scientific Reports, 2017, 7, 6251.	1.6	15
1089	Occurrence and expression of novel methyl-coenzyme M reductase gene (mcrA) variants in hot spring sediments. Scientific Reports, 2017, 7, 7252.	1.6	37

#	Article	IF	Citations
1090	Dramatic Differences in Gut Bacterial Densities Correlate with Diet and Habitat in Rainforest Ants. Integrative and Comparative Biology, 2017, 57, 705-722.	0.9	77
1091	Symbiont dynamics and strain diversity in the defensive mutualism between <i>Lagria</i> beetles and <i>Burkholderia</i>. Environmental Microbiology, 2017, 19, 3674-3688.	1.8	42
1092	An underappreciated hotspot of antibiotic resistance: The groundwater near the municipal solid waste landfill. Science of the Total Environment, 2017, 609, 966-973.	3.9	133
1093	High-grain diets altered rumen fermentation and epithelial bacterial community and resulted in rumen epithelial injuries of goats. Applied Microbiology and Biotechnology, 2017, 101, 6981-6992.	1.7	46
1094	The role of microbial diversity and composition in minimizing sludge production in the oxic-settling-anoxic process. Science of the Total Environment, 2017, 607-608, 558-567.	3.9	28
1095	Microbial association with the dynamics of particulate organic carbon in response to the amendment of elevated CO2-derived wheat residue into a Mollisol. Science of the Total Environment, 2017, 607-608, 972-981.	3.9	38
1096	Effects of Disodium Fumarate on In Vitro Rumen Fermentation, The Production of Lipopolysaccharide and Biogenic Amines, and The Rumen Bacterial Community. Current Microbiology, 2017, 74, 1337-1342.	1.0	10
1097	The Skin Microbiome of Cohabiting Couples. MSystems, 2017, 2, .	1.7	87
1098	Insights into Butyrate Production in a Controlled Fermentation System via Gene Predictions. MSystems, 2017, 2, .	1.7	169
1099	Effect of membrane material chemistry and properties on biofouling susceptibility during milk and cheese whey ultrafiltration. Journal of Membrane Science, 2017, 542, 208-216.	4.1	16
1100	Microbes Facilitate Mineral Deposition in Bioelectrochemical Systems. ACS Earth and Space Chemistry, 2017, 1, 277-287.	1.2	12
1101	Effects of over 30-year of different fertilization regimes on fungal community compositions in the black soils of northeast China. Agriculture, Ecosystems and Environment, 2017, 248, 113-122.	2.5	105
1102	Methane-metabolizing microbial communities in sediments of the Haima cold seep area, northwest slope of the South China Sea. FEMS Microbiology Ecology, 2017, 93, .	1.3	44
1103	Navy and black bean supplementation primes the colonic mucosal microenvironment to improve gut health. Journal of Nutritional Biochemistry, 2017, 49, 89-100.	1.9	59
1104	Intestinal Dysbiosis and Biotin Deprivation Induce Alopecia through Overgrowth of Lactobacillus murinus in Mice. Cell Reports, 2017, 20, 1513-1524.	2.9	93
1105	Predicting Microbial Fuel Cell Biofilm Communities and Bioreactor Performance using Artificial Neural Networks. Environmental Science & Technology, 2017, 51, 10881-10892.	4.6	64
1106	Incorporation of bean plant residue in soil with different agricultural practices and its effect on the soil bacteria. Applied Soil Ecology, 2017, 119, 417-427.	2.1	40
1107	A wellness study of 108 individuals using personal, dense, dynamic data clouds. Nature Biotechnology, 2017, 35, 747-756.	9.4	340

#	ARTICLE	IF	CITATIONS
1108	Consumption of kiwifruit capsules increases <i>Faecalibacterium prausnitzii</i> abundance in functionally constipated individuals: a randomised controlled human trial. Journal of Nutritional Science, 2017, 6, e52.	0.7	34
1109	Archaeal and Bacterial Community Structure in an Anaerobic Digestion Reactor (Lagoon Type) Used for Biogas Production at a Pig Farm. Journal of Molecular Microbiology and Biotechnology, 2017, 27, 306-317.	1.0	33
1110	Carbonate-rich dendrolitic cones: insights into a modern analog for incipient microbialite formation, Little Hot Creek, Long Valley Caldera, California. Npj Biofilms and Microbiomes, 2017, 3, 32.	2.9	30
1111	High-resolution bacterial 16S rRNA gene profile meta-analysis and biofilm status reveal common colorectal cancer consortia. Npj Biofilms and Microbiomes, 2017, 3, 34.	2.9	237
1112	Stromatolites on the rise in peat-bound karstic wetlands. Scientific Reports, 2017, 7, 15384.	1.6	28
1113	Salt-responsive gut commensal modulates TH17 axis and disease. Nature, 2017, 551, 585-589.	13.7	896
1114	Microbe biogeography tracks water masses in a dynamic oceanic frontal system. Royal Society Open Science, 2017, 4, 170033.	1.1	46
1115	Does noncontact lowâ€frequency ultrasound therapy contribute to wound healing at the molecular level?. Wound Repair and Regeneration, 2017, 25, 871-882.	1.5	9
1116	An intact gut microbiota may be required for lactoferrin-driven immunomodulation in rats. Journal of Functional Foods, 2017, 39, 268-278.	1.6	13
1117	A High-Throughput DNA-Sequencing Approach for Determining Sources of Fecal Bacteria in a Lake Superior Estuary. Environmental Science & Technology, 2017, 51, 8263-8271.	4.6	54
1118	Vertical and horizontal assemblage patterns of bacterial communities in a eutrophic river receiving domestic wastewater in southeast China. Environmental Pollution, 2017, 230, 469-478.	3.7	65
1119	Effect of cytomegalovirus and Epsteinâ€“Barr virus replication on intestinal mucosal gene expression and microbiome composition of HIV-infected and uninfected individuals. Aids, 2017, 31, 2059-2067.	1.0	26
1120	Application of the entomogenous fungus, Metarhizium anisopliae, for leafroller (Cnaphalocrocis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2 Biotechnology, 2017, 101, 6793-6807.	1.7	26
1121	SigTree : A Microbial Community Analysis Tool to Identify and Visualize Significantly Responsive Branches in a Phylogenetic Tree. Computational and Structural Biotechnology Journal, 2017, 15, 372-378.	1.9	5
1122	The gut eukaryotic microbiota influences the growth performance among cohabitating shrimp. Applied Microbiology and Biotechnology, 2017, 101, 6447-6457.	1.7	77
1123	Polydextrose changes the gut microbiome and attenuates fasting triglyceride and cholesterol levels in Western diet fed mice. Scientific Reports, 2017, 7, 5294.	1.6	71
1124	Robustness and Microbial Diversity of a Fluidized Bed Reactor Employed for the Removal and Degradation of an Anionic Surfactant from Laundry Wastewater. Journal of Environmental Engineering, ASCE, 2017, 143, .	0.7	10
1125	Natural products and morphogenic activity of Î³-Proteobacteria associated with the marine hydroid polyp Hydractinia echinata. Bioorganic and Medicinal Chemistry, 2017, 25, 6088-6097.	1.4	15

#	ARTICLE	IF	CITATIONS
1126	Bifidobacterium animalis subsp. lactis LKM512 reduces levels of intestinal trimethylamine produced by intestinal microbiota in healthy volunteers: A double-blind, placebo-controlled study. Journal of Functional Foods, 2017, 36, 94-101.	1.6	30
1127	Bacterial profile in human atherosclerotic plaques. Atherosclerosis, 2017, 263, 177-183.	0.4	49
1128	Inter-personal diversity and temporal dynamics of dental, tongue, and salivary microbiota in the healthy oral cavity. Npj Biofilms and Microbiomes, 2017, 3, 2.	2.9	158
1129	Diversity and Persistence of the Gut Microbiome of the Giant Neotropical Bullet Ant. Integrative and Comparative Biology, 2017, 57, 682-689.	0.9	21
1130	Community analysis of biofilms on flame-oxidized stainless steel anodes in microbial fuel cells fed with different substrates. BMC Microbiology, 2017, 17, 145.	1.3	22
1131	Direct treatment of high-strength soft drink wastewater using a down-flow hanging sponge reactor: performance and microbial community dynamics. Applied Microbiology and Biotechnology, 2017, 101, 5925-5936.	1.7	10
1132	Social Influences on Prevotella and the Gut Microbiome of Young Monkeys. Psychosomatic Medicine, 2017, 79, 888-897.	1.3	47
1133	Microbial composition of spiny ants (Hymenoptera: Formicidae: Polyrhachis) across their geographic range. BMC Evolutionary Biology, 2017, 17, 96.	3.2	42
1134	Bacterial and fungal core microbiomes associated with small grain silages during ensiling and aerobic spoilage. BMC Microbiology, 2017, 17, 50.	1.3	116
1135	Dominant bacterial phyla in caves and their predicted functional roles in C and N cycle. BMC Microbiology, 2017, 17, 90.	1.3	70
1136	Temperature drives the assembly of endophytic communities' seasonal succession. Environmental Microbiology, 2017, 19, 3353-3364.	1.8	54
1137	Influence of water management on the active root-associated microbiota involved in arsenic, iron, and sulfur cycles in rice paddies. Applied Microbiology and Biotechnology, 2017, 101, 6725-6738.	1.7	32
1138	Dietary fructose causes defective insulin signalling and ceramide accumulation in the liver that can be reversed by gut microbiota modulation. Food and Nutrition Research, 2017, 61, 1331657.	1.2	44
1139	Bacterial community composition and diversity in Kalakuli, an alpine glacial-fed lake in Muztagh Ata of the westernmost Tibetan Plateau. FEMS Microbiology Ecology, 2017, 93, .	1.3	23
1140	Early-Life Diet Affects Host Microbiota and Later-Life Defenses Against Parasites in Frogs. Integrative and Comparative Biology, 2017, 57, 732-742.	0.9	44
1141	White Syndrome-Affected Corals Have a Distinct Microbiome at Disease Lesion Fronts. Applied and Environmental Microbiology, 2017, 83, .	1.4	52
1142	Features of the bronchial bacterial microbiome associated with atopy, asthma, and responsiveness to inhaled corticosteroid treatment. Journal of Allergy and Clinical Immunology, 2017, 140, 63-75.	1.5	222
1143	Thirty-one years of rice-rice-green manure rotations shape the rhizosphere microbial community and enrich beneficial bacteria. Soil Biology and Biochemistry, 2017, 104, 208-217.	4.2	205

#	ARTICLE	IF	CITATIONS
1144	Microbial community analysis of pH 4 thermal springs in Yellowstone National Park. Extremophiles, 2017, 21, 135-152.	0.9	30
1145	Exploring lot-to-lot variation in spoilage bacterial communities on commercial modified atmosphere packaged beef. Food Microbiology, 2017, 62, 147-152.	2.1	49
1146	Individualization of pubic hair bacterial communities and the effects of storage time and temperature. Forensic Science International: Genetics, 2017, 26, 12-20.	1.6	26
1147	Gut microbiome in children with enthesitis-related arthritis in a developing country and the effect of probiotic administration. Clinical and Experimental Immunology, 2017, 187, 480-489.	1.1	53
1148	The rectal mucosa and condomless receptive anal intercourse in HIV-negative MSM: implications for HIV transmission and prevention. Mucosal Immunology, 2017, 10, 996-1007.	2.7	135
1149	The bacterial community associated with rose-scented geranium (Pelargonium graveolens) leaves responds to anthracnose symptoms. Plant and Soil, 2017, 414, 69-79.	1.8	5
1150	Genome reduction in an abundant and ubiquitous soil bacterium â€˜Candidatus Udaeobacter copiosusâ€™. Nature Microbiology, 2017, 2, 16198.	5.9	168
1151	Mannan- and xylooligosaccharides modulate caecal microbiota and expression of inflammatory-related cytokines and reduce caecal<i>Salmonella</i>Enteritidis colonisation in young chickens. FEMS Microbiology Ecology, 2017, 93, fiw226.	1.3	50
1152	Dry Season Constrains Bacterial Phylogenetic Diversity in a Semi-Arid Rhizosphere System. Microbial Ecology, 2017, 73, 153-161.	1.4	86
1153	The Cervicovaginal Microbiota in Women Notified for<i>Chlamydia trachomatis</i>Infection: A Case-Control Study at the Sexually Transmitted Infection Outpatient Clinic in Amsterdam, The Netherlands. Clinical Infectious Diseases, 2017, 64, 24-31.	2.9	66
1154	Flowers and Wild Megachilid Bees Share Microbes. Microbial Ecology, 2017, 73, 188-200.	1.4	128
1155	The microbial degradation of 2,4,6-tribromophenol (TBP) in water/sediments interface: Investigating bioaugmentation using Bacillus sp. GZT. Science of the Total Environment, 2017, 575, 573-580.	3.9	23
1156	Iron oxide magnetic nanoparticles deteriorate the mutual interaction between arbuscular mycorrhizal fungi and plant. Journal of Soils and Sediments, 2017, 17, 841-851.	1.5	44
1157	Effects of polysaccharide from mycelia of Ganoderma lucidum on intestinal barrier functions of rats. International Journal of Biological Macromolecules, 2017, 94, 1-9.	3.6	102
1158	Analysis of bacterial composition in marine sponges reveals the influence of host phylogeny and environment. FEMS Microbiology Ecology, 2017, 93, fiw204.	1.3	31
1159	The influence of the autochthonous wastewater microbiota and gene host on the fate of invasive antibiotic resistance genes. Science of the Total Environment, 2017, 575, 932-940.	3.9	11
1160	Characterization of the Cutaneous Bacterial Communities of Two Giant Salamander Subspecies. Microbial Ecology, 2017, 73, 445-454.	1.4	27
1161	Addition of arabinoxylan and mixed linkage glucans in porcine diets affects the large intestinal bacterial populations. European Journal of Nutrition, 2017, 56, 2193-2206.	1.8	27

#	Article	IF	Citations
1162	Metaâ€omic analyses of Baltic Sea cyanobacteria: diversity, community structure and salt acclimation. Environmental Microbiology, 2017, 19, 673-686.	1.8	65
1163	Fire modifies the phylogenetic structure of soil bacterial coâ€occurrence networks. Environmental Microbiology, 2017, 19, 317-327.	1.8	48
1164	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. Nature Microbiology, 2017, 2, 16221.	5.9	138
1165	Composition and diversity of mucosaâ€associated microbiota along the entire length of the pig gastrointestinal tract; dietary influences. Environmental Microbiology, 2017, 19, 1425-1438.	1.8	120
1166	Insight into the long-term effect of mangrove species on removal of polybrominated diphenyl ethers (PBDEs) from BDE-47 contaminated sediments. Science of the Total Environment, 2017, 575, 390-399.	3.9	51
1167	Monitoring the mycobiota during Greco di Tufo and Aglianico wine fermentation by 18S rRNA gene sequencing. Food Microbiology, 2017, 63, 117-122.	2.1	35
1168	Contribution of different dispersal sources to the metabolic response of lake bacterioplankton following a salinity change. Environmental Microbiology, 2017, 19, 251-260.	1.8	19
1169	Honey bee gut microbial communities are robust to the fungicide PristineÂ® consumed in pollen. Apidologie, 2017, 48, 340-352.	0.9	21
1170	Changes in the bacterial microbiome of patients with chronic rhinosinusitis after endoscopic sinus surgery. International Forum of Allergy and Rhinology, 2017, 7, 7-15.	1.5	39
1171	Interleukin-15 promotes intestinal dysbiosis with butyrate deficiency associated with increased susceptibility to colitis. ISME Journal, 2017, 11, 15-30.	4.4	68
1172	Intraruminal infusion of oligofructose alters ruminal microbiota and induces acute laminitis in sheep1,2. Journal of Animal Science, 2017, 95, 5407-5419.	0.2	5
1173	Eikelboom filamentous morphotypes 0675 and 0041 embrace members of the Chloroflexi: resolving their phylogeny, and design of fluorescence in situ hybridisation probes for their identification. FEMS Microbiology Ecology, 2017, 93, .	1.3	17
1174	Food-grade cationic antimicrobial Îµ-polylysine transiently alters the gut microbial community and predicted metagenome function in CD-1 mice. Npj Science of Food, 2017, 1, 8.	2.5	31
1175	Bioinformatics in Microbiome Analysis. Methods in Microbiology, 2017, 44, 1-18.	0.4	4
1176	Microbial diversity in an intensively managed landscape is structured by landscape connectivity. FEMS Microbiology Ecology, 2017, 93, .	1.3	30
1177	A comprehensive evaluation of the sl1p pipeline for 16S rRNA gene sequencing analysis. Microbiome, 2017, 5, 100.	4.9	82
1178	High Organic Loading Treatment of Synthetic Soy-sauce Production Wastewater Using a Combined System Consisting of a Psychrophilic (20 ºC) UASB Reactor and a DHS Reactor at Ambient Temperature. Journal of Japan Society on Water Environment, 2017, 40, 67-75.	0.1	1
1179	Effects of kelp<i>Ecklonia maxima</i>inclusion in formulated feed on the growth, feed utilisation and gut microbiota of South African abalone<i>Haliotis midae</i>. African Journal of Marine Science, 2017, 39, 183-192.	0.4	9

#	ARTICLE	IF	CITATIONS
1180	Impact of hypoxia on gene expression patterns by the human pathogen, Vibrio vulnificus , and bacterial community composition in a North Carolina estuary. GeoHealth, 2017, 1, 37-50.	1.9	7
1181	Geographical variation in soil bacterial community structure in tropical forests in Southeast Asia and temperate forests in Japan based on pyrosequencing analysis of 16S rRNA. Genes and Genetic Systems, 2017, 92, 1-20.	0.2	11
1182	Climate controls prokaryotic community composition in desert soils of the southwestern United States. FEMS Microbiology Ecology, 2017, 93, .	1.3	26
1183	Influence of short-term dietary starch inclusion on the equine cecal microbiome1. Journal of Animal Science, 2017, 95, 5077-5090.	0.2	33
1184	Pearl Millet Genetic Traits Shape Rhizobacterial Diversity and Modulate Rhizosphere Aggregation. Frontiers in Plant Science, 2017, 8, 1288.	1.7	23
1185	Individual Signatures Define Canine Skin Microbiota Composition and Variability. Frontiers in Veterinary Science, 2017, 4, 6.	0.9	26
1186	Starter feeding altered ruminal epithelial bacterial communities and some key immune-related genes' expression before weaning in lambs1. Journal of Animal Science, 2017, 95, 910-921.	0.2	21
1187	A Metagenomic and in Silico Functional Prediction of Gut Microbiota Profiles May Concur in Discovering New Cystic Fibrosis Patient-Targeted Probiotics. Nutrients, 2017, 9, 1342.	1.7	24
1188	Assessment of Bifidobacterium Species Using groEL Gene on the Basis of Illumina MiSeq High-Throughput Sequencing. Genes, 2017, 8, 336.	1.0	38
1189	Optimisation of 16S rRNA gut microbiota profiling of extremely low birth weight infants. BMC Genomics, 2017, 18, 841.	1.2	47
1190	16S rRNA Gene-Based Metagenomic Analysis of Ozark Cave Bacteria. Diversity, 2017, 9, 31.	0.7	30
1191	Delivery Mode and the Transition of Pioneering Gut-Microbiota Structure, Composition and Predicted Metabolic Function. Genes, 2017, 8, 364.	1.0	55
1192	Regulation of life span by the gut microbiota in the short-lived African turquoise killifish. ELife, 2017, 6, .	2.8	317
1193	Reactivation of Intestinal Inflammation Is Suppressed by Catestatin in a Murine Model of Colitis via M1 Macrophages and Not the Gut Microbiota. Frontiers in Immunology, 2017, 8, 985.	2.2	38
1194	Seasonal and Interannual Changes in Ciliate and Dinoflagellate Species Assemblages in the Arctic Ocean (Amundsen Gulf, Beaufort Sea, Canada). Frontiers in Marine Science, 2017, 4, .	1.2	35
1195	Changes in Marine Prokaryote Composition with Season and Depth Over an Arctic Polar Year. Frontiers in Marine Science, 2017, 4, .	1.2	73
1196	Characterization of Gut Microbiome Dynamics in Developing Pekin Ducks and Impact of Management System. Frontiers in Microbiology, 2016, 7, 2125.	1.5	46
1197	Nutritional Models of Experimentally-Induced Subacute Ruminal Acidosis (SARA) Differ in Their Impact on Rumen and Hindgut Bacterial Communities in Dairy Cows. Frontiers in Microbiology, 2016, 7, 2128.	1.5	97

#	ARTICLE	IF	CITATIONS
1198	Sampling Modification Effects in the Subgingival Microbiome Profile of Healthy Children. Frontiers in Microbiology, 2017, 7, 2142.	1.5	13
1199	Linking Peripartal Dynamics of Ruminal Microbiota to Dietary Changes and Production Parameters. Frontiers in Microbiology, 2017, 7, 2143.	1.5	58
1200	Human Catestatin Alters Gut Microbiota Composition in Mice. Frontiers in Microbiology, 2016, 7, 2151.	1.5	37
1201	Temporal Stability and the Effect of Transgenerational Transfer on Fecal Microbiota Structure in a Long Distance Migratory Bird. Frontiers in Microbiology, 2017, 8, 50.	1.5	70
1202	Metabolomic and Metagenomic Analysis of Two Crude Oil Production Pipelines Experiencing Differential Rates of Corrosion. Frontiers in Microbiology, 2017, 8, 99.	1.5	38
1203	Changes in Metabolically Active Bacterial Community during Rumen Development, and Their Alteration by Rhubarb Root Powder Revealed by 16S rRNA Amplicon Sequencing. Frontiers in Microbiology, 2017, 8, 159.	1.5	34
1204	Broadcast Spawning Coral Mussismilia hispida Can Vertically Transfer its Associated Bacterial Core. Frontiers in Microbiology, 2017, 8, 176.	1.5	81
1205	Bacterial Community and PHB-Accumulating Bacteria Associated with the Wall and Specialized Niches of the Hindgut of the Forest Cockchafer (Melolontha hippocastani). Frontiers in Microbiology, 2017, 8, 291.	1.5	24
1206	Compositional Stability of the Bacterial Community in a Climate-Sensitive Sub-Arctic Peatland. Frontiers in Microbiology, 2017, 8, 317.	1.5	20
1207	Different Bacterial Communities Involved in Peptide Decomposition between Normoxic and Hypoxic Coastal Waters. Frontiers in Microbiology, 2017, 8, 353.	1.5	26
1208	Starter Feeding Supplementation Alters Colonic Mucosal Bacterial Communities and Modulates Mucosal Immune Homeostasis in Newborn Lambs. Frontiers in Microbiology, 2017, 8, 429.	1.5	60
1209	Reducing Salinity by Flooding an Extremely Alkaline and Saline Soil Changes the Bacterial Community but Its Effect on the Archaeal Community Is Limited. Frontiers in Microbiology, 2017, 8, 466.	1.5	42
1210	Comparative Evaluation of Four Bacteria-Specific Primer Pairs for 16S rRNA Gene Surveys. Frontiers in Microbiology, 2017, 8, 494.	1.5	242
1211	Inferring Microbial Interactions in the Gut of the Hong Kong Whipping Frog (Polypedates) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.5	37
1212	Microbial Diversity of Browning Peninsula, Eastern Antarctica Revealed Using Molecular and Cultivation Methods. Frontiers in Microbiology, 2017, 8, 591.	1.5	66
1213	The Type of Forage Substrate Preparation Included as Substrate in a RUSITEC System Affects the Ruminal Microbiota and Fermentation Characteristics. Frontiers in Microbiology, 2017, 8, 704.	1.5	44
1214	Biogeographic Comparison of Lophelia-Associated Bacterial Communities in the Western Atlantic Reveals Conserved Core Microbiome. Frontiers in Microbiology, 2017, 8, 796.	1.5	50
1215	A Phloem-Feeding Insect Transfers Bacterial Endophytic Communities between Grapevine Plants. Frontiers in Microbiology, 2017, 8, 834.	1.5	56

#	Article	IF	Citations
1216	Diversity and Activity of Diazotrophs in Great Barrier Reef Surface Waters. Frontiers in Microbiology, 2017, 8, 967.	1.5	23
1217	Survey of Antibiotic-producing Bacteria Associated with the Epidermal Mucus Layers of Rays and Skates. Frontiers in Microbiology, 2017, 8, 1050.	1.5	23
1218	Incubation Temperature, But Not Pequi Oil Supplementation, Affects Methane Production, and the Ruminal Microbiota in a Rumen Simulation Technique (Rusitec) System. Frontiers in Microbiology, 2017, 8, 1076.	1.5	24
1219	The Impact of Hydration and Temperature on Bacterial Diversity in Arid Soil Mesocosms. Frontiers in Microbiology, 2017, 8, 1078.	1.5	25
1220	Monensin and Nisin Affect Rumen Fermentation and Microbiota Differently In Vitro. Frontiers in Microbiology, 2017, 8, 1111.	1.5	63
1221	Effects of Physiochemical Factors on Prokaryotic Biodiversity in Malaysian Circumneutral Hot Springs. Frontiers in Microbiology, 2017, 8, 1252.	1.5	49
1222	Nutrient and Rainfall Additions Shift Phylogenetically Estimated Traits of Soil Microbial Communities. Frontiers in Microbiology, 2017, 8, 1271.	1.5	25
1223	Microbial Communities and Their Predicted Metabolic Functions in Growth Laminae of a Unique Large Conical Mat from Lake Untersee, East Antarctica. Frontiers in Microbiology, 2017, 8, 1347.	1.5	51
1224	Temporal Microbial Community Dynamics in Microbial Electrolysis Cells â€“ Influence of Acetate and Propionate Concentration. Frontiers in Microbiology, 2017, 8, 1371.	1.5	27
1225	Cutaneous Microbial Community Variation across Populations of Eastern Hellbenders (Cryptobranchus alleganiensis alleganiensis). Frontiers in Microbiology, 2017, 8, 1379.	1.5	39
1226	Bacteria Associated to Plants Naturally Selected in a Historical PCB Polluted Soil Show Potential to Sustain Natural Attenuation. Frontiers in Microbiology, 2017, 8, 1385.	1.5	33
1227	The Cyanobacteria-Dominated Sponge Dactylospongia elegans in the South China Sea: Prokaryotic Community and Metagenomic Insights. Frontiers in Microbiology, 2017, 8, 1387.	1.5	15
1228	Wood Ash Induced pH Changes Strongly Affect Soil Bacterial Numbers and Community Composition. Frontiers in Microbiology, 2017, 8, 1400.	1.5	74
1229	Effects of 1,1,1-Trichloroethane and Triclocarban on Reductive Dechlorination of Trichloroethene in a TCE-Reducing Culture. Frontiers in Microbiology, 2017, 8, 1439.	1.5	17
1230	Watershed Urbanization Linked to Differences in Stream Bacterial Community Composition. Frontiers in Microbiology, 2017, 8, 1452.	1.5	94
1231	Culture Media and Individual Hosts Affect the Recovery of Culturable Bacterial Diversity from Amphibian Skin. Frontiers in Microbiology, 2017, 8, 1574.	1.5	35
1232	High-Resolution Microbiome Profiling for Detection and Tracking of Salmonella enterica. Frontiers in Microbiology, 2017, 8, 1587.	1.5	31
1233	Shifts in Host Mucosal Innate Immune Function Are Associated with Ruminal Microbial Succession in Supplemental Feeding and Grazing Goats at Different Ages. Frontiers in Microbiology, 2017, 8, 1655.	1.5	19

#	ARTICLE	IF	CITATIONS
1234	Bacterial, Archaeal, and Eukaryotic Diversity across Distinct Microhabitats in an Acid Mine Drainage. Frontiers in Microbiology, 2017, 8, 1756.	1.5	88
1235	A Novel Lactobacilli-Based Teat Disinfectant for Improving Bacterial Communities in the Milks of Cow Teats with Subclinical Mastitis. Frontiers in Microbiology, 2017, 8, 1782.	1.5	27
1236	Legacy Effects on the Recovery of Soil Bacterial Communities from Extreme Temperature Perturbation. Frontiers in Microbiology, 2017, 8, 1832.	1.5	89
1237	In Vivo Isotopic Labeling of Symbiotic Bacteria Involved in Cellulose Degradation and Nitrogen Recycling within the Gut of the Forest Cockchafer (Melolontha hippocastani). Frontiers in Microbiology, 2017, 8, 1970.	1.5	28
1238	Diet, Environments, and Gut Microbiota. A Preliminary Investigation in Children Living in Rural and Urban Burkina Faso and Italy. Frontiers in Microbiology, 2017, 8, 1979.	1.5	222
1239	The Low-Diversity Fecal Microbiota of the Critically Endangered KÄ·kÄ·pÅ·Is Robust to Anthropogenic Dietary and Geographic Influences. Frontiers in Microbiology, 2017, 8, 2033.	1.5	15
1240	A High Grain Diet Dynamically Shifted the Composition of Mucosa-Associated Microbiota and Induced Mucosal Injuries in the Colon of Sheep. Frontiers in Microbiology, 2017, 8, 2080.	1.5	62
1241	Effect of Dietary Forage to Concentrate Ratios on Dynamic Profile Changes and Interactions of Ruminal Microbiota and Metabolites in Holstein Heifers. Frontiers in Microbiology, 2017, 8, 2206.	1.5	155
1242	Parallelized, Aerobic, Single Carbon-Source Enrichments from Different Natural Environments Contain Divergent Microbial Communities. Frontiers in Microbiology, 2017, 8, 2321.	1.5	21
1243	Phylogenetic Structure and Metabolic Properties of Microbial Communities in Arsenic-Rich Waters of Geothermal Origin. Frontiers in Microbiology, 2017, 8, 2468.	1.5	17
1244	Seasonal Changes in a Maize-Based Polyculture of Central Mexico Reshape the Co-occurrence Networks of Soil Bacterial Communities. Frontiers in Microbiology, 2017, 8, 2478.	1.5	36
1245	Temporal Variation of the Skin Bacterial Community and Batrachochytrium dendrobatidis Infection in the Terrestrial Cryptic Frog Philoria loveridgei. Frontiers in Microbiology, 2017, 8, 2535.	1.5	33
1246	Host Specificity for Bacterial, Archaeal and Fungal Communities Determined for High- and Low-Microbial Abundance Sponge Species in Two Genera. Frontiers in Microbiology, 2017, 8, 2560.	1.5	47
1247	16S rRNA Next Generation Sequencing Analysis Shows Bacteria in Alzheimerâ€™s Post-Mortem Brain. Frontiers in Aging Neuroscience, 2017, 9, 195.	1.7	234
1248	Serotonin Transporter Genotype Modulates the Gut Microbiota Composition in Young Rats, an Effect Augmented by Early Life Stress. Frontiers in Cellular Neuroscience, 2017, 11, 222.	1.8	65
1249	Independent Effects of a Herbivoreâ€™s Bacterial Symbionts on Its Performance and Induced Plant Defences. International Journal of Molecular Sciences, 2017, 18, 182.	1.8	40
1250	Comparison of bacterial communities from lava cave microbial mats to overlying surface soils from Lava Beds National Monument, USA. PLoS ONE, 2017, 12, e0169339.	1.1	59
1251	Olive oil bioactives protect pigs against experimentally-induced chronic inflammation independently of alterations in gut microbiota. PLoS ONE, 2017, 12, e0174239.	1.1	35

#	ARTICLE	IF	CITATIONS
1252	Crude oil impairs immune function and increases susceptibility to pathogenic bacteria in southern flounder. PLoS ONE, 2017, 12, e0176559.	1.1	38
1253	The feline skin microbiota: The bacteria inhabiting the skin of healthy and allergic cats. PLoS ONE, 2017, 12, e0178555.	1.1	41
1254	Variation between the oral and faecal microbiota in a free-living passerine bird, the great tit (Parus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	24
1255	Species-specific signatures of the microbiome from Camponotus and Colobopsis ants across developmental stages. PLoS ONE, 2017, 12, e0187461.	1.1	36
1256	Microbiomes associated with infective stages of root-knot and lesion nematodes in soil. PLoS ONE, 2017, 12, e0177145.	1.1	113
1257	Comparison of rumen bacterial communities in dairy herds of different production. BMC Microbiology, 2017, 17, 190.	1.3	62
1258	Faecal bacterial microbiota in patients with cirrhosis and the effect of lactulose administration. BMC Gastroenterology, 2017, 17, 125.	0.8	37
1259	High-throughput sequencing technology reveals that continuous cropping of American ginseng results in changes in the microbial community in arable soil. Chinese Medicine, 2017, 12, 18.	1.6	72
1260	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
1261	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. Microbiome, 2017, 5, 84.	4.9	247
1262	Space-type radiation induces multimodal responses in the mouse gut microbiome and metabolome. Microbiome, 2017, 5, 105.	4.9	81
1263	Individual signatures and environmental factors shape skin microbiota in healthy dogs. Microbiome, 2017, 5, 139.	4.9	38
1264	Indoor microbiota in severely moisture damaged homes and the impact of interventions. Microbiome, 2017, 5, 138.	4.9	40
1265	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. Microbiome, 2017, 5, 156.	4.9	73
1266	Comparing microbiota profiles in induced and spontaneous sputum samples in COPD patients. Respiratory Research, 2017, 18, 164.	1.4	24
1267	Identifying predictive features of Clostridium difficile infection recurrence before, during, and after primary antibiotic treatment. Microbiome, 2017, 5, 148.	4.9	36
1268	Evaluating the accuracy of amplicon-based microbiome computational pipelines on simulated human gut microbial communities. BMC Bioinformatics, 2017, 18, 283.	1.2	51
1269	Increasing corn distillers solubles alters the liquid fraction of the ruminal microbiome. Journal of Animal Science, 2017, 95, 3540-3551.	0.2	2

#	ARTICLE	IF	CITATIONS
1270	Gut microbial diversity analysis using Illumina sequencing for functional dyspepsia with liver depression-spleen deficiency syndrome and the interventional Xiaoyaosan in a rat model. World Journal of Gastroenterology, 2017, 23, 810.	1.4	38
1272	Characterisation of Arctic Bacterial Communities in the Air above Svalbard. Biology, 2017, 6, 29.	1.3	35
1273	Alteration of gut microbial community after N,N-Dimethylformamide exposure. Journal of Toxicological Sciences, 2017, 42, 241-250.	0.7	10
1274	Biofilm formation and potential for iron cycling in serpentinization-influenced groundwater of the Zambales and Coast Range ophiolites. Extremophiles, 2018, 22, 407-431.	0.9	9
1275	The vertical distribution of prokaryotes in the surface sediment of Jiaolong cold seep at the northern South China Sea. Extremophiles, 2018, 22, 499-510.	0.9	24
1276	Porcine Response to a Multidrug-Resistant <i>Salmonella enterica</i> serovar I 4,[5],12:i:- Outbreak Isolate. Foodborne Pathogens and Disease, 2018, 15, 253-261.	0.8	18
1277	Integrating molecular and ecological approaches to identify potential polymicrobial pathogens over a shrimp disease progression. Applied Microbiology and Biotechnology, 2018, 102, 3755-3764.	1.7	44
1278	Fragile skin microbiomes in megacities are assembled by a predominantly niche-based process. Science Advances, 2018, 4, e1701581.	4.7	70
1279	Bacterial community changes in an industrial algae production system. Algal Research, 2018, 31, 147-156.	2.4	55
1280	Depth matters: effects of precipitation regime on soil microbial activity upon rewetting of a plant-soil system. ISME Journal, 2018, 12, 1061-1071.	4.4	94
1281	Grape seed proanthocyanidins influence gut microbiota and enteroendocrine secretions in female rats. Food and Function, 2018, 9, 1672-1682.	2.1	87
1282	Dog introduction alters the home dust microbiota. Indoor Air, 2018, 28, 539-547.	2.0	46
1283	Dietary live yeast and increased water temperature influence the gut microbiota of rainbow trout. Journal of Applied Microbiology, 2018, 124, 1377-1392.	1.4	112
1284	Large Blooms of <i>Bacillales</i> (<i>Firmicutes</i>) Underlie the Response to Wetting of Cyanobacterial Biocrusts at Various Stages of Maturity. MBio, 2018, 9, .	1.8	28
1285	Evaluation of the nutrition and function of cow and goat milk based on intestinal microbiota by metagenomic analysis. Food and Function, 2018, 9, 2320-2327.	2.1	33
1286	Effects of nutrient loading on sediment bacterial and pathogen communities within seagrass meadows. MicrobiologyOpen, 2018, 7, e00600.	1.2	34
1287	Rhizospheric microbial communities are driven by Panax ginseng at different growth stages and biocontrol bacteria alleviates replanting mortality. Acta Pharmaceutica Sinica B, 2018, 8, 272-282.	5.7	122
1288	Quantitative prediction of shrimp disease incidence via the profiles of gut eukaryotic microbiota. Applied Microbiology and Biotechnology, 2018, 102, 3315-3326.	1.7	40

#	Article	IF	Citations
1289	Estimating taxonâ€specific population dynamics in diverse microbial communities. Ecosphere, 2018, 9, e02090.	1.0	85
1290	One-time phosphate fertilizer application to grassland columns modifies the soil microbiota and limits its role in ecosystem services. Science of the Total Environment, 2018, 630, 849-858.	3.9	87
1291	Biodegradation of Poly(3-hydroxybutyrate-<i>co</i>-3-hydroxyhexanoate) Plastic under Anaerobic Sludge and Aerobic Seawater Conditions: Gas Evolution and Microbial Diversity. Environmental Science & Technology, 2018, 52, 5700-5709.	4.6	72
1292	Impacts of Glutaraldehyde on Microbial Community Structure and Degradation Potential in Streams Impacted by Hydraulic Fracturing. Environmental Science & Technology, 2018, 52, 5989-5999.	4.6	35
1293	Microbiota-accessible carbohydrates suppress Clostridium difficile infection in a murine model. Nature Microbiology, 2018, 3, 662-669.	5.9	185
1294	Competition and habitat filtering jointly explain phylogenetic structure of soil bacterial communities across elevational gradients. Environmental Microbiology, 2018, 20, 2386-2396.	1.8	26
1295	Ecology determines how low antibiotic concentration impacts community composition and horizontal transfer of resistance genes. Communications Biology, 2018, 1, 35.	2.0	80
1296	Inferring Roles in Defense from Metabolic Allocation of Rice Diterpenoids. Plant Cell, 2018, 30, 1119-1131.	3.1	55
1297	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. MSystems, 2018, 3, .	1.7	376
1298	River Flow Impacts Bacterial and Archaeal Community Structure in Surface Sediments in the Northern Gulf of Mexico. Microbial Ecology, 2018, 76, 941-953.	1.4	4
1299	Tracing of the fecal microbiota of commercial pigs at five growth stages from birth to shipment. Scientific Reports, 2018, 8, 6012.	1.6	100
1300	High-throughput sequencing for algal systematics. European Journal of Phycology, 2018, 53, 256-272.	0.9	33
1301	Investigation of the core microbiome in main soil types from the East European plain. Science of the Total Environment, 2018, 631-632, 1421-1430.	3.9	43
1302	Antibiotic distribution, risk assessment, and microbial diversity in river water and sediment in Hong Kong. Environmental Geochemistry and Health, 2018, 40, 2191-2203.	1.8	41
1303	Monomorphic pathogens: The case of Candidatus Xenohaliotis californiensis from abalone in California, USA and Baja California, Mexico. Journal of Invertebrate Pathology, 2018, 154, 19-23.	1.5	5
1304	Effects of Lactogen 13, a New Probiotic Preparation, on Gut Microbiota and Endocrine Signals Controlling Growth and Appetite of Oreochromis niloticus Juveniles. Microbial Ecology, 2018, 76, 1063-1074.	1.4	23
1305	High diversity and variability in the bacterial microbiota of the coffee berry borer (<i>Coleoptera</i>:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.4	15
1306	Yeast culture dietary supplementation modulates gut microbiota, growth and biochemical parameters of grass carp. Microbial Biotechnology, 2018, 11, 551-565.	2.0	36

#	Article	IF	Citations
1307	Altered fecal microbiota composition in all male aggressorâ€exposed rodent model simulating features of postâ€traumatic stress disorder. Journal of Neuroscience Research, 2018, 96, 1311-1323.	1.3	54
1308	A large-scale survey of the postmortem human microbiome, and its potential to provide insight into the living health condition. Scientific Reports, 2018, 8, 5724.	1.6	102
1309	Dietary supplementation with flaxseed meal and oat hulls modulates intestinal histomorphometric characteristics, digesta- and mucosa-associated microbiota in pigs. Scientific Reports, 2018, 8, 5880.	1.6	30
1310	Cadmium Exposure-Sedum alfredii Planting Interactions Shape the Bacterial Community in the Hyperaccumulator Plant Rhizosphere. Applied and Environmental Microbiology, 2018, 84, .	1.4	60
1311	No Significant Association Between the Fecal Microbiome and the Presence of Irritable Bowel Syndrome-type Symptoms in Patients with Quiescent Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2018, 24, 1597-1605.	0.9	20
1312	Interaction of genotype and diet on small intestine microbiota of Japanese quail fed a cholesterol enriched diet. Scientific Reports, 2018, 8, 2381.	1.6	14
1313	Feedstock determines biocharâ€induced soil priming effects by stimulating the activity of specific microorganisms. European Journal of Soil Science, 2018, 69, 521-534.	1.8	112
1314	Delayed gut microbiota development in high-risk for asthma infants is temporarily modifiable by Lactobacillus supplementation. Nature Communications, 2018, 9, 707.	5.8	158
1315	Shift in the microbial community composition of surface water and sediment along an urban river. Science of the Total Environment, 2018, 627, 600-612.	3.9	172
1316	Transient influence of blood meal and natural environment on blacklegged tick bacterial communities. Ticks and Tick-borne Diseases, 2018, 9, 563-572.	1.1	41
1317	Impact of beneficial bacteria supplementation on the gut microbiota, colony development and productivity of Apis mellifera L.. Beneficial Microbes, 2018, 9, 269-278.	1.0	56
1318	Longitudinal Effects of Supplemental Forage on the Honey Bee (Apis mellifera) Microbiota and Inter- and Intra-Colony Variability. Microbial Ecology, 2018, 76, 814-824.	1.4	36
1319	Distribution of thermophilic endospores in a temperate estuary indicate that dispersal history structures sediment microbial communities. Environmental Microbiology, 2018, 20, 1134-1147.	1.8	25
1320	In children, the microbiota of the nasopharynx and bronchoalveolar lavage fluid are both similar and different. Pediatric Pulmonology, 2018, 53, 475-482.	1.0	31
1321	Microbiome assembly of avian eggshells and their potential as transgenerational carriers of maternal microbiota. ISME Journal, 2018, 12, 1375-1388.	4.4	53
1322	Microbial rRNA Synthesis and Growth Compared through Quantitative Stable Isotope Probing with H ₂ ¹⁸ O. Applied and Environmental Microbiology, 2018, 84, .	1.4	27
1323	Bioaugmentation of sidestream nitrifying-denitrifying phosphorus-accumulating granules in a low-SRT activated sludge system at low temperature. Water Research, 2018, 135, 241-250.	5.3	46
1324	Influence of immunogenetics, sex and body condition on the cutaneous microbial communities of two giant salamanders. Molecular Ecology, 2018, 27, 1915-1929.	2.0	21

#	ARTICLE	IF	CITATIONS
1325	Microbial community and short-chain fatty acid profile in gastrointestinal tract of goose. Poultry Science, 2018, 97, 1420-1428.	1.5	46
1326	Specific plasmid patterns and high rates of bacterial coâ€occurrence within the coral holobiont. Ecology and Evolution, 2018, 8, 1818-1832.	0.8	27
1327	Root-Associated Bacterial and Fungal Community Profiles of <i>Arabidopsis thaliana</i> Are Robust Across Contrasting Soil P Levels. Phytobiomes Journal, 2018, 2, 24-34.	1.4	37
1328	Predator identity more than predator richness structures aquatic microbial assemblages in <i>Sarracenia purpurea</i> leaves. Ecology, 2018, 99, 652-660.	1.5	17
1329	Mosquito vectorâ€associated microbiota: Metabarcoding bacteria and eukaryotic symbionts across habitat types in Thailand endemic for dengue and other arthropodâ€borne diseases. Ecology and Evolution, 2018, 8, 1352-1368.	0.8	99
1330	Aberrant intestinal microbiota in individuals with prediabetes. Diabetologia, 2018, 61, 810-820.	2.9	313
1331	Antibiotics Disturb the Microbiome and Increase the Incidence of Resistance Genes in the Gut of a Common Soil Collembolan. Environmental Science & Technology, 2018, 52, 3081-3090.	4.6	162
1332	Bacteria and fungi in day-old turkeys vary among companies, collection periods, and breeder flocks. Poultry Science, 2018, 97, 1400-1411.	1.5	9
1333	Effect of snowpack on the soil bacteria of alpine meadows in the Qinghai-Tibetan Plateau of China. Catena, 2018, 164, 13-22.	2.2	33
1334	Identification of active denitrifiers by DNA-stable isotope probing and amplicon sequencing reveals Betaproteobacteria as responsible for attenuation of nitrate contamination in a low impacted aquifer. FEMS Microbiology Ecology, 2018, 94, .	1.3	24
1335	Highâ€throughput environmental sequencing reveals high diversity of litter and moss associated protist communities along a gradient of drainage and tree productivity. Environmental Microbiology, 2018, 20, 1185-1203.	1.8	45
1336	Bacterial diversity and community structure in Chongqing radish paocai brines revealed using PacBio singleâ€molecule realâ€time sequencing technology. Journal of the Science of Food and Agriculture, 2018, 98, 3234-3245.	1.7	43
1337	Metabolic Fate of ¹³C-Labeled Polydextrose and Impact on the Gut Microbiome: A Triple-Phase Study in a Colon Simulator. Journal of Proteome Research, 2018, 17, 1041-1053.	1.8	17
1338	Co-occurring Mangroves and Salt Marshes Differ in Microbial Community Composition. Wetlands, 2018, 38, 497-508.	0.7	36
1339	The Combined Effect of Temperature and Host Clonal Line on the Microbiota of a Planktonic Crustacean. Microbial Ecology, 2018, 76, 506-517.	1.4	28
1340	Key microbial taxa in the rhizosphere of sorghum and sunflower grown in crop rotation. Science of the Total Environment, 2018, 624, 530-539.	3.9	69
1341	Degradation of Deepwater Horizon oil buried in a Florida beach influenced by tidal pumping. Marine Pollution Bulletin, 2018, 126, 488-500.	2.3	40
1342	A year in the life of a thrombolite: comparative metatranscriptomics reveals dynamic metabolic changes over diel and seasonal cycles. Environmental Microbiology, 2018, 20, 842-861.	1.8	24

#	ARTICLE	IF	CITATIONS
1343	An Attenuated Salmonella enterica Serovar Typhimurium Strain and Galacto-Oligosaccharides Accelerate Clearance of Salmonella Infections in Poultry through Modifications to the Gut Microbiome. Applied and Environmental Microbiology, 2018, 84, .	1.4	59
1344	Short-term particulate matter exposure influences nasal microbiota in a population of healthy subjects. Environmental Research, 2018, 162, 119-126.	3.7	56
1345	Correlation between system performance and bacterial composition under varied mixing intensity in thermophilic anaerobic digestion of food waste. Journal of Environmental Management, 2018, 206, 472-481.	3.8	22
1346	Vitamin B12 effects on chlorinated methanes-degrading microcosms: Dual isotope and metabolically active microbial populations assessment. Science of the Total Environment, 2018, 621, 1615-1625.	3.9	16
1347	Responses of the soil microbial community to nitrogen fertilizer regimes and historical exposure to extreme weather events: Flooding or prolonged-drought. Soil Biology and Biochemistry, 2018, 118, 227-236.	4.2	68
1348	Responses of bulk and rhizosphere soil microbial communities to thermoclimatic changes in a Mediterranean ecosystem. Soil Biology and Biochemistry, 2018, 118, 130-144.	4.2	23
1349	Associations between <i>Escherichia coli</i> O157 shedding and the faecal microbiota of dairy cows. Journal of Applied Microbiology, 2018, 124, 881-898.	1.4	15
1350	Oxygen barrier and catalytic effect of the cathodic biofilm in single chamber microbial fuel cells. Journal of Chemical Technology and Biotechnology, 2018, 93, 2199-2207.	1.6	17
1351	Bifidobacteria or Fiber Protects against Diet-Induced Microbiota-Mediated Colonic Mucus Deterioration. Cell Host and Microbe, 2018, 23, 27-40.e7.	5.1	477
1352	Rifampicin treatment of Blattella germanica evidences a fecal transmission route of their gut microbiota. FEMS Microbiology Ecology, 2018, 94, .	1.3	43
1353	Intraspecies variation in a widely distributed tree species regulates the responses of soil microbiome to different temperature regimes. Environmental Microbiology Reports, 2018, 10, 167-178.	1.0	8
1354	Impact of dietary induced precocious gut maturation on cecal microbiota and its relation to the bloodâ€brain barrier during the postnatal period in rats. Neurogastroenterology and Motility, 2018, 30, e13285.	1.6	15
1355	Profiling of metabolome and bacterial community dynamics in ensiled Medicago sativa inoculated without or with Lactobacillus plantarum or Lactobacillus buchneri. Scientific Reports, 2018, 8, 357.	1.6	118
1356	The role of ozone pretreatment on optimization of membrane bioreactor for treatment of oil sands process-affected water. Journal of Hazardous Materials, 2018, 347, 470-477.	6.5	22
1357	Online Bayesian Phylogenetic Inference: Theoretical Foundations via Sequential Monte Carlo. Systematic Biology, 2018, 67, 503-517.	2.7	21
1358	Prolonged exposure does not increase soil microbial community compositional response to warming along geothermal gradients. FEMS Microbiology Ecology, 2018, 94, .	1.3	29
1359	Soil bacterial community responses to altered precipitation and temperature regimes in an old field grassland are mediated by plants. FEMS Microbiology Ecology, 2018, 94, .	1.3	54
1360	The commensal microbiome is associated with antiâ€“PD-1 efficacy in metastatic melanoma patients. Science, 2018, 359, 104-108.	6.0	2,027

#	ARTICLE	IF	CITATIONS
1361	Diversity patterns of microbial eukaryotes mirror those of bacteria in Antarctic cryoconite holes. FEMS Microbiology Ecology, 2018, 94, .	1.3	65
1362	Enhancement of volatile fatty acid production and biogas yield from food waste following sonication pretreatment. Journal of Environmental Management, 2018, 217, 797-804.	3.8	30
1363	A microbiome case-control study of recurrent acute otitis media identified potentially protective bacterial genera. BMC Microbiology, 2018, 18, 13.	1.3	126
1364	Sediment bacterial community structures and their predicted functions implied the impacts from natural processes and anthropogenic activities in coastal area. Marine Pollution Bulletin, 2018, 131, 481-495.	2.3	92
1365	Stochastic processes govern bacterial communities from the blood of pikas and from their arthropod vectors. FEMS Microbiology Ecology, 2018, 94, .	1.3	14
1366	Predator and prey biodiversity relationship and its consequences on marine ecosystem functioningâ€"interplay between nanoflagellates and bacterioplankton. ISME Journal, 2018, 12, 1532-1542.	4.4	63
1367	Comparison of rhizosphere and endophytic microbial communities of Chinese leek through high-throughput 16S rRNA gene Illumina sequencing. Journal of Integrative Agriculture, 2018, 17, 359-367.	1.7	23
1368	A town on fire! Integrating 16S rRNA gene amplicon analyses into an undergraduate microbiology lecture class. FEMS Microbiology Letters, 2018, 365, .	0.7	5
1369	Guano exposed: Impact of aerobic conditions on bat fecal microbiota. Ecology and Evolution, 2018, 8, 5563-5574.	0.8	11
1370	Synthesis of multi-omic data and community metabolic models reveals insights into the role of hydrogen sulfide in colon cancer. Methods, 2018, 149, 59-68.	1.9	63
1371	Methodology challenges in studying human gut microbiota â€" effects of collection, storage, DNA extraction and next generation sequencing technologies. Scientific Reports, 2018, 8, 5143.	1.6	146
1372	Kenaf addition has mixed effects on process performance of sequencing batch reactors treating municipal wastewater. Environmental Science: Water Research and Technology, 2018, 4, 711-720.	1.2	1
1373	Frontline Science: Microbiota reconstitution restores intestinal integrity after cisplatin therapy. Journal of Leukocyte Biology, 2018, 103, 799-805.	1.5	72
1374	Impact of oxytetracycline and bacterial bioaugmentation on the efficiency and microbial community structure of a pesticide-degrading biomixture. Environmental Science and Pollution Research, 2018, 25, 11787-11799.	2.7	18
1375	Host range of antibiotic resistance genes in wastewater treatment plant influent and effluent. FEMS Microbiology Ecology, 2018, 94, .	1.3	148
1376	Incubation with macroalgae induces large shifts in water column microbiota, but minor changes to the epibiota of coâ€occurring macroalgae. Molecular Ecology, 2018, 27, 1966-1979.	2.0	50
1377	Microbial community and metagenome dynamics during biodegradation of dispersed oil reveals potential key-players in cold Norwegian seawater. Marine Pollution Bulletin, 2018, 129, 370-378.	2.3	91
1378	Use of an improved high-throughput absolute abundance quantification method to characterize soil bacterial community and dynamics. Science of the Total Environment, 2018, 633, 360-371.	3.9	42

#	Article	IF	Citations
1379	A Method to Define the Effects of Environmental Enrichment on Colon Microbiome Biodiversity in a Mouse Colon Tumor Model. Journal of Visualized Experiments, 2018, , .	0.2	3
1380	The impact of depuration on mussel hepatopancreas bacteriome composition and predicted metagenome. Antonie Van Leeuwenhoek, 2018, 111, 1117-1129.	0.7	13
1381	Nutrient-Dependent Impact of Microbes on <i>Drosophila suzukii</i> Development. MBio, 2018, 9, .	1.8	109
1382	Microbial communities in seawater from an Arctic and a temperate Norwegian fjord and their potentials for biodegradation of chemically dispersed oil at low seawater temperatures. Marine Pollution Bulletin, 2018, 129, 308-317.	2.3	35
1383	Oyster microbial communities and implications for chalky deposit formation. Hydrobiologia, 2018, 816, 121-135.	1.0	22
1384	Influence of fecal collection conditions and 16S rRNA gene sequencing at two centers on human gut microbiota analysis. Scientific Reports, 2018, 8, 4386.	1.6	46
1385	Physiological Regulation of Drug Metabolism and Transport: Pregnancy, Microbiome, Inflammation, Infection, and Fasting. Drug Metabolism and Disposition, 2018, 46, 503-513.	1.7	40
1386	Microbiome Dynamics in a Large Artificial Seawater Aquarium. Applied and Environmental Microbiology, 2018, 84, .	1.4	33
1387	Dietary Changes Impact the Gut Microbe Composition in Overweight and Obese MenÂwith Prostate Cancer Undergoing RadicalÂProstatectomy. Journal of the Academy of Nutrition and Dietetics, 2018, 118, 714-723.e1.	0.4	25
1388	Gut microbial communities of American pikas (<i><scp>O</scp>chotona princeps</i>): Evidence for phylosymbiosis and adaptations to novel diets. Journal of Animal Ecology, 2018, 87, 323-330.	1.3	85
1389	Characteristics of microbial community involved in early biofilms formation under the influence of wastewater treatment plant effluent. Journal of Environmental Sciences, 2018, 66, 113-124.	3.2	33
1390	The Cucurbita pepo seed microbiome: genotype-specific composition and implications for breeding. Plant and Soil, 2018, 422, 35-49.	1.8	131
1391	Communities of arbuscular mycorrhizal fungi under Picconia azorica in native forests of Azores. Symbiosis, 2018, 74, 43-54.	1.2	10
1392	The seed endosphere of Anadenanthera colubrina is inhabited by a complex microbiota, including Methylobacteriumspp. and Staphylococcus spp. with potential plant-growth promoting activities. Plant and Soil, 2018, 422, 81-99.	1.8	44
1393	Metagenomic analysis reveals changes of the <i>Drosophila suzukii</i> microbiota in the newly colonized regions. Insect Science, 2018, 25, 833-846.	1.5	25
1394	Community structure and diversity of endophytic bacteria in seeds of three consecutive generations of Crotalaria pumila growing on metal mine residues. Plant and Soil, 2018, 422, 51-66.	1.8	70
1395	Drivers of coastal bacterioplankton community diversity and structure along a nutrient gradient in the East China Sea. Journal of Oceanology and Limnology, 2018, 36, 329-340.	0.6	3
1396	Burying beetles regulate the microbiome of carcasses and use it to transmit a core microbiota to their offspring. Molecular Ecology, 2018, 27, 1980-1991.	2.0	71

#	ARTICLE	IF	CITATIONS
1397	Diet Versus Phylogeny: a Comparison of Gut Microbiota in Captive Colobine Monkey Species. Microbial Ecology, 2018, 75, 515-527.	1.4	106
1398	Simultaneous fermentation of cellulose and current production with an enriched mixed culture of thermophilic bacteria in a microbial electrolysis cell. Microbial Biotechnology, 2018, 11, 63-73.	2.0	26
1399	Effects of host species and environment on the skin microbiome of Plethodontid salamanders. Journal of Animal Ecology, 2018, 87, 341-353.	1.3	120
1400	Rifaximin has minor effects on bacterial composition, inflammation, and bacterial translocation in cirrhosis: A randomized trial. Journal of Gastroenterology and Hepatology (Australia), 2018, 33, 307-314.	1.4	51
1401	Lung Microbiota Is Related to Smoking Status and to Development of Acute Respiratory Distress Syndrome in Critically Ill Trauma Patients. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 621-631.	2.5	114
1402	Gut microbiome modulates response to antiâ€“PD-1 immunotherapy in melanoma patients. Science, 2018, 359, 97-103.	6.0	3,126
1403	CORK Study in Cystic Fibrosis. Chest, 2018, 153, 395-403.	0.4	74
1404	A comparison of bioinformatic approaches for 16S rRNA gene profiling of food bacterial microbiota. International Journal of Food Microbiology, 2018, 265, 9-17.	2.1	35
1405	Supplementation of pancreatic digestive enzymes alters the composition of intestinal microbiota in mice. Biochemical and Biophysical Research Communications, 2018, 495, 273-279.	1.0	43
1406	Long-term industrial metal contamination unexpectedly shaped diversity and activity response of sediment microbiome. Journal of Hazardous Materials, 2018, 344, 299-307.	6.5	86
1407	Host effects on microbiota community assembly. Journal of Animal Ecology, 2018, 87, 331-340.	1.3	39
1408	Do hostâ€associated gut microbiota mediate the effect of an herbicide on disease risk in frogs?. Journal of Animal Ecology, 2018, 87, 489-499.	1.3	45
1409	Arbuscular mycorrhizal fungi promote coexistence and niche divergence of sympatric palm species on a remote oceanic island. New Phytologist, 2018, 217, 1254-1266.	3.5	36
1410	A randomised trial of the effect of omega-3 polyunsaturated fatty acid supplements on the human intestinal microbiota. Gut, 2018, 67, 1974-1983.	6.1	332
1411	The bacterial composition of ventilation filter dust in Norwegian pre-school nurseries. Indoor and Built Environment, 2018, 27, 1392-1404.	1.5	9
1412	Fecal microbiota of lambs fed purple prairie clover (Dalea purpurea Vent.) and alfalfa (Medicago) Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	26
1413	Diversity and the environmental drivers of spatial variation in Bacteria and micro-Eukarya communities from the Hawaiian anchialine ecosystem. Hydrobiologia, 2018, 806, 265-282.	1.0	14
1414	Microbial Lineages in Sarcoidosis. A Metagenomic Analysis Tailored for Lowâ€“Microbial Content Samples. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 225-234.	2.5	59

#	ARTICLE	IF	CITATIONS
1415	Soil Microbiomes Associated with Verticillium Wilt-Suppressive Broccoli and Chitin Amendments are Enriched with Potential Biocontrol Agents. Phytopathology, 2018, 108, 31-43.	1.1	71
1416	Alterations in ruminal bacterial populations at induction and recovery from diet-induced milk fat depression in dairy cows. Journal of Dairy Science, 2018, 101, 295-309.	1.4	45
1417	VMG II transport medium stabilises oral microbiome samples for Next-Generation Sequencing. Journal of Microbiological Methods, 2018, 144, 91-98.	0.7	5
1418	Gut microbes limit growth in house sparrow nestlings (<i>Passer domesticus</i>) but not through limitations in digestive capacity. Integrative Zoology, 2018, 13, 139-151.	1.3	42
1419	Distribution and Diversity of Ocular Microbial Communities in Diabetic Patients Compared with Healthy Subjects. Current Eye Research, 2018, 43, 314-324.	0.7	49
1420	Diazotroph Community Characterization via a High-Throughput <i>nifH</i> Amplicon Sequencing and Analysis Pipeline. Applied and Environmental Microbiology, 2018, 84, .	1.4	78
1421	Effects of dietary raffinose on growth, non-specific immunity, intestinal morphology and microbiome of juvenile hybrid sturgeon (Acipenser baeri Brandt â™€ Ã— A. schrenckii Brandt â™‚). Fish and Shellfish Immunology, 2018, 72, 237-246.	1.6	29
1422	Homogenization of lake cyanobacterial communities over a century of climate change and eutrophication. Nature Ecology and Evolution, 2018, 2, 317-324.	3.4	133
1423	Forest conversion induces seasonal variation in microbial Î²â€diversity. Environmental Microbiology, 2018, 20, 111-123.	1.8	33
1424	Microbial communities exhibit host species distinguishability and phylosymbiosis along the length of the gastrointestinal tract. Molecular Ecology, 2018, 27, 1874-1883.	2.0	73
1425	Associations between infant fungal and bacterial dysbiosis and childhood atopic wheeze in a nonindustrialized setting. Journal of Allergy and Clinical Immunology, 2018, 142, 424-434.e10.	1.5	181
1426	Biological crusts of serpentine and nonâ€serpentine soils from the Barberton Greenstone Belt of South Africa. Ecological Research, 2018, 33, 629-640.	0.7	16
1427	Optical fiber-mediated photosynthesis for enhanced subsurface oxygen delivery. Chemosphere, 2018, 195, 742-748.	4.2	8
1428	Temporal characterization and statistical analysis of flowback and produced waters and their potential for reuse. Science of the Total Environment, 2018, 619-620, 654-664.	3.9	69
1429	Compositional and functional variations of oral microbiota associated with the mutational changes in oral cancer. Oral Oncology, 2018, 77, 1-8.	0.8	95
1430	Response of marine bacteria to oil contamination and to high pressure and low temperature deep sea conditions. MicrobiologyOpen, 2018, 7, e00550.	1.2	22
1431	Exposure of soil collembolans to microplastics perturbs their gut microbiota and alters their isotopic composition. Soil Biology and Biochemistry, 2018, 116, 302-310.	4.2	385
1432	Roles of different active metal-reducing bacteria in arsenic release from arsenic-contaminated paddy soil amended with biochar. Journal of Hazardous Materials, 2018, 344, 958-967.	6.5	123

#	Article	IF	Citations
1433	Effect of vacuum and modified atmosphere packaging on the microbiological, chemical and sensory properties of tropical red drum (Sciaenops ocellatus) fillets stored at 4 Â°C. International Journal of Food Microbiology, 2018, 266, 31-41.	2.1	45
1434	<i>Wolbachia</i> infection alters the relative abundance of resident bacteria in adult <i>Aedes aegypti</i> mosquitoes, but not larvae. Molecular Ecology, 2018, 27, 297-309.	2.0	85
1435	Sympatric kelp species share a large portion of their surface bacterial communities. Environmental Microbiology, 2018, 20, 658-670.	1.8	65
1436	A study of microbial communities on terracotta separator and on biocathode of air breathing microbial fuel cells. Bioelectrochemistry, 2018, 120, 18-26.	2.4	48
1437	Cryogenic Minerals in Hawaiian Lava Tubes: A Geochemical and Microbiological Exploration. Geomicrobiology Journal, 2018, 35, 227-241.	1.0	15
1438	Host Differentiation and Compartmentalization of Microbial Communities in the Azooxanthellate Cupcorals Tubastrea coccinea and Rhizopsammia goesi in the Caribbean. Frontiers in Marine Science, 2018, 5, .	1.2	25
1439	Quantitative Genetics of the Maize Leaf Microbiome. Phytobiomes Journal, 2018, 2, 208-224.	1.4	110
1440	Filtration artefacts in bacterial community composition can affect the outcome of dissolved organic matter biolability assays. Biogeosciences, 2018, 15, 7141-7154.	1.3	9
1441	Bacterial microbiota composition of fermented fruit and vegetable juices (<i>jiaosu</i>) analyzed by single-molecule, real-time (SMRT) sequencing. CYTA - Journal of Food, 2018, 16, 950-956.	0.9	7
1442	Similarities and differences in gut microbiome composition correlate with dietary patterns of Indian and Chinese adults. AMB Express, 2018, 8, 104.	1.4	55
1443	Response of the Bacterial Communities Associated With Maize Rhizosphere to Poultry Litter as an Organomineral Fertilizer. Frontiers in Environmental Science, 2018, 6, .	1.5	16
1444	Culture-independent Profiling of the Fecal Microbiome to Identify Microbial Species Associated with a Diarrheal Outbreak in Immunocompromised Mice. Comparative Medicine, 2018, 68, 261-268.	0.4	6
1445	Soil Bacterial Communities Under Different Long-Term Fertilization Regimes in Three Locations Across the Black Soil Region of Northeast China. Pedosphere, 2018, 28, 751-763.	2.1	32
1446	Metagenomic analysis and the functional profiles of traditional fermented pork fat â€˜sa-umâ€™ of Northeast India. AMB Express, 2018, 8, 163.	1.4	18
1447	Microbiome shifts with onset and progression of Sea Star Wasting Disease revealed through time course sampling. Scientific Reports, 2018, 8, 16476.	1.6	34
1448	Dynamic Distribution of Gut Microbiota in Goats at Different Ages and Health States. Frontiers in Microbiology, 2018, 9, 2509.	1.5	91
1449	Comparative Analysis of the Microbial Profiles in Supragingival Plaque Samples Obtained From Twins With Discordant Caries Phenotypes and Their Mothers. Frontiers in Cellular and Infection Microbiology, 2018, 8, 361.	1.8	12
1450	High Microbial Diversity Despite Extremely Low Biomass in a Deep Karst Aquifer. Frontiers in Microbiology, 2018, 9, 2823.	1.5	34

#	Article	IF	Citations
1451	Land Use Influences Antibiotic Resistance in the Microbiome of Soil Collembolans <i>Orchesellides sinensis</i>. Environmental Science & Technology, 2018, 52, 14088-14098.	4.6	46
1452	Evaluation of Bacterial Contamination in Goat Milk Powder Using PacBio Single Molecule Real-Time Sequencing and Droplet Digital PCR. Journal of Food Protection, 2018, 81, 1791-1799.	0.8	3
1453	Compounded Disturbance Chronology Modulates the Resilience of Soil Microbial Communities and N-Cycle Related Functions. Frontiers in Microbiology, 2018, 9, 2721.	1.5	23
1454	Coral-associated bacteria demonstrate phylosymbiosis and cophylogeny. Nature Communications, 2018, 9, 4921.	5.8	264
1455	The Microbial Metabolite Butyrate Stimulates Bone Formation via T Regulatory Cell-Mediated Regulation of WNT10B Expression. Immunity, 2018, 49, 1116-1131.e7.	6.6	288
1456	Characterization of the Microbiome at the Worldâ€™s Largest Potable Water Reuse Facility. Frontiers in Microbiology, 2018, 9, 2435.	1.5	43
1457	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. Science Translational Medicine, 2018, 10, .	5.8	121
1458	Fecal microbiota associated with phytohaemagglutininâ€induced immune response in nestlings of a passerine bird. Ecology and Evolution, 2018, 8, 9793-9802.	0.8	10
1459	Enrichment of Bacterioplankton Able to Utilize One-Carbon and Methylated Compounds in the Coastal Pacific Ocean. Frontiers in Marine Science, 2018, 5, .	1.2	12
1460	Free D-amino acids produced by commensal bacteria in the colonic lumen. Scientific Reports, 2018, 8, 17915.	1.6	55
1461	Gut microbiota profiling in Norwegian weaner pigs reveals potentially beneficial effects of a high-fiber rapeseed diet. PLoS ONE, 2018, 13, e0209439.	1.1	26
1462	Low-Temperature Sulfidic-Ice Microbial Communities, Borup Fiord Pass, Canadian High Arctic. Frontiers in Microbiology, 2018, 9, 1622.	1.5	10
1463	Stability and resilience of the intestinal microbiota in children in daycare â€“ a 12â€‰month cohort study. BMC Microbiology, 2018, 18, 223.	1.3	15
1464	Phosphorus-mineralizing Communities Reflect Nutrient-Rich Characteristics in Japanese Arable Andisols. Microbes and Environments, 2018, 33, 282-289.	0.7	17
1465	Impact of Individual Traits, Saturated Fat, and Protein Source on the Gut Microbiome. MBio, 2018, 9, .	1.8	70
1466	New Insights into Human Nostril Microbiome from the Expanded Human Oral Microbiome Database (eHOMD): a Resource for the Microbiome of the Human Aerodigestive Tract. MSystems, 2018, 3, .	1.7	346
1467	<i>Toxoplasma gondii-</i>Induced Long-Term Changes in the Upper Intestinal Microflora during the Chronic Stage of Infection. Scientifica, 2018, 2018, 1-11.	0.6	11
1468	Bacterial microbiome of the chigger mite Leptotrombidium imphalum varies by life stage and infection with the scrub typhus pathogen Orientia tsutsugamushi. PLoS ONE, 2018, 13, e0208327.	1.1	16

#	ARTICLE	IF	CITATIONS
1469	Monomethylmercury degradation by the human gut microbiota is stimulated by protein amendments. Journal of Toxicological Sciences, 2018, 43, 717-725.	0.7	22
1470	Characterization of gut bacterial community associated with worker and soldier castes of Globitermes sulphureus Haviland (Blattodea: Termitidae) using 16S rRNA metagenomic. Journal of Asia-Pacific Entomology, 2018, 21, 1268-1274.	0.4	7
1471	Loss of murine Paneth cell function alters the immature intestinal microbiome and mimics changes seen in neonatal necrotizing enterocolitis. PLoS ONE, 2018, 13, e0204967.	1.1	53
1472	Bacterial Microbiota and Metabolic Character of Traditional Sour Cream and Butter in Buryatia, Russia. Frontiers in Microbiology, 2018, 9, 2496.	1.5	18
1473	Characterization of the vaginal microbiota of Japanese women. Anaerobe, 2018, 54, 172-177.	1.0	20
1474	Obesity-Linked Gut Microbiome Dysbiosis Associated with Derangements in Gut Permeability and Intestinal Cellular Homeostasis Independent of Diet. Journal of Diabetes Research, 2018, 2018, 1-9.	1.0	116
1475	Analysis of microbial communities in natural halite springs reveals a domainâ€dependent relationship of species diversity to osmotic stress. Environmental Microbiology Reports, 2018, 10, 695-703.	1.0	10
1476	Host diet mediates a negative relationship between abundance and diversity of <i>Drosophila</i> gut microbiota. Ecology and Evolution, 2018, 8, 9491-9502.	0.8	29
1477	The impact of epidermal growth factor supernatant on pig performance and ileal microbiota1. Translational Animal Science, 2018, 2, 184-194.	0.4	7
1478	Monosodium glutamate induces limited modulation in gut microbiota. Journal of Functional Foods, 2018, 49, 493-500.	1.6	18
1479	Effects of an oral synbiotic on the gastrointestinal immune system and microbiota in patients with diarrhea-predominant irritable bowel syndrome. European Journal of Nutrition, 2018, 58, 2767-2778.	1.8	21
1480	Diet induced changes in the microbiota and cell composition of rabbit gut associated lymphoid tissue (GALT). Scientific Reports, 2018, 8, 14103.	1.6	18
1481	First insight into microbiome profile of fungivorous thrips Hoplothrips carpathicus (Insecta:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 T Scientific Reports, 2018, 8, 14376.	1.6	24
1482	Local confinement of disease-related microbiome facilitates recovery of gorgonian sea fans from necrotic-patch disease. Scientific Reports, 2018, 8, 14636.	1.6	17
1483	Soil amendment with sewage sludge affects soil prokaryotic community composition, mobilome and resistome. FEMS Microbiology Ecology, 2019, 95, .	1.3	12
1484	An assessment of the microbial community in an urban fringing tidal marsh with an emphasis on petroleum hydrocarbon degradative genes. Marine Pollution Bulletin, 2018, 136, 351-364.	2.3	4
1485	Biases in Prokaryotic Community Amplicon Sequencing Affected by DNA Extraction Methods in Both Saline and Non-saline Soil. Frontiers in Microbiology, 2018, 9, 1796.	1.5	12
1486	A Natural History of Actinic Keratosis and Cutaneous Squamous Cell Carcinoma Microbiomes. MBio, 2018, 9, .	1.8	37

#	Article	IF	Citations
1487	Differences in the fecal microbiota of neonates born at home or in the hospital. Scientific Reports, 2018, 8, 15660.	1.6	38
1488	Two key features influencing community assembly processes at regional scale: Initial state and degree of change in environmental conditions. Molecular Ecology, 2018, 27, 5238-5251.	2.0	147
1489	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dysbiosis and alteration of community structure. Microbiome, 2018, 6, 180.	4.9	23
1490	Exposure of a Soil Collembolan to Ag Nanoparticles and AgNO₃ Disturbs Its Associated Microbiota and Lowers the Incidence of Antibiotic Resistance Genes in the Gut. Environmental Science & Technology, 2018, 52, 12748-12756.	4.6	67
1491	Bacterial and archaeal community structures in perennial cave ice. Scientific Reports, 2018, 8, 15671.	1.6	30
1492	Repeated rectal application of a hyperosmolar lubricant is associated with microbiota shifts but does not affect Pr<scp>EP</scp> drug concentrations: results from a randomized trial in men who have sex with men. Journal of the International AIDS Society, 2018, 21, e25199.	1.2	13
1493	Microbial Interkingdom Interactions in Roots Promote Arabidopsis Survival. Cell, 2018, 175, 973-983.e14.	13.5	707
1494	The severity of human periâ€implantitis lesions correlates with the level of submucosal microbial dysbiosis. Journal of Clinical Periodontology, 2018, 45, 1498-1509.	2.3	60
1495	Characterization of bacterial and microbial eukaryotic communities associated with an ephemeral hypoxia event in Taihu Lake, a shallow eutrophic Chinese lake. Environmental Science and Pollution Research, 2018, 25, 31543-31557.	2.7	20
1496	Poisoning with Soman, an Organophosphorus Nerve Agent, Alters Fecal Bacterial Biota and Urine Metabolites: a Case for Novel Signatures for Asymptomatic Nerve Agent Exposure. Applied and Environmental Microbiology, 2018, 84, .	1.4	6
1497	Biodegradability of polar compounds formed from weathered diesel. Biodegradation, 2018, 29, 443-461.	1.5	10
1498	HmmUFOtu: An HMM and phylogenetic placement based ultra-fast taxonomic assignment and OTU picking tool for microbiome amplicon sequencing studies. Genome Biology, 2018, 19, 82.	3.8	32
1499	Oil type and temperature dependent biodegradation dynamics - Combining chemical and microbial community data through multivariate analysis. BMC Microbiology, 2018, 18, 83.	1.3	59
1500	Effect of humic substances on rumen fermentation, nutrient digestibility, methane emissions, and rumen microbiota in beef heifers1. Journal of Animal Science, 2018, 96, 3863-3877.	0.2	20
1501	Alteration of the cutaneous microbiome in psoriasis and potential role in Th17 polarization. Microbiome, 2018, 6, 154.	4.9	190
1502	Assessment of Bacterial Communities Associated With the Skin of Costa Rican Amphibians at La Selva Biological Station. Frontiers in Microbiology, 2018, 9, 2001.	1.5	21
1503	Exposures Related to House Dust Microbiota in a U.S. Farming Population. Environmental Health Perspectives, 2018, 126, 067001.	2.8	23
1504	Direct-fed microbial supplementation influences the bacteria community composition of the gastrointestinal tract of pre- and post-weaned calves. Scientific Reports, 2018, 8, 14147.	1.6	50

#	ARTICLE	IF	CITATIONS
1505	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. Scientific Reports, 2018, 8, 13314.	1.6	54
1506	Diverse Bacteria Utilize Alginate Within the Microbiome of the Giant Kelp Macrocystis pyrifera. Frontiers in Microbiology, 2018, 9, 1914.	1.5	38
1507	Comparison of microbial community dynamics induced by distinct crude oil dispersions reveals compositional differences. Journal of Sea Research, 2018, 141, 112-118.	0.6	5
1508	Gut Bacterial Communities of Dendroctonus valens and D. mexicanus (Curculionidae: Scolytinae): A Metagenomic Analysis across Different Geographical Locations in Mexico. International Journal of Molecular Sciences, 2018, 19, 2578.	1.8	25
1509	Associations between the gut microbiota and host responses to high altitude. American Journal of Physiology - Renal Physiology, 2018, 315, G1003-G1015.	1.6	48
1510	Diversity and antimicrobial potential in sea anemone and holothurian microbiomes. PLoS ONE, 2018, 13, e0196178.	1.1	30
1511	Local and Regional Scale Heterogeneity Drive Bacterial Community Diversity and Composition in a Polar Desert. Frontiers in Microbiology, 2018, 9, 1928.	1.5	34
1512	Composition of the teat canal and intramammary microbiota of dairy cows subjected to antimicrobial dry cow therapy and internal teat sealant. Journal of Dairy Science, 2018, 101, 10191-10205.	1.4	46
1513	Spatial and temporal characterization of epiphytic microbial communities associated with Eurasian watermilfoil: a highly invasive macrophyte in North America. FEMS Microbiology Ecology, 2018, 94, .	1.3	6
1514	Changes in rumen bacterial and archaeal communities over the transition period in primiparous Holstein dairy cows. Journal of Dairy Science, 2018, 101, 9847-9862.	1.4	38
1515	Impact of xylanases on gut microbiota of growing pigs fed corn- or wheat-based diets. Animal Nutrition, 2018, 4, 339-350.	2.1	41
1516	Diet Modifies Colonic Microbiota and CD4+ T-Cell Repertoire to Induce Flares of Colitis in Mice With Myeloid-Cell Expression of Interleukin 23. Gastroenterology, 2018, 155, 1177-1191.e16.	0.6	32
1517	The Use of a Mini-Bioreactor Fermentation System as a Reproducible, High-Throughput ex vivo Batch Model of the Distal Colon. Frontiers in Microbiology, 2018, 9, 1844.	1.5	36
1518	Insights into the Populations of Proteolytic and Amino Acid-Fermenting Bacteria from Microbiota Analysis Using In Vitro Enrichment Cultures. Current Microbiology, 2018, 75, 1543-1550.	1.0	7
1519	Reduced-Particle-Size Wheat Bran Is Efficiently Colonized by a Lactic Acid-Producing Community and Reduces Levels of Enterobacteriaceae in the Cecal Microbiota of Broilers. Applied and Environmental Microbiology, 2018, 84, .	1.4	18
1520	Restoration with pioneer plants changes soil properties and remodels the diversity and structure of bacterial communities in rhizosphere and bulk soil of copper mine tailings in Jiangxi Province, China. Environmental Science and Pollution Research, 2018, 25, 22106-22119.	2.7	60
1521	Starvation stress affects the interplay among shrimp gut microbiota, digestion and immune activities. Fish and Shellfish Immunology, 2018, 80, 191-199.	1.6	61
1522	Dynamic bacterial and fungal microbiomes during sweet sorghum ensiling impact bioethanol production. Bioresource Technology, 2018, 264, 163-173.	4.8	37

#	ARTICLE	IF	CITATIONS
1523	Resilience to fire of phylogenetic diversity across biological domains. Molecular Ecology, 2018, 27, 2896-2908.	2.0	49
1524	Deterministic mechanisms define the long-term anaerobic digestion microbiome and its functionality regardless of the initial microbial community. Water Research, 2018, 141, 366-376.	5.3	82
1525	Effects of Immunonutrition in Advanced Human Immunodeficiency Virus Disease: A Randomized Placebo-controlled Clinical Trial (Promaltia Study). Clinical Infectious Diseases, 2019, 68, 120-130.	2.9	31
1526	Inhalational exposure to particulate matter air pollution alters the composition of the gut microbiome. Environmental Pollution, 2018, 240, 817-830.	3.7	181
1527	Food Starch Structure Impacts Gut Microbiome Composition. MSphere, 2018, 3, .	1.3	106
1528	Short communication: Variability in fermentation end-products and methanogen communities in different rumen sites of dairy cows. Journal of Dairy Science, 2018, 101, 5153-5158.	1.4	23
1529	Bangladeshi children with acute diarrhoea show faecal microbiomes with increased <i>Streptococcus</i> abundance, irrespective of diarrhoea aetiology. Environmental Microbiology, 2018, 20, 2256-2269.	1.8	33
1530	The Transplantation of Ï‰3 PUFAâ€“Altered Gut Microbiota of fat-1 Mice to Wild-Type Littermates Prevents Obesity and Associated Metabolic Disorders. Diabetes, 2018, 67, 1512-1523.	0.3	65
1531	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. Applied and Environmental Microbiology, 2018, 84, .	1.4	63
1532	Dysbiosis of microbiome and probiotic treatment in a genetic model of autism spectrum disorders. Brain, Behavior, and Immunity, 2018, 73, 310-319.	2.0	130
1533	Application of PacBio Single Molecule Real-Time (SMRT) sequencing in bacterial source tracking analysis during milk powder production. Food Control, 2018, 93, 226-234.	2.8	12
1534	Impact of Iron-Enriched <i>Aspergillus oryzae</i> on Iron Bioavailability, Safety, and Gut Microbiota in Rats. Journal of Agricultural and Food Chemistry, 2018, 66, 6213-6218.	2.4	14
1535	Microbiome dynamics during spontaneous fermentations of sound grapes in comparison with sour rot and Botrytis infected grapes. International Journal of Food Microbiology, 2018, 281, 36-46.	2.1	34
1536	Limited influence of hospital wastewater on the microbiome and resistome of wastewater in a community sewerage system. FEMS Microbiology Ecology, 2018, 94, .	1.3	72
1537	Bacterial endophyte communities in Pinus flexilis are structured by host age, tissue type, and environmental factors. Plant and Soil, 2018, 428, 335-352.	1.8	32
1538	Gut microflora may facilitate adaptation to anthropic habitat: A comparative study in <i>Rattus</i>. Ecology and Evolution, 2018, 8, 6463-6472.	0.8	4
1539	Interactive network configuration maintains bacterioplankton community structure under elevated CO&lt;sub&gt;2&lt;/sub&gt; in a eutrophic coastal mesocosm experiment. Biogeosciences, 2018, 15, 551-565.	1.3	9
1540	Antimicrobial peptide expression in a wild tobacco plant reveals the limits of host-microbe-manipulations in the field. ELife, 2018, 7, .	2.8	19

#	ARTICLE	IF	CITATIONS
1541	AnalyticÂMethods in Microbiome Studies. , 2018, , 29-42.		0
1542	Viral community predicts the geographical origin of fermented vegetable foods more precisely than bacterial community. Food Microbiology, 2018, 76, 319-327.	2.1	28
1543	Predators and nutrient availability favor protozoa-resisting bacteria in aquatic systems. Scientific Reports, 2018, 8, 8415.	1.6	20
1544	Perennials but not slope aspect affect the diversity of soil bacterial communities in the northern Negev Desert, Israel. Soil Research, 2018, 56, 123.	0.6	5
1545	Grape Sour Rot: A Four-Way Interaction Involving the Host, Yeast, Acetic Acid Bacteria, and Insects. Phytopathology, 2018, 108, 1429-1442.	1.1	40
1546	Analysis of Bacterial Diversity in Different Heavy Oil Wells of a Reservoir in South Oman with Alkaline pH. Scientifica, 2018, 2018, 1-10.	0.6	4
1547	Relationships among introduced parasites, host defenses, and gut microbiota of Galapagos birds. Ecosphere, 2018, 9, e02286.	1.0	21
1548	Linking patterns of net community production and marine microbial community structure in the western North Atlantic. ISME Journal, 2018, 12, 2582-2595.	4.4	15
1549	Alterations in the gut bacterial microbiome in fungal Keratitis patients. PLoS ONE, 2018, 13, e0199640.	1.1	65
1550	Influence of gender and menopausal status on gut microbiota. Maturitas, 2018, 116, 43-53.	1.0	153
1551	Types of tobacco consumption and the oral microbiome in the United Arab Emirates Healthy Future (UAEHFS) Pilot Study. Scientific Reports, 2018, 8, 11327.	1.6	51
1552	How wastewater with different nutrient levels influences microbial degradation of 2,2â€²,4,4â€²-tetrabromodiphenyl ether (BDE-47) in anaerobic sediments. Chemosphere, 2018, 211, 128-138.	4.2	9
1553	Alternate life history phases of a common seaweed have distinct microbial surface communities. Molecular Ecology, 2018, 27, 3555-3568.	2.0	41
1554	Characterization of the fecal microbiota of healthy horses. American Journal of Veterinary Research, 2018, 79, 811-819.	0.3	37
1555	Microbial connectivity and sorting in a High Arctic watershed. ISME Journal, 2018, 12, 2988-3000.	4.4	33
1556	A meta-analysis reveals universal gut bacterial signatures for diagnosing the incidence of shrimp disease. FEMS Microbiology Ecology, 2018, 94, .	1.3	33
1557	Responses of Intestinal Mucosal Barrier Functions of Rats to Simulated Weightlessness. Frontiers in Physiology, 2018, 9, 729.	1.3	27
1558	Metagenomic and Metatranscriptomic Analyses of Diverse Watermelon Cultivars Reveal the Role of Fruit Associated Microbiome in Carbohydrate Metabolism and Ripening of Mature Fruits. Frontiers in Plant Science, 2018, 9, 4.	1.7	43

#	Article	IF	Citations
1559	Trichoderma-Inoculated Miscanthus Straw Can Replace Peat in Strawberry Cultivation, with Beneficial Effects on Disease Control. Frontiers in Plant Science, 2018, 9, 213.	1.7	28
1560	Core Microbiome of Medicinal Plant Salvia miltiorrhiza Seed: A Rich Reservoir of Beneficial Microbes for Secondary Metabolism?. International Journal of Molecular Sciences, 2018, 19, 672.	1.8	109
1561	Microbial biogeography of 925 geothermal springs in New Zealand. Nature Communications, 2018, 9, 2876.	5.8	163
1562	Microbial community changes during a toxic cyanobacterial bloom in an alkaline Hungarian lake. Antonie Van Leeuwenhoek, 2018, 111, 2425-2440.	0.7	12
1563	The effect of dietary lipid on gut microbiota in a senescence-accelerated prone mouse model (SAMP8). Biogerontology, 2018, 19, 367-383.	2.0	10
1564	The impact of Clostridium butyricum MIYAIRI 588 on the murine gut microbiome and colonic tissue. Anaerobe, 2018, 54, 8-18.	1.0	45
1565	Sinus Microanatomy and Microbiota in a Rabbit Model of Rhinosinusitis. Frontiers in Cellular and Infection Microbiology, 2017, 7, 540.	1.8	31
1566	Soil Salinity Controls Relative Abundance of Specific Bacterial Groups Involved in the Decomposition of Maize Plant Residues. Frontiers in Ecology and Evolution, 2018, 6, .	1.1	25
1567	Estimating the Intra-taxa Diversity, Population Genetic Structure, and Evolutionary Pathways of Cryptococcus neoformans and Cryptococcus gattii. Frontiers in Genetics, 2018, 9, 148.	1.1	30
1568	Respiratory Disease following Viral Lung Infection Alters the Murine Gut Microbiota. Frontiers in Immunology, 2018, 9, 182.	2.2	178
1569	Holobiont Diversity in a Reef-Building Coral over Its Entire Depth Range in the Mesophotic Zone. Frontiers in Marine Science, 2018, 5, .	1.2	47
1570	Differential Responses of Eukaryotic Phytoplankton to Nitrogenous Nutrients in the North Pacific Subtropical Gyre. Frontiers in Marine Science, 2018, 5, .	1.2	16
1571	Low Light Availability Alters Root Exudation and Reduces Putative Beneficial Microorganisms in Seagrass Roots. Frontiers in Microbiology, 2017, 8, 2667.	1.5	88
1572	Diversity of Rare and Abundant Prokaryotic Phylotypes in the Prony Hydrothermal Field and Comparison with Other Serpentinite-Hosted Ecosystems. Frontiers in Microbiology, 2018, 9, 102.	1.5	23
1573	Interspecific Plant Interactions Reflected in Soil Bacterial Community Structure and Nitrogen Cycling in Primary Succession. Frontiers in Microbiology, 2018, 9, 128.	1.5	57
1574	Ammonia-Oxidizing Archaea Show More Distinct Biogeographic Distribution Patterns than Ammonia-Oxidizing Bacteria across the Black Soil Zone of Northeast China. Frontiers in Microbiology, 2018, 9, 171.	1.5	51
1575	Soil Bacterial Community Was Changed after Brassicaceous Seed Meal Application for Suppression of Fusarium Wilt on Pepper. Frontiers in Microbiology, 2018, 9, 185.	1.5	22
1576	Comparison of Meconium DNA Extraction Methods for Use in Microbiome Studies. Frontiers in Microbiology, 2018, 9, 270.	1.5	53

#	ARTICLE	IF	CITATIONS
1577	Physiological and Metagenomic Characterizations of the Synergistic Relationships between Ammonia- and Nitrite-Oxidizing Bacteria in Freshwater Nitrification. Frontiers in Microbiology, 2018, 9, 280.	1.5	15
1578	Environmental and Host Effects on Skin Bacterial Community Composition in Panamanian Frogs. Frontiers in Microbiology, 2018, 9, 298.	1.5	49
1579	Watershed-Induced Limnological and Microbial Status in Two Oligotrophic Andean Lakes Exposed to the Same Climatic Scenario. Frontiers in Microbiology, 2018, 9, 357.	1.5	11
1580	Unique Microbial Diversity and Metabolic Pathway Features of Fermented Vegetables From Hainan, China. Frontiers in Microbiology, 2018, 9, 399.	1.5	53
1581	Skin Microbiomes of California Terrestrial Salamanders Are Influenced by Habitat More Than Host Phylogeny. Frontiers in Microbiology, 2018, 9, 442.	1.5	58
1582	Gut Microbiota Profiling and Gutâ€"Brain Crosstalk in Children Affected by Pediatric Acute-Onset Neuropsychiatric Syndrome and Pediatric Autoimmune Neuropsychiatric Disorders Associated With Streptococcal Infections. Frontiers in Microbiology, 2018, 9, 675.	1.5	88
1583	Rearing Water Treatment Induces Microbial Selection Influencing the Microbiota and Pathogen Associated Transcripts of Cod (Gadus morhua) Larvae. Frontiers in Microbiology, 2018, 9, 851.	1.5	33
1584	Variation in Bat Guano Bacterial Community Composition With Depth. Frontiers in Microbiology, 2018, 9, 914.	1.5	20
1585	Effect of Limit-Fed Diets With Different Forage to Concentrate Ratios on Fecal Bacterial and Archaeal Community Composition in Holstein Heifers. Frontiers in Microbiology, 2018, 9, 976.	1.5	37
1586	Microscale Biosignatures and Abiotic Mineral Authigenesis in Little Hot Creek, California. Frontiers in Microbiology, 2018, 9, 997.	1.5	35
1587	Microbiomes of North American Triatominae: The Grounds for Chagas Disease Epidemiology. Frontiers in Microbiology, 2018, 9, 1167.	1.5	57
1588	Effectiveness of Interventions to Modulate the Rumen Microbiota Composition and Function in Pre-ruminant and Ruminant Lambs. Frontiers in Microbiology, 2018, 9, 1273.	1.5	52
1589	Exposure to Arsenic Alters the Microbiome of Larval Zebrafish. Frontiers in Microbiology, 2018, 9, 1323.	1.5	42
1590	Persistence of Cellulolytic Bacteria Fibrobacter and Treponema After Short-Term Corn Stover-Based Dietary Intervention Reveals the Potential to Improve Rumen Fibrolytic Function. Frontiers in Microbiology, 2018, 9, 1363.	1.5	92
1591	Lab to Field Assessment of the Ecotoxicological Impact of Chlorpyrifos, Isoproturon, or Tebuconazole on the Diversity and Composition of the Soil Bacterial Community. Frontiers in Microbiology, 2018, 9, 1412.	1.5	46
1592	Gut Microbiome Composition in Non-human Primates Consuming a Western or Mediterranean Diet. Frontiers in Nutrition, 2018, 5, 28.	1.6	125
1593	Maternal diet during pregnancy is related with the infant stool microbiome in a delivery mode-dependent manner. Microbiome, 2018, 6, 109.	4.9	168
1594	Modulation of the honey bee queen microbiota: Effects of early social contact. PLoS ONE, 2018, 13, e0200527.	1.1	43

#	Article	IF	Citations
1595	Massive Sequencing: A New Tool for the Control of Alcoholic Fermentation in Wine?. Fermentation, 2018, 4, 7.	1.4	10
1596	Drosophila melanogaster establishes a species-specific mutualistic interaction with stable gut-colonizing bacteria. PLoS Biology, 2018, 16, e2005710.	2.6	173
1597	Bioturbation by the razor clam (Sinonovacula constricta) on the microbial community and enzymatic activities in the sediment of an ecological aquaculture wastewater treatment system. Science of the Total Environment, 2018, 643, 1098-1107.	3.9	57
1598	Manipulation of microbial community in the rhizosphere alleviates the replanting issues in Panax ginseng. Soil Biology and Biochemistry, 2018, 125, 64-74.	4.2	64
1599	A Long-Standing Complex Tropical Dipole Shapes Marine Microbial Biogeography. Applied and Environmental Microbiology, 2018, 84, .	1.4	6
1600	Dietary Supplementation with a Magnesium-Rich Marine Mineral Blend Enhances the Diversity of Gastrointestinal Microbiota. Marine Drugs, 2018, 16, 216.	2.2	41
1601	Bioleaching potential of bacterial communities in historic mine waste areas. Environmental Earth Sciences, 2018, 77, 1.	1.3	7
1602	Effect of Dietary Fructooligosaccharide (FOS) Supplementation on Ileal Microbiota in Broiler Chickens. Poultry Science, 2018, 97, 3622-3634.	1.5	48
1603	Developing climateâ€smart restoration: Can plant microbiomes be hardened against heat waves?. Ecological Applications, 2018, 28, 1594-1605.	1.8	8
1604	Metabolic Biosynthesis Pathways Identified from Fecal Microbiome Associated with Prostate Cancer. European Urology, 2018, 74, 575-582.	0.9	117
1605	Microbial communities in the rhizosphere and the root of lettuce as affected by Salmonella-contaminated irrigation water. FEMS Microbiology Ecology, 2018, 94, .	1.3	13
1606	Microbial community response to growing season and plant nutrient optimisation in a boreal Norway spruce forest. Soil Biology and Biochemistry, 2018, 125, 197-209.	4.2	64
1607	Mapping the Bacterial Community in Digboi Oil Refinery, India by High-Throughput Sequencing Approach. Current Microbiology, 2018, 75, 1441-1446.	1.0	5
1608	Host genotype-specific microbiota do not influence the susceptibility of D. magna to a bacterial pathogen. Scientific Reports, 2018, 8, 9407.	1.6	19
1609	Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. Biotechnology for Biofuels, 2018, 11, 200.	6.2	99
1610	Phylogenetic convolutional neural networks in metagenomics. BMC Bioinformatics, 2018, 19, 49.	1.2	75
1611	Organic acid production from potato starch waste fermentation by rumen microbial communities from Dutch and Thai dairy cows. Biotechnology for Biofuels, 2018, 11, 13.	6.2	30
1612	Influenza A virus infection impacts systemic microbiota dynamics and causes quantitative enteric dysbiosis. Microbiome, 2018, 6, 9.	4.9	194

#	Article	IF	Citations
1613	Crawling-induced floor dust resuspension affects the microbiota of the infant breathing zone. Microbiome, 2018, 6, 25.	4.9	40
1614	Effect of heat shock on hot water plumbing microbiota and Legionella pneumophila control. Microbiome, 2018, 6, 30.	4.9	20
1615	Disruption of bacterial balance in the gut of Portunus trituberculatus induced by Vibrio alginolyticus infection. Journal of Oceanology and Limnology, 2018, 36, 1891-1898.	0.6	8
1616	Feminizing Wolbachia influence microbiota composition in the terrestrial isopod Armadillidium vulgare. Scientific Reports, 2018, 8, 6998.	1.6	45
1617	Tracking antibiotic resistome during wastewater treatment using high throughput quantitative PCR. Environment International, 2018, 117, 146-153.	4.8	152
1618	Comparative study on the gut microbiotas of four economically important Asian carp species. Science China Life Sciences, 2018, 61, 696-705.	2.3	52
1619	Exposure to toxic metals triggers unique responses from the rat gut microbiota. Scientific Reports, 2018, 8, 6578.	1.6	95
1620	Effects of dietary supplementation of Ulva pertusa and non-starch polysaccharide enzymes on gut microbiota of Siganus canaliculatus. Journal of Oceanology and Limnology, 2018, 36, 438-449.	0.6	28
1621	Near full-length 16S rRNA gene next-generation sequencing revealed Asaia as a common midgut bacterium of wild and domesticated Queensland fruit fly larvae. Microbiome, 2018, 6, 85.	4.9	82
1622	<i>Archaea</i>are prominent members of the prokaryotic communities colonizing common forest mushrooms. Canadian Journal of Microbiology, 2018, 64, 716-726.	0.8	9
1623	Exploring the pathology of an epidermal disease affecting a circum-Antarctic sea star. Scientific Reports, 2018, 8, 11353.	1.6	19
1624	Diversity and composition of bacterial endophytes among plant parts of Panax notoginseng. Chinese Medicine, 2018, 13, 41.	1.6	53
1625	Bacterial biogeography of adult airways in atopic asthma. Microbiome, 2018, 6, 104.	4.9	93
1626	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. Journal of Functional Foods, 2018, 49, 96-104.	1.6	3
1627	Effects of Different Doses of Fructooligosaccharides (FOS) on the Composition of Mice Fecal Microbiota, Especially the Bifidobacterium Composition. Nutrients, 2018, 10, 1105.	1.7	69
1628	Coâ€occurrence network analysis reveals thermodynamicsâ€driven microbial interactions in methanogenic bioreactors. Environmental Microbiology Reports, 2018, 10, 673-685.	1.0	22
1629	Microbial Community Composition Reveals Spatial Variation and Distinctive Core Microbiome of the Weaver Ant Oecophylla smaragdina in Malaysia. Scientific Reports, 2018, 8, 10777.	1.6	22
1630	Sex-specific associations of infantsâ€™ gut microbiome with arsenic exposure in a US population. Scientific Reports, 2018, 8, 12627.	1.6	47

#	ARTICLE	IF	CITATIONS
1631	Comparison of microbiomes of cold-water corals Primnoa pacifica and Primnoa resedaeformis, with possible link between microbiome composition and host genotype. Scientific Reports, 2018, 8, 12383.	1.6	25
1632	The response of ruminal fermentation, epithelium-associated microbiota, and epithelial barrier function to severe feed restriction in pregnant ewes. Journal of Animal Science, 2018, 96, 4293-4305.	0.2	28
1633	Comparative evaluation of a new magnetic bead-based DNA extraction method from fecal samples for downstream next-generation 16S rRNA gene sequencing. PLoS ONE, 2018, 13, e0202858.	1.1	15
1634	Insect exclusion limits variation in bacterial microbiomes of tomato flowers and fruit. Journal of Applied Microbiology, 2018, 125, 1749-1760.	1.4	23
1635	The treatment of flowback water in a sequencing batch reactor with aerobic granular sludge: Performance and microbial community structure. Chemosphere, 2018, 211, 1065-1072.	4.2	25
1636	Comparison of Fecal Collection Methods for Microbiome and Metabolomics Studies. Frontiers in Cellular and Infection Microbiology, 2018, 8, 301.	1.8	114
1637	Microbiome Composition in Both Wild-Type and Disease Model Mice Is Heavily Influenced by Mouse Facility. Frontiers in Microbiology, 2018, 9, 1598.	1.5	60
1638	Substrate-Induced Response in Biogas Process Performance and Microbial Community Relates Back to Inoculum Source. Microorganisms, 2018, 6, 80.	1.6	21
1639	Petroleum hydrocarbon and microbial community structure successions in marine oil-related aggregates associated with diatoms relevant for Arctic conditions. Marine Pollution Bulletin, 2018, 135, 759-768.	2.3	13
1640	Diet and other environmental factors shape the bacterial communities of fish gut in an eutrophic lake. Journal of Applied Microbiology, 2018, 125, 1626-1641.	1.4	47
1641	Metagenomic analysis of rhizosphere microflora of oil-contaminated soil planted with barley and alfalfa. PLoS ONE, 2018, 13, e0202127.	1.1	45
1642	Dissolved Carbon Dynamics in Meltwaters From the Russell Glacier, Greenland Ice Sheet. Journal of Geophysical Research G: Biogeosciences, 2018, 123, 2922-2940.	1.3	17
1643	Metabolic Capability and Phylogenetic Diversity of Mono Lake during a Bloom of the Eukaryotic Phototroph Picocystis sp. Strain ML. Applied and Environmental Microbiology, 2018, 84, .	1.4	18
1644	The Performance of an Oral Microbiome Biomarker Panel in Predicting Oral Cavity and Oropharyngeal Cancers. Frontiers in Cellular and Infection Microbiology, 2018, 8, 267.	1.8	83
1645	Sample size effects on the assessment of eukaryotic diversity and community structure in aquatic sediments using high-throughput sequencing. Scientific Reports, 2018, 8, 11737.	1.6	55
1646	Temporal dynamics of microbiota before and after host death. ISME Journal, 2018, 12, 2076-2085.	4.4	21
1647	Composition and richness of the serum microbiome differ by age and link to systemic inflammation. GeroScience, 2018, 40, 257-268.	2.1	63
1648	Comprehensive skin microbiome analysis reveals the uniqueness of human skin and evidence for phylosymbiosis within the class Mammalia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5786-E5795.	3.3	184

#	Article	IF	Citations
1649	Deciphering the Rhizosphere and Geocaulosphere Microbiomes of Potato Following Inoculation with the Biocontrol Agent <i>Pseudomonas fluorescens</i> Strain LBUM223. Phytobiomes Journal, 2018, 2, 92-99.	1.4	27
1650	Seasonal shifts in the insect gut microbiome are concurrent with changes in cold tolerance and immunity. Functional Ecology, 2018, 32, 2357-2368.	1.7	105
1651	Oral administration of Bifidobacterium bifidum TMC3115 to neonatal mice may alleviate IgE-mediated allergic risk in adulthood. Beneficial Microbes, 2018, 9, 815-828.	1.0	22
1652	Analysis of the Gut Microbial Diversity of Dairy Cows During Peak Lactation by PacBio Single-Molecule Real-Time (SMRT) Sequencing. Current Microbiology, 2018, 75, 1316-1323.	1.0	13
1653	Impact of Gut Microbiota and Diet on the Development of Atherosclerosis in <i>Apoe</i> ^{â^'/â^'} Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 2318-2326.	1.1	123
1654	A comparative study of prokaryotic diversity and physicochemical characteristics of Devils Hole and the Ash Meadows Fish Conservation Facility, a constructed analog. PLoS ONE, 2018, 13, e0194404.	1.1	13
1655	Host: Microbiome co-metabolic processing of dietary polyphenols â€" An acute, single blinded, cross-over study with different doses of apple polyphenols in healthy subjects. Food Research International, 2018, 112, 108-128.	2.9	67
1656	Diversity, specificity, co-occurrence and hub taxa of the bacterialâ€"fungal pollen microbiome. FEMS Microbiology Ecology, 2018, 94, .	1.3	68
1657	Bacterial lineages putatively associated with the dissemination of antibiotic resistance genes in a full-scale urban wastewater treatment plant. Environment International, 2018, 118, 179-188.	4.8	93
1658	Environmental legacy contributes to the resilience of methane consumption in a laboratory microcosm system. Scientific Reports, 2018, 8, 8862.	1.6	12
1659	Effect of antibiotic withdrawal in feed on chicken gut microbial dynamics, immunity, growth performance and prevalence of foodborne pathogens. PLoS ONE, 2018, 13, e0192450.	1.1	112
1660	<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. Helicobacter, 2018, 23, e12498.	1.6	66
1661	The benign helminth <i>Hymenolepis diminuta</i> ameliorates chemically induced colitis in a rat model system. Parasitology, 2018, 145, 1324-1335.	0.7	13
1662	Ageâ€related changes in the gut microbiota of wild House Sparrow nestlings. Ibis, 2019, 161, 184-191.	1.0	39
1663	What Can Environmental Sequences Tell Us About the Distribution of Lowâ€Rank Taxa? The Case of <i>Euplotes</i> (Ciliophora, Spirotrichea), Including a Description of <i>Euplotes enigma</i> sp. nov.. Journal of Eukaryotic Microbiology, 2019, 66, 281-293.	0.8	17
1664	The Impact of Anthropogenic Disturbance on Bacterioplankton Communities During the Construction of Donghu Tunnel (Wuhan, China). Microbial Ecology, 2019, 77, 277-287.	1.4	17
1665	Occurrence of antibiotic resistance genes and bacterial pathogens in water and sediment in urban recreational water. Journal of Environmental Sciences, 2019, 77, 65-74.	3.2	46
1666	Assessment of the non-lactic acid bacteria microbiota in fresh cucumbers and commercially fermented cucumber pickles brined with 6% NaCl. Food Microbiology, 2019, 77, 10-20.	2.1	34

#	Article	IF	Citations
1667	The biology of fog: results from coastal Maine and Namib Desert reveal common drivers of fog microbial composition. Science of the Total Environment, 2019, 647, 1547-1556.	3.9	40
1668	Profiling the Gut Microbiome: Practice and Potential. , 2019, , 200-217.		0
1669	Loss of HDAC6 alters gut microbiota and worsens obesity. FASEB Journal, 2019, 33, 1098-1109.	0.2	36
1670	Dietary specialization in mutualistic acaciaâ€ants affects relative abundance but not identity of hostâ€associated bacteria. Molecular Ecology, 2019, 28, 900-916.	2.0	34
1671	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. ISME Journal, 2019, 13, 576-587.	4.4	236
1672	Effects of moderate, voluntary ethanol consumption on the rat and human gut microbiome. Addiction Biology, 2019, 24, 617-630.	1.4	46
1673	Species-specific effects of arsenic on the soil collembolan gut microbiota. Ecotoxicology and Environmental Safety, 2019, 183, 109538.	2.9	6
1674	Continental scale structuring of forest and soil diversity via functional traits. Nature Ecology and Evolution, 2019, 3, 1298-1308.	3.4	34
1675	Environmental filtering increases with elevation for the assembly of gut microbiota in wild pikas. Microbial Biotechnology, 2019, 12, 976-992.	2.0	55
1676	Understanding soil biodiversity using two orthogonal 1000km transects across New South Wales, Australia. Geoderma, 2019, 354, 113860.	2.3	10
1677	Dynamics of Vaginal and Rectal Microbiota Over Several Menstrual Cycles in Female Cynomolgus Macaques. Frontiers in Cellular and Infection Microbiology, 2019, 9, 188.	1.8	24
1678	Cooked Red Lentils Dose-Dependently Modulate the Colonic Microenvironment in Healthy C57Bl/6 Male Mice. Nutrients, 2019, 11, 1853.	1.7	12
1679	Spatial variations of microbial communities in abyssal and hadal sediments across the Challenger Deep. PeerJ, 2019, 7, e6961.	0.9	48
1680	Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes. Cell, 2019, 178, 795-806.e12.	13.5	830
1681	The microbiology, pH, and oxidation reduction potential of larval masses in decomposing carcasses on Oahu, Hawaii. Journal of Clinical Forensic and Legal Medicine, 2019, 67, 37-48.	0.5	19
1682	Age and Mothers: Potent Influences of Childrenâ€™s Skin Microbiota. Journal of Investigative Dermatology, 2019, 139, 2497-2505.e6.	0.3	46
1683	Biogeographical patterns in soil bacterial communities across the Arctic region. FEMS Microbiology Ecology, 2019, 95, .	1.3	53
1684	Arsenic and Sulfamethoxazole Increase the Incidence of Antibiotic Resistance Genes in the Gut of Earthworm. Environmental Science & Technology, 2019, 53, 10445-10453.	4.6	59

#	ARTICLE	IF	CITATIONS
1685	A diet of U.S. military food rations alters gut microbiota composition and does not increase intestinal permeability. Journal of Nutritional Biochemistry, 2019, 72, 108217.	1.9	13
1686	Dietary probiotic <i>Pediococcus acidilactici</i> MA18/5M modulates the intestinal microbiota and stimulates intestinal immunity in rainbow trout (<i>Oncorhynchus mykiss</i>). Journal of the World Aquaculture Society, 2019, 50, 1133-1151.	1.2	41
1687	Composition of the mucosaâ€associated microbiota along the entire gastrointestinal tract of human individuals. United European Gastroenterology Journal, 2019, 7, 897-907.	1.6	70
1688	A Metagenomics Study on Hirschsprung's Disease Associated Enterocolitis: Biodiversity and Gut Microbial Homeostasis Depend on Resection Length and Patient's Clinical History. Frontiers in Pediatrics, 2019, 7, 326.	0.9	19
1689	Crypt- and Mucosa-Associated Core Microbiotas in Humans and Their Alteration in Colon Cancer Patients. MBio, 2019, 10, .	1.8	94
1690	Collembolans accelerate the dispersal of antibiotic resistance genes in the soil ecosystem. Soil Ecology Letters, 2019, 1, 14-21.	2.4	7
1691	Novel production of natural bacteriocin via internalization of dextran nanoparticles into probiotics. Biomaterials, 2019, 218, 119360.	5.7	23
1692	Bifidobacterium and Lactobacillus Composition at Species Level and Gut Microbiota Diversity in Infants before 6 Weeks. International Journal of Molecular Sciences, 2019, 20, 3306.	1.8	61
1693	Diversity of Gut Microbiota Affecting Serum Level of Undercarboxylated Osteocalcin in Patients with Crohnâ€™s Disease. Nutrients, 2019, 11, 1541.	1.7	17
1694	Effects of starter feeding on caecal mucosal bacterial composition and expression of genes involved in immune and tight junctions in pre-weaned twin lambs. Anaerobe, 2019, 59, 167-175.	1.0	5
1695	Saline stress modifies the effect of cadmium toxicity on soil archaeal communities. Ecotoxicology and Environmental Safety, 2019, 182, 109431.	2.9	25
1696	Incense Burning is Associated with Human Oral Microbiota Composition. Scientific Reports, 2019, 9, 10039.	1.6	12
1697	Multiple Data Analyses and Statistical Approaches for Analyzing Data from Metagenomic Studies and Clinical Trials. Methods in Molecular Biology, 2019, 1910, 605-634.	0.4	8
1698	Nieves penitentes are a new habitat for snow algae in one of the most extreme high-elevation environments on Earth. Arctic, Antarctic, and Alpine Research, 2019, 51, 190-200.	0.4	16
1699	The fungicide azoxystrobin perturbs the gut microbiota community and enriches antibiotic resistance genes in Enchytraeus crypticus. Environment International, 2019, 131, 104965.	4.8	64
1700	Improvement of pesticide removal in contaminated media using aqueous extracts from contaminated biopurification systems. Science of the Total Environment, 2019, 691, 749-759.	3.9	12
1701	Dissecting the Heterogeneous Population Genetic Structure of Candida albicans: Limitations and Constraints of the Multilocus Sequence Typing Scheme. Frontiers in Microbiology, 2019, 10, 1052.	1.5	9
1702	The responses of a soil bacterial community under saline stress are associated with Cd availability in long-term wastewater-irrigated field soil. Chemosphere, 2019, 236, 124372.	4.2	41

#	ARTICLE	IF	CITATIONS
1703	Combining stable isotope analysis with DNA metabarcoding improves inferences of trophic ecology. PLoS ONE, 2019, 14, e0219070.	1.1	15
1704	Effect of live yeast Saccharomyces cerevisiae supplementation on the performance and cecum microbial profile of suckling piglets. PLoS ONE, 2019, 14, e0219557.	1.1	43
1705	Relationship between the structure and composition of rumen microorganisms and the digestibility of neutral detergent fibre in goats. Asian-Australasian Journal of Animal Sciences, 2019, 32, 82-91.	2.4	8
1706	High-quality treated wastewater causes remarkable changes in natural microbial communities and intI1 gene abundance. Water Research, 2019, 167, 114895.	5.3	33
1707	Cover Crop Management Practices Rather Than Composition of Cover Crop Mixtures Affect Bacterial Communities in No-Till Agroecosystems. Frontiers in Microbiology, 2019, 10, 1618.	1.5	64
1708	The disappearing periglacial ecosystem atop Mt. Kilimanjaro supports both cosmopolitan and endemic microbial communities. Scientific Reports, 2019, 9, 10676.	1.6	21
1709	Establishment of Coral-Bacteria Symbioses Reveal Changes in the Core Bacterial Community With Host Ontogeny. Frontiers in Microbiology, 2019, 10, 1529.	1.5	50
1710	Regulation of the Phytoplankton Heme b Iron Pool During the North Atlantic Spring Bloom. Frontiers in Microbiology, 2019, 10, 1566.	1.5	4
1711	The Seasonal Dynamics and the Influence of Human Activities on Campus Outdoor Microbial Communities. Frontiers in Microbiology, 2019, 10, 1579.	1.5	7
1712	Plant Diversity and Fertilizer Management Shape the Belowground Microbiome of Native Grass Bioenergy Feedstocks. Frontiers in Plant Science, 2019, 10, 1018.	1.7	19
1713	Autochthonous probiotic bacteria modulate intestinal microbiota of Pirarucu, <i>Arapaima gigas</i>. Journal of the World Aquaculture Society, 2019, 50, 1152-1167.	1.2	9
1714	Identification of methanogenesis and syntrophy as important microbial metabolic processes for optimal thermophilic anaerobic digestion of energy cane thin stillage. Bioresource Technology Reports, 2019, 7, 100254.	1.5	17
1715	DNA extraction and amplicon production strategies deeply infâ€Šluence the outcome of gut mycobiome studies. Scientific Reports, 2019, 9, 9328.	1.6	51
1716	Arthropodâ€“bacteria interactions influence assembly of aquatic host microbiome and pathogen defense. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190924.	1.2	27
1717	Above-below surface interactions mediate effects of seagrass disturbance on meiobenthic diversity, nematode and polychaete trophic structure. Communications Biology, 2019, 2, 362.	2.0	6
1718	Seasonal blooms of neutrophilic Betaproteobacterial Fe(II) oxidizers and Chlorobi in iron-rich coal mine drainage sediments. FEMS Microbiology Ecology, 2019, 95, .	1.3	3
1719	Polymorphic Immune Mechanisms Regulate Commensal Repertoire. Cell Reports, 2019, 29, 541-550.e4.	2.9	55
1720	Viral respiratory infections and the oropharyngeal bacterial microbiota in acutely wheezing children. PLoS ONE, 2019, 14, e0223990.	1.1	14

#	Article	IF	Citations
1721	Influence of Dietary Supplementation of Probiotic Pediococcus acidilactici MA18/5M During the Transition From Freshwater to Seawater on Intestinal Health and Microbiota of Atlantic Salmon (Salmo salar L.). Frontiers in Microbiology, 2019, 10, 2243.	1.5	45
1722	Characterization of Microbial Communities Populating the Inflorescences of <i>Humulus lupulus</i> L.. Journal of the American Society of Brewing Chemists, 2019, 77, 243-250.	0.8	7
1723	Floral organs act as environmental filters and interact with pollinators to structure the yellow monkeyflower (<i>Mimulus guttatus</i>) floral microbiome. Molecular Ecology, 2019, 28, 5155-5171.	2.0	32
1724	Phytoremediation potential of Miscanthus sinensis for mercury-polluted sites and its impacts on soil microbial community. Environmental Science and Pollution Research, 2019, 26, 34818-34829.	2.7	35
1725	Bacterial Community on a Guyot in the Northwest Pacific Ocean Influenced by Physical Dynamics and Environmental Variables. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 2883-2897.	1.3	14
1726	Metagenomic Analyses of Microbial and Carbohydrate-Active Enzymes in the Rumen of Holstein Cows Fed Different Forage-to-Concentrate Ratios. Frontiers in Microbiology, 2019, 10, 649.	1.5	90
1727	Adsorption of NO Gas Molecules on Monolayer Arsenene Doped with Al, B, S and Si: A First-Principles Study. Processes, 2019, 7, 538.	1.3	8
1728	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. Genome Biology, 2019, 20, 219.	3.8	94
1729	Changed Caecal Microbiota and Fermentation Contribute to the Beneficial Effects of Early Weaning with Alfalfa Hay, Starter Feed, and Milk Replacer on the Growth and Organ Development of Yak Calves. Animals, 2019, 9, 921.	1.0	10
1730	Prokaryotic and eukaryotic microbiomes associated with blooms of the ichthyotoxic dinoflagellate Cochlodinium (Margalefidinium) polykrikoides in New York, USA, estuaries. PLoS ONE, 2019, 14, e0223067.	1.1	16
1731	Illumina-based Analysis of Endophytic Bacterial Diversity of four Allium species. Scientific Reports, 2019, 9, 15271.	1.6	19
1732	Trichinella spiralis infection decreases the diversity of the intestinal flora in the infected mouse. Journal of Microbiology, Immunology and Infection, 2021, 54, 490-500.	1.5	12
1733	Gut microbiota and their putative metabolic functions in fragmented Bengal tiger population of Nepal. PLoS ONE, 2019, 14, e0221868.	1.1	13
1734	Compositional and predicted functional dynamics of soil bacterial community in response to single pulse and repeated dosing of titanium dioxide nanoparticles. NanoImpact, 2019, 16, 100187.	2.4	6
1735	A novel calreticulin-related molecule that interacts with bacteria and enhances host resistance against bacterial infection in black rockfish, Sebastes schlegeli. Fish and Shellfish Immunology, 2019, 93, 823-831.	1.6	6
1736	Incorporating phylogenetic metrics to microbial coâ€occurrence networks based on amplicon sequences to discern community assembly processes. Molecular Ecology Resources, 2019, 19, 1552-1564.	2.2	41
1737	Tuning the Optical and Electrical Properties of Fewâ€Layer Black Phosphorus via Physisorption of Small Solvent Molecules. Small, 2019, 15, e1903432.	5.2	21
1738	13C-DNA-SIP Distinguishes the Prokaryotic Community That Metabolizes Soybean Residues Produced Under Different CO2 Concentrations. Frontiers in Microbiology, 2019, 10, 2184.	1.5	5

#	ARTICLE	IF	CITATIONS
1739	Community Structure Analyses of Anodic Biofilms in a Bioelectrochemical System Combined with an Aerobic Reactor. Energies, 2019, 12, 3643.	1.6	3
1740	High-throughput DNA sequencing reveals the dominance of pico- and other filamentous cyanobacteria in an urban freshwater Lake. Science of the Total Environment, 2019, 661, 465-480.	3.9	28
1741	Effect of Re-acidification on Buffalo Grass Rhizosphere and Bulk Microbial Communities During Phytostabilization of Metalliferous Mine Tailings. Frontiers in Microbiology, 2019, 10, 1209.	1.5	24
1742	Dose-Dependent Alterations to In Vitro Human Microbiota Composition and Butyrate Inhibition by a Supercritical Carbon Dioxide Hops Extract. Biomolecules, 2019, 9, 390.	1.8	9
1743	Bacterial but Not Fungal Gut Microbiota Alterations Are Associated With Common Variable Immunodeficiency (CVID) Phenotype. Frontiers in Immunology, 2019, 10, 1914.	2.2	37
1744	A Microbiomic Analysis of a Pasture-Raised Broiler Flock Elucidates Foodborne Pathogen Ecology Along the Farm-To-Fork Continuum. Frontiers in Veterinary Science, 2019, 6, 260.	0.9	18
1745	Effects of Land Transport Stress on Variations in Ruminal Microbe Diversity and Immune Functions in Different Breeds of Cattle. Animals, 2019, 9, 599.	1.0	26
1746	Bacterioplankton community in response to biological filters (clam, biofilm, and macrophytes) in an integrated aquaculture wastewater bioremediation system. Environmental Pollution, 2019, 254, 113035.	3.7	22
1747	A high-sugar diet rapidly enhances susceptibility to colitis via depletion of luminal short-chain fatty acids in mice. Scientific Reports, 2019, 9, 12294.	1.6	115
1748	Highly Reproducible 16S Sequencing Facilitates Measurement of Host Genetic Influences on the Stickleback Gut Microbiome. MSystems, 2019, 4, .	1.7	8
1749	Surface Water Microbial Community Response to the Biocide 2,2-Dibromo-3-Nitrilopropionamide, Used in Unconventional Oil and Gas Extraction. Applied and Environmental Microbiology, 2019, 85, .	1.4	12
1750	Conservation of Endophyte Bacterial Community Structure Across Two Panicum Grass Species. Frontiers in Microbiology, 2019, 10, 2181.	1.5	19
1751	Identification of Initial Colonizing Bacteria in Dental Plaques from Young Adults Using Full-Length 16S rRNA Gene Sequencing. MSystems, 2019, 4, .	1.7	22
1752	Long-term nitrogen fertilization indirectly affects soil fungi community structure by changing soil and pruned litter in a subtropical tea (Camellia sinensis L.) plantation in China. Plant and Soil, 2019, 444, 409-426.	1.8	44
1753	Fish oil supplementation to a high-fat diet improves both intestinal health and the systemic obese phenotype. Journal of Nutritional Biochemistry, 2019, 72, 108216.	1.9	26
1754	Dietary intake influences gut microbiota development of healthy Australian children from the age of one to two years. Scientific Reports, 2019, 9, 12476.	1.6	28
1755	Culture-dependent and metagenomic analysis of lesser horseshoe batsâ€™ gut microbiome revealing unique bacterial diversity and signatures of potential human pathogens. Microbial Pathogenesis, 2019, 137, 103675.	1.3	18
1756	Untapped sponge microbiomes: structure specificity at host order and family levels. FEMS Microbiology Ecology, 2019, 95, .	1.3	14

#	ARTICLE	IF	CITATIONS
1757	Network Analysis Reveals Seasonal Patterns of Bacterial Community Networks in Lake Taihu under Aquaculture Conditions. Water (Switzerland), 2019, 11, 1868.	1.2	13
1758	Methane-based denitrification kinetics and syntrophy in a membrane biofilm reactor at low methane pressure. Science of the Total Environment, 2019, 695, 133818.	3.9	18
1759	The microbiome of the footrot lesion in Merino sheep is characterized by a persistent bacterial dysbiosis. Veterinary Microbiology, 2019, 236, 108378.	0.8	10
1760	Long-Term N Fertilization Decreased Diversity and Altered the Composition of Soil Bacterial and Archaeal Communities. Agronomy, 2019, 9, 574.	1.3	22
1761	Antarctic tundra soil metagenome as useful natural resources of cold-active lignocelluolytic enzymes. Journal of Microbiology, 2019, 57, 865-873.	1.3	18
1762	Spatial variation of sediment bacterial community in an acid mine drainage contaminated area and surrounding river basin. Journal of Environmental Management, 2019, 251, 109542.	3.8	25
1763	Next-generation sequencing and waste/wastewater treatment: a comprehensive overview. Reviews in Environmental Science and Biotechnology, 2019, 18, 635-680.	3.9	32
1764	The Gut Microbiome and Metabolome of Two Riparian Communities in the Amazon. Frontiers in Microbiology, 2019, 10, 2003.	1.5	10
1765	Microbiomes in Soils Exposed to Naturally High Concentrations of CO2 (Bossoleto Mofette Tuscany,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	11
1766	Community characteristics and ecological roles of bacterial biofilms associated with various algal settlements on coastal reefs. Journal of Environmental Management, 2019, 250, 109459.	3.8	16
1767	Biogeographic Distribution Patterns of the Archaeal Communities Across the Black Soil Zone of Northeast China. Frontiers in Microbiology, 2019, 10, 23.	1.5	27
1768	Microbial community and fermentation characteristic of Italian ryegrass silage prepared with corn stover and lactic acid bacteria. Bioresource Technology, 2019, 279, 166-173.	4.8	138
1769	The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. GigaScience, 2019, 8, .	3.3	143
1770	Retention of Microbiota Diversity by Lactose-Free Milk in a Mouse Model of Elderly Gut Microbiota. Journal of Agricultural and Food Chemistry, 2019, 67, 2098-2112.	2.4	11
1771	Genomic Analyses of Acute Flaccid Myelitis Cases among a Cluster in Arizona Provide Further Evidence of Enterovirus D68 Role. MBio, 2019, 10, .	1.8	15
1772	Population structure of human gut bacteria in a diverse cohort from rural Tanzania and Botswana. Genome Biology, 2019, 20, 16.	3.8	66
1773	Effects of urea plus nitrate pretreated rice straw and corn oil supplementation on fiber digestibility, nitrogen balance, rumen fermentation, microbiota and methane emissions in goats. Journal of Animal Science and Biotechnology, 2019, 10, 6.	2.1	18
1774	<scp>d</scp>- and<scp>l</scp>-Aspartate regulates growth performance, inflammation and intestinal microbial community in young pigs. Food and Function, 2019, 10, 1028-1037.	2.1	21

#	ARTICLE	IF	CITATIONS
1775	A high linoleic acid diet exacerbates metabolic responses and gut microbiota dysbiosis in obese rats with diabetes mellitus. Food and Function, 2019, 10, 786-798.	2.1	41
1776	High dispersal levels and lake warming are emergent drivers of cyanobacterial community assembly in peri-Alpine lakes. Scientific Reports, 2019, 9, 7366.	1.6	18
1777	Comparison of Bacterial Populations in the Ceca of Swine at Two Different Stages and Their Functional Annotations. Genes, 2019, 10, 382.	1.0	13
1778	Ultra-small microorganisms in the polyextreme conditions of the Dallol volcano, Northern Afar, Ethiopia. Scientific Reports, 2019, 9, 7907.	1.6	28
1779	New Microbial Lineages Capable of Carbon Fixation and Nutrient Cycling in Deep-Sea Sediments of the Northern South China Sea. Applied and Environmental Microbiology, 2019, 85, .	1.4	36
1780	Evolutionary history constrains microbial traits across environmental variation. Nature Ecology and Evolution, 2019, 3, 1064-1069.	3.4	76
1781	The Relative Abundance of Benthic Bacterial Phyla Along a Water-Depth Gradient in a Plateau Lake: Physical, Chemical, and Biotic Drivers. Frontiers in Microbiology, 2019, 10, 1521.	1.5	28
1782	Comparison of the microbiomes of two drinking water distribution systemsâ€"with and without residual chloramine disinfection. Microbiome, 2019, 7, 87.	4.9	63
1783	Microbiota data from low biomass milk samples is markedly affected by laboratory and reagent contamination. PLoS ONE, 2019, 14, e0218257.	1.1	36
1784	Assessment of bacterial diversity in western Accra, Ghana, drinking water samples. Journal of Water Sanitation and Hygiene for Development, 2019, 9, 644-661.	0.7	2
1785	Biodiversity patterns across taxonomic groups along a lake water-depth gradient: Effects of abiotic and biotic drivers. Science of the Total Environment, 2019, 686, 1262-1271.	3.9	22
1786	Responses of soil microbial communities and their network interactions to saline-alkaline stress in Cd-contaminated soils. Environmental Pollution, 2019, 252, 1609-1621.	3.7	135
1787	Microbial Community Structure and Metabolic Potential of the Hyporheic Zone of a Large Mid-Stream Channel Bar. Geomicrobiology Journal, 2019, 36, 765-776.	1.0	12
1788	Microbial Associations of Four Species of Algal Symbiont-bearing Foraminifers from the Florida Reef Tract, Usa. Journal of Foraminiferal Research, 2019, 49, 178-190.	0.1	3
1789	Trophic Transfer of Antibiotic Resistance Genes in a Soil Detritus Food Chain. Environmental Science & Technology, 2019, 53, 7770-7781.	4.6	69
1790	The Successional Changes in the Gut Microbiome of Pasture-Raised Chickens Fed Soy-Containing and Soy-Free Diets. Frontiers in Sustainable Food Systems, 2019, 3, .	1.8	16
1791	Classification of individuals and the potential to detect sexual contact using the microbiome of the pubic region. Forensic Science International: Genetics, 2019, 41, 177-187.	1.6	21
1792	Unveiled feather microcosm: feather microbiota of passerine birds is closely associated with host species identity and bacteriocin-producing bacteria. ISME Journal, 2019, 13, 2363-2376.	4.4	38

#	ARTICLE	IF	CITATIONS
1793	Microbiological profiles in clinical and subclinical cases of mastitis in milking Jafarabadi buffalo. Research in Veterinary Science, 2019, 125, 94-99.	0.9	13
1794	Biofertilizers regulate the soil microbial community and enhance Panax ginseng yields. Chinese Medicine, 2019, 14, 20.	1.6	54
1795	A specific synbiotic-containing amino acid-based formula restores gut microbiota in non-IgE mediated cowâ€™s milk allergic infants: a randomized controlled trial. Clinical and Translational Allergy, 2019, 9, 27.	1.4	24
1797	Fecal Microbial Communities in a Large Representative Cohort of California Dairy Cows. Frontiers in Microbiology, 2019, 10, 1093.	1.5	60
1798	Bovine milk microbiome: a more complex issue than expected. Veterinary Research, 2019, 50, 44.	1.1	67
1799	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
1800	Effect of the Degree of Polymerization of Fructans on Ex Vivo Fermented Human Gut Microbiome. Nutrients, 2019, 11, 1293.	1.7	23
1801	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
1802	GenPipes: an open-source framework for distributed and scalable genomic analyses. GigaScience, 2019, 8, .	3.3	121
1803	Shortâ€term and longâ€term impacts of <scp><i>Helicobacter pylori</i></scp> eradication with reverse hybrid therapy on the gut microbiota. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 1968-1976.	1.4	39
1804	Mycobiome of Brevipalpus Mite Strains and Insights on Metabolic Function in the Bacteriome of the Tetranychoidea Mites. , 2019, , 79-91.		1
1805	Soil bacterial community dynamics following surfactant addition and bioaugmentation in pyrene-contaminated soils. Chemosphere, 2019, 231, 93-102.	4.2	35
1806	Phyllosphere of staple crops under pig manure fertilization, a reservoir of antibiotic resistance genes. Environmental Pollution, 2019, 252, 227-235.	3.7	62
1807	Hindgut microbiota in laboratory-reared and wild Triatoma infestans. PLoS Neglected Tropical Diseases, 2019, 13, e0007383.	1.3	39
1808	Using fecal microbiota as biomarkers for predictions of performance in the selective breeding process of pedigree broiler breeders. PLoS ONE, 2019, 14, e0216080.	1.1	27
1809	Manure and Doxycycline Affect the Bacterial Community and Its Resistome in Lettuce Rhizosphere and Bulk Soil. Frontiers in Microbiology, 2019, 10, 725.	1.5	46
1810	Interpreting distanceâ€decay pattern of soil bacteria via quantifying the assembly processes at multiple spatial scales. MicrobiologyOpen, 2019, 8, e00851.	1.2	42
1811	Bioturbation of blood clam Tegillarca granosa on benthic nutrient fluxes and microbial community in an aquaculture wastewater treatment system. International Biodeterioration and Biodegradation, 2019, 142, 73-82.	1.9	27

#	ARTICLE	IF	CITATIONS
1812	The impact of probiotic Clostridium butyricum MIYAIRI 588 on murine gut metabolic alterations. Journal of Infection and Chemotherapy, 2019, 25, 571-577.	0.8	17
1813	Vanishing benefits - The loss of actinobacterial symbionts at elevated temperatures. Journal of Thermal Biology, 2019, 82, 222-228.	1.1	16
1814	Navy bean supplemented high-fat diet improves intestinal health, epithelial barrier integrity and critical aspects of the obese inflammatory phenotype. Journal of Nutritional Biochemistry, 2019, 70, 91-104.	1.9	41
1815	Organotrophic acid-tolerant microorganisms enriched from an acid mine drainage affected environment as inoculum for microbial fuel cells. Science of the Total Environment, 2019, 678, 639-646.	3.9	16
1816	Mineral and organic fertilization alters the microbiome of a soil nematode Dorylaimus stagnalis and its resistome. Science of the Total Environment, 2019, 680, 70-78.	3.9	35
1817	Microbial Communities in Sediments From Four Mildly Acidic Ephemeral Salt Lakes in the Yilgarn Craton (Australia) â€“ Terrestrial Analogs to Ancient Mars. Frontiers in Microbiology, 2019, 10, 779.	1.5	15
1818	Differential Effects of Bacitracin Methylene Disalicylate (BMD) on the Distal Colon and Cecal Microbiota of Young Broiler Chickens. Frontiers in Veterinary Science, 2019, 6, 114.	0.9	36
1819	Recently duplicated sesterterpene (C25) gene clusters in Arabidopsis thaliana modulate root microbiota. Science China Life Sciences, 2019, 62, 947-958.	2.3	52
1820	Malaria vector species in Amazonian Peru co-occur in larval habitats but have distinct larval microbial communities. PLoS Neglected Tropical Diseases, 2019, 13, e0007412.	1.3	22
1821	Extent of the annual Gulf of Mexico hypoxic zone influences microbial community structure. PLoS ONE, 2019, 14, e0209055.	1.1	15
1822	Butyrate Protects Mice from Clostridium difficile-Induced Colitis through an HIF-1-Dependent Mechanism. Cell Reports, 2019, 27, 750-761.e7.	2.9	212
1823	[NiFe]-hydrogenases are constitutively expressed in an enriched Methanobacterium sp. population during electromethanogenesis. PLoS ONE, 2019, 14, e0215029.	1.1	10
1824	Uncovering the hidden marine sponge microbiome by applying a multi-primer approach. Scientific Reports, 2019, 9, 6214.	1.6	12
1825	Thermal disruption of soil bacterial assemblages decreases diversity and assemblage similarity. Ecosphere, 2019, 10, e02598.	1.0	2
1826	Comparison of the rumen bacterial community, rumen fermentation and growth performance of fattening lambs fed low-grain, pelleted or non-pelleted high grain total mixed ration. Animal Feed Science and Technology, 2019, 253, 1-12.	1.1	40
1827	Multiple stressors interact primarily through antagonism to drive changes in the coral microbiome. Scientific Reports, 2019, 9, 6834.	1.6	64
1828	Exposure to microplastics lowers arsenic accumulation and alters gut bacterial communities of earthworm Metaphire californica. Environmental Pollution, 2019, 251, 110-116.	3.7	171
1829	Unraveling the diversity of sedimentary sulfate-reducing prokaryotes (SRP) across Tibetan saline lakes using epicPCR. Microbiome, 2019, 7, 71.	4.9	16

#	Article	IF	Citations
1830	Structure and stability of the coral microbiome in space and time. Scientific Reports, 2019, 9, 6785.	1.6	74
1831	Phosphate depletion controls lipid content and accumulation of heterotrophic bacteria during growth of Synechocystis sp. PCC 6803. Applied Microbiology and Biotechnology, 2019, 103, 5007-5014.	1.7	6
1832	Pyrolysis biochar has negligible effects on soil greenhouse gas production, microbial communities, plant germination, and initial seedling growth. Chemosphere, 2019, 228, 565-576.	4.2	30
1833	Different response of bacteria, archaea and fungi to process parameters in nine fullâ€scale anaerobic digesters. Microbial Biotechnology, 2019, 12, 1210-1225.	2.0	23
1834	Unprecedented bacterial community richness in soybean nodules vary with cultivar and water status. Microbiome, 2019, 7, 63.	4.9	51
1835	Agricultural Risk Factors Influence Microbial Ecology in Honghu Lake. Genomics, Proteomics and Bioinformatics, 2019, 17, 76-90.	3.0	31
1836	Roots Mediate the Effects of Snowpack Decline on Soil Bacteria, Fungi, and Nitrogen Cycling in a Northern Hardwood Forest. Frontiers in Microbiology, 2019, 10, 926.	1.5	9
1837	The Association Between the Developing Nasal Microbiota of Hospitalized Neonates and <i>Staphylococcus aureus</i> Colonization. Open Forum Infectious Diseases, 2019, 6, ofz062.	0.4	12
1838	New Insights into Sediment Transport in Interconnected Riverâ€"Lake Systems Through Tracing Microorganisms. Environmental Science & Technology, 2019, 53, 4099-4108.	4.6	47
1839	Integrating the role of antifungal bacteria into skin symbiotic communities of three Neotropical frog species. ISME Journal, 2019, 13, 1763-1775.	4.4	31
1840	Characterization of the rumen and fecal microbiome in bloated and non-bloated cattle grazing alfalfa pastures and subjected to bloat prevention strategies. Scientific Reports, 2019, 9, 4272.	1.6	20
1841	Comparative analysis of bacterial community compositions between sediment and water in different types of wetlands of northeast China. Journal of Soils and Sediments, 2019, 19, 3083-3097.	1.5	18
1842	Gut eukaryotic disease-discriminatory taxa are indicative of Pacific white shrimp (Litopenaeus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.7	29
1843	Microbial Profile and Genetic Polymorphism of Predominant Species in Some Traditional Fermented Seafoods of the Hainan Area in China. Frontiers in Microbiology, 2019, 10, 564.	1.5	14
1844	Exploring the links between bacterial communities and magnetic susceptibility in bulk soil and rhizosphere of beech (Fagus sylvatica L.). Applied Soil Ecology, 2019, 138, 69-79.	2.1	6
1845	Initial Evidence of the Relationships between the Human Postmortem Microbiome and Neighborhood Blight and Greening Efforts. Annals of the American Association of Geographers, 2019, 109, 958-978.	1.5	18
1846	Relative abundance of Akkermansia spp. and other bacterial phylotypes correlates with anxiety- and depressive-like behavior following social defeat in mice. Scientific Reports, 2019, 9, 3281.	1.6	85
1847	Effects of Sulfates on Enhanced Biological Phosphorus Removal in Three Waste Water Treatment Plants. Journal of Water and Environment Technology, 2019, 17, 54-65.	0.3	2

#	ARTICLE	IF	CITATIONS
1848	Evidence for Biotic Perchlorate Reduction in Naturally Perchlorate-Rich Sediments of Pilot Valley Basin, Utah. Astrobiology, 2019, 19, 629-641.	1.5	15
1849	Spatial Variability of Antarctic Surface Snow Bacterial Communities. Frontiers in Microbiology, 2019, 10, 461.	1.5	20
1850	An integrated microbiological and electrochemical approach to determine distributions of Fe metabolism in acid mine drainage-induced â€œiron moundâ€• sediments. PLoS ONE, 2019, 14, e0213807.	1.1	6
1851	Insight Into Dynamics of Gut Microbial Community of Broilers Fed With Fructooligosaccharides Supplemented Low Calcium and Phosphorus Diets. Frontiers in Veterinary Science, 2019, 6, 95.	0.9	14
1852	The epiphytic microbiota of sour rot-affected grapes differs minimally from that of healthy grapes, indicating causal organisms are already present on healthy berries. PLoS ONE, 2019, 14, e0211378.	1.1	10
1853	Effects of wild blueberry (Vaccinium angustifolium) pomace feeding on gut microbiota and blood metabolites in free-range pastured broiler chickens. Poultry Science, 2019, 98, 3739-3755.	1.5	29
1854	Fur seal microbiota are shaped by the social and physical environment, show motherâ€“offspring similarities and are associated with host genetic quality. Molecular Ecology, 2019, 28, 2406-2422.	2.0	27
1855	Different host-specific responses in thyroid function and gut microbiota modulation between diet-induced obese and normal mice given the same dose of iodine. Applied Microbiology and Biotechnology, 2019, 103, 3537-3547.	1.7	22
1856	Soil bacterial diversity is positively associated with air temperature in the maritime Antarctic. Scientific Reports, 2019, 9, 2686.	1.6	37
1857	Temporal variability of diazotroph community composition in the upwelling region off NW Iberia. Scientific Reports, 2019, 9, 3737.	1.6	18
1858	Differential Sensitivity to Plasmodium yoelii Infection in C57BL/6 Mice Impacts Gut-Liver Axis Homeostasis. Scientific Reports, 2019, 9, 3472.	1.6	30
1859	Microbial composition changes on the surface of strawberries from the field and market by 16SrDNA sequencing. Journal of Food Safety, 2019, 39, e12630.	1.1	4
1860	Contributions of the microbial community to algal biomass and biofuel productivity in a wastewater treatment lagoon system. Algal Research, 2019, 39, 101461.	2.4	8
1861	Investigating the bacterial microbiota of traditional fermented dairy products using propidium monoazide with single-molecule real-time sequencing. Journal of Dairy Science, 2019, 102, 3912-3923.	1.4	17
1862	Comparison of Microbial Communities in the Sediments and Water Columns of Frozen Cryoconite Holes in the McMurdo Dry Valleys, Antarctica. Frontiers in Microbiology, 2019, 10, 65.	1.5	36
1863	Symbiontâ€mediated chemical defense in the invasive ladybird <i>Harmonia axyridis</i>. Ecology and Evolution, 2019, 9, 1715-1729.	0.8	18
1864	Evolution of hierarchy in bacterial metabolic networks. BioSystems, 2019, 180, 71-78.	0.9	3
1865	The fecal, oral, and skin microbiota of children with Chagas disease treated with benznidazole. PLoS ONE, 2019, 14, e0212593.	1.1	21

#	Article	IF	Citations
1866	High total dissolved solids in shale gas wastewater inhibit biodegradation of alkyl and nonylphenol ethoxylate surfactants. Science of the Total Environment, 2019, 668, 1094-1103.	3.9	27
1867	Effects of Arsenic on Gut Microbiota and Its Biotransformation Genes in Earthworm <i>Metaphire sieboldi</i>. Environmental Science & Technology, 2019, 53, 3841-3849.	4.6	78
1868	Microbiome diversity in carriers of fluoroquinolone resistant<i>Escherichia coli</i>. Investigative and Clinical Urology, 2019, 60, 75.	1.0	3
1869	Elevated CO₂ alters the structure of the bacterial community assimilating plantâ€derived carbon in the rhizosphere of soya bean. European Journal of Soil Science, 2019, 70, 1212-1220.	1.8	15
1870	Bacterial colonisation of reeds and cottonseed hulls in the rumen of Tarim red deer (Cervus elaphus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	12
1871	Effects of Nanoparticles on Plant Growth-Promoting Bacteria in Indian Agricultural Soil. Agronomy, 2019, 9, 140.	1.3	61
1872	Diurnal Temperature Variation and Plants Drive Latitudinal Patterns in Seasonal Dynamics of Soil Microbial Community. Frontiers in Microbiology, 2019, 10, 674.	1.5	27
1873	Recovery of Benthic Microalgal Biomass and Community Structure Following Beach Renourishment at Folly Beach, South Carolina. Estuaries and Coasts, 2019, 42, 157-172.	1.0	12
1874	Ecological Correlates of Large-Scale Turnover in the Dominant Members of Pseudacris crucifer Skin Bacterial Communities. Microbial Ecology, 2019, 78, 832-842.	1.4	7
1875	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. FASEB Journal, 2019, 33, 8453-8467.	0.2	23
1876	Microbiota in the apical root canal system of tooth with apical periodontitis. BMC Genomics, 2019, 20, 189.	1.2	37
1877	Impact of Saskatoon berry powder on insulin resistance and relationship with intestinal microbiota in high fatâ€“high sucrose diet-induced obese mice. Journal of Nutritional Biochemistry, 2019, 69, 130-138.	1.9	25
1878	Assessing Microbial Community Patterns During Incipient Soil Formation From Basalt. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 941-958.	1.3	16
1879	Microbial Community Analysis Provides Insights into the Effects of Tetrahydrofuran on 1,4-Dioxane Biodegradation. Applied and Environmental Microbiology, 2019, 85, .	1.4	20
1880	The Charosphere Promotes Mineralization of ¹³Câ€Phenanthrene by Psychrotrophic Microorganisms in Greenland Soils. Journal of Environmental Quality, 2019, 48, 559-567.	1.0	6
1881	Oral Administration of Compound Probiotics Improved Canine Feed Intake, Weight Gain, Immunity and Intestinal Microbiota. Frontiers in Immunology, 2019, 10, 666.	2.2	53
1882	Combining electrokinetic transport and bioremediation for enhanced removal of crude oil from contaminated marine sediments: Results of a long-term, mesocosm-scale experiment. Water Research, 2019, 157, 381-395.	5.3	38
1883	Bamboo lignocellulose degradation by gut symbiotic microbiota of the bamboo snout beetle Cyrtotrachelus buqueti. Biotechnology for Biofuels, 2019, 12, 70.	6.2	48

#	ARTICLE	IF	CITATIONS
1884	Effect of the sulfation pattern of sea cucumber-derived fucoidan oligosaccharides on modulating metabolic syndromes and gut microbiota dysbiosis caused by HFD in mice. Journal of Functional Foods, 2019, 55, 193-210.	1.6	38
1885	A Haemophilus sp. dominates the microbiota of sputum from UK adults with non-severe community acquired pneumonia and chronic lung disease. Scientific Reports, 2019, 9, 2388.	1.6	12
1886	Fecal transplant modifies urine chemistry risk factors for urinary stone disease. Physiological Reports, 2019, 7, e14012.	0.7	18
1887	Influence of pH control on material characteristics, bacterial community composition and BNR performance of mature aerobic granules. Chemical Engineering Research and Design, 2019, 124, 158-166.	2.7	6
1888	Electronâ€acceptor loadings affect chloroform dechlorination in a hydrogenâ€based membrane biofilm reactor. Biotechnology and Bioengineering, 2019, 116, 1439-1448.	1.7	13
1889	Prokaryotic and viral community structure in the singular chaotropic salt lake Salar de Uyuni. Environmental Microbiology, 2019, 21, 2029-2042.	1.8	22
1890	Evaluation of Oral Cavity DNA Extraction Methods on Bacterial and Fungal Microbiota. Scientific Reports, 2019, 9, 1531.	1.6	31
1891	Distinct microbiotas of anatomical gut regions display idiosyncratic seasonal variation in an avian folivore. Animal Microbiome, 2019, 1, 2.	1.5	21
1892	Effect of the extraction and purification of soil<scp>DNA</scp>and pooling of<scp>PCR</scp>amplification products on the description of bacterial and archaeal communities. Journal of Applied Microbiology, 2019, 126, 1454-1467.	1.4	26
1893	Performance of Microbiome Sequence Inference Methods in Environments with Varying Biomass. MSystems, 2019, 4, .	1.7	118
1894	No difference in 4â€nitroquinoline induced tumorigenesis between germâ€free and colonized mice. Molecular Carcinogenesis, 2019, 58, 627-632.	1.3	2
1895	Methane oxidation coupled to perchlorate reduction in a membrane biofilm batch reactor. Science of the Total Environment, 2019, 667, 9-15.	3.9	46
1896	Loading ceftriaxone, vancomycin, and Bifidobacteria bifidum TMC3115 to neonatal mice could differently and consequently affect intestinal microbiota and immunity in adulthood. Scientific Reports, 2019, 9, 3254.	1.6	27
1897	Antagonistic effects of<i>Streptococcus</i>and<i>Lactobacillus</i>probiotics in pharyngeal biofilms. Letters in Applied Microbiology, 2019, 68, 303-312.	1.0	26
1898	Bacterial Community Diversity Associated With Different Utilization Efficiencies of Nitrogen in the Gastrointestinal Tract of Goats. Frontiers in Microbiology, 2019, 10, 239.	1.5	41
1899	Biochar as a management tool for soilborne diseases affecting early stage nursery seedling production. Crop Protection, 2019, 120, 34-42.	1.0	36
1900	Gut Mucosal Proteins and Bacteriome Are Shaped by the Saturation Index of Dietary Lipids. Nutrients, 2019, 11, 418.	1.7	41
1901	Anaerobic degradation of hexadecane and phenanthrene coupled to sulfate reduction by enriched consortia from northern Gulf of Mexico seafloor sediment. Scientific Reports, 2019, 9, 1239.	1.6	31

#	Article	IF	Citations
1902	Enhancement of gasworks groundwater remediation by coupling a bio-electrochemical and activated carbon system. Environmental Science and Pollution Research, 2019, 26, 9981-9991.	2.7	7
1903	Probiotic or synbiotic alters the gut microbiota and metabolism in a randomised controlled trial of weight management in overweight adults. Beneficial Microbes, 2019, 10, 121-135.	1.0	118
1904	Microbial Population Change in Anaerobic Digestion during Copper Sulfate Inhibition and Recovery. Transactions of the ASABE, 2019, 62, 1231-1241.	1.1	2
1905	Validating DNA Extraction Protocols for Bentonite Clay. MSphere, 2019, 4, .	1.3	12
1906	Fecal Components Modulate Human Astrovirus Infectivity in Cells and Reconstituted Intestinal Tissues. MSphere, 2019, 4, .	1.3	12
1907	5. Metagenomics of extreme environments: methods and applications. , 2019, , 93-126.		0
1908	Fetal exposure to maternal inflammation interrupts murine intestinal development and increases susceptibility to neonatal intestinal injury. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	22
1909	Importance of Farm Environment to Shape Poultry-Related Microbiomes Throughout the Farm-to-Fork Continuum of Pasture-Raised Broiler Flocks. Frontiers in Sustainable Food Systems, 2019, 3, .	1.8	11
1910	Assessing the Diversity and Distribution of Apicomplexans in Host and Free-Living Environments Using High-Throughput Amplicon Data and a Phylogenetically Informed Reference Framework. Frontiers in Microbiology, 2019, 10, 2373.	1.5	33
1911	Latitudinal Distributions and Controls of Bacterial Community Composition during the Summer of 2017 in Western Arctic Surface Waters (from the Bering Strait to the Chukchi Borderland). Scientific Reports, 2019, 9, 16822.	1.6	12
1912	Group I alkenones and Isochrysidales in the worldâ€™s largest maar lakes and their potential paleoclimate applications. Organic Geochemistry, 2019, 138, 103924.	0.9	7
1913	Descriptive Bacterial and Fungal Characterization of Propolis Using Ultra-High-Throughput Marker Gene Sequencing. Insects, 2019, 10, 402.	1.0	10
1914	Comparison of specific endophytic bacterial communities in different developmental stages ofPassiflora incarnatausing cultureâ€dependent and cultureâ€independent analysis. MicrobiologyOpen, 2019, 8, e896.	1.2	13
1915	Segregation of age-related skin microbiome characteristics by functionality. Scientific Reports, 2019, 9, 16748.	1.6	77
1916	Corn oil supplementation enhances hydrogen use for biohydrogenation, inhibits methanogenesis, and alters fermentation pathways and the microbial community in the rumen of goats. Journal of Animal Science, 2019, 97, 4999-5008.	0.2	17
1917	Airâ€side ammonia stripping coupled to anaerobic digestion indirectly impacts anaerobic microbiome. Microbial Biotechnology, 2019, 12, 1403-1416.	2.0	19
1918	Comparative study on the effects of different feeding habits and diets on intestinal microbiota in Acipenser baeri Brandt and Huso huso. BMC Microbiology, 2019, 19, 297.	1.3	17
1919	Compositional homogeneity in the pathobiome of a new, slow-spreading coral disease. Microbiome, 2019, 7, 139.	4.9	32

#	Article	IF	Citations
1920	Blueberry Attenuates Liver Fibrosis, Protects Intestinal Epithelial Barrier, and Maintains Gut Microbiota Homeostasis. Canadian Journal of Gastroenterology and Hepatology, 2019, 2019, 1-11.	0.8	21
1921	Prokaryotic Diversity in Mangrove Sediments across Southeastern China Fundamentally Differs from That in Other Biomes. MSystems, 2019, 4, .	1.7	57
1922	Acute changes in the colonic microbiota are associated with large intestinal forms of surgical colic. BMC Veterinary Research, 2019, 15, 468.	0.7	11
1923	Community Structure and Abundance of Archaea in a <i>Zostera marina</i> Meadow: A Comparison between Seagrass-Colonized and Bare Sediment Sites. Archaea, 2019, 2019, 1-11.	2.3	20
1924	Oral administration of vancomycin to neonatal mice could alter their immunity and allergic sensibility late in adulthood. Bioscience of Microbiota, Food and Health, 2019, 38, 129-139.	0.8	2
1925	Distinct gut microbiota profile in antiretroviral therapy-treated perinatally HIV-infected patients associated with cardiac and inflammatory biomarkers. Aids, 2019, 33, 1001-1011.	1.0	31
1926	Microbial Communities in Human Milk Relate to Measures of Maternal Weight. Frontiers in Microbiology, 2019, 10, 2886.	1.5	28
1927	Fasting challenges human gut microbiome resilience and reduces Fusobacterium. Medicine in Microecology, 2019, 1-2, 100003.	0.7	10
1928	Potassium sorbate suppresses intestinal microbial activity and triggers immune regulation in zebrafish (<i>Danio rerio</i>). Food and Function, 2019, 10, 7164-7173.	2.1	15
1929	Related Enteric Viruses Have Different Requirements for Host Microbiota in Mice. Journal of Virology, 2019, 93, .	1.5	30
1930	Differences in the equine faecal microbiota between horses presenting to a tertiary referral hospital for colic compared with an elective surgical procedure. Equine Veterinary Journal, 2019, 51, 336-342.	0.9	42
1931	Bacterial community structure in a sympagic habitat expanding with global warming: brackish ice brine at 85â€“90 Â°N. ISME Journal, 2019, 13, 316-333.	4.4	18
1932	Captivity-Induced Changes in the Skin Microbial Communities of Hellbenders (Cryptobranchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.4	18
1933	Microbiota of eggs revealed by 16S rRNA-based sequencing: From raw materials produced by different suppliers to chilled pasteurized liquid products. Food Control, 2019, 96, 194-204.	2.8	17
1934	Assessment of the ecotoxicological impact of natural and synthetic Î²-triketone herbicides on the diversity and activity of the soil bacterial community using omic approaches. Science of the Total Environment, 2019, 651, 241-249.	3.9	28
1935	Temporal Variability and Stability of the Fecal Microbiome: The Multiethnic Cohort Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 154-162.	1.1	31
1936	Manipulation of the rhizosphere bacterial community by biofertilizers is associated with mitigation of cadmium phytotoxicity. Science of the Total Environment, 2019, 649, 413-421.	3.9	61
1937	Intestinal luminal putrescine is produced by collective biosynthetic pathways of the commensal microbiome. Gut Microbes, 2019, 10, 159-171.	4.3	56

#	ARTICLE	IF	CITATIONS
1938	Effects of past and current drought on the composition and diversity of soil microbial communities. Soil Biology and Biochemistry, 2019, 131, 28-39.	4.2	141
1939	Contrasting patterns of plant and microbial diversity during longâ€term ecosystem development. Journal of Ecology, 2019, 107, 606-621.	1.9	48
1940	Effects of the Wastewater Flow Rate on Interactions between the Genus <i>Nitrosomonas</i> and Diverse Populations in an Activated Sludge Microbiome. Microbes and Environments, 2019, 34, 89-94.	0.7	6
1941	Influence of Library Composition on SourceTracker Predictions for Community-Based Microbial Source Tracking. Environmental Science & Technology, 2019, 53, 60-68.	4.6	33
1942	Variations in Microbial Diversity and Metabolite Profiles of the Tropical Marine Sponge Xestospongia muta with Season and Depth. Microbial Ecology, 2019, 78, 243-256.	1.4	25
1943	Importance of soil texture to the fate of pathogens introduced by irrigation with treated wastewater. Science of the Total Environment, 2019, 653, 886-896.	3.9	21
1944	Microbiome of drinking water: A full-scale spatio-temporal study to monitor water quality in the Paris distribution system. Water Research, 2019, 149, 375-385.	5.3	81
1945	Consumption of florfenicol-medicated feed alters the composition of the channel catfish intestinal microbiota including enriching the relative abundance of opportunistic pathogens. Aquaculture, 2019, 501, 111-118.	1.7	39
1946	Exopolysaccharides from Leuconostoc mesenteroides attenuate chronic kidney disease in mice by protecting the intestinal barrier. Journal of Functional Foods, 2019, 52, 276-283.	1.6	10
1947	Host selectively contributes to shaping intestinal microbiota of carnivorous and omnivorous fish. Journal of General and Applied Microbiology, 2019, 65, 129-136.	0.4	11
1948	Elevational patterns and hierarchical determinants of biodiversity across microbial taxonomic scales. Molecular Ecology, 2019, 28, 86-99.	2.0	34
1949	Effects of organic loading rates on microbial communities and biogas production from water hyacinth: a case of monoâ€•and coâ€digestion. Journal of Chemical Technology and Biotechnology, 2019, 94, 1294-1304.	1.6	23
1950	Zengye decoction induces alterations to metabolically active gut microbiota in aged constipated rats. Biomedicine and Pharmacotherapy, 2019, 109, 1361-1371.	2.5	26
1951	Changes in long chain alkenone distributions and Isochrysidales groups along the Baltic Sea salinity gradient. Organic Geochemistry, 2019, 127, 92-103.	0.9	31
1952	The microbiome of Escherichia coli and culture-negative nonsevere clinical mastitis: Characterization and associations with linear score and milk production. Journal of Dairy Science, 2019, 102, 578-594.	1.4	12
1953	Breastfeeding: a key modulator of gut microbiota characteristics in late infancy. Journal of Developmental Origins of Health and Disease, 2019, 10, 206-213.	0.7	15
1954	Alleviation of cadmium toxicity to tobacco (Nicotiana tabacum) by biofertilizers involves the changes of soil aggregates and bacterial communities. Ecotoxicology and Environmental Safety, 2019, 169, 240-247.	2.9	17
1955	The Influence of Habitat and Phylogeny on the Skin Microbiome of Amphibians in Guatemala and Mexico. Microbial Ecology, 2019, 78, 257-267.	1.4	34

#	ARTICLE	IF	CITATIONS
1956	Identification and Frequencies of Endophytic Microbes within Healthy Grape Berries. American Journal of Enology and Viticulture, 2019, 70, 212-219.	0.9	21
1957	Galaxy mothur Toolset (GmT): a user-friendly application for 16S rRNA gene sequencing analysis using mothur. GigaScience, 2019, 8, .	3.3	17
1958	Analysis of viral and bacterial communities in groundwater associated with contaminated land. Science of the Total Environment, 2019, 656, 1413-1426.	3.9	18
1959	Delayed differentiation of vaginal and uterine microbiomes in dairy cows developing postpartum endometritis. PLoS ONE, 2019, 14, e0200974.	1.1	57
1960	Bacterial Communities in the Alpaca Gastrointestinal Tract Vary With Diet and Body Site. Frontiers in Microbiology, 2019, 9, 3334.	1.5	7
1961	Effects of light intensity on soluble microbial products produced by Synechocystis sp. PCC 6803 and associated heterotrophic communities. Algal Research, 2019, 38, 101409.	2.4	4
1962	Microbial recycling cells: First steps into a new type of microbial electrochemical technologies, aimed at recovering nutrients from wastewater. Bioresource Technology, 2019, 277, 117-127.	4.8	20
1963	Seasonal dynamics of the coastal bacterioplankton at intensive fish-farming areas of the Yellow Sea, China revealed by high-throughput sequencing. Marine Pollution Bulletin, 2019, 139, 366-375.	2.3	9
1964	Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. Environmental Science & Technology, 2019, 53, 1315-1324.	4.6	109
1965	Healthy infants harbor intestinal bacteria that protect against food allergy. Nature Medicine, 2019, 25, 448-453.	15.2	306
1966	The Metabolic Response to a Low Amino Acid Diet is Independent of Diet-Induced Shifts in the Composition of the Gut Microbiome. Scientific Reports, 2019, 9, 67.	1.6	16
1967	OTUX: V-region specific OTU database for improved 16S rRNA OTU picking and efficient cross-study taxonomic comparison of microbiomes. DNA Research, 2019, 26, 147-156.	1.5	18
1968	Transitions in microbial communities along a 1600â€‰km freshwater trophic gradient. Journal of Great Lakes Research, 2019, 45, 263-276.	0.8	10
1969	Daily Consumption of Orange Juice from <i>Citrus sinensis</i> L. Osbeck cv. Cara Cara and cv. Bahia Differently Affects Gut Microbiota Profiling as Unveiled by an Integrated Meta-Omics Approach. Journal of Agricultural and Food Chemistry, 2019, 67, 1381-1391.	2.4	39
1970	Bioelectrochemical Nitrogen fixation (e-BNF): Electro-stimulation of enriched biofilm communities drives autotrophic nitrogen and carbon fixation. Bioelectrochemistry, 2019, 125, 105-115.	2.4	28
1971	High-throughput sequencing of gut microbiota in rainbow trout (Oncorhynchus mykiss) fed larval and pre-pupae stages of black soldier fly (Hermetia illucens). Aquaculture, 2019, 500, 485-491.	1.7	135
1972	Oxygen loss from seagrass roots coincides with colonisation of sulphide-oxidising cable bacteria and reduces sulphide stress. ISME Journal, 2019, 13, 707-719.	4.4	89
1973	Impact of highâ€grain diet feeding on mucosaâ€associated bacterial community and gene expression of tight junction proteins in the small intestine of goats. MicrobiologyOpen, 2019, 8, e00745.	1.2	19

#	ARTICLE	IF	CITATIONS
1974	Unlocking and functional profiling of the bacterial communities in diesel tanks upon additive treatment. Fuel, 2019, 236, 1311-1320.	3.4	9
1975	Dietary shifts influenced by livestock grazing shape the gut microbiota composition and coâ€occurrence networks in a local rodent species. Journal of Animal Ecology, 2019, 88, 302-314.	1.3	36
1976	Lower perinatal exposure to Proteobacteria is an independent predictor of early childhood wheezing. Journal of Allergy and Clinical Immunology, 2019, 143, 419-421.e5.	1.5	6
1977	Comparative study of gut microbiota in wild and captive Malaysian Mahseer (<i>Tor tambroides</i>). MicrobiologyOpen, 2019, 8, e00734.	1.2	30
1978	Structure and Diversity of the Bacterial Communities in the Acid and Thermophilic Crater-Lake of the Volcano â€œEl ChichÃ³nâ€, Mexico. Geomicrobiology Journal, 2019, 36, 97-109.	1.0	14
1979	Prokaryotic Diversity and Distribution in Different Habitats of an Alpine Rock Glacier-Pond System. Microbial Ecology, 2019, 78, 70-84.	1.4	12
1980	Secondary successional forests undergo tightly-coupled changes in soil microbial community structure and soil organic matter. Soil Biology and Biochemistry, 2019, 128, 56-65.	4.2	91
1981	Comparative Analysis of Anuran Amphibian Skin Microbiomes Across Inland and Coastal Wetlands. Microbial Ecology, 2019, 78, 348-360.	1.4	16
1982	Koumiss consumption modulates gut microbiota, increases plasma high density cholesterol, decreases immunoglobulin G and albumin. Journal of Functional Foods, 2019, 52, 469-478.	1.6	38
1983	Metagenome tracking biogeographic agroecology: Phytobiota of tomatoes from Virginia, Maryland, North Carolina and California. Food Microbiology, 2019, 79, 132-136.	2.1	19
1984	Identification of Specific Oral and Gut Pathogens in Full Thickness Colon of Colitis Patients: Implications for Colon Motility. Frontiers in Microbiology, 2018, 9, 3220.	1.5	57
1985	Reduced skin bacterial diversity correlates with increased pathogen infection intensity in an endangered amphibian host. Molecular Ecology, 2019, 28, 127-140.	2.0	41
1986	Loss of Microbial Niche Specificity Between the Upper and Lower Airways in Patients With Cystic Fibrosis. Laryngoscope, 2019, 129, 544-550.	1.1	35
1987	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
1988	Novel T4 bacteriophages associated with black band disease in corals. Environmental Microbiology, 2019, 21, 1969-1979.	1.8	13
1989	Evaluation of anionic surfactant removal by anaerobic degradation of commercial laundry wastewater and domestic sewage. Environmental Technology (United Kingdom), 2019, 40, 988-996.	1.2	28
1990	Exercise prevents high fat diet-induced bone loss, marrow adiposity and dysbiosis in male mice. Bone, 2019, 118, 20-31.	1.4	69
1991	A membrane aerated biofilm reactor for sulfide control from anaerobically treated wastewater. Environmental Technology (United Kingdom), 2019, 40, 2354-2363.	1.2	11

#	ARTICLE	IF	CITATIONS
1992	Computational profiling of the gutâ€"brain axis: microflora dysbiosis insights to neurological disorders. Briefings in Bioinformatics, 2019, 20, 825-841.	3.2	27
1993	Midtrimester microbial DNA variations in maternal serum of women who experience spontaneous preterm birth. Journal of Maternal-Fetal and Neonatal Medicine, 2020, 33, 359-367.	0.7	5
1994	Lingonberries and their two separated fractions differently alter the gut microbiota, improve metabolic functions, reduce gut inflammatory properties, and improve brain function in ApoEâˆ'/âˆ' mice fed high-fat diet. Nutritional Neuroscience, 2020, 23, 600-612.	1.5	25
1995	Effects of a polysaccharide-rich extract derived from Irish-sourced Laminaria digitata on the composition and metabolic activity of the human gut microbiota using an in vitro colonic model. European Journal of Nutrition, 2020, 59, 309-325.	1.8	22
1996	The microbial community in an alkaline saline sediment of a former maar lake bed. Journal of Soils and Sediments, 2020, 20, 542-555.	1.5	9
1997	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota Î±-Diversity: An Individual-level Meta-analysis. Clinical Infectious Diseases, 2020, 70, 615-627.	2.9	65
1998	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. Food Microbiology, 2020, 86, 103340.	2.1	52
1999	The aeroponic rhizosphere microbiome: community dynamics in early succession suggest strong selectional forces. Antonie Van Leeuwenhoek, 2020, 113, 83-99.	0.7	10
2000	Degree of lipid saturation affects depressive-like behaviour and gut microbiota in mice. International Journal of Food Sciences and Nutrition, 2020, 71, 440-452.	1.3	5
2001	Genderâ€related characterization of sensitive skin in normal young Chinese. Journal of Cosmetic Dermatology, 2020, 19, 1137-1142.	0.8	14
2002	Glucose triggers strong taxonâ€specific responses in microbial growth and activity: insights from <scp>DNA</scp> and <scp>RNA qSIP</scp>. Ecology, 2020, 101, e02887.	1.5	20
2003	Antibiotic resistome in a landfill leachate treatment plant and effluent-receiving river. Chemosphere, 2020, 242, 125207.	4.2	41
2004	Selection and propagation of IncP conjugative plasmids following long-term anthropogenic metal pollution in river sediments. Journal of Hazardous Materials, 2020, 382, 121173.	6.5	9
2005	Chemical and biological dispersants differently affect the bacterial communities of uncontaminated and oil-contaminated marine water. Brazilian Journal of Microbiology, 2020, 51, 691-700.	0.8	4
2006	A Tripartite Microbial-Environment Network Indicates How Crucial Microbes Influence the Microbial Community Ecology. Microbial Ecology, 2020, 79, 342-356.	1.4	7
2007	Metformin and Dipeptidyl Peptidase-4 Inhibitor Differentially Modulate the Intestinal Microbiota and Plasma Metabolome of Metabolically Dysfunctional Mice. Canadian Journal of Diabetes, 2020, 44, 146-155.e2.	0.4	41
2009	Targeting the Cutaneous Microbiota in Atopic Dermatitis by Coal Tar via AHR-Dependent Induction of Antimicrobial Peptides. Journal of Investigative Dermatology, 2020, 140, 415-424.e10.	0.3	57
2010	Dietary administration of resistant starch improved caecal barrier function by enhancing intestinal morphology and modulating microbiota composition in meat duck. British Journal of Nutrition, 2020, 123, 172-181.	1.2	24

#	Article	IF	Citations
2011	Bacterial Succession in Salt Marsh Soils Along a Short-term Invasion Chronosequence of Spartina alterniflora in the Yellow River Estuary, China. Microbial Ecology, 2020, 79, 644-661.	1.4	33
2012	Blood clams (Tegillarca granosa) bioturbation alter succession of bacterioplankton community and nutrient removal performance in an aquaculture wastewater bioremediation system. Aquaculture, 2020, 516, 734520.	1.7	7
2013	Analyses of physicochemical properties, bacterial microbiota, and lactic acid bacteria of fresh camel milk collected in Inner Mongolia. Journal of Dairy Science, 2020, 103, 106-116.	1.4	41
2014	Linking rhizosphere soil biochemical and microbial community characteristics across different land use systems in mountainous region in Northeast India. Meta Gene, 2020, 23, 100625.	0.3	12
2015	Composition of the microbial communities in the gastrointestinal tract of perch (<i>Perca) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td 2020, 43, 23-38.	0.9	17
2016	Profiling soil free-living nematodes in the Namib Desert, Namibia. Journal of Arid Land, 2020, 12, 130-143.	0.9	2
2017	Ecological processes underlying community assembly of aquatic bacteria and macroinvertebrates under contrasting climates on the Tibetan Plateau. Science of the Total Environment, 2020, 702, 134974.	3.9	15
2018	Unlinked rRNA genes are widespread among bacteria and archaea. ISME Journal, 2020, 14, 597-608.	4.4	30
2019	Diversity and dynamics of microbial communities in brown planthopper at different developmental stages revealed by highâ€throughput amplicon sequencing. Insect Science, 2020, 27, 883-894.	1.5	28
2020	Increased loading stress leads to convergence of microbial communities and high methane yields in adapted anaerobic co-digesters. Water Research, 2020, 169, 115155.	5.3	13
2021	Evaluation of the Bacterial Diversity of Inner Mongolian Acidic Gruel Using Illumina MiSeq and PCR-DGGE. Current Microbiology, 2020, 77, 434-442.	1.0	13
2022	Comparisons of protective effects between two sea cucumber hydrolysates against diet induced hyperuricemia and renal inflammation in mice. Food and Function, 2020, 11, 1074-1086.	2.1	59
2023	Betaine addition as a potent ruminal fermentation modulator under hyperthermal and hyperosmotic conditions <i>in vitro</i>. Journal of the Science of Food and Agriculture, 2020, 100, 2261-2271.	1.7	13
2024	Influence of non-dechlorinating microbes on trichloroethene reduction based on vitamin B12 synthesis in anaerobic cultures. Environmental Pollution, 2020, 259, 113947.	3.7	14
2025	How nitrate affects perchlorate reduction in a methane-based biofilm batch reactor. Water Research, 2020, 171, 115397.	5.3	48
2026	Beyond host regulation: Changes in gut microbiome of permissive and non-permissive hosts following parasitization by the wasp Cotesia flavipes. FEMS Microbiology Ecology, 2020, 96, .	1.3	11
2027	Analyses of environmental sequences and two regions of chloroplast genomes revealed the presence of new clades of photosynthetic euglenids in marine environments. Environmental Microbiology Reports, 2020, 12, 78-91.	1.0	5
2028	Root microbiomes as indicators of seagrass health. FEMS Microbiology Ecology, 2020, 96, .	1.3	38

#	Article	IF	Citations
2029	Gut butyrate-producing organisms correlate to Placenta Specific 8 protein: Importance to colorectal cancer progression. Journal of Advanced Research, 2020, 22, 7-20.	4.4	22
2030	Mechanisms of water regime effects on uptake of cadmium and nitrate by two ecotypes of water spinach (Ipomoea aquatica Forsk.) in contaminated soil. Chemosphere, 2020, 246, 125798.	4.2	24
2031	The global <i>Microcystis</i> interactome. Limnology and Oceanography, 2020, 65, S194-S207.	1.6	63
2032	Environmental Controls on Microbial Diversity in Arctic Lakes of West Greenland. Microbial Ecology, 2020, 80, 60-72.	1.4	9
2033	Long-term administration of Lactobacillus casei Zhang stabilized gut microbiota of adults and reduced gut microbiota age index of older adults. Journal of Functional Foods, 2020, 64, 103682.	1.6	16
2034	Resilience of planktonic bacterial community structure in response to short-term weather deterioration during the growing season in an alpine lake. Hydrobiologia, 2020, 847, 535-548.	1.0	6
2035	Investigation into the microbial communities and associated crude oil-contamination along a Gulf War impacted groundwater system in Kuwait. Water Research, 2020, 170, 115314.	5.3	19
2036	Functional Genomics of a Symbiotic Community: Shared Traits in the Olive Fruit Fly Gut Microbiota. Genome Biology and Evolution, 2020, 12, 3778-3791.	1.1	16
2037	Diversity and flexibility of the bacterial communities on Cancer pagurus at different temperatures. Journal of Sea Research, 2020, 156, 101827.	0.6	8
2038	Cascade dam impoundments restrain the trophic transfer efficiencies in benthic microbial food web. Water Research, 2020, 170, 115351.	5.3	40
2039	Unexpected mitochondrial genome diversity revealed by targeted single-cell genomics of heterotrophic flagellated protists. Nature Microbiology, 2020, 5, 154-165.	5.9	44
2040	Metagenomic insights unveil the dominance of undescribed Actinobacteria in pond ecosystem of an Indian shrine. Meta Gene, 2020, 23, 100639.	0.3	4
2041	Water and sediment act as reservoirs for microbial taxa associated with invasive dreissenid mussels. Science of the Total Environment, 2020, 703, 134915.	3.9	8
2042	Microbial associations and spatial proximity predict North American moose (<i>Alces alces</i>) gastrointestinal community composition. Journal of Animal Ecology, 2020, 89, 817-828.	1.3	16
2043	Hydrogeochemical and microbiological effects of simulated recharge and drying within a 2D meso-scale aquifer. Chemosphere, 2020, 241, 125116.	4.2	7
2044	Influence of operating conditions on sulfate reduction from real mining process water by membrane biofilm reactors. Chemosphere, 2020, 244, 125508.	4.2	18
2045	The microbiota influences the <i>Drosophila melanogaster</i> life history strategy. Molecular Ecology, 2020, 29, 639-653.	2.0	65
2046	Effects of feeding strategy and duration of the dry period on the rumen microbiota of dairy cows. Canadian Journal of Animal Science, 2020, 100, 346-358.	0.7	0

#	ARTICLE	IF	CITATIONS
2047	Effect of 2-hydroxy-4-(methylthio) butanoate (HMTBa) supplementation on rumen bacterial populations in dairy cows when exposed to diets with risk for milk fat depression. Journal of Dairy Science, 2020, 103, 2718-2730.	1.4	16
2048	PacBio sequencing reveals bacterial community diversity in cheeses collected from different regions. Journal of Dairy Science, 2020, 103, 1238-1249.	1.4	30
2049	Influence of Sampling Site and other Environmental Factors on the Bacterial Community Composition of Domestic Washing Machines. Microorganisms, 2020, 8, 30.	1.6	22
2050	Integrative description of bisexual Paramacrobiotus experimentalis sp. nov. (Macrobiotidae) from republic of Madagascar (Africa) with microbiome analysis. Molecular Phylogenetics and Evolution, 2020, 145, 106730.	1.2	34
2051	Seasonality in Spatial Turnover of Bacterioplankton Along an Ecological Gradient in the East China Sea: Biogeographic Patterns, Processes and Drivers. Microorganisms, 2020, 8, 1484.	1.6	8
2052	Sertraline inhibits top-down forces (predation) in microbial food web and promotes nitrification in sediment. Environmental Pollution, 2020, 267, 115580.	3.7	16
2053	Whole Blueberry and Isolated Polyphenol-Rich Fractions Modulate Specific Gut Microbes in an In Vitro Colon Model and in a Pilot Study in Human Consumers. Nutrients, 2020, 12, 2800.	1.7	30
2054	Analysis of 16S rRNA genes reveals reduced Fusobacterial community diversity when translocating from saliva to GI sites. Gut Microbes, 2020, 12, 1814120.	4.3	13
2055	Interpretations of Environmental Microbial Community Studies Are Biased by the Selected 16S rRNA (Gene) Amplicon Sequencing Pipeline. Frontiers in Microbiology, 2020, 11, 550420.	1.5	113
2056	The effects of mowing and multi-level N fertilization on soil bacterial and fungal communities in a semiarid grassland are year-dependent. Soil Biology and Biochemistry, 2020, 151, 108040.	4.2	25
2057	Soil structure, nutrient status and water holding capacity shape Uruguayan grassland prokaryotic communities. FEMS Microbiology Ecology, 2020, 96, .	1.3	9
2058	An Assessment of the Stability of the Canine Oral Microbiota After Probiotic Administration in Healthy Dogs Over Time. Frontiers in Veterinary Science, 2020, 7, 616.	0.9	11
2059	Metagenomic studies of SAR202 bacteria at the full-ocean depth in the Mariana Trench. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 165, 103396.	0.6	14
2060	Fecal Microbiota Transplant in Two Ulcerative Colitis Pediatric Cases: Gut Microbiota and Clinical Course Correlations. Microorganisms, 2020, 8, 1486.	1.6	18
2061	Modulation of the bacterial population in commercial cucumber fermentations by brining salt type. Journal of Applied Microbiology, 2020, 128, 1678-1693.	1.4	11
2062	Saccharomyces cerevisiae fermentation products (SCFP) stabilize the ruminal microbiota of lactating dairy cows during periods of a depressed rumen pH. BMC Veterinary Research, 2020, 16, 237.	0.7	22
2063	The supplementation of a corn/barley-based diet with bacterial xylanase did not prevent diarrhoea of ETEC susceptible piglets, but favoured the persistence of Lactobacillus reuteri in the gut. Livestock Science, 2020, 240, 104161.	0.6	4
2064	The gut microbiota structure of the terrestrial isopod <i>Porcellionides pruinosus</i> (Isopoda:) Tj ETQq1 1 0.784314 rgBT /Overlock		10

#	Article	IF	Citations
2065	Gut microbiota in a hostâ€"brood parasite system: insights from common cuckoos raised by two warbler species. FEMS Microbiology Ecology, 2020, 96, .	1.3	9
2066	Influence of inoculum selection on the utilisation of volatile fatty acid and glucose in sulfate reducing reactors. Environmental Technology (United Kingdom), 2020, , 1-12.	1.2	1
2067	Microbial biodiversity in the throats of pulmonary tuberculosis patients and tuberculin skin test (TST) positive and negative healthy individuals in Malaysia. Tuberculosis, 2020, 124, 101965.	0.8	0
2068	Lifestyle preferences drive the structure and diversity of bacterial and archaeal communities in a small riverine reservoir. Scientific Reports, 2020, 10, 11288.	1.6	8
2069	Viral control of biomass and diversity of bacterioplankton in the deep sea. Communications Biology, 2020, 3, 256.	2.0	18
2070	Type VI secretion systems of plantâ€pathogenic <i>Burkholderia glumae</i> BGR1 play a functionally distinct role in interspecies interactions and virulence. Molecular Plant Pathology, 2020, 21, 1055-1069.	2.0	20
2071	Effects of Bacterial Supplementation on Black Soldier Fly Growth and Development at Benchtop and Industrial Scale. Frontiers in Microbiology, 2020, 11, 587979.	1.5	23
2072	Network Analysis of Gut Microbiome and Metabolome to Discover Microbiota-Linked Biomarkers in Patients Affected by Non-Small Cell Lung Cancer. International Journal of Molecular Sciences, 2020, 21, 8730.	1.8	75
2073	Gut Microbiota Predict Enterococcus Expansion but Not Vancomycin-Resistant Enterococcus Acquisition. MSphere, 2020, 5, .	1.3	11
2074	Carbon and nitrogen cycling in Yedoma permafrost controlled by microbial functional limitations. Nature Geoscience, 2020, 13, 794-798.	5.4	45
2075	Adjunctive treatment with probiotics partially alleviates symptoms and reduces inflammation in patients with irritable bowel syndrome. European Journal of Nutrition, 2020, 60, 2553-2565.	1.8	31
2076	Methanogen Abundance Thresholds Capable of Differentiating In Vitro Methane Production in Human Stool Samples. Digestive Diseases and Sciences, 2020, 66, 3822-3830.	1.1	3
2077	The Duration of Increased Grain Feeding Affects the Microbiota throughout the Digestive Tract of Yearling Holstein Steers. Microorganisms, 2020, 8, 1854.	1.6	5
2078	Highly Branched Neo-Fructans (Agavins) Attenuate Metabolic Endotoxemia and Low-Grade Inflammation in Association with Gut Microbiota Modulation on High-Fat Diet-Fed Mice. Foods, 2020, 9, 1792.	1.9	22
2079	Response of Horticultural Soil Microbiota to Different Fertilization Practices. Plants, 2020, 9, 1501.	1.6	12
2080	Comparison of Bacterial Microbiota in Raw Mareâ€™s Milk and Koumiss Using PacBio Single Molecule Real-Time Sequencing Technology. Frontiers in Microbiology, 2020, 11, 581610.	1.5	12
2081	Parental Care Alters the Egg Microbiome of Maritime Earwigs. Microbial Ecology, 2020, 80, 920-934.	1.4	10
2082	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

#	Article	IF	Citations
2083	NOD1 deficiency promotes an imbalance of thyroid hormones and microbiota homeostasis in mice fed high fat diet. Scientific Reports, 2020, 10, 12317.	1.6	15
2084	Elevation rather than season determines the assembly and co-occurrence patterns of soil bacterial communities in forest ecosystems of Mount Gongga. Applied Microbiology and Biotechnology, 2020, 104, 7589-7602.	1.7	28
2085	Has compost with biochar applied during the process added value over biochar or compost for increasing soil quality in an arable cropping system?. Applied Soil Ecology, 2020, 156, 103706.	2.1	16
2086	Limited Response of Indigenous Microbes to Water and Nutrient Pulses in High-Elevation Atacama Soils: Implications for the Coldâ€“Dry Limits of Life on Earth. Microorganisms, 2020, 8, 1061.	1.6	2
2087	Diversity of Gut Microbiota and Bifidobacterial Community of Chinese Subjects of Different Ages and from Different Regions. Microorganisms, 2020, 8, 1108.	1.6	15
2088	Nitrogen Removal Efficiency and Microbial Community Analysis of a High-Efficiency Honeycomb Fixed-Bed Bioreactor. Water (Switzerland), 2020, 12, 1832.	1.2	2
2089	Effects of oligochitosan on the growth, immune responses and gut microbes of tilapia (Oreochromis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	21
2090	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
2091	Soil microbiome drives the recovery of ecosystem functions after fire. Soil Biology and Biochemistry, 2020, 149, 107948.	4.2	40
2092	Effect of increasing precipitation and warming on microbial community in Tibetan alpine steppe. Environmental Research, 2020, 189, 109917.	3.7	32
2093	Domestication-driven changes in plant traits associated with changes in the assembly of the rhizosphere microbiota in tetraploid wheat. Scientific Reports, 2020, 10, 12234.	1.6	38
2094	Physicochemical Parameters Affecting the Distribution and Diversity of the Water Column Microbial Community in the High-Altitude Andean Lake System of La Brava and La Punta. Microorganisms, 2020, 8, 1181.	1.6	18
2095	Developmental stage-associated microbiota profile of the peach fruit fly, Bactrocera zonata (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 2020, 10, 390.	1.1	5
2096	Oral and vaginal microbiota in selected field mice of the genus Apodemus: a wild population study. Scientific Reports, 2020, 10, 13246.	1.6	8
2097	Compositional and Functional Characteristics of Swine Slurry Microbes through 16S rRNA Metagenomic Sequencing Approach. Animals, 2020, 10, 1372.	1.0	12
2098	Differences in honey bee bacterial diversity and composition in agricultural and pristine environments â€“ a field study. Apidologie, 2020, 51, 1018-1037.	0.9	23
2099	Differential Responses to Dietary Protein and Carbohydrate Ratio on Gut Microbiome in Obese vs. Lean Cats. Frontiers in Microbiology, 2020, 11, 591462.	1.5	7
2100	Changes in serum inflammatory cytokine levels and intestinal flora in a self-healing dextran sodium sulfate-induced ulcerative colitis murine model. Life Sciences, 2020, 263, 118587.	2.0	52

#	Article	IF	Citations
2101	The Rumen Specific Bacteriome in Dry Dairy Cows and Its Possible Relationship with Phenotypes. Animals, 2020, 10, 1791.	1.0	9
2102	Maternal and cord blood vitamin D level and the infant gut microbiota in a birth cohort study. Maternal Health, Neonatology and Perinatology, 2020, 6, 5.	1.0	9
2103	Identification and functional assessment of endophytic bacterial diversity in Ageratina adenophora (Sprengel) and their interactions with the host plant. South African Journal of Botany, 2020, 134, 99-108.	1.2	2
2104	Physicochemical stressors and mixed alkaloid supplementation modulate ruminal microbiota and fermentation inÂvitro. Anaerobe, 2020, 65, 102263.	1.0	10
2105	Effects of sodium citrate on the structure and microbial community composition of an early-stage multispecies biofilm model. Scientific Reports, 2020, 10, 16585.	1.6	3
2106	Phytoplankton composition in a eutrophic estuary: Comparison of multiple taxonomic approaches and influence of environmental factors. Environmental Microbiology, 2020, 22, 4718-4731.	1.8	19
2107	Microbial environment shapes immune function and cloacal microbiota dynamics in zebra finches Taeniopygia guttata. Animal Microbiome, 2020, 2, 21.	1.5	21
2108	Poorly known microbial taxa dominate the microbiome of hypersaline Sambhar Lake salterns in India. Extremophiles, 2020, 24, 875-885.	0.9	15
2109	Modulation of gut mucosal microbiota as a mechanism of probioticsâ€based adjunctive therapy for ulcerative colitis. Microbial Biotechnology, 2020, 13, 2032-2043.	2.0	45
2110	Disruption of ruminal homeostasis by malnutrition involved in systemic ruminal microbiota-host interactions in a pregnant sheep model. Microbiome, 2020, 8, 138.	4.9	30
2111	Mucosa-Associated Microbiota in Barrett's Esophagus, Dysplasia, and Esophageal Adenocarcinoma Differ Similarly Compared With Healthy Controls. Clinical and Translational Gastroenterology, 2020, 11, e00199.	1.3	15
2112	<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. Food and Function, 2020, 11, 8939-8950.	2.1	27
2113	Biological observations in microbiota analysis are robust to the choice of 16S rRNA gene sequencing processing algorithm: case study on human milk microbiota. BMC Microbiology, 2020, 20, 290.	1.3	15
2114	Rehydration of dry corn preserves the desirable bacterial community during ensiling. FEMS Microbiology Letters, 2020, 367, .	0.7	1
2115	Community assembly of bacteria and archaea in coastal waters governed by contrasting mechanisms: A seasonal perspective. Molecular Ecology, 2020, 29, 3762-3776.	2.0	35
2116	NC10 bacteria promoted methane oxidation coupled to chlorate reduction. Biodegradation, 2020, 31, 319-329.	1.5	6
2117	Dolosigranulum pigrum Cooperation and Competition in Human Nasal Microbiota. MSphere, 2020, 5, .	1.3	65
2118	Metrics for Evaluating Inundation Impacts on the Decomposer Communities in a Southern California Coastal Salt Marsh. Wetlands, 2020, 40, 2443-2459.	0.7	6

#	Article	IF	Citations
2119	The Use of Bioinformatic Tools in Symbiosis and Co-Evolution Studies. , 0, , .		1
2120	Rumen Microbiome and Metabolome of Tibetan Sheep (Ovis aries) Reflect Animal Age and Nutritional Requirement. Frontiers in Veterinary Science, 2020, 7, 609.	0.9	25
2121	Integration of molecular profiles in a longitudinal wellness profiling cohort. Nature Communications, 2020, 11, 4487.	5.8	66
2122	Actinobacteria from Antarctica as a source for anticancer discovery. Scientific Reports, 2020, 10, 13870.	1.6	38
2123	Abrupt dietary changes between grass and hay alter faecal microbiota of ponies. PLoS ONE, 2020, 15, e0237869.	1.1	16
2124	Antibiotic Resistance in the Collembolan Gut Microbiome Accelerated by the Nonantibiotic Drug Carbamazepine. Environmental Science & Technology, 2020, 54, 10754-10762.	4.6	25
2125	Comparing the Bacterial Community in the Gastrointestinal Tracts Between Growth-Retarded and Normal Yaks on the Qinghaiâ€“Tibetan Plateau. Frontiers in Microbiology, 2020, 11, 600516.	1.5	24
2126	Curing piglets from diarrhea and preparation of a healthy microbiome with Bacillus treatment for industrial animal breeding. Scientific Reports, 2020, 10, 19476.	1.6	25
2127	An unusual microbiome characterises a spatially-aggressive crustose alga rapidly overgrowing shallow Caribbean reefs. Scientific Reports, 2020, 10, 20949.	1.6	8
2128	An iron corrosion-assisted H2-supplying system: a culture method for methanogens and acetogens under low H2 pressures. Scientific Reports, 2020, 10, 19124.	1.6	6
2129	Cascabel: A Scalable and Versatile Amplicon Sequence Data Analysis Pipeline Delivering Reproducible and Documented Results. Frontiers in Genetics, 2020, 11, 489357.	1.1	19
2130	Influence of Lab Adapted Natural Diet and Microbiota on Life History and Metabolic Phenotype of Drosophila melanogaster. Microorganisms, 2020, 8, 1972.	1.6	2
2131	In situ Assemblies of Bacteria and Nutrient Dynamics in Response to an Ecosystem Engineer, Marine Clam Scapharca subcrenata, in the Sediment of an Aquaculture Bioremediation System. Journal of Ocean University of China, 2020, 19, 1447-1460.	0.6	6
2132	Host-Specificity and Core Taxa of Seagrass Leaf Microbiome Identified Across Tissue Age and Geographical Regions. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	12
2133	The effects of taxonomy, diet, and ecology on the microbiota of riverine macroinvertebrates. Ecology and Evolution, 2020, 10, 14000-14019.	0.8	5
2134	The microbiota of the <i>Lasius fuliginosus</i> â€“ <i>Pella laticollis</i> myrmecophilous interaction. , 2020, 87, 754-769.		2
2135	Intramuscular injection of tetracycline decreased gut microbial diversity in mouse. Mammalian Genome, 2020, 31, 295-308.	1.0	2
2136	Prokaryotic Community Compositions of the Hypersaline Sediments of Tuz Lake Demonstrated by Cloning and High-Throughput Sequencing. Microbiology, 2020, 89, 756-768.	0.5	10

#	Article	IF	Citations
2137	The Composition and Predictive Function of the Fecal Microbiota Differ Between Young and Adult Donkeys. Frontiers in Microbiology, 2020, 11, 596394.	1.5	6
2138	Sialic Acids: An Important Family of Carbohydrates Overlooked in Environmental Biofilms. Applied Sciences (Switzerland), 2020, 10, 7694.	1.3	7
2139	Soluble Immune Checkpoints, Gut Metabolites and Performance Status as Parameters of Response to Nivolumab Treatment in NSCLC Patients. Journal of Personalized Medicine, 2020, 10, 208.	1.1	23
2140	Highâ€throughput sequencingâ€based analysis of fungal diversity and taste quality evaluation of Douchi, a traditional fermented food. Food Science and Nutrition, 2020, 8, 6612-6620.	1.5	5
2141	The Bacterial Microbiome in the Small Intestine of Hooded Seals (Cystophora cristata). Microorganisms, 2020, 8, 1664.	1.6	5
2142	Phenotypic Comparability from Genotypic Variability among Physically Structured Microbial Consortia. Integrative and Comparative Biology, 2020, 60, 288-303.	0.9	5
2143	Microbial predictors of healing and short-term effect of debridement on the microbiome of chronic wounds. Npj Biofilms and Microbiomes, 2020, 6, 21.	2.9	86
2144	Seasonal habitat drives intestinal microbiome composition in anadromous Arctic char (<i>Salvelinus) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	19
2145	Undernutrition shifted colonic fermentation and digest-associated bacterial communities in pregnant ewes. Applied Microbiology and Biotechnology, 2020, 104, 5973-5984.	1.7	12
2146	The Effects of the Marine-Derived Polysaccharides Laminarin and Chitosan on Aspects of Colonic Health in Pigs Challenged with Dextran Sodium Sulphate. Marine Drugs, 2020, 18, 262.	2.2	15
2147	Nitrogen and water addition regulate soil fungal diversity and co-occurrence networks. Journal of Soils and Sediments, 2020, 20, 3192-3203.	1.5	18
2148	Biogeography of microbiome and short-chain fatty acids in the gastrointestinal tract of duck. Poultry Science, 2020, 99, 4016-4027.	1.5	21
2149	A powerful microbial group association test based on the higher criticism analysis for sparse microbial association signals. Microbiome, 2020, 8, 63.	4.9	9
2150	Effects of soybean lecithin supplementation on growth performance, serum metabolites, ruminal fermentation and microbial flora of beef steers. Livestock Science, 2020, 240, 104121.	0.6	9
2151	Microbial diversity analysis of jiaoke from Xilingol, Inner Mongolia. Journal of Dairy Science, 2020, 103, 5893-5905.	1.4	1
2152	The probiotic <i>L. casei</i> LC-XCALâ„¢ improves metabolic health in a diet-induced obesity mouse model without altering the microbiome. Gut Microbes, 2020, 12, 1747330.	4.3	16
2153	Composition and co-occurrence patterns of the microbiota of different niches of the bovine mammary gland: potential associations with mastitis susceptibility, udder inflammation, and teat-end hyperkeratosis. Animal Microbiome, 2020, 2, 11.	1.5	32
2154	Insights into the Function and Horizontal Transfer of Isoproturon Degradation Genes (<i>pdmAB</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.4	5

#	Article	IF	Citations
2155	Unraveling the Complexity of Soil Microbiomes in a Large-Scale Study Subjected to Different Agricultural Management in Styria. Frontiers in Microbiology, 2020, 11, 1052.	1.5	32
2156	Study on the experimental performance by electrolysis-integrated ecological floating bed for nitrogen and phosphorus removal in eutrophic water. Scientific Reports, 2020, 10, 7619.	1.6	5
2157	Microorganisms Move a Short Distance into an Almond Orchard from an Adjacent Upwind Poultry Operation. Applied and Environmental Microbiology, 2020, 86, .	1.4	11
2158	Using molecular microbial ecology to define differential responses to the inoculation of barley silage. Canadian Journal of Animal Science, 2020, 100, 703-715.	0.7	3
2159	Wet or dry sowing had a larger effect on the soil bacterial community composition than tillage practices in an arid irrigated agro-ecosystem. Journal of Soils and Sediments, 2020, 20, 3316-3329.	1.5	2
2160	Metagenomics analysis of rhizospheric bacterial communities of Saccharum arundinaceum growing on organometallic sludge of sugarcane molasses-based distillery. 3 Biotech, 2020, 10, 316.	1.1	47
2161	Effects of hydraulic retention time on the process performance and microbial community structure of an anaerobic single-stage semi-pilot scale reactor for the treatment of food waste. International Biodeterioration and Biodegradation, 2020, 152, 104999.	1.9	12
2162	Soil metabolome correlates with bacterial diversity and co-occurrence patterns in root-associated soils on the Tibetan Plateau. Science of the Total Environment, 2020, 735, 139572.	3.9	26
2163	The Snowmelt Niche Differentiates Three Microbial Life Strategies That Influence Soil Nitrogen Availability During and After Winter. Frontiers in Microbiology, 2020, 11, 871.	1.5	32
2164	Rapeseed-based diet modulates the imputed functions of gut microbiome in growing-finishing pigs. Scientific Reports, 2020, 10, 9372.	1.6	13
2165	A prospective longitudinal study on the microbiota composition in amyotrophic lateral sclerosis. BMC Medicine, 2020, 18, 153.	2.3	78
2166	Microbiota Composition of Breast Milk from Women of Different Ethnicity from the Manawatuâ€"Wanganui Region of New Zealand. Nutrients, 2020, 12, 1756.	1.7	10
2167	Habitat Disturbances Modulate the Barrier Effect of Resident Soil Microbiota on Listeria monocytogenes Invasion Success. Frontiers in Microbiology, 2020, 11, 927.	1.5	14
2168	Effect of Rhizophora apiculata plantation for improving water quality, growth, and health of mud crab. Applied Microbiology and Biotechnology, 2020, 104, 6813-6824.	1.7	7
2169	Metagenomics based approach to reveal the secrets of unculturable microbial diversity from aquatic environment. , 2020, , 537-559.		3
2170	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. British Poultry Science, 2020, 61, 590-598.	0.8	12
2171	Effect of Alfalfa Hay and Starter Feeding Intervention on Gastrointestinal Microbial Community, Growth and Immune Performance of Yak Calves. Frontiers in Microbiology, 2020, 11, 994.	1.5	27
2172	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. Sustainability, 2020, 12, 4209.	1.6	2

#	ARTICLE	IF	CITATIONS
2173	Intestinal Microbiota Analyses of Litopenaeus vannamei During a Case of Atypical Massive Mortality in Northwestern Mexico. Current Microbiology, 2020, 77, 2312-2321.	1.0	3
2174	Biosignature Analysis of Mars Soil Analogs from the Atacama Desert: Challenges and Implications for Future Missions to Mars. Astrobiology, 2020, 20, 766-784.	1.5	17
2175	Leucine-Rich Immune Factor APL1 Is Associated With Specific Modulation of Enteric Microbiome Taxa in the Asian Malaria Mosquito Anopheles stephensi. Frontiers in Microbiology, 2020, 11, 306.	1.5	20
2176	Sequential hydrotalcite precipitation and biological sulfate reduction for acid mine drainage treatment. Chemosphere, 2020, 252, 126570.	4.2	35
2177	Exploring intestinal microbiome composition in three Indian major carps under polyculture system: A high-throughput sequencing based approach. Aquaculture, 2020, 524, 735206.	1.7	18
2178	Taxon-specific microbial growth and mortality patterns reveal distinct temporal population responses to rewetting in a California grassland soil. ISME Journal, 2020, 14, 1520-1532.	4.4	67
2179	Role of the intestinal microbiome in low-density polyethylene degradation by caterpillar larvae of the greater wax moth, <i>Galleria mellonella</i>. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200112.	1.2	77
2180	Rhizosphere Microbial Community Structure Is Selected by Habitat but Not Plant Species in Two Tropical Seagrass Beds. Frontiers in Microbiology, 2020, 11, 161.	1.5	33
2181	Probiotic-directed modulation of gut microbiota is basal microbiome dependent. Gut Microbes, 2020, 12, 1736974.	4.3	69
2182	A potential alternative to traditional antibiotics in aquaculture: Yeast glycoprotein exhibits antimicrobial effect in vivo and in vitro on <i>Aeromonas caviae</i> isolated from <i>Carassius auratus gibelio</i>. Veterinary Medicine and Science, 2020, 6, 639-648.	0.6	8
2183	The Influence of O2 on the Enrichment and Activities of Acidophilic Fe(III) Reducing Bacteria. Geomicrobiology Journal, 2020, 37, 564-571.	1.0	0
2184	Isolation of Exopolysaccharide-Producing Yeast and Lactic Acid Bacteria from Quinoa (Chenopodium) Tj ETQq1 1 0.784314 rgBT /Over	1.9	25
2185	Dynamic microbial assembly processes correspond to soil fertility in sustainable paddy agroecosystems. Functional Ecology, 2020, 34, 1244-1256.	1.7	36
2186	Murine Gut Microbiome Association With APOE Alleles. Frontiers in Immunology, 2020, 11, 200.	2.2	37
2187	Nitrogen and Phosphorus Absorption and Yield of Tomato Increased by Regulating the Bacterial Community under Greenhouse Conditions via the Alternate Drip Irrigation Method. Agronomy, 2020, 10, 315.	1.3	7
2188	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. Cell Reports, 2020, 30, 2909-2922.e6.	2.9	85
2189	Modulation of the intestinal microbiota and the metabolites produced by the administration of ice cream and a dietary supplement containing the same probiotics. British Journal of Nutrition, 2020, 124, 57-68.	1.2	20
2190	Taxonomic dependency of beta diversity components in benthic communities of bacteria, diatoms and chironomids along a water-depth gradient. Science of the Total Environment, 2020, 741, 140462.	3.9	23

#	Article	IF	Citations
2191	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. BMC Genomics, 2020, 21, 408.	1.2	65
2192	Energy-Efficient Single-Stage Nitrite Shunt Denitrification with Saline Sewage through Concise Dissolved Oxygen (DO) Supply: Process Performance and Microbial Communities. Microorganisms, 2020, 8, 919.	1.6	9
2193	Dietary organic cranberry pomace influences multiple blood biochemical parameters and cecal microbiota in pasture-raised broiler chickens. Journal of Functional Foods, 2020, 72, 104053.	1.6	21
2194	Bacterial ecotoxicity and shifts in bacterial communities associated with the removal of ibuprofen, diclofenac and triclosan in biopurification systems. Science of the Total Environment, 2020, 741, 140461.	3.9	20
2195	How being synanthropic affects the gut bacteriome and mycobiome: comparison of two mouse species with contrasting ecologies. BMC Microbiology, 2020, 20, 194.	1.3	14
2196	Unraveling DMPSA nitrification inhibitor impact on soil bacterial consortia under different tillage systems. Agriculture, Ecosystems and Environment, 2020, 301, 107029.	2.5	16
2197	The effect of supplementing pony diets with yeast on 2. The faecal microbiome. Animal, 2020, 14, 2493-2502.	1.3	5
2198	Relationship between the Oral and Vaginal Microbiota of South African Adolescents with High Prevalence of Bacterial Vaginosis. Microorganisms, 2020, 8, 1004.	1.6	13
2199	Fragmentation of plastic objects in a laboratory seawater microcosm. Scientific Reports, 2020, 10, 10945.	1.6	101
2200	Comparison of Rumen Microbiota and Serum Biochemical Indices in White Cashmere Goats Fed Ensiled or Sun-Dried Mulberry Leaves. Microorganisms, 2020, 8, 981.	1.6	16
2201	Repeated inoculation with fresh rumen fluid before or during weaning modulates the microbiota composition and co-occurrence of the rumen and colon of lambs. BMC Microbiology, 2020, 20, 29.	1.3	41
2202	Environmental influences on and antimicrobial activity of the skin microbiota of <i>Proceratophrys boiei</i> (Amphibia, Anura) across forest fragments. Ecology and Evolution, 2020, 10, 901-913.	0.8	8
2203	Profiling of the viable bacterial and fungal microbiota in fermented feeds using single-molecule real-time sequencing. Journal of Animal Science, 2020, 98, .	0.2	5
2204	Amplicon sequencing reveals the bacterial diversity in milk, dairy premises and Serra da Canastra artisanal cheeses produced by three different farms. Food Microbiology, 2020, 89, 103453.	2.1	38
2205	Immune and gut bacterial successions of large yellow croaker (Larimichthys crocea) during Pseudomonas plecoglossicida infection. Fish and Shellfish Immunology, 2020, 99, 176-183.	1.6	20
2206	Constraints on microbial communities, decomposition and methane production in deep peat deposits. PLoS ONE, 2020, 15, e0223744.	1.1	13
2207	First Insight into Microbiome Profiles of Myrmecophilous Beetles and Their Host, Red Wood Ant Formica polyctena (Hymenoptera: Formicidae)â€"A Case Study. Insects, 2020, 11, 134.	1.0	9
2208	Bacterioplankton community variation in Bohai Bay (China) is explained by joint effects of environmental and spatial factors. MicrobiologyOpen, 2020, 9, e997.	1.2	12

#	Article	IF	Citations
2209	Effect of pelleted high-grain total mixed ration on rumen morphology, epithelium-associated microbiota and gene expression of proinflammatory cytokines and tight junction proteins in Hu sheep. Animal Feed Science and Technology, 2020, 263, 114453.	1.1	21
2210	Comparative immunophenotyping of Saccharomyces cerevisiae and Candida spp. strains from Crohnâ€™s disease patients and their interactions with the gut microbiome. Journal of Translational Autoimmunity, 2020, 3, 100036.	2.0	24
2211	Plant communities mediate the interactive effects of invasion and drought on soil microbial communities. ISME Journal, 2020, 14, 1396-1409.	4.4	53
2212	Genome-Centered Metagenomics Analysis Reveals the Microbial Interactions of a Syntrophic Consortium during Methane Generation in a Decentralized Wastewater Treatment System. Applied Sciences (Switzerland), 2020, 10, 135.	1.3	13
2213	Methane emission suppression in flooded soil from Amazonia. Chemosphere, 2020, 250, 126263.	4.2	19
2214	Pectin drives microbial phosphorus solubilization in soil: Evidence from isolation-based and community-scale approaches. European Journal of Soil Biology, 2020, 97, 103169.	1.4	7
2215	Biodegradability of woody film produced by solvent volatilisation of Japanese Beech solution. Scientific Reports, 2020, 10, 476.	1.6	2
2216	Pyrodextrin enhances intestinal function through changing the intestinal microbiota composition and metabolism in early weaned piglets. Applied Microbiology and Biotechnology, 2020, 104, 4141-4154.	1.7	18
2217	Meiofaunal diversity at a seamount in the pacific ocean: A comprehensive study using environmental DNA and RNA. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 160, 103253.	0.6	10
2218	Decoupled diversity patterns in bacteria and fungi across continental forest ecosystems. Soil Biology and Biochemistry, 2020, 144, 107763.	4.2	78
2219	Impact of acid mine drainage chemistry and microbiology on the development of efficient Fe removal activities. Chemosphere, 2020, 249, 126117.	4.2	11
2220	Rain induces temporary shifts in epiphytic bacterial communities of cucumber and tomato fruit. Scientific Reports, 2020, 10, 1765.	1.6	25
2221	Cloacal bacterial communities of tree swallows (Tachycineta bicolor): Similarity within a population, but not between pair-bonded social partners. PLoS ONE, 2020, 15, e0228982.	1.1	8
2222	OGG1 deficiency alters the intestinal microbiome and increases intestinal inflammation in a mouse model. PLoS ONE, 2020, 15, e0227501.	1.1	18
2223	Prenatal Transfer of Gut Bacteria in Rock Pigeon. Microorganisms, 2020, 8, 61.	1.6	19
2224	Geographic Patterns of Bacterioplankton among Lakes of the Middle and Lower Reaches of the Yangtze River Basin, China. Applied and Environmental Microbiology, 2020, 86, .	1.4	25
2225	High-throughput Sequencing-based Analysis of Microbial Diversity in Rice Wine Koji from Different Areas. Current Microbiology, 2020, 77, 882-889.	1.0	23
2226	Response of bacterial communities from Kongsfjorden (Svalbard, Arctic Ocean) to macroalgal polysaccharide amendments. Marine Environmental Research, 2020, 155, 104874.	1.1	26

#	ARTICLE	IF	CITATIONS
2227	Gut bacteria of field-collected larvae of Spodoptera frugiperda undergo selection and are more diverse and active in metabolizing multiple insecticides than laboratory-selected resistant strains. Journal of Pest Science, 2020, 93, 833-851.	1.9	57
2228	Influence of contaminant exposure on the development of aerobic ETBE biodegradation potential in microbial communities from a gasoline-impacted aquifer. Journal of Hazardous Materials, 2020, 388, 122022.	6.5	9
2229	Opposing effects of bacterial endophytes on biomass allocation of a wild donor and agricultural recipient. FEMS Microbiology Ecology, 2020, 96, .	1.3	4
2230	Digestive tract microbiota of beef cattle that differed in feed efficiency. Journal of Animal Science, 2020, 98, .	0.2	35
2231	Endogenous FGF21-signaling controls paradoxical obesity resistance of UCP1-deficient mice. Nature Communications, 2020, 11, 624.	5.8	60
2232	Shotgun metagenomics approach reveals the bacterial community and metabolic pathways in commercial hongeo product, a traditional Korean fermented skate product. Food Research International, 2020, 131, 109030.	2.9	25
2233	Microbial Community Changes in the Rhizosphere Soil of Healthy and Rusty <i>Panax ginseng</i> and Discovery of Pivotal Fungal Genera Associated with Rusty Roots. BioMed Research International, 2020, 2020, 1-13.	0.9	41
2234	Gut metabolomics profiling of non-small cell lung cancer (NSCLC) patients under immunotherapy treatment. Journal of Translational Medicine, 2020, 18, 49.	1.8	114
2235	Gut Microbiota as Diagnostic Tools for Mirroring Disease Progression and Circulating Nephrotoxin Levels in Chronic Kidney Disease: Discovery and Validation Study. International Journal of Biological Sciences, 2020, 16, 420-434.	2.6	64
2236	Comparison of the Bacterial Gut Microbiome of North American Triatoma spp. With and Without Trypanosoma cruzi. Frontiers in Microbiology, 2020, 11, 364.	1.5	20
2237	Multiple Factors Determine the Structure of Bacterial Communities Associated With Aedes albopictus Under Artificial Rearing Conditions. Frontiers in Microbiology, 2020, 11, 605.	1.5	23
2238	Effects of Earthworms on the Microbiomes and Antibiotic Resistomes of Detritus Fauna and Phyllospheres. Environmental Science & Technology, 2020, 54, 6000-6008.	4.6	41
2239	Methodological Insight Into Mosquito Microbiome Studies. Frontiers in Cellular and Infection Microbiology, 2020, 10, 86.	1.8	15
2240	Source identification of phosphorus in the river-lake interconnected system using microbial community fingerprints. Environmental Research, 2020, 186, 109498.	3.7	16
2241	Microbiota stratification and succession of amylaseâ€producing <i>Bacillus</i> in traditional Chinese Jiuqu (fermentation starters). Journal of the Science of Food and Agriculture, 2020, 100, 3544-3553.	1.7	18
2242	Cottonseed meal fermented by Candida tropical reduces the fat deposition in white-feather broilers through cecum bacteria-host metabolic cross-talk. Applied Microbiology and Biotechnology, 2020, 104, 4345-4357.	1.7	14
2243	Dynamic shifts within volatile fatty acidâ€“degrading microbial communities indicate process imbalance in anaerobic digesters. Applied Microbiology and Biotechnology, 2020, 104, 4563-4575.	1.7	11
2244	Rhizosphere bacteria are more strongly related to plant root traits than fungi in temperate montane forests: insights from closed and open forest patches along an elevational gradient. Plant and Soil, 2020, 450, 183-200.	1.8	24

#	ARTICLE	IF	CITATIONS
2245	Site-specific molecular analysis of the bacteriota on worn spectacles. Scientific Reports, 2020, 10, 5577.	1.6	4
2246	Tracking the Dairy Microbiota from Farm Bulk Tank to Skimmed Milk Powder. MSystems, 2020, 5, .	1.7	45
2247	Effect of Supplemental Protease on Growth Performance and Excreta Microbiome of Broiler Chicks. Microorganisms, 2020, 8, 475.	1.6	14
2248	Thermophilic bio-electro CO₂ recycling into organic compounds. Green Chemistry, 2020, 22, 2947-2955.	4.6	16
2249	Unraveling Heterogeneity of Coral Microbiome Assemblages in Tropical and Subtropical Corals in the South China Sea. Microorganisms, 2020, 8, 604.	1.6	12
2250	Microbial Diversity and Physicochemical Characteristics of the Maotai-Flavored Liquor Fermentation Process. Journal of Nanoscience and Nanotechnology, 2020, 20, 4097-4109.	0.9	26
2251	Multiple in situ Nucleic Acid Collections (MISNAC) From Deep-Sea Waters. Frontiers in Marine Science, 2020, 7, .	1.2	13
2252	Different community assembly mechanisms underlie similar biogeography of bacteria and microeukaryotes in Tibetan lakes. FEMS Microbiology Ecology, 2020, 96, .	1.3	43
2253	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. Frontiers in Microbiology, 2020, 11, 485.	1.5	27
2254	Identifying Potential Polymicrobial Pathogens: Moving Beyond Differential Abundance to Driver Taxa. Microbial Ecology, 2020, 80, 447-458.	1.4	26
2255	Effect of phosphorus amendments on rice rhizospheric methanogens and methanotrophs in a phosphorus deficient soil. Geoderma, 2020, 368, 114312.	2.3	17
2256	Temporal changes in microbial communities attached to forages with different lignocellulosic compositions in cattle rumen. FEMS Microbiology Ecology, 2020, 96, .	1.3	32
2257	Microbial ecology and biogeochemistry of hypersaline sediments in Orca Basin. PLoS ONE, 2020, 15, e0231676.	1.1	14
2258	Dysbiosis of saliva microbiome in patients with oral lichen planus. BMC Microbiology, 2020, 20, 75.	1.3	30
2259	Lower airway bacterial microbiome may influence recurrence after resection of early-stage nonâ€“small cell lung cancer. Journal of Thoracic and Cardiovascular Surgery, 2021, 161, 419-429.e16.	0.4	37
2260	Biogeographic patterns of abundant and rare bacterial and microeukaryotic subcommunities in connected freshwater lake zones subjected to different levels of nutrient loading. Journal of Applied Microbiology, 2021, 130, 123-132.	1.4	6
2261	Oral microbial dysbiosis and its performance in predicting oral cancer. Carcinogenesis, 2021, 42, 127-135.	1.3	70
2262	House dust microbiota in relation to adult asthma and atopy in a US farming population. Journal of Allergy and Clinical Immunology, 2021, 147, 910-920.	1.5	21

#	ARTICLE	IF	CITATIONS
2263	Metagenomics reveals the diversity and taxonomy of antibiotic resistance genes in sufu bacterial communities. Food Control, 2021, 121, 107641.	2.8	9
2264	Microeukaryotic Communities Associated With the Seagrass <i>Zostera marina</i> Are Spatially Structured. Journal of Eukaryotic Microbiology, 2021, 68, e12827.	0.8	12
2265	Effects of activated carbon on the in-situ control of odorous gases emitted from anaerobic digestion of food waste and the microbial community response. Environmental Technology and Innovation, 2021, 21, 101170.	3.0	7
2266	Salinity controls soil microbial community structure and function in coastal estuarine wetlands. Environmental Microbiology, 2021, 23, 1020-1037.	1.8	109
2267	Soil carbon and associated bacterial community shifts driven by fine root traits along a chronosequence of Moso bamboo (Phyllostachys edulis) plantations in subtropical China. Science of the Total Environment, 2021, 752, 142333.	3.9	30
2268	Influence of Environmental Stressors on the Microbiota of Zebra Mussels (Dreissena polymorpha). Microbial Ecology, 2021, 81, 1042-1053.	1.4	6
2269	Seasonal changes and the unexpected impact of environmental disturbance on skin bacteria of individual amphibians in a natural habitat. FEMS Microbiology Ecology, 2021, 97, .	1.3	10
2270	Balanced stochastic versus deterministic assembly processes benefit diverse yet uneven ecosystem functions in representative agroecosystems. Environmental Microbiology, 2021, 23, 391-404.	1.8	42
2271	Microbial diversity and activity assessment in a 100-year-old lead mine. Journal of Hazardous Materials, 2021, 410, 124618.	6.5	24
2272	Comparative study of the bacterial communities throughout the gastrointestinal tract in two beef cattle breeds. Applied Microbiology and Biotechnology, 2021, 105, 313-325.	1.7	14
2273	Changes in the bacterial community structure in soil under conventional and conservation practices throughout a complete maize (Zea mays L.) crop cycle. Applied Soil Ecology, 2021, 157, 103733.	2.1	10
2274	Maize endophytic microbial-communities revealed by removing PCR and 16S rRNA sequencing and their synthetic applications to suppress maize banded leaf and sheath blight. Microbiological Research, 2021, 242, 126639.	2.5	17
2275	Effects of Antibiotic Treatment with Piperacillin/Tazobactam versus Ceftriaxone on the Composition of the Murine Gut Microbiota. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	17
2276	Distribution of physiochemically defined soil organic carbon pools and their relationship to the soil microbial community in grasslands. Pedobiologia, 2021, 84, 150704.	0.5	4
2277	Microbial diversity and structure in the gastrointestinal tracts of two stranded shortâ€finned pilot whales (<i>Globicephala macrorhynchus</i>) and a pygmy sperm whale (<i>Kogia breviceps</i>). Integrative Zoology, 2021, 16, 324-335.	1.3	16
2278	Influence of seasonality on the aerosol microbiome of the Amazon rainforest. Science of the Total Environment, 2021, 760, 144092.	3.9	13
2279	Bacterial epibiont communities of panmictic Antarctic krill are spatially structured. Molecular Ecology, 2021, 30, 1042-1052.	2.0	6
2280	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. Molecular Ecology, 2021, 30, 1072-1085.	2.0	43

#	Article	IF	Citations
2281	Composition and interaction frequencies in soil bacterial communities change in association with urban park age in Beijing. Pedobiologia, 2021, 84, 150699.	0.5	12
2282	Linking bacterial diversity to floral identity in the bumble bee pollen basket. Environmental DNA, 2021, 3, 669-680.	3.1	8
2283	Community assembly processes underlying the temporal dynamics of glacial stream and lake bacterial communities. Science of the Total Environment, 2021, 761, 143178.	3.9	22
2284	Sediment resuspension drives protist metacommunity structure and assembly in grass carp (Ctenopharyngodon idella) aquaculture ponds. Science of the Total Environment, 2021, 764, 142840.	3.9	19
2285	Pollution shapes the microbial communities in river water and sediments from the Olifants River catchment, South Africa. Archives of Microbiology, 2021, 203, 295-303.	1.0	3
2286	High-resolution taxonomic examination of the oral microbiome after oil pulling with standardized sunflower seed oil and healthy participants: a pilot study. Clinical Oral Investigations, 2021, 25, 2689-2703.	1.4	9
2287	Fermented Soybean Meal Replacement in the Diet of Lactating Holstein Dairy Cows: Modulated Rumen Fermentation and Ruminal Microflora. Frontiers in Microbiology, 2021, 12, 625857.	1.5	15
2288	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
2289	Host-Plant Induced Shifts in Microbial Community Structure in Small Brown Planthopper, <i>Laodelphax striatellus</i> (Homoptera: Delphacidae). Journal of Economic Entomology, 2021, 114, 937-946.	0.8	4
2290	Diversity of microbes colonizing forages of varying lignocellulose properties in the sheep rumen. PeerJ, 2021, 9, e10463.	0.9	18
2291	Systemic Metabolic Alterations Correlate with Islet-Level Prostaglandin E2 Production and Signaling Mechanisms That Predict Î²-Cell Dysfunction in a Mouse Model of Type 2 Diabetes. Metabolites, 2021, 11, 58.	1.3	16
2292	Development of gut microbiota and bifidobacterial communities of neonates in the first 6 weeks and their inheritance from mother. Gut Microbes, 2021, 13, 1-13.	4.3	15
2293	Subgingival microbiota of dogs with healthy gingiva or early periodontal disease from different geographical locations. BMC Veterinary Research, 2021, 17, 7.	0.7	14
2294	Group 2i Isochrysidales produce characteristic alkenones reflecting sea ice distribution. Nature Communications, 2021, 12, 15.	5.8	33
2295	Short-Term Exposure to Sterile Seawater Reduces Bacterial Community Diversity in the Sea Anemone, Exaiptasia diaphana. Frontiers in Marine Science, 2021, 7, .	1.2	11
2296	Assessment of Bacterial Community Structure in Saline Sediment Microcosms Exposed for the First Time to the Ionic Liquid 1-Ethyl-3-Methylimidazolium Chloride. Water, Air, and Soil Pollution, 2021, 232, 1.	1.1	3
2297	High Taxonomic and Functional Diversity of Bacterial Communities Associated with Melon Fly, Zeugodacus cucurbitae (Diptera: Tephritidae). Current Microbiology, 2021, 78, 611-623.	1.0	9
2298	Proteomics, Lipidomics, Metabolomics, and 16S DNA Sequencing of Dental Plaque From Patients With Diabetes and Periodontal Disease. Molecular and Cellular Proteomics, 2021, 20, 100126.	2.5	19

#	ARTICLE	IF	CITATIONS
2299	The ultra-structural, metabolomic and metagenomic characterisation of the sudanese smokeless tobacco â€˜Toombakâ€™. Toxicology Reports, 2021, 8, 1498-1512.	1.6	10
2300	Microbial diversity of co-occurring heterotrophs in cultures of marine picocyanobacteria. Environmental Microbiomes, 2021, 16, 1.	2.2	28
2301	Ã‡EÅžÄ°TLÄ° SUCUL HÄ°PERSALÄ°N HABÄ°TATLARDAKÄ° (TÃœRKÄ°YE) PROKARYOTÄ°K TOPLULUKLARIN VE NANOHALOARKEAL SOYLARIN Ã‡EÅžÄ°TLÄ°LÄ°ÄžÄ°NÄ°N YÃœKSEK-VERÄ°MLÄ° DÄ°ZÄ°LEME VE KLONLAMA KULLANILARAK DEÄžERLENDÄ°RÄ°LMESÄ°. Es Ãœniversitesi Bilim Ve Teknoloji Dergisi - C YaÅŸam Bilimleri Ve Biyoteknoloji, 2021, 10, 57-68.	0.1	2
2302	The Alteration of Intestinal Microbiota Profile and Immune Response in Epinephelus coioides during Pathogen Infection. Life, 2021, 11, 99.	1.1	16
2303	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
2304	The gut microbiota is a transmissible determinant of skeletal maturation. ELife, 2021, 10, .	2.8	25
2305	Intestinal microbiome and metabolome analyses reveal metabolic disorders in the early stage of renal transplantation. Molecular Omics, 2021, 17, 985-996.	1.4	2
2306	Infant gut microbiota modulation by human milk disaccharides in humanized microbiome mice. Gut Microbes, 2021, 13, 1-20.	4.3	15
2307	Structure and diversity of bacterial community in semiarid soils cultivated with prickly-pear cactus (Opuntia ficus-indica (L.) Mill.). Anais Da Academia Brasileira De Ciencias, 2021, 93, e20190183.	0.3	3
2308	Characterization and comparison of the bacterial community between complete intensive and extensive feeding patterns in pigs. AMB Express, 2021, 11, 32.	1.4	3
2309	Evaluation of Microbe-Driven Soil Organic Matter Quantity and Quality by Thermodynamic Theory. MBio, 2021, 12, .	1.8	7
2310	The Butyrate-Producing Bacterium <i>Clostridium butyricum</i> Suppresses <i>Clostridioides difficile</i> Infection via Neutrophil- and Antimicrobial Cytokineâ€"Dependent but GPR43/109a-Independent Mechanisms. Journal of Immunology, 2021, 206, 1576-1585.	0.4	47
2311	Bacterial dynamics of sugarcane silage in the tropics. Environmental Microbiology, 2021, 23, 5979-5991.	1.8	13
2312	Influence of Spatial Scale on Structure of Soil Bacterial Communities across an Arctic Landscape. Applied and Environmental Microbiology, 2021, 87, .	1.4	6
2313	Chemoradiation therapy changes oral microbiome and metabolomic profiles in patients with oral cavity cancer and oropharyngeal cancer. Head and Neck, 2021, 43, 1521-1534.	0.9	17
2314	Supplement of High Protein-Enriched Diet Modulates the Diversity of Gut Microbiota in WT or PD-1H-Depleted Mice. Journal of Microbiology and Biotechnology, 2021, 31, 207-216.	0.9	4
2315	The Lung Microbiome in Young Children with Cystic Fibrosis: A Prospective Cohort Study. Microorganisms, 2021, 9, 492.	1.6	12
2316	Early life dietary intervention in dairy calves results in a long-term reduction in methane emissions. Scientific Reports, 2021, 11, 3003.	1.6	32

#	Article	IF	Citations
2317	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
2318	Loss of Î±-gal during primate evolution enhanced antibody-effector function and resistance to bacterial sepsis. Cell Host and Microbe, 2021, 29, 347-361.e12.	5.1	14
2319	Metaâ€analysis methods for multiple related markers: Applications to microbiome studies with the results on multiple Î± â€diversity indices. Statistics in Medicine, 2021, 40, 2859-2876.	0.8	3
2320	Placentas delivered by preâ€pregnant obese women have reduced abundance and diversity in the microbiome. FASEB Journal, 2021, 35, e21524.	0.2	14
2321	Temperate southern Australian coastal waters are characterised by surprisingly high rates of nitrogen fixation and diversity of diazotrophs. PeerJ, 2021, 9, e10809.	0.9	12
2322	Effect of alfalfa hay and starter feed supplementation on caecal microbiota and fermentation, growth, and health of yak calves. Animal, 2021, 15, 100019.	1.3	8
2323	Lactulose significantly increased the relative abundance of <i>Bifidobacterium</i> and <i>Blautia</i> in mice feces as revealed by 16S rRNA amplicon sequencing. Journal of the Science of Food and Agriculture, 2021, 101, 5721-5729.	1.7	6
2324	The temperature sensitivity of soil: microbial biodiversity, growth, and carbon mineralization. ISME Journal, 2021, 15, 2738-2747.	4.4	65
2325	Characterization and association of bacterial communities and nonvolatile components in spontaneously fermented cow milk at different geographical distances. Journal of Dairy Science, 2021, 104, 2594-2605.	1.4	9
2326	Dysbiosis of the shrimp (<i>Penaeus monodon</i>) gut microbiome with AHPND outbreaks revealed by 16S rRNA metagenomics analysis. Aquaculture Research, 2021, 52, 3336-3349.	0.9	19
2327	Nonlinear machine learning pattern recognition and bacteria-metabolite multilayer network analysis of perturbed gastric microbiome. Nature Communications, 2021, 12, 1926.	5.8	22
2328	Rhizosphere microbiome modulated effects of biochar on ryegrass 15N uptake and rhizodeposited 13C allocation in soil. Plant and Soil, 2021, 463, 359-377.	1.8	17
2329	Fecal microbiota signatures of insulin resistance, inflammation, and metabolic syndrome in youth with obesity: a pilot study. Acta Diabetologica, 2021, 58, 1009-1022.	1.2	32
2330	Bacterial diversity and flavor profile of Zha-Chili, a traditional fermented food in China. Food Research International, 2021, 141, 110112.	2.9	57
2331	Microbial community structure in a hostâ€“parasite system: the case of Prussian carp and its parasitic crustaceans. Journal of Applied Microbiology, 2021, 131, 1722-1741.	1.4	10
2332	Enterolignan Production in a Flaxseed Intervention Study in Postmenopausal US Women of African Ancestry and European Ancestry. Nutrients, 2021, 13, 919.	1.7	9
2333	A Comparison of the Colonic Microbiome and Volatile Organic Compound Metabolome of Anoplocephala perfoliata Infected and Non-Infected Horses: A Pilot Study. Animals, 2021, 11, 755.	1.0	5
2334	Niche Selection by Soil Bacterial Community of Disturbed Subalpine Forests in Western Sichuan. Forests, 2021, 12, 505.	0.9	6

#	ARTICLE	IF	CITATIONS
2335	Diversity of microbial community and its metabolic potential for nitrogen and sulfur cycling in sediments of Phu Quoc island, Gulf of Thailand. Brazilian Journal of Microbiology, 2021, 52, 1385-1395.	0.8	2
2337	Streptomyces strains modulate dynamics of soil bacterial communities and their efficacy in disease suppression caused by Phytophthora capsici. Scientific Reports, 2021, 11, 9317.	1.6	25
2338	The G proteinâ€coupled receptor 15 (GPR15) regulates cutaneous immunology by maintaining dendritic epidermal T cells and regulating the skin microbiome. European Journal of Immunology, 2021, 51, 1390-1398.	1.6	4
2339	Orange Juice and Yogurt Carrying Probiotic Bacillus coagulans GBI-30 6086: Impact of Intake on Wistar Male Rats Health Parameters and Gut Bacterial Diversity. Frontiers in Microbiology, 2021, 12, 623951.	1.5	13
2340	Paraprobiotics obtained by six different inactivation processes: impacts on the biochemical parameters and intestinal microbiota of Wistar male rats. International Journal of Food Sciences and Nutrition, 2021, 72, 1057-1070.	1.3	10
2341	Diet-ruminal microbiome-host crosstalk contributes to differential effects of calf starter and alfalfa hay on rumen epithelial development and pancreatic Î±-amylase activity in yak calves. Journal of Dairy Science, 2021, 104, 4326-4340.	1.4	11
2342	Salt-induced recruitment of specific root-associated bacterial consortium capable of enhancing plant adaptability to salt stress. ISME Journal, 2021, 15, 2865-2882.	4.4	104
2343	Active Microbiome Structure and Functional Analyses of Freshwater Benthic Biofilm Samples Influenced by RNA Extraction Methods. Frontiers in Microbiology, 2021, 12, 588025.	1.5	2
2344	When your host shuts down: larval diapause impacts host-microbiome interactions in Nasonia vitripennis. Microbiome, 2021, 9, 85.	4.9	18
2345	The sugar composition of the fibre in selected plant foods modulates weaning infantsâ€™ gut microbiome composition and fermentation metabolites in vitro. Scientific Reports, 2021, 11, 9292.	1.6	9
2346	Collection of a Bacterial Community Reconstructed from Marine Metagenomes Derived from Jinhae Bay, South Korea. Data, 2021, 6, 44.	1.2	0
2347	Evaluation of bacterial diversity of traditional cheese in Tarbagatay Prefecture, China, and its correlation with cheese quality. Food Science and Nutrition, 2021, 9, 3155-3164.	1.5	10
2348	Simultaneous PAHs degradation, odour mitigation and energy harvesting by sediment microbial fuel cell coupled with nitrate-induced biostimulation. Journal of Environmental Management, 2021, 284, 112045.	3.8	11
2349	Monitoring of antimicrobial resistance genes in the spotted sea bass (): Association with the microbiome and its environment in aquaculture ponds. Environmental Pollution, 2021, 276, 116714.	3.7	17
2350	Rhizosphere Bacterial Networks, but Not Diversity, Are Impacted by Pea-Wheat Intercropping. Frontiers in Microbiology, 2021, 12, 674556.	1.5	23
2351	Microscopic Colitis Patients Possess a Perturbed and Inflammatory Gut Microbiota. Digestive Diseases and Sciences, 2022, 67, 2433-2443.	1.1	13
2352	Developmental trajectory of the healthy human gut microbiota during the first 5 years of life. Cell Host and Microbe, 2021, 29, 765-776.e3.	5.1	208
2353	Dominant egg surface bacteria of Holotrichia oblita (Coleoptera: Scarabaeidae) inhibit the multiplication of Bacillus thuringiensis and Beauveria bassiana. Scientific Reports, 2021, 11, 9499.	1.6	2

#	Article	IF	Citations
2354	Deciphering Potential Roles of Earthworms in Mitigation of Antibiotic Resistance in the Soils from Diverse Ecosystems. Environmental Science & Technology, 2021, 55, 7445-7455.	4.6	49
2355	Extraction and characterisation of arabinoxylan from brewers spent grain and investigation of microbiome modulation potential. European Journal of Nutrition, 2021, 60, 4393-4411.	1.8	24
2356	Bacterial diversity and predicted enzymatic function in a multipurpose surface water system â€" from wastewater effluent discharges to drinking water production. Environmental Microbiomes, 2021, 16, 11.	2.2	17
2357	Different Associations between Tonsil Microbiome, Chronic Tonsillitis, and Intermittent Hypoxemia among Obstructive Sleep Apnea Children of Different Weight Status: A Pilot Case-Control Study. Journal of Personalized Medicine, 2021, 11, 486.	1.1	8
2358	Using PacBio sequencing to investigate the effects of treatment with lactic acid bacteria or antibiotics on cow endometritis. Electronic Journal of Biotechnology, 2021, 51, 67-78.	1.2	4
2359	Melatonin Regulates the Neurotransmitter Secretion Disorder Induced by Caffeine Through the Microbiota-Gut-Brain Axis in Zebrafish (Danio rerio). Frontiers in Cell and Developmental Biology, 2021, 9, 678190.	1.8	13
2360	Shiftwork, functional bowel symptoms, and the microbiome. PeerJ, 2021, 9, e11406.	0.9	5
2362	Comprehensive Ecological and Geographic Characterization of Eukaryotic and Prokaryotic Microbiomes in African Anopheles. Frontiers in Microbiology, 2021, 12, 635772.	1.5	5
2363	In-code citation practices in open research software libraries. Journal of Informetrics, 2021, 15, 101139.	1.4	0
2365	Linkages between soil respiration and microbial communities following afforestation of alpine grasslands in the northeastern Tibetan Plateau. Applied Soil Ecology, 2021, 161, 103882.	2.1	35
2366	Functional redundancy and specific taxa modulate the contribution of prokaryotic diversity and composition to multifunctionality. Molecular Ecology, 2021, 30, 2915-2930.	2.0	38
2367	Effects of the dietary grain content on rumen and fecal microbiota of dairy cows. Canadian Journal of Animal Science, 2021, 101, 274-286.	0.7	10
2368	Sweet Sorghum Genotypes Tolerant and Sensitive to Nitrogen Stress Select Distinct Root Endosphere and Rhizosphere Bacterial Communities. Microorganisms, 2021, 9, 1329.	1.6	10
2369	Impact of a bacterial consortium on the soil bacterial community structure and maize (Zea mays L.) cultivation. Scientific Reports, 2021, 11, 13092.	1.6	16
2370	Niche partitioning of bacterial communities along the stratified water column in the Black Sea. MicrobiologyOpen, 2021, 10, e1195.	1.2	7
2371	Mediterranean Diet to Prevent the Development of Colon Diseases: A Meta-Analysis of Gut Microbiota Studies. Nutrients, 2021, 13, 2234.	1.7	42
2372	Modulation of human gut microbiota by dietary fibers from unripe and ripe papayas: Distinct polysaccharide degradation using a colonic in vitro fermentation model. Food Chemistry, 2021, 348, 129071.	4.2	20
2373	Activity of Fengycin and Iturin A Isolated From Bacillus subtilis Z-14 on Gaeumannomyces graminis Var. tritici and Soil Microbial Diversity. Frontiers in Microbiology, 2021, 12, 682437.	1.5	37

#	Article	IF	Citations
2374	Bacterial Communities in Alkaline Saline Soils Amended with Young Maize Plants or Its (Hemi)Cellulose Fraction. Microorganisms, 2021, 9, 1297.	1.6	1
2375	The gut microbiome and type 2 diabetes status in the Multiethnic Cohort. PLoS ONE, 2021, 16, e0250855.	1.1	30
2376	Deciphering Historical Water-Quality Changes Recorded in Sediments Using eDNA. Frontiers in Environmental Science, 2021, 9, .	1.5	2
2377	Cross-taxon congruence of aquatic microbial communities across geological ages in Iceland: Stochastic and deterministic processes. Science of the Total Environment, 2021, 774, 145103.	3.9	2
2378	Characterization of the microbiome of the invasive Asian toad in Madagascar across the expansion range and comparison with a native co-occurring species. PeerJ, 2021, 9, e11532.	0.9	7
2379	Removal of nitrogen and phosphorus from sediment and overlying water by double electrolytic-driven remediation and its effect on microbial community structure in sediment. Biogeochemistry, 2021, 155, 205-218.	1.7	0
2380	Bacteroides uniformis CECT 7771 alleviates inflammation within the gut-adipose tissue axis involving TLR5 signaling in obese mice. Scientific Reports, 2021, 11, 11788.	1.6	33
2381	Glutamine supplementation affected the gut bacterial community and fermentation leading to improved nutrient digestibility in growth-retarded yaks. FEMS Microbiology Ecology, 2021, 97, .	1.3	8
2382	Using Structural Equation Modeling to Understand Interactions Between Bacterial and Archaeal Populations and Volatile Fatty Acid Proportions in the Rumen. Frontiers in Microbiology, 2021, 12, 611951.	1.5	10
2384	Soy whey as a promising substrate in the fermentation of soy sauce: a study of microbial community and volatile compounds. International Journal of Food Science and Technology, 2021, 56, 5799.	1.3	5
2385	Temperature and microbial interactions drive the deterministic assembly processes in sediments of hot springs. Science of the Total Environment, 2021, 772, 145465.	3.9	85
2386	Oral Ferric Maltol Does Not Adversely Affect the Intestinal Microbiome of Patients or Mice, but Ferrous Sulphate Does. Nutrients, 2021, 13, 2269.	1.7	10
2387	Tick Ecdysteroid Hormone, Global Microbiota/Rickettsia Signaling in the Ovary versus Carcass during Vitellogenesis in Part-Fed (Virgin) American Dog Ticks, Dermacentor variabilis. Microorganisms, 2021, 9, 1242.	1.6	2
2388	AB-Kefir Reduced Body Weight and Ameliorated Inflammation in Adipose Tissue of Obese Mice Fed a High-Fat Diet, but Not a High-Sucrose Diet. Nutrients, 2021, 13, 2182.	1.7	12
2389	Endophytes isolated from <i>Panax notoginseng</i> converted ginsenosides. Microbial Biotechnology, 2021, 14, 1730-1746.	2.0	26
2390	Structure of Chimpanzee Gut Microbiomes across Tropical Africa. MSystems, 2021, 6, e0126920.	1.7	8
2391	Changes in physico-chemical characteristics and viable bacterial communities during fermentation of alfalfa silages inoculated with Lactobacillus plantarum. World Journal of Microbiology and Biotechnology, 2021, 37, 127.	1.7	11
2392	Performance of five typical warmâ€season turfgrasses and their influence on soil bacterial community under a simulated tropical coral island environment. Land Degradation and Development, 2021, 32, 3920-3929.	1.8	2

#	ARTICLE	IF	CITATIONS
2393	Food colorants metabolized by commensal bacteria promote colitis in mice with dysregulated expression of interleukin-23. Cell Metabolism, 2021, 33, 1358-1371.e5.	7.2	49
2394	Long-Term Effects of Bariatric Surgery on Gut Microbiota Composition and Faecal Metabolome Related to Obesity Remission. Nutrients, 2021, 13, 2519.	1.7	27
2395	Host habitat is the major determinant of the gut microbiome of fish. Microbiome, 2021, 9, 166.	4.9	100
2396	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. Nature Medicine, 2021, 27, 1432-1441.	15.2	216
2397	Unraveling negative biotic interactions determining soil microbial community assembly and functioning. ISME Journal, 2022, 16, 296-306.	4.4	80
2398	Seasonal Shifts in Cold Tolerance and the Composition of the Gut Microbiome of Dendroctonus valens LeConte Occur Concurrently. Forests, 2021, 12, 888.	0.9	8
2399	Soil Properties and Bacterial Community Dynamics in a Coal Mining Subsidence Area: Active Versus Passive Revegetation. Journal of Soil Science and Plant Nutrition, 2021, 21, 2573-2585.	1.7	6
2400	Bacteroides uniformis CECT 7771 Modulates the Brain Reward Response to Reduce Binge Eating and Anxiety-Like Behavior in Rat. Molecular Neurobiology, 2021, 58, 4959-4979.	1.9	20
2401	Salamander loss alters litter decomposition dynamics. Science of the Total Environment, 2021, 776, 145994.	3.9	6
2402	Clostridium butyricum enhances colonization resistance against Clostridioides difficile by metabolic and immune modulation. Scientific Reports, 2021, 11, 15007.	1.6	23
2403	Deep-Sea Carbonates Are a Reservoir of Fossil Microbes Previously Inhabiting Cold Seeps. Frontiers in Marine Science, 2021, 8, .	1.2	1
2404	Native Yeasts and Lactic Acid Bacteria Isolated from Spontaneous Fermentation of Seven Grape Cultivars from the Maule Region (Chile). Foods, 2021, 10, 1737.	1.9	10
2405	Soil pH and Organic Carbon Properties Drive Soil Bacterial Communities in Surface and Deep Layers Along an Elevational Gradient. Frontiers in Microbiology, 2021, 12, 646124.	1.5	36
2406	Wolbachia Strain wGri From the Tea Geometrid Moth Ectropis grisescens Contributes to Its Hostâ€™s Fecundity. Frontiers in Microbiology, 2021, 12, 694466.	1.5	5
2407	Gut Microbiota and Related Electronic Multisensorial System Changes in Subjects With Symptomatic Uncomplicated Diverticular Disease Undergoing Rifaximin Therapy. Frontiers in Medicine, 2021, 8, 655474.	1.2	6
2408	Nutrient resource availability mediates niche differentiation and temporal co-occurrence of soil bacterial communities. Applied Soil Ecology, 2021, 163, 103965.	2.1	13
2409	An Exploratory Study for the Association of Gut Microbiome with Efficacy of Immune Checkpoint Inhibitor in Patients with Hepatocellular Carcinoma. Journal of Hepatocellular Carcinoma, 2021, Volume 8, 809-822.	1.8	17
2410	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	3.8	51

#	ARTICLE	IF	CITATIONS
2411	Characterizing the Cattle Gut Microbiome in Farms with a High and Low Prevalence of Shiga Toxin Producing Escherichia coli. Microorganisms, 2021, 9, 1737.	1.6	8
2412	Steering bio-electro recycling of carbon dioxide towards target compounds through novel inoculation and feeding strategies. Journal of Environmental Chemical Engineering, 2021, 9, 105549.	3.3	6
2413	Two community types occur in gut microbiota of largeâ€sample wild plateau pikas (<i>Ochotona) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.3	14
2414	Biosorption of Copper in Swine Manure Using Aspergillus and Yeast: Characterization and Its Microbial Diversity Study. Frontiers in Microbiology, 2021, 12, 687533.	1.5	2
2415	Potential for Passive Treatment of Coal Mine-derived Acid Mine Drainage in Abandoned Stream Channels. Mine Water and the Environment, 0, , 1.	0.9	1
2416	Microbial analysis of sewage sludge shows closer monitoring needed for landfill waste. Proceedings of Institution of Civil Engineers: Waste and Resource Management, 0, , 1-7.	0.9	2
2417	Seasonal Variation in the Faecal Microbiota of Mature Adult Horses Maintained on Pasture in New Zealand. Animals, 2021, 11, 2300.	1.0	5
2418	Temporal changes in total and metabolically active ruminal methanogens in dairy cows supplemented with 3-nitrooxypropanol. Journal of Dairy Science, 2021, 104, 8721-8735.	1.4	18
2419	Changes in Bacterial Communities During Treatment of Municipal Wastewater in Arctic Wastewater Stabilization Ponds. Frontiers in Water, 2021, 3, .	1.0	2
2420	Matrix Effects on the Delivery Efficacy of Bifidobacterium animalis subsp. <i>lactis</i> BB-12 on Fecal Microbiota, Gut Transit Time, and Short-Chain Fatty Acids in Healthy Young Adults. MSphere, 2021, 6, e0008421.	1.3	11
2422	Potential of preventive bioremediation to reduce environmental contamination by pesticides in an agricultural context: A case study with the herbicide 2,4-D. Journal of Hazardous Materials, 2021, 416, 125740.	6.5	23
2423	Endophytic Microbiome Variation Among Single Plant Seeds. Phytobiomes Journal, 2022, 6, 45-55.	1.4	24
2424	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. Canadian Journal of Animal Science, 2021, 101, 493-506.	0.7	3
2425	Anoxic storage to promote arsenic removal with groundwater-native iron. Water Research, 2021, 202, 117404.	5.3	8
2426	Distinct intestinal microbial communities of two sympatric anadromous Arctic salmonids and the effects of migration and feeding. Arctic Science, 2021, 7, 634-654.	0.9	11
2427	Efficacy of Zhuyu Pill Intervention in a Cholestasis Rat Model: Mutual Effects on Fecal Metabolism and Microbial Diversity. Frontiers in Pharmacology, 2021, 12, 695035.	1.6	11
2428	Dietary grape seed proanthocyanidins improved growth, immunity, antioxidant, digestive enzymes activities, and intestinal microbiota of juvenile hybrid sturgeon (<i>Acipenser baeri</i> Brandt â™€ÂÃ—Â <i>A.) Tj ETQq0 0 0 rgBT /Over	1.1	11
2429	Sustained Ability of a Natural Microbial Community to Remove Nitrate from Groundwater. Ground Water, 2022, 60, 99-111.	0.7	6

#	Article	IF	Citations
2430	Differences of Gut Microbiota in the Freshwater Blackworm (Lumbriculus variegatus: Oligochaeta) in Two Different Habitat Conditions. International Journal of Environmental Research and Public Health, 2021, 18, 10298.	1.2	2
2431	Gut Microbiota Associated With Different Sea Lamprey (Petromyzon marinus) Life Stages. Frontiers in Microbiology, 2021, 12, 706683.	1.5	3
2432	Diversity and Taxonomic Distribution of Endophytic Bacterial Community in the Rice Plant and Its Prospective. International Journal of Molecular Sciences, 2021, 22, 10165.	1.8	30
2433	Structural, functional, resistome and pathogenicity profiling of the Cooum river. Microbial Pathogenesis, 2021, 158, 105048.	1.3	8
2434	Chitosan-chelated zinc modulates ileal microbiota, ileal microbial metabolites, and intestinal function in weaned piglets challenged with Escherichia coli K88. Applied Microbiology and Biotechnology, 2021, 105, 7529-7544.	1.7	9
2435	The Effect of Disinfectants on the Microbial Community on Environmental Healthcare Surfaces using Next Generation Sequencing. American Journal of Infection Control, 2021, , .	1.1	7
2436	Agricultural Management Affects the Active Rhizosphere Bacterial Community Composition and Nitrification. MSystems, 2021, 6, e0065121.	1.7	15
2437	The Bacterial Diversity of Spontaneously Fermented Dairy Products Collected in Northeast Asia. Foods, 2021, 10, 2321.	1.9	14
2438	The short-term effect of residential home energy retrofits on indoor air quality and microbial exposure: A case-control study. PLoS ONE, 2021, 16, e0230700.	1.1	2
2439	Trophic level drives the host microbiome of soil invertebrates at a continental scale. Microbiome, 2021, 9, 189.	4.9	18
2440	Enhanced diversity and rock-weathering potential of bacterial communities inhabiting potash trachyte surface beneath mosses and lichens â€" A case study in Nanjing, China. Science of the Total Environment, 2021, 785, 147357.	3.9	7
2441	Linking pollution to biodiversity and ecosystem multifunctionality across benthic-pelagic habitats of a large eutrophic lake: A whole-ecosystem perspective. Environmental Pollution, 2021, 285, 117501.	3.7	23
2442	Arsenic bioaccumulation in the soil fauna alters its gut microbiome and microbial arsenic biotransformation capacity. Journal of Hazardous Materials, 2021, 417, 126018.	6.5	19
2443	Plant legacies and soil microbial community dynamics control soil respiration. Soil Biology and Biochemistry, 2021, 160, 108350.	4.2	10
2444	Effects of tea polyphenols and EGCG on glucose metabolism and intestinal flora in diabetic mice fed a cornstarch-based functional diet. Food Science and Technology, 0, , .	0.8	1
2445	Microbes on decomposing litter in streams: entering on the leaf or colonizing in the water?. ISME Journal, 2022, 16, 717-725.	4.4	14
2446	Distinct patterns of abundant and rare subcommunities in paddy soil during wettingâ€"drying cycles. Science of the Total Environment, 2021, 785, 147298.	3.9	14
2447	Paleoecological evidence for a multi-trophic regime shift in a perialpine lake (Lake Joux, Switzerland). Anthropocene, 2021, 35, 100301.	1.6	12

#	ARTICLE	IF	CITATIONS
2448	Active methane processing microbes and the disproportionate role of NC10 phylum in methane mitigation in Amazonian floodplains. Biogeochemistry, 2021, 156, 293-317.	1.7	7
2449	Ecotoxicological risk assessment of wastewater irrigation on soil microorganisms: Fate and impact of wastewater-borne micropollutants in lettuce-soil system. Ecotoxicology and Environmental Safety, 2021, 223, 112595.	2.9	12
2450	Soil pH has a stronger effect than arsenic content on shaping plastisphere bacterial communities in soil. Environmental Pollution, 2021, 287, 117339.	3.7	35
2451	Soil microbial and chemical responses to foliar EpichloÃ« fungal infection in Lolium perenne, Hordeum brevisubulatum and Achnatherum inebrians. Fungal Ecology, 2021, 53, 101091.	0.7	3
2452	Both sampling seasonality and geographic origin contribute significantly to variations in raw milk microbiota, but sampling seasonality is the more determining factor. Journal of Dairy Science, 2021, 104, 10609-10627.	1.4	8
2453	Microbial diversity of marine shrimp pond sediment and its variability due to the effect of immobilized media in biohydrogen and biohythane production. Journal of Environmental Chemical Engineering, 2021, 9, 106166.	3.3	7
2454	Impact of dimethylpyrazole-based nitrification inhibitors on soil-borne bacteria. Science of the Total Environment, 2021, 792, 148374.	3.9	18
2455	Alterations of gut microbiota and metabolome with Parkinson's disease. Microbial Pathogenesis, 2021, 160, 105187.	1.3	38
2456	The dominance of Ligularia spp. related to significant changes in soil microenvironment. Ecological Indicators, 2021, 131, 108183.	2.6	9
2457	How can fertilization regimes and durations shape earthworm gut microbiota in a long-term field experiment?. Ecotoxicology and Environmental Safety, 2021, 224, 112643.	2.9	9
2458	Combined pollution of arsenic and Polymyxin B enhanced arsenic toxicity and enriched ARG abundance in soil and earthworm gut microbiotas. Journal of Environmental Sciences, 2021, 109, 171-180.	3.2	17
2459	Chiral enantiomers of the plant growth regulator paclobutrazol selectively affect community structure and diversity of soil microorganisms. Science of the Total Environment, 2021, 797, 148942.	3.9	12
2460	Lowered water table causes species substitution while nitrogen amendment causes species loss in alpine wetland microbial communities. Pedosphere, 2021, 31, 912-922.	2.1	6
2461	Responses of earthworm Metaphire vulgaris gut microbiota to arsenic and nanoplastics contamination. Science of the Total Environment, 2022, 806, 150279.	3.9	9
2462	Oral azoxystrobin driving the dynamic change in resistome by disturbing the stability of the gut microbiota of Enchytraeus crypticus. Journal of Hazardous Materials, 2022, 423, 127252.	6.5	15
2463	Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. Annals of Translational Medicine, 2021, 9, 32-32.	0.7	16
2464	Fecal microbiome and metabolome differ in healthy and food-allergic twins. Journal of Clinical Investigation, 2021, 131, .	3.9	69
2465	Insights into Bacterial Community Involved in Bioremediation of Aged Oil-Contaminated Soil in Arid Environment. Evolutionary Bioinformatics, 2021, 17, 117693432110168.	0.6	4

#	ARTICLE	IF	CITATIONS
2466	Co-digestion of Dairy Cattle Waste in a Pilot-Scale Thermophilic Digester Adapted to Poultry Litter Feedstock: Stress, Recovery, and Microbiome Response. Bioenergy Research, 2021, 14, 1349.	2.2	3
2467	Phytophthora Root Rot Modifies the Composition of the Avocado Rhizosphere Microbiome and Increases the Abundance of Opportunistic Fungal Pathogens. Frontiers in Microbiology, 2020, 11, 574110.	1.5	40
2468	Host development overwhelms environmental dispersal in governing the ecological succession of zebrafish gut microbiota. Npj Biofilms and Microbiomes, 2021, 7, 5.	2.9	64
2469	Analysis of microbial diversity and functional differences in different types of highâ€temperature Daqu. Food Science and Nutrition, 2021, 9, 1003-1016.	1.5	54
2470	Effect of storage, temperature, and extraction kit on the phylogenetic composition detected in the human milk microbiota. MicrobiologyOpen, 2021, 10, e1127.	1.2	14
2471	Resting Stage of PlanktonÂDiversity from SingaporeÂCoastal Water: Implications for Harmful Algae Blooms and Coastal Management. Environmental Management, 2018, 61, 275-290.	1.2	12
2472	Benthic microbial biogeography along the continental shelf shaped by substrates from the Changjiang River plume. Acta Oceanologica Sinica, 2022, 41, 118-131.	0.4	7
2473	Microbial inoculant and garbage enzyme reduced cadmium (Cd) uptake in Salvia miltiorrhiza (Bge.) under Cd stress. Ecotoxicology and Environmental Safety, 2020, 192, 110311.	2.9	31
2474	Does reduced usage of antibiotics in livestock production mitigate the spread of antibiotic resistance in soil, earthworm guts, and the phyllosphere?. Environment International, 2020, 136, 105359.	4.8	47
2475	Fetal and early postnatal lead exposure measured in teeth associates with infant gut microbiota. Environment International, 2020, 144, 106062.	4.8	21
2476	Meteorological factors had more impact on airborne bacterial communities than air pollutants. Science of the Total Environment, 2017, 601-602, 703-712.	3.9	138
2477	Tagging the vanA gene in wastewater microbial communities for cell sorting and taxonomy of vanA carrying cells. Science of the Total Environment, 2020, 732, 138865.	3.9	4
2478	Oil-Spill Triggered Shift in Indigenous Microbial Structure and Functional Dynamics in Different Marine Environmental Matrices. Scientific Reports, 2019, 9, 1354.	1.6	71
2479	Effect of mannan oligosaccharides on the microbiota and productivity parameters of Litopenaeus vannamei shrimp under intensive cultivation in Ecuador. Scientific Reports, 2020, 10, 2719.	1.6	36
2480	Skin microbiome correlates with bioclimate and Batrachochytrium dendrobatidis infection intensity in Brazilâ€™s Atlantic Forest treefrogs. Scientific Reports, 2020, 10, 22311.	1.6	19
2481	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
2482	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
2483	Isolation and characterization of Flexilinea flocculi gen. nov., sp. nov., a filamentous, anaerobic bacterium belonging to the class Anaerolineae in the phylum Chloroflexi. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 988-996.	0.8	75

#	Article	IF	Citations
2484	Lentimicrobium saccharophilum gen. nov., sp. nov., a strictly anaerobic bacterium representing a new family in the phylum Bacteroidetes, and proposal of Lentimicrobiaceae fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2635-2642.	0.8	177
2485	First insight into the faecal microbiota of the high Arctic muskoxen (Ovibos moschatus). Microbial Genomics, 2016, 2, e000066.	1.0	18
2486	The comparative genomics of Bifidobacterium callitrichos reflects dietary carbohydrate utilization within the common marmoset gut. Microbial Genomics, 2018, 4, .	1.0	16
2487	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. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlock	0.7	46
2518	Soil microbes of an urban remnant riparian zone have greater potential for N removal than a degraded riparian zone. Environmental Microbiology, 2020, 22, 3302-3314.	1.8	7
2519	Does a carbonatite deposit influence its surrounding ecosystem?. Facets, 2019, 4, 389-406.	1.1	2
2520	Gut microbiota modulates adoptive cell therapy via CD8Î± dendritic cells and IL-12. JCI Insight, 2018, 3, .	2.3	111
2521	Gut microbiota modulate dendritic cell antigen presentation and radiotherapy-induced antitumor immune response. Journal of Clinical Investigation, 2019, 130, 466-479.	3.9	159
2523	Structure and diversity of native bacterial communities in soils contaminated with polychlorinated biphenyls. AMB Express, 2020, 10, 124.	1.4	10
2524	Disordered Microbial Communities in the Upper Respiratory Tract of Cigarette Smokers. PLoS ONE, 2010, 5, e15216.	1.1	350
2525	Microbial Biogeography of Public Restroom Surfaces. PLoS ONE, 2011, 6, e28132.	1.1	222
2526	Composition and Similarity of Bovine Rumen Microbiota across Individual Animals. PLoS ONE, 2012, 7, e33306.	1.1	508
2527	Proof of Concept of Microbiome-Metabolome Analysis and Delayed Gluten Exposure on Celiac Disease Autoimmunity in Genetically At-Risk Infants. PLoS ONE, 2012, 7, e33387.	1.1	219
2528	Office Space Bacterial Abundance and Diversity in Three Metropolitan Areas. PLoS ONE, 2012, 7, e37849.	1.1	114
2529	Dramatic Shifts in Benthic Microbial Eukaryote Communities following the Deepwater Horizon Oil Spill. PLoS ONE, 2012, 7, e38550.	1.1	139
2530	Metagenomics of the Svalbard Reindeer Rumen Microbiome Reveals Abundance of Polysaccharide Utilization Loci. PLoS ONE, 2012, 7, e38571.	1.1	190
2531	Assessing Bacterial Populations in the Lung by Replicate Analysis of Samples from the Upper and Lower Respiratory Tracts. PLoS ONE, 2012, 7, e42786.	1.1	126
2532	Compositional Stability of a Salivary Bacterial Population against Supragingival Microbiota Shift following Periodontal Therapy. PLoS ONE, 2012, 7, e42806.	1.1	66

#	ARTICLE	IF	CITATIONS
2533	Gut Microbiota Composition Is Correlated to Grid Floor Induced Stress and Behavior in the BALB/c Mouse. PLoS ONE, 2012, 7, e46231.	1.1	254
2534	Upper Airways Microbiota in Antibiotic-NaÃ¯ve Wheezing and Healthy Infants from the Tropics of Rural Ecuador. PLoS ONE, 2012, 7, e46803.	1.1	89
2535	Characterization of the Fecal Microbiota Using High-Throughput Sequencing Reveals a Stable Microbial Community during Storage. PLoS ONE, 2012, 7, e46953.	1.1	190
2536	A Jungle in There: Bacteria in Belly Buttons are Highly Diverse, but Predictable. PLoS ONE, 2012, 7, e47712.	1.1	69
2537	Short-Read Assembly of Full-Length 16S Amplicons Reveals Bacterial Diversity in Subsurface Sediments. PLoS ONE, 2013, 8, e56018.	1.1	153
2538	Control of Temperature on Microbial Community Structure in Hot Springs of the Tibetan Plateau. PLoS ONE, 2013, 8, e62901.	1.1	157
2539	A Filtering Method to Generate High Quality Short Reads Using Illumina Paired-End Technology. PLoS ONE, 2013, 8, e66643.	1.1	282
2540	Bacterial Community Mapping of the Mouse Gastrointestinal Tract. PLoS ONE, 2013, 8, e74957.	1.1	363
2541	A Cross-Sectional Survey of Bacterial Species in Plaque from Client Owned Dogs with Healthy Gingiva, Gingivitis or Mild Periodontitis. PLoS ONE, 2013, 8, e83158.	1.1	76
2542	Evidence of a Putative Deep Sea Specific Microbiome in Marine Sponges. PLoS ONE, 2014, 9, e91092.	1.1	79
2543	Mycoplasma salivarium as a Dominant Coloniser of Fanconi Anaemia Associated Oral Carcinoma. PLoS ONE, 2014, 9, e92297.	1.1	32
2544	Comparative Analysis of Functional Metagenomic Annotation and the Mappability of Short Reads. PLoS ONE, 2014, 9, e105776.	1.1	58
2545	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
2546	Bacterial Endophytic Communities in the Grapevine Depend on Pest Management. PLoS ONE, 2014, 9, e112763.	1.1	125
2547	Effects of a Ciliate Protozoa Predator on Microbial Communities in Pitcher Plant (Sarracenia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T	1.1	20
2548	Biochar in Co-Contaminated Soil Manipulates Arsenic Solubility and Microbiological Community Structure, and Promotes Organochlorine Degradation. PLoS ONE, 2015, 10, e0125393.	1.1	45
2549	Effects of Long Term Antibiotic Therapy on Human Oral and Fecal Viromes. PLoS ONE, 2015, 10, e0134941.	1.1	119
2550	Cloacal Microbiome Structure in a Long-Distance Migratory Bird Assessed Using Deep 16sRNA Pyrosequencing. PLoS ONE, 2015, 10, e0137401.	1.1	70

#	ARTICLE	IF	CITATIONS
2551	Zonation of Microbial Communities by a Hydrothermal Mound in the Atlantis II Deep (the Red Sea). PLoS ONE, 2015, 10, e0140766.	1.1	6
2552	Methanosarcina Play an Important Role in Anaerobic Co-Digestion of the Seaweed Ulva lactuca: Taxonomy and Predicted Metabolism of Functional Microbial Communities. PLoS ONE, 2015, 10, e0142603.	1.1	33
2553	Functional Metagenomics of the Bronchial Microbiome in COPD. PLoS ONE, 2015, 10, e0144448.	1.1	40
2554	Pglyrp-Regulated Gut Microflora Prevotella falsenii, Parabacteroides distasonis and Bacteroides eggerthii Enhance and Alistipes finegoldii Attenuates Colitis in Mice. PLoS ONE, 2016, 11, e0146162.	1.1	259
2555	Resistant Starch Alters the Microbiota-Gut Brain Axis: Implications for Dietary Modulation of Behavior. PLoS ONE, 2016, 11, e0146406.	1.1	45
2556	Microbial Community Profile and Water Quality in a Protected Area of the Caatinga Biome. PLoS ONE, 2016, 11, e0148296.	1.1	20
2557	Variability of Bacterial Communities in the Moth Heliothis virescens Indicates Transient Association with the Host. PLoS ONE, 2016, 11, e0154514.	1.1	89
2558	Rumen and Cecum Microbiomes in Reindeer (Rangifer tarandus tarandus) Are Changed in Response to a Lichen Diet and May Affect Enteric Methane Emissions. PLoS ONE, 2016, 11, e0155213.	1.1	42
2559	Dietary Regulation of the Gut Microbiota Engineered by a Minimal Defined Bacterial Consortium. PLoS ONE, 2016, 11, e0155620.	1.1	16
2560	Bacterial and Archaeal Diversity in the Gastrointestinal Tract of the North American Beaver (Castor) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	35
2561	Early Gut Microbiota Perturbations Following Intrapartum Antibiotic Prophylaxis to Prevent Group B Streptococcal Disease. PLoS ONE, 2016, 11, e0157527.	1.1	81
2562	Seasonality and Locality Affect the Diversity of Anopheles gambiae and Anopheles coluzzii Midgut Microbiota from Ghana. PLoS ONE, 2016, 11, e0157529.	1.1	58
2563	Dysbiosis of the Fecal Microbiota in Cattle Infected with Mycobacterium avium subsp. paratuberculosis. PLoS ONE, 2016, 11, e0160353.	1.1	44
2564	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
2565	Changes in the Bacterial Community Structure of Remediated Anthracene-Contaminated Soils. PLoS ONE, 2016, 11, e0160991.	1.1	21
2566	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
2567	Using a Control to Better Understand Phyllosphere Microbiota. PLoS ONE, 2016, 11, e0163482.	1.1	52
2568	Microbiota of the Small Intestine Is Selectively Engulfed by Phagocytes of the Lamina Propria and Peyerâ€™s Patches. PLoS ONE, 2016, 11, e0163607.	1.1	53

#	Article	IF	Citations
2569	Chronic Opisthorchis viverrini Infection Changes the Liver Microbiome and Promotes Helicobacter Growth. PLoS ONE, 2016, 11, e0165798.	1.1	40
2570	Ontogenetic Characterization of the Intestinal Microbiota of Channel Catfish through 16S rRNA Gene Sequencing Reveals Insights on Temporal Shifts and the Influence of Environmental Microbes. PLoS ONE, 2016, 11, e0166379.	1.1	102
2571	A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. PLoS ONE, 2016, 11, e0167788.	1.1	46
2572	Distinctive Feature of Microbial Communities and Bacterial Functional Profiles in Tricholoma matsutake Dominant Soil. PLoS ONE, 2016, 11, e0168573.	1.1	39
2573	Effectiveness of Devices to Monitor Biofouling and Metals Deposition on Plumbing Materials Exposed to a Full-Scale Drinking Water Distribution System. PLoS ONE, 2017, 12, e0169140.	1.1	27
2574	Changes in bacterial community composition of Escherichia coli O157:H7 super-shedder cattle occur in the lower intestine. PLoS ONE, 2017, 12, e0170050.	1.1	25
2575	Investigation of bacterial communities within the digestive organs of the hydrothermal vent shrimp Rimicaris exoculata provide insights into holobiont geographic clustering. PLoS ONE, 2017, 12, e0172543.	1.1	23
2576	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
2577	Seasonal changes in the digesta-adherent rumen bacterial communities of dairy cattle grazing pasture. PLoS ONE, 2017, 12, e0173819.	1.1	35
2578	The preservation of microbial DNA in archived soils of various genetic types. PLoS ONE, 2017, 12, e0173901.	1.1	17
2579	Comparative analysis of bacterial community structure in the rhizosphere of maize by high-throughput pyrosequencing. PLoS ONE, 2017, 12, e0178425.	1.1	147
2580	Host niche may determine disease-driven extinction risk. PLoS ONE, 2017, 12, e0181051.	1.1	14
2581	The microbiota of water buffalo milk during mastitis. PLoS ONE, 2017, 12, e0184710.	1.1	58
2582	Phylogenic inference using alignment-free methods for applications in microbial community surveys using 16s rRNA gene. PLoS ONE, 2017, 12, e0187940.	1.1	5
2583	Analysis of the tonsillar microbiome in young adults with sore throat reveals a high relative abundance of Fusobacterium necrophorum with low diversity. PLoS ONE, 2018, 13, e0189423.	1.1	18
2584	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
2585	Variation in the microbiome of the urogenital tract of Chlamydia-free female koalas (Phascolarctos) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	14
2586	Nutritional combinatorial impact on the gut microbiota and plasma short-chain fatty acids levels in the prevention of mammary cancer in Her2/neu estrogen receptor-negative transgenic mice. PLoS ONE, 2020, 15, e0234893.	1.1	18

#	Article	IF	Citations
2587	Species-dependent variation of the gut bacterial communities across Trypanosoma cruzi insect vectors. PLoS ONE, 2020, 15, e0240916.	1.1	6
2588	Longitudinal analysis reveals characteristically high proportions of bacterial vaginosis-associated bacteria and temporal variability of vaginal microbiota in northern pig-tailed macaques (Macaca) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.4	6
2589	Effects of triclosan on bacterial community composition and <i>Vibrio</i> populations in natural seawater microcosms. Elementa, 2017, 5, 1-16.	1.1	5
2590	An altered fecal microbiota profile in patients with non-alcoholic fatty liver disease (NAFLD) associated with obesity. Revista Espanola De Enfermedades Digestivas, 2019, 111, 275-282.	0.1	41
2591	Breast tissue, oral and urinary microbiomes in breast cancer. Oncotarget, 2017, 8, 88122-88138.	0.8	134
2592	Diversity and Metabolic Potential of Earthworm Gut Microbiota in Indo-Myanmar Biodiversity Hotspot. Journal of Pure and Applied Microbiology, 2020, 14, 1503-1511.	0.3	4
2593	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
2594	Environmental controls on estuarine nitrifying communities along a salinity gradient. Aquatic Microbial Ecology, 2017, 80, 167-180.	0.9	8
2595	Comparing the community structure of Bacteria and micro-Eukarya from the Hawaiian anchialine ecosystem during wet and dry seasons. Aquatic Microbial Ecology, 2018, 82, 87-104.	0.9	6
2596	Meiobenthic community composition and biodiversity along a 5500 km transect of Western Antarctica: a metabarcoding analysis. Marine Ecology - Progress Series, 2018, 603, 47-60.	0.9	26
2597	A Unique Benthic Microbial Community Underlying the Phaeocystis antarctica-Dominated Amundsen Sea Polynya, Antarctica: A Proxy for Assessing the Impact of Global Changes. Frontiers in Marine Science, 2020, 6, .	1.2	6
2598	Regular Biochar and Bacteria-Inoculated Biochar Alter the Composition of the Microbial Community in the Soil of a Chinese Fir Plantation. Forests, 2020, 11, 951.	0.9	13
2599	Effects of a Synbiotic Formula on Functional Bowel Disorders and Gut Microbiota Profile during Long-Term Home Enteral Nutrition (LTHEN): A Pilot Study. Nutrients, 2021, 13, 87.	1.7	3
2600	A Hybrid DNA Extraction Method for the Qualitative and Quantitative Assessment of Bacterial Communities from Poultry Production Samples. Journal of Visualized Experiments, 2014, , .	0.2	22
2601	Vaginal Microbiota Profiles of Native Korean Women and Associations with High-Risk Pregnancy. Journal of Microbiology and Biotechnology, 2020, 30, 248-258.	0.9	27
2602	Association between Gut Microbiome Composition and Rotavirus Vaccine Response among Nicaraguan Infants. American Journal of Tropical Medicine and Hygiene, 2020, 102, 213-219.	0.6	35
2605	The impact of diet on the composition and relative abundance of rumen microbes in goat. Asian-Australasian Journal of Animal Sciences, 2017, 30, 531-537.	2.4	47
2606	Enterotype Variations of the Healthy Human Gut Microbiome in Different Geographical Regions. Bioinformation, 2018, 14, 560-573.	0.2	65

#	ARTICLE	IF	CITATIONS
2609	Bidirectional interactions between indomethacin and the murine intestinal microbiota. ELife, 2015, 4, e08973.	2.8	80
2610	Respiratory tissue-associated commensal bacteria offer therapeutic potential against pneumococcal colonization. ELife, 2020, 9, .	2.8	22
2611	Response of the rare biosphere to environmental stressors in a highly diverse ecosystem (Zodletone) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	40
2612	Characterization of the salivary microbiome in patients with pancreatic cancer. PeerJ, 2015, 3, e1373.	0.9	150
2613	A comparison of rumen microbial profiles in dairy cows as retrieved by 454 Roche and Ion Torrent (PGM) sequencing platforms. PeerJ, 2016, 4, e1599.	0.9	17
2614	The impact of freeze-drying infant fecal samples on measures of their bacterial community profiles and milk-derived oligosaccharide content. PeerJ, 2016, 4, e1612.	0.9	13
2615	Microbial diversity of extreme habitats in human homes. PeerJ, 2016, 4, e2376.	0.9	21
2616	Bacterial community diversity of the deep-sea octocoral<i>Paramuricea placomus</i>. PeerJ, 2016, 4, e2529.	0.9	56
2617	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
2618	Effect of freshwater mussels on the vertical distribution of anaerobic ammonia oxidizers and other nitrogen-transforming microorganisms in upper Mississippi river sediment. PeerJ, 2017, 5, e3536.	0.9	22
2619	A longitudinal study of the diabetic skin and wound microbiome. PeerJ, 2017, 5, e3543.	0.9	93
2620	Skin bacterial microbiome of a generalist Puerto Rican frog varies along elevation and land use gradients. PeerJ, 2017, 5, e3688.	0.9	75
2621	Fungi found in Mediterranean and North Sea sponges: how specific are they?. PeerJ, 2017, 5, e3722.	0.9	26
2622	Distribution of bacterial communities along the spatial and environmental gradients from Bohai Sea to northern Yellow Sea. PeerJ, 2018, 6, e4272.	0.9	38
2623	Evaluation of a therapy for Idiopathic Chronic Enterocolitis in rhesus macaques (<i>Macaca) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T	0.9	5
2624	Fine grained compositional analysis of Port Everglades Inlet microbiome using high throughput DNA sequencing. PeerJ, 2018, 6, e4671.	0.9	4
2625	Salt marsh sediment bacterial communities maintain original population structure after transplantation across a latitudinal gradient. PeerJ, 2018, 6, e4735.	0.9	14
2626	The bacterial communities of<i>Drosophila suzukii</i>collected from undamaged cherries. PeerJ, 2014, 2, e474.	0.9	62

#	ARTICLE	IF	CITATIONS
2627	Effects of agricultural management on phyllosphere fungal diversity in vineyards and the association with adjacent native forests. PeerJ, 2018, 6, e5715.	0.9	27
2628	Structure, dynamics and predicted functional role of the gut microbiota of the blue (<i>Haliotis) Tj ETQq1 1 0.784314 rgBT /Overlock e5830.	0.9	26
2629	Bacterial and archaeal spatial distribution and its environmental drivers in an extremely haloalkaline soil at the landscape scale. PeerJ, 2019, 7, e6127.	0.9	8
2630	The role of macrobiota in structuring microbial communities along rocky shores. PeerJ, 2014, 2, e631.	0.9	19
2631	Diverse microbial communities hosted by the model carnivorous pitcher plant <i>Sarracenia purpurea</i>: analysis of both bacterial and eukaryotic composition across distinct host plant populations. PeerJ, 2019, 7, e6392.	0.9	10
2632	Biodegradation of thiocyanate by a native groundwater microbial consortium. PeerJ, 2019, 7, e6498.	0.9	10
2633	The Koala (<i>Phascolarctos cinereus</i>) faecal microbiome differs with diet in a wild population. PeerJ, 2019, 7, e6534.	0.9	46
2634	A longitudinal study of the faecal microbiome and metabolome of periparturient mares. PeerJ, 2019, 7, e6687.	0.9	14
2635	Skin bacterial communities of neotropical treefrogs vary with local environmental conditions at the time of sampling. PeerJ, 2019, 7, e7044.	0.9	22
2636	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 2015, 3, e740.	0.9	157
2637	Factors associated with the composition and diversity of the cervical microbiota of reproductive-age Black South African women: a retrospective cross-sectional study. PeerJ, 2019, 7, e7488.	0.9	19
2638	Effects of particle size of ground alfalfa hay on caecal bacteria and archaea populations of rabbits. PeerJ, 2019, 7, e7910.	0.9	2
2639	Different nitrogen sources speed recovery from corallivory and uniquely alter the microbiome of a reef-building coral. PeerJ, 2019, 7, e8056.	0.9	20
2640	Microbial communities on fish eggs from <i>Acanthopagrus schlegelii</i> and <i>Halichoeres nigrescens</i> at the XuWen coral reef in the Gulf of Tonkin. PeerJ, 2020, 8, e8517.	0.9	5
2641	Pyrosequencing revealed shifts of prokaryotic communities between healthy and disease-like tissues of the Red Sea sponge<i>Crella cyathophora</i>. PeerJ, 2015, 3, e890.	0.9	20
2642	Loss OfÂ Tet2 Âln T Cells Drives Translocated Pathobiont Derived Aryl Hydrocarbon Receptor Agonist-Induced Tc1 Cell Autoimmune Hepatitis. SSRN Electronic Journal, 0, , .	0.4	0
2643	Towards bacterioplankton composition as indicator of environmental status: proof of principle using indicator value analysis of estuarine communities. Aquatic Microbial Ecology, 0, , .	0.9	4
2644	Neonatal Piglets Are Protected from Clostridioides difficile Infection by Age-Dependent Increase in Intestinal Microbial Diversity. Microbiology Spectrum, 2021, 9, e0124321.	1.2	4

#	Article	IF	Citations
2645	Longitudinal Multi-Omics Study of a Mother-Infant Dyad from Breastfeeding to Weaning: An Individualized Approach to Understand the Interactions Among Diet, Fecal Metabolome and Microbiota Composition. Frontiers in Molecular Biosciences, 2021, 8, 688440.	1.6	14
2646	The diversity and composition of the human gut lactic acid bacteria and bifidobacterial microbiota vary depending on age. Applied Microbiology and Biotechnology, 2021, 105, 8427-8440.	1.7	13
2647	Effect of the skincare product on facial skin microbial structure and biophysical parameters: A pilot study. MicrobiologyOpen, 2021, 10, e1236.	1.2	6
2648	Winter Rye Cover Cropping Changes Squash (<i>Cucurbita pepo</i>) Phyllosphere Microbiota and Reduces <i>Pseudomonas syringae</i> Symptoms. Phytobiomes Journal, 2022, 6, 3-12.	1.4	2
2649	Microbial chemolithotrophic oxidation of pyrite in a subsurface shale weathering environment: Geologic considerations and potential mechanisms. Geobiology, 2022, 20, 271-291.	1.1	4
2650	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
2652	Unveiling metabolic characteristics of an uncultured Gammaproteobacterium responsible for <i>in situ</i>â€‰<scp>PAH</scp> biodegradation in petroleum polluted soil. Environmental Microbiology, 2021, 23, 7093-7104.	1.8	4
2653	Effect of the administration of probiotics on the fecal microbiota of adult individuals. Food Science and Nutrition, 2021, 9, 6471-6479.	1.5	4
2654	Raw milk processing by highâ€intensity ultrasound and conventional heat treatments: Microbial profile by amplicon sequencing and physical stability during storage. International Journal of Dairy Technology, 2022, 75, 115-128.	1.3	10
2655	Comparison of Gut Bacterial Communities of Fall Armyworm (Spodoptera frugiperda) Reared on Different Host Plants. International Journal of Molecular Sciences, 2021, 22, 11266.	1.8	24
2656	Particulate Matter Exposure and Allergic Rhinitis: The Role of Plasmatic Extracellular Vesicles and Bacterial Nasal Microbiome. International Journal of Environmental Research and Public Health, 2021, 18, 10689.	1.2	6
2657	Compartment Niche Shapes the Assembly and Network of Cannabis sativa-Associated Microbiome. Frontiers in Microbiology, 2021, 12, 714993.	1.5	26
2658	Ulmus macrocarpa Hance extract modulates intestinal microbiota in healthy adults: a randomized, placebo-controlled clinical trial. Journal of Microbiology, 2021, 59, 1150-1156.	1.3	5
2659	New Arsenite Oxidase Gene (aioA) PCR Primers for Assessing Arsenite-Oxidizer Diversity in the Environment Using High-Throughput Sequencing. Frontiers in Microbiology, 2021, 12, 691913.	1.5	2
2661	Assembly and co-occurrence patterns of rare and abundant bacterial sub-communities in rice rhizosphere soil under short-term nitrogen deep placement. Journal of Integrative Agriculture, 2021, 20, 3299-3311.	1.7	6
2662	Dynamics of the ruminal microbial ecosystem, and inhibition of methanogenesis and propiogenesis in response to nitrate feeding to Holstein calves. Animal Nutrition, 2021, 7, 1205-1218.	2.1	6
2664	The faecal flora: a source of healthcare-associated infections and antibiotic resistance. , 2013, , .		0
2679	Study of Periplaneta Americana Microbial Community Structure and Diversity by 16S rRNA High-Throughput Sequencing. Sustainability in Environment, 2017, 2, 350.	0.2	0

#	ARTICLE	IF	CITATIONS
2700	Using <i>Ipomoea aquatic</i> as an environmental-friendly alternative to <i>Elodea nuttallii</i> for the aquaculture of Chinese mitten crab. PeerJ, 2019, 7, e6785.	0.9	6
2702	Composition and dynamics of the bacterial communities present in the post-slaughter environment of farmed Atlantic salmon (Salmo salarL.) and correlations to gelatin degrading activity. PeerJ, 2019, 7, e7040.	0.9	1
2706	Succession of bacteria and fungi in leaf litter of tree hole habitats: responses of diversity to mosquito larvae. Aquatic Microbial Ecology, 2019, 83, 237-250.	0.9	0
2710	Xenobioticsâ€™ impact on black sea prokaryotic communitiesâ€™ qualitative composition. Biological Systems Theory and Innovation, 2020, 11, 50-59.	0.1	0
2714	Differential nasopharyngeal microbiota composition in children according to respiratory health status. Microbial Genomics, 2021, 7, .	1.0	9
2715	Ecosystem functioning is linked to microbial evenness and community composition along depth gradient in a semiarid lake. Ecological Indicators, 2021, 132, 108314.	2.6	10
2716	Biogeochemical Controls on the Potential for Long-Term Contaminant Leaching from Soils Developing on Historic Coal Mine Spoil. Soil Systems, 2021, 5, 3.	1.0	6
2719	Labile carbon feedstocks trigger a priming effect in anaerobic digestion: An insight into microbial mechanisms. Bioresource Technology, 2022, 344, 126243.	4.8	5
2720	Evolutionary and dietary relationships of wild mammals based on the gut microbiome. Gene, 2022, 808, 145999.	1.0	11
2721	A review on recent advancements in bioenergy production using microbial fuel cells. Chemosphere, 2022, 288, 132512.	4.2	59
2722	Influences of phosphorus and potassium deficiencies on the methanotrophic communities in rice rhizosphere. Applied Soil Ecology, 2022, 170, 104265.	2.1	5
2723	Long-term combined application of chemical fertilizers and organic manure shapes the gut microbial diversity and functional community structures of earthworms. Applied Soil Ecology, 2022, 170, 104250.	2.1	10
2724	Long-term management drives divergence in soil microbial biomass, richness, and composition among upper Midwest, USA cropping systems. Agriculture, Ecosystems and Environment, 2022, 325, 107718.	2.5	9
2725	CHARACTERIZATION OF MICROBIAL POPULATIONS OF LAKE VAN BY 16S METAGENOMICS STUDY. EskiÅŸehir Teknik Ãœniversitesi Bilim Ve Teknoloji Dergisi - C YaÅŸam Bilimleri Ve Biyoteknoloji, 0, , .	0.1	1
2730	Legacy Effects of Intercropping and Nitrogen Fertilization on Soil N Cycling, Nitrous Oxide Emissions, and the Soil Microbial Community in Tropical Maize Production. Frontiers in Soil Science, 2021, 1, .	0.8	6
2732	Energy savings with a biochemical oxygen demand (BOD)- and pH-based intermittent aeration control system using a BOD biosensor for swine wastewater treatment. Biochemical Engineering Journal, 2022, 177, 108266.	1.8	14
2734	Rhizospheric bacterial community structure of <i>Triticum</i> and <i>Aegilops</i> revealed by pyrosequencing analysis of the 16S rRNA gene: dominance of the A genome over the B and D genomes. Genes and Genetic Systems, 2020, 95, 249-268.	0.2	4
2735	Potential Risk for Localized Aggressive Periodontitis in African American Preadolescent Children. Pediatric Dentistry (discontinued), 2017, 39, 294-298.	0.4	4

#	Article	IF	Citations
2736	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
2737	Environmental harshness mediates the relationship between aboveground and belowground communities in Antarctica. Soil Biology and Biochemistry, 2022, 164, 108493.	4.2	9
2738	Distinctive roles between rumen epimural and content bacterial communities on beef cattle feed efficiency: A combined analysis. Current Research in Microbial Sciences, 2021, 2, 100085.	1.4	5
2739	Contrasting Community Assembly Forces Drive Microbial Structural and Potential Functional Responses to Precipitation in an Incipient Soil System. Frontiers in Microbiology, 2021, 12, 754698.	1.5	4
2740	Changes to human faecal microbiota after international travel. Travel Medicine and Infectious Disease, 2021, 44, 102199.	1.5	4
2741	Mono-specific algal diets shape microbial networking in the gut of the sea urchin Tripneustes gratilla elatensis. Animal Microbiome, 2021, 3, 79.	1.5	7
2742	A correlational study of Weifuchun and its clinical effect on intestinal flora in precancerous lesions of gastric cancer. Chinese Medicine, 2021, 16, 120.	1.6	13
2743	Responses of Soil Bacterial Diversity to Fertilization are Driven by Local Environmental Context Across China. Engineering, 2022, 12, 164-170.	3.2	12
2744	Microbial regulation of hexokinase 2 links mitochondrial metabolism and cell death in colitis. Cell Metabolism, 2021, 33, 2355-2366.e8.	7.2	40
2745	Impact of Electrolyzed Water on the Microbial Spoilage Profile of Piedmontese Steak Tartare. Microbiology Spectrum, 2021, 9, e0175121.	1.2	4
2746	Ubiquitous flocculation activity and flocculation production basis of the conglutination mud from Ruditapes philippinarum along the coast of China. PLoS ONE, 2021, 16, e0256013.	1.1	0
2747	Alone Yet Not Alone: Frankia Lives Under the Same Roof With Other Bacteria in Actinorhizal Nodules. Frontiers in Microbiology, 2021, 12, 749760.	1.5	10
2748	The gut microbiota of Cystidicola farionis parasitizing the swim bladder of the nosed charr morph Salvelinus malma complex in Lake Kronotskoe (Kamchatka, Russia). Journal of Nematology, 2021, 53, 1-15.	0.4	1
2749	Bacterial Diversity, Organic Acid, and Flavor Analysis of Dacha and Ercha Fermented Grains of Fen Flavor Baijiu. Frontiers in Microbiology, 2021, 12, 769290.	1.5	7
2750	Diallyl Disulfide (DADS) Ameliorates Intestinal Candida albicans Infection by Modulating the Gut microbiota and Metabolites and Providing Intestinal Protection in Mice. Frontiers in Cellular and Infection Microbiology, 2021, 11, 743454.	1.8	10
2751	Comparison and Analysis of Gut Microbiota in Children With IgA Vasculitis With Different Clinical Symptoms. Frontiers in Pediatrics, 2021, 9, 800677.	0.9	5
2752	Eutrophication causes microbial community homogenization via modulating generalist species. Water Research, 2022, 210, 118003.	5.3	46
2753	Maternal pre-pregnancy overweight and neonatal gut bacterial colonization are associated with cognitive development and gut microbiota composition in pre-school-age offspring. Brain, Behavior, and Immunity, 2022, 100, 311-320.	2.0	32

#	Article	IF	Citations
2754	Gut microbiome composition likely affects the growth of razor clam Sinonovacula constricta. Aquaculture, 2022, 550, 737847.	1.7	13
2755	Sulfate-reduction behavior in waste-leachate transition zones of landfill sites. Journal of Hazardous Materials, 2022, 428, 128199.	6.5	14
2756	The Synbiotic Combination of Akkermansia muciniphila and Quercetin Ameliorates Early Obesity and NAFLD through Gut Microbiota Reshaping and Bile Acid Metabolism Modulation. Antioxidants, 2021, 10, 2001.	2.2	47
2757	Bacterial Communities and Prediction of Microbial Metabolic Pathway in Rice Wine Koji From Different Regions in China. Frontiers in Microbiology, 2021, 12, 748779.	1.5	9
2758	Land-use intensification differentially affects bacterial, fungal and protist communities and decreases microbiome network complexity. Environmental Microbiomes, 2022, 17, 1.	2.2	48
2759	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. Food and Function, 2022, 13, 1860-1880.	2.1	11
2760	16S rRNA Gene-Based Metagenomic Analysis of Rhizosphere Soil Bacteria in Arkansas Rice Crop Fields. Agronomy, 2022, 12, 222.	1.3	8
2761	Maize/peanut intercropping improves nutrient uptake of side-row maize and system microbial community diversity. BMC Microbiology, 2022, 22, 14.	1.3	34
2762	The bacterial density of clinical rectal swabs is highly variable, correlates with sequencing contamination, and predicts patient risk of extraintestinal infection. Microbiome, 2022, 10, 2.	4.9	8
2763	Gut microbe-targeted choline trimethylamine lyase inhibition improves obesity via rewiring of host circadian rhythms. ELife, 2022, 11, .	2.8	27
2764	A randomized double-blind cross-over trial to study the effects of resistant starch prebiotic in chronic kidney disease (ReSPECKD). Trials, 2022, 23, 72.	0.7	5
2766	Increased Yield and High Resilience of Microbiota Representatives With Organic Soil Amendments in Smallholder Farms of Uganda. Frontiers in Plant Science, 2021, 12, 815377.	1.7	0
2767	Bacterial distribution on the ocular surface of patients with primary SjÃ¶grenâ€™s syndrome. Scientific Reports, 2022, 12, 1715.	1.6	7
2768	Factors affecting the isolation and diversity of marine sponge-associated bacteria. Applied Microbiology and Biotechnology, 2022, 106, 1729-1744.	1.7	4
2769	Spatio-temporal variation of bacterioplankton community structure in the Pearl River: impacts of artificial fishery habitat and physicochemical factors. Bmc Ecology and Evolution, 2022, 22, 10.	0.7	0
2770	New insights into identifying sediment phosphorus sources in river-lake coupled system: A framework for optimizing microbial community fingerprints. Environmental Research, 2022, 209, 112854.	3.7	7
2771	Cervicovaginal Microbiota Predicts Neisseria gonorrhoeae Clinical Presentation. Frontiers in Microbiology, 2021, 12, 790531.	1.5	4
2772	Dietary Intake Mediates Ethnic Differences in Gut Microbial Composition. Nutrients, 2022, 14, 660.	1.7	17

#	Article	IF	Citations
2773	Inhibition of gut microbial Î²-glucuronidase effectively prevents carcinogen-induced microbial dysbiosis and intestinal tumorigenesis. Pharmacological Research, 2022, 177, 106115.	3.1	10
2774	A Novel and Affordable Bioaugmentation Strategy with Microbial Extracts to Accelerate the Biodegradation of Emerging Contaminants in Different Media. SSRN Electronic Journal, 0, , .	0.4	0
2776	The Phylosymbiosis Pattern Between the Fig Wasps of the Same Genus and Their Associated Microbiota. Frontiers in Microbiology, 2021, 12, 800190.	1.5	1
2777	Amplicon sequencing of <i>Fusarium</i> translation elongation factor 1Î± reveals that soil communities of <i>Fusarium</i> species are resilient to disturbances caused by crop and tillage practices. Phytobiomes Journal, 0, , .	1.4	1
2778	Microbiome Resilience and Health Implications for People in Half-Year Travel. Frontiers in Immunology, 2022, 13, 848994.	2.2	2
2779	Sargasso Sea bacterioplankton community structure and drivers of variance as revealed by DNA metabarcoding analysis. PeerJ, 2022, 10, e12835.	0.9	2
2780	Performance, Rumen Microbial Community and Immune Status of Goat Kids Fed Leucaena leucocephala Post-weaning as Affected by Prenatal and Early Life Nutritional Interventions. Frontiers in Microbiology, 2021, 12, 769438.	1.5	2
2781	Murine Model for Measuring Effects of Humanized-Dosing of Antibiotics on the Gut Microbiome. Frontiers in Microbiology, 2022, 13, 813849.	1.5	1
2782	Community Structure and Functional Annotations of the Skin Microbiome in Healthy and Diseased Catfish, Heteropneustes fossilis. Frontiers in Microbiology, 2022, 13, 856014.	1.5	4
2783	Changes in root microbiome during wheat evolution. BMC Microbiology, 2022, 22, 64.	1.3	12
2784	Limits to the three domains of life: lessons from community assembly along an Antarctic salinity gradient. Extremophiles, 2022, 26, 15.	0.9	7
2785	Effects of Long-Term Enclosed Environment on Human Health Based on the Analysis of Salivary Microbiota and Cytokines. Microbiology Spectrum, 2022, 10, e0025422.	1.2	3
2786	Soil bacterial community responses to cadmium and lead stabilization during ecological restoration of an abandoned mine. Soil Use and Management, 2022, 38, 1459-1469.	2.6	15
2787	Linking photoacclimation responses and microbiome shifts between depth-segregated sibling species of reef corals. Royal Society Open Science, 2022, 9, 211591.	1.1	3
2788	Microbial Co-occurrence Network and Fermentation Information of Natural Woody-Plant Silage Prepared With Grass and Crop By-Product in Southern Africa. Frontiers in Microbiology, 2022, 13, 756209.	1.5	9
2790	Normal Light-Dark and Short-Light Cycles Regulate Intestinal Inflammation, Circulating Short-chain Fatty Acids and Gut Microbiota in Period2 Gene Knockout Mice. Frontiers in Immunology, 2022, 13, 848248.	2.2	14
2792	Microbial phylogenetic relatedness links to distinct successional patterns of bacterial and fungal communities. Environmental Microbiology, 2022, 24, 3985-4000.	1.8	11
2793	Dynamics of the normal gut microbiota: A longitudinal one-year population study in Sweden. Cell Host and Microbe, 2022, 30, 726-739.e3.	5.1	64

#	ARTICLE	IF	CITATIONS
2794	Microbial Community Composition in Explanted Cystic Fibrosis and Control Donor Lungs. Frontiers in Cellular and Infection Microbiology, 2021, 11, 764585.	1.8	1
2795	Comparison of changes in fecal microbiota of calves with and without dam. PeerJ, 2022, 10, e12826.	0.9	2
2796	Abiotic Treatment to Common Bean Plants Results in an Altered Endophytic Seed Microbiome. Microbiology Spectrum, 2022, 10, e0021021.	1.2	12
2797	The human milk microbiome aligns with lactation stage and not birth mode. Scientific Reports, 2022, 12, 5598.	1.6	16
2798	Sediment prokaryotic assembly, methane cycling, and ammonia oxidation potentials in response to increasing antibiotic pollution at shrimp aquafarm. Journal of Hazardous Materials, 2022, 434, 128885.	6.5	7
2799	The Bacterial Microbiota of Edible Insects Acheta domesticus and Gryllus assimilis Revealed by High Content Analysis. Foods, 2022, 11, 1073.	1.9	9
2801	Microbial communities in sandy beaches from the three domains of life differ by microhabitat and intertidal location. Molecular Ecology, 2022, 31, 3210-3227.	2.0	6
2802	Metataxonomic signature of beef burger perishability depends on the meat origin prior grinding. Food Research International, 2022, 156, 111103.	2.9	6
2803	A win-win solution to chromate removal by sulfidated nanoscale zero-valent iron in sludge. Journal of Hazardous Materials, 2022, 432, 128683.	6.5	16
2804	Topographic attributes override impacts of agronomic practices on prokaryotic community structure. Applied Soil Ecology, 2022, 175, 104446.	2.1	2
2805	Microbial habitat specificity largely affects microbial co-occurrence patterns and functional profiles in wetland soils. Geoderma, 2022, 418, 115866.	2.3	20
2806	Evaluation of lactic acid bacterial communities in spontaneously-fermented dairy products from Tajikistan, Kyrgyzstan and Uzbekistan using culture-dependent and culture-independent methods. International Dairy Journal, 2022, 130, 105281.	1.5	7
2807	Gut Microbial Dysbiosis Associated with Type 2 Diabetes Aggravates Acute Ischemic Stroke. MSystems, 2021, 6, e0130421.	1.7	9
2808	Interaction between bacterial diversity and biogenic amines production in a salted mackerel stored at soft frozen (âˆ’7â„ƒâ€“0â„ƒ) storage. Food Science and Nutrition, 2022, 10, 412-421.	1.5	0
2809	Associations of physical activity with gut microbiota in pre-adolescent children. Physical Activity and Nutrition, 2021, 25, 24-37.	0.4	6
2810	Moraxella-dominated pediatric nasopharyngeal microbiota associate with upper respiratory infection and sinusitis. PLoS ONE, 2021, 16, e0261179.	1.1	11
2811	Antimicrobial Late Cornified Envelope Proteins: The Psoriasis Risk Factor Deletion of LCE3B/C Genes Affects Microbiota Composition. Journal of Investigative Dermatology, 2022, 142, 1947-1955.e6.	0.3	5
2812	The Impact of Pre-Slaughter Fasting on the Ruminal Microbial Population of Commercial Angus Steers. Microorganisms, 2021, 9, 2625.	1.6	7

#	ARTICLE	IF	CITATIONS
2813	A novel and affordable bioaugmentation strategy with microbial extracts to accelerate the biodegradation of emerging contaminants in different media. Science of the Total Environment, 2022, 834, 155234.	3.9	5
2814	Altered Gut Microbiota as an Auxiliary Diagnostic Indicator for Patients With Fracture-Related Infection. Frontiers in Microbiology, 2022, 13, 723791.	1.5	2
2815	Early-life gut microbiota and attention deficit hyperactivity disorder in preadolescents. Pediatric Research, 2023, 93, 2051-2060.	1.1	5
2816	Community Assembly and Stability in the Root Microbiota During Early Plant Development. Frontiers in Microbiology, 2022, 13, 826521.	1.5	7
2817	Bacillus cereus (EG-Q3) in the Gut of Ectropis grisescens Contributes to Host Response to Starvation Conditions. Frontiers in Microbiology, 2022, 13, 785415.	1.5	1
2818	Microbial Community Composition and Activity in Saline Soils of Coastal Agroâ€"Ecosystems. Microorganisms, 2022, 10, 835.	1.6	11
2819	Bacteria in (vermi)composted organic wastes mostly survive when applied to an arable soil cultivated with wheat (Triticum sp. L.). Environmental Monitoring and Assessment, 2022, 194, 363.	1.3	2
2820	Application of fast expectation-maximization microbial source tracking to discern fecal contamination in rivers exposed to low fecal inputs. Journal of Microbiology, 2022, , 1.	1.3	3
2821	Ammonia volatilization and Sporosarcina genus abundance in an Oxisol enriched with urea, compost and biochar. Applied Soil Ecology, 2022, 176, 104494.	2.1	5
3208	Gut Microbiome-Induced Ï‰-3 Fatty Acid, 18-HEPE, Elicits Anti-Influenza Virus Pneumonia Effects Through Interferon-Î» Upregulation. SSRN Electronic Journal, 0, , .	0.4	0
3209	Bacterial communities in soils as indicators of the potential of syenite as an agromineral. Pesquisa Agropecuaria Brasileira, 0, 57, .	0.9	1
3210	Biochar accelerates soil organic carbon mineralization via rhizodeposit-activated Actinobacteria. Biology and Fertility of Soils, 2022, 58, 565-577.	2.3	22
3211	Gut Microbiota and Subjective Memory Complaints in Older Women. Journal of Alzheimer's Disease, 2022, , 1-12.	1.2	3
3212	Plant diversity improves resistance of plant biomass and soil microbial communities to drought. Journal of Ecology, 2022, 110, 1656-1672.	1.9	9
3213	Glycyrrhiza uralensis Fisch. Root-associated microbiota: the multifaceted hubs associated with environmental factors, growth status and accumulation of secondary metabolites. Environmental Microbiomes, 2022, 17, 23.	2.2	7
3214	Microbiota Comparison of Amur ide (Leuciscus waleckii) Intestine and Waters at Alkaline Water and Freshwater as the Living Environment. Frontiers in Microbiology, 2022, 13, .	1.5	3
3215	Repeated hydrogen peroxide dosing briefly reduces cyanobacterial blooms and microcystin while increasing fecal bacteria indicators in a eutrophic pond. Journal of Environmental Sciences, 2023, 124, 522-543.	3.2	11
3216	Effects of Different Sources of Calcium in the Diet on Growth Performance, Blood Metabolic Parameters, and Intestinal Bacterial Community and Function of Weaned Piglets. Frontiers in Nutrition, 2022, 9, 885497.	1.6	4

#	ARTICLE	IF	CITATIONS
3217	Multimodal Data Integration Reveals Mode of Delivery and Snack Consumption Outrank Salivary Microbiome in Association With Caries Outcome in Thai Children. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	1.8	6
3218	Interaction effect between NAFLD severity and high carbohydrate diet on gut microbiome alteration and hepatic <i>de novo</i> lipogenesis. Gut Microbes, 2022, 14, .	4.3	18
3219	The Gut Microbiome of Preterm Infants Treated With Aminophylline Is Closely Related to the Occurrence of Feeding Intolerance and the Weight Gain. Frontiers in Nutrition, 2022, 9, .	1.6	3
3220	High-throughput sequencing to evaluate the effects of methamphetamine on the succession of the bacterial community to estimate the postmortem interval. Forensic Sciences Research, 0, , 1-12.	0.9	3
3221	Shared Microbial Taxa Respond Predictably to Cyclic Time-Varying Oxygen Limitation in Two Disparate Soils. Frontiers in Microbiology, 2022, 13, .	1.5	1
3222	Tet2 deficiency drives liver microbiome dysbiosis triggering Tc1 cell autoimmune hepatitis. Cell Host and Microbe, 2022, 30, 1003-1019.e10.	5.1	24
3223	Integrated analysis of changes in soil microbiota and metabolites following long-term fertilization in a subtropical maize-wheat agroecosystem. Pedosphere, 2023, 33, 521-533.	2.1	2
3224	Landscape Composition and Soil Physicalâ€"Chemical Properties Drive the Assemblages of Bacteria and Fungi in Conventional Vegetable Fields. Microorganisms, 2022, 10, 1202.	1.6	14
3225	Effects of Dietary Antimicrobial Growth Promoters on Performance Parameters and Abundance and Diversity of Broiler Chicken Gut Microbiome and Selection of Antibiotic Resistance Genes. Frontiers in Microbiology, 0, 13, .	1.5	10
3226	Physical Process Controlling the Surface Bacterial Community Composition in the Ulleung Basin of East Sea. Frontiers in Marine Science, 0, 9, .	1.2	2
3227	Linkages of Various Calcium Sources on Immune Performance, Diarrhea Rate, Intestinal Barrier, and Post-gut Microbial Structure and Function in Piglets. Frontiers in Nutrition, 0, 9, .	1.6	4
3228	Evaluation of different primers of the 18S rRNA gene to profile amoeba communities in environmental samples. , 2022, 1, 100057.		5
3229	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
3230	Gut microbiota in mucosa and feces of newly diagnosed, treatment-naÃ¯ve adult inflammatory bowel disease and irritable bowel syndrome patients. Gut Microbes, 2022, 14, .	4.3	20
3231	Impact of Intestinal Microbiota on Cognitive Flexibility by a Novel Touch Screen Operant System Task in Mice. Frontiers in Neuroscience, 0, 16, .	1.4	4
3232	Prior exposure to ciprofloxacin disrupts intestinal homeostasis and predisposes ayu (<i>Plecoglossus altivelis</i>) to subsequent <i>Pseudomonas plecoglossicida</i>-induced infection. Zoological Research, 2022, 43, 648-665.	0.9	3
3233	Identification of Nordic Berries with Beneficial Effects on Cognitive Outcomes and Gut Microbiota in High-Fat-Fed Middle-Aged C57BL/6J Mice. Nutrients, 2022, 14, 2734.	1.7	8
3234	Bacterial Community Dynamics in Kumamoto Oyster Crassostrea sikamea Hatchery During Larval Development. Frontiers in Microbiology, 0, 13, .	1.5	4

#	ARTICLE	IF	CITATIONS
3235	A single respiratory tract infection early in life reroutes healthy microbiome development and affects adult metabolism in a preclinical animal model. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	1
3236	Effects of Different Native Plants on Soil Remediation and Microbial Diversity in Jiulong Iron Tailings Area, Jiangxi. Forests, 2022, 13, 1106.	0.9	3
3237	Depth-depended quality comparison of light-flavor fermented grains from two fermentation rounds. Food Research International, 2022, 159, 111587.	2.9	9
3238	The Fate and Distribution of Microalgal Nitrogen When Applied as an Agricultural Soil Fertiliser and Its Effect on Soil Microbial Communities. Phycology, 2022, 2, 297-318.	1.7	4
3239	The Fecal Metabolome Links Diet Composition, Foacidic positive ion conditions, chromatographicallyod Processing, and the Gut Microbiota to Gastrointestinal Health in a Randomized Trial of Adults Consuming a Processed Diet. Journal of Nutrition, 2022, 152, 2343-2357.	1.3	4
3240	Differential richness inference for 16S rRNA marker gene surveys. Genome Biology, 2022, 23, .	3.8	5
3241	Involvement of toll-like receptor 5 on mouse model of colonic hypersensitivity induced by neonatal maternal separation. World Journal of Gastroenterology, 2022, 28, 3903-3916.	1.4	3
3242	Bacterial Community with Plant Growth-Promoting Potential Associated to Pioneer Plants from an Active Mexican Volcanic Complex. Microorganisms, 2022, 10, 1568.	1.6	6
3243	Does Plant Identity Affect the Dispersal of Resistomes Above and Below Ground?. Environmental Science & Technology, 2022, 56, 14904-14912.	4.6	8
3244	In Situ Genomics and Transcriptomics of SAR202 Subclusters Revealed Subtle Distinct Activities in Deep-Sea Water. Microorganisms, 2022, 10, 1629.	1.6	2
3245	Different feeding strategies can affect growth performance and rumen functions in Gangba sheep as revealed by integrated transcriptome and microbiome analyses. Frontiers in Microbiology, 0, 13, .	1.5	9
3246	<scp>SAR11</scp> clade microdiversity and activity during the early spring blooms off Kerguelen Island, Southern Ocean. Environmental Microbiology Reports, 0, , .	1.0	2
3247	Molecular evidence for stimulation of methane oxidation in Amazonian floodplains by ammonia-oxidizing communities. Frontiers in Microbiology, 0, 13, .	1.5	1
3248	Intraamniotic Administration (Gallus gallus) of Genistein Alters Mineral Transport, Intestinal Morphology, and Gut Microbiota. Nutrients, 2022, 14, 3473.	1.7	8
3249	Succession of the soil bacterial community as resource utilization shifts from plant residues to rhizodeposits. Soil Biology and Biochemistry, 2022, 173, 108785.	4.2	13
3250	Preparation of liquid bacteria fertilizer with phosphate-solubilizing bacteria cultured by food wastewater and the promotion on the soil fertility and plants biomass. Journal of Cleaner Production, 2022, 370, 133328.	4.6	8
3251	nTiO2 alleviates the toxic effects of TCPP on mussels by adjusting respiratory metabolism and gut microbiota. Science of the Total Environment, 2022, 851, 158176.	3.9	7
3252	Microbiome Changes during Regenerative Endodontic Treatment Using Different Methods of Disinfection. Journal of Endodontics, 2022, 48, 1273-1284.	1.4	16

#	ARTICLE	IF	CITATIONS
3253	Chemical and volatile composition, and microbial communities in edible purple flowers (Torenia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7 111973.	2.9	1
3254	Warming Alters Cascading Effects of a Dominant Arthropod Predator on Microbial Community Composition in the Arctic. SSRN Electronic Journal, 0, , .	0.4	0
3255	Associating changes in the bacterial community of rumen and faeces and milk fatty acid profiles in dairy cows fed high-starch or starch and oil-supplemented diets. Journal of Dairy Research, 0, , 1-10.	0.7	0
3256	Frequent antibiotic exposure stabilized the associated bacterial community while altering physiological and biochemical characteristics of the coccolithophore Chrysotila roscoffensis. Algal Research, 2022, 67, 102807.	2.4	3
3257	The effects of epiphytic microbiota and chemical composition of Italian ryegrass harvested at different growth stages on silage fermentation. Journal of the Science of Food and Agriculture, 2023, 103, 1385-1393.	1.7	5
3258	Influence of planting yellowhorn (<i>Xanthoceras sorbifolium</i> Bunge) on the bacterial and fungal diversity of fly ash. PeerJ, 0, 10, e14015.	0.9	0
3259	Growth Promotion of Guava â€œPearâ€•(Psidium guajava cv.) by Sinorhizobium mexicanum in Southern Mexican Agricultural Fields. Sustainability, 2022, 14, 12391.	1.6	1
3260	Alterations in the Gut Microbiota and Metabolomics of Seafarers after a Six-Month Sea Voyage. Microbiology Spectrum, 0, , .	1.2	0
3261	Postmortem submersion interval estimation of cadavers recovered from freshwater based on gut microbial community succession. Frontiers in Microbiology, 0, 13, .	1.5	6
3262	An exploratory to analysis the effects of the dirrerent roles of mathca on lipid metabolism and intestinal flora regulation between normal and diabetic mice fed a high-fat diet. Food Science and Technology, 0, 42, .	0.8	0
3263	Land-use change alters the bacterial community structure, but not forest management. Folia Microbiologica, 2023, 68, 277-290.	1.1	2
3264	Association between Gut Microbiota and Emotional-Behavioral Symptoms in Children with Attention-Deficit/Hyperactivity Disorder. Journal of Personalized Medicine, 2022, 12, 1634.	1.1	3
3266	Taxonomic dependency of beta diversity for bacteria, archaea, and fungi in a semi-arid lake. Frontiers in Microbiology, 0, 13, .	1.5	3
3267	Rationale and study protocol for a randomized controlled feeding study to determine the structural- and functional-level effects of diet-specific interventions on the gut microbiota of non-Hispanic black and white adults. Contemporary Clinical Trials, 2022, 123, 106968.	0.8	0
3268	Contrasting diversity patterns and community assembly mechanisms of bacterioplankton among different aquatic habitats in Lake Taihu, a large eutrophic shallow lake in China. Environmental Pollution, 2022, 315, 120342.	3.7	4
3269	Oral vaccination with feed-based live attenuated vaccine protects large yellow croaker against Pseudomonas plecoglossicida infection. Aquaculture, 2023, 563, 738932.	1.7	1
3270	Association of intestinal microbiota markers and dietary pattern in Chinese patients with type 2 diabetes: The Henan rural cohort study. Frontiers in Public Health, 0, 10, .	1.3	2
3271	Composition and factors influencing community structure of lactic acid bacterial in dairy products from Nyingchi Prefecture of Tibet. Journal of Bioscience and Bioengineering, 2023, 135, 44-53.	1.1	2

#	Article	IF	Citations
3272	Dietary L-Arginine or N-Carbamylglutamate Alleviates Colonic Barrier Injury, Oxidative Stress, and Inflammation by Modulation of Intestinal Microbiota in Intrauterine Growth-Retarded Suckling Lambs. Antioxidants, 2022, 11, 2251.	2.2	7
3273	Effects of Intestinal Bacterial Hydrogen Gas Production on Muscle Recovery following Intense Exercise in Adult Men: A Pilot Study. Nutrients, 2022, 14, 4875.	1.7	1
3274	Unraveling the effect of the combination of modified atmosphere packaging and Îµ-polylysine on the physicochemical properties and bacterial community of greater amberjack (Seriola dumerili). Frontiers in Nutrition, 0, 9, .	1.6	0
3275	Tilapia processing byproduct treated with enzymatic hydrolysis and Rhodopseudomonas palustris is feasible for live feed culturing:ÂPathogen inhibition in vitro, live feeds microbiota, and Bidyanus bidyanus larviculture. Aquaculture Reports, 2023, 28, 101439.	0.7	0
3276	Community adaptation to temperature explains abrupt soil bacterial community shift along a geothermal gradient on Iceland. Soil Biology and Biochemistry, 2023, 177, 108914.	4.2	2
3277	<i>Bifidobacterium lactis</i> Probio-M8 ameliorated the symptoms of type 2 diabetes mellitus mice by changing ileum FXR-CYP7A1. Open Medicine (Poland), 2022, 17, 2072-2084.	0.6	0
3278	Polyphenol-Rich Liupao Tea Extract Prevents High-Fat Diet-Induced MAFLD by Modulating the Gut Microbiota. Nutrients, 2022, 14, 4930.	1.7	3
3279	AMF colonization affects allelopathic effects of Zea mays L. root exudates and community structure of rhizosphere bacteria. Frontiers in Plant Science, 0, 13, .	1.7	6
3280	Dynamics of rumen microbiome in sika deer (Cervus nippon yakushimae) from unique subtropical ecosystem in Yakushima Island, Japan. Scientific Reports, 2022, 12, .	1.6	3
3281	The Quality and Bacterial Community Changes in Freshwater Crawfish Stored at 4 Â°C in Vacuum Packaging. Molecules, 2022, 27, 8618.	1.7	6
3282	Dark Matter Enhances Interactions within Both Microbes and Dissolved Organic Matter under Global Change. Environmental Science & Technology, 2023, 57, 761-769.	4.6	4
3283	Microbiota-dependent proteolysis of gluten subverts diet-mediated protection against type 1 diabetes. Cell Host and Microbe, 2023, 31, 213-227.e9.	5.1	3
3284	Glucose addition improves the culture performance of Pacific white shrimp by regulating the assembly of Rhodobacteraceae taxa in gut bacterial community. Aquaculture, 2023, 567, 739254.	1.7	6
3285	Spatio-temporal patterns of Synechococcus oligotypes in Moroccan lagoonal environments. Scientific Reports, 2023, 13, .	1.6	1
3286	New Insights into the Effect of Fipronil on the Soil Bacterial Community. Microorganisms, 2023, 11, 52.	1.6	2
3287	The ground beetle Pseudoophonus rufipes gut microbiome is influenced by the farm management system. Scientific Reports, 2022, 12, .	1.6	3
3288	Elevated temperature and CO2 strongly affect the growth strategies of soil bacteria. Nature Communications, 2023, 14, .	5.8	10
3289	Biogeography and potential ecological functions of prokaryotes in the hydrothermal and non-hydrothermal field sediments of the Indian Ocean Ridges. Frontiers in Marine Science, 0, 9, .	1.2	2

#	Article	IF	Citations
3290	Dynamic changes in fecal microbiota in donkey foals during weaning: From pre-weaning to post-weaning. Frontiers in Microbiology, 0, 14, .	1.5	3
3291	More Robust Co-Occurrence Patterns and Stronger Dispersal Limitations of Bacterial Communities in Wet than Dry Seasons of Riparian Wetlands. MSystems, 2023, 8, .	1.7	9
3292	Short-chain n-alkanes in benthic mats and mosses from the Larsemann Hills, East Antarctica. Organic Geochemistry, 2023, 179, 104587.	0.9	0
3293	Limosilactobacillus reuteri ameliorates preeclampsia in mice via improving gut dysbiosis and endothelial dysfunction. Biomedicine and Pharmacotherapy, 2023, 161, 114429.	2.5	2
3294	Fecal microbiota transplantation affects the recovery of AD-skin lesions and enhances gut microbiota homeostasis. International Immunopharmacology, 2023, 118, 110005.	1.7	5
3295	An in vitro model of the chicken gastrointestinal tract with special emphasis to the cecal microbiota. Poultry Science, 2023, 102, 102654.	1.5	1
3296	Immune priming prior to pathogen exposure sheds light on the relationship between host, microbiome and pathogen in disease. Royal Society Open Science, 2023, 10, .	1.1	2
3297	Dark Fermentation of Arundo donax: Characterization of the Anaerobic Microbial Consortium. Energies, 2023, 16, 1813.	1.6	0
3298	The Pathogen Aeromonas salmonicida achromogenes Induces Fast Immune and Microbiota Modifications in Rainbow Trout. Microorganisms, 2023, 11, 539.	1.6	3
3300	16S rRNA Gene Amplicon Sequencing Data for Pteris vittata Rhizosphere Soils. Microbiology Resource Announcements, 2023, 12, .	0.3	0
3301	Compositional Alteration of Gut Microbiota in Psoriasis Treated with IL-23 and IL-17 Inhibitors. International Journal of Molecular Sciences, 2023, 24, 4568.	1.8	4
3302	Comparison of Fecal Microbiota Communities between Primiparous and Multiparous Cows during Non-Pregnancy and Pregnancy. Animals, 2023, 13, 869.	1.0	3
3303	Habitat severity characteristics structure soil communities at regional and local spatial scales along the Antarctica Peninsula. Antarctic Science, 2023, 35, 103-119.	0.5	2
3304	Polybacterial shift in benthic river biofilms attributed to organic pollution â€“ a prospect of a new biosentinel?. Hydrology Research, 2023, 54, 348-359.	1.1	1
3305	Microbial diversity and metabolic function in duodenum, jejunum and ileum of emu (Dromaius) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	1.6	2
3306	Gut Microbiota Dysbiosis and Increased NLRP3 Levels in Patients with Pregnancy-Induced Hypertension. Current Microbiology, 2023, 80, .	1.0	2
3307	Age Rather Than Supplementation with Oat Î²-Glucan Influences Development of the Intestinal Microbiota and SCFA Concentrations in Suckling Piglets. Animals, 2023, 13, 1349.	1.0	1
3308	Habitats shape root-associated fungal and bacterial communities of Minjiang fir saplings. Journal of Forestry Research, 2023, 34, 1491-1502.	1.7	1

#	ARTICLE	IF	CITATIONS
3309	Photobacterium predominate the microbial communities of muscle of European plaice (Pleuronectes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf storage conditions. International Journal of Food Microbiology, 2023, 397, 110222.	2.1	3
3331	Introduction to QIIME 2. , 2023, , 1-9.		0
3357	Towards Optimal Microbiome to Inhibit Multidrug Resistance. , 2023, , .		0