Chimeric 16S rRNA sequence formation and detection is amplicons

Genome Research 21, 494-504 DOI: 10.1101/gr.112730.110

Citation Report

		REDORT	
#	Article	IF	CITATIONS
1	UCHIME improves sensitivity and speed of chimera detection. Bioinformatics, 2011, 27, 2194-2200.	1.8	13,241
2	2,4,5-Trichlorophenol Degradation Using a Novel TiO ₂ -Coated Biofilm Carrier: Roles of Adsorption, Photocatalysis, and Biodegradation. Environmental Science & Technology, 2011, 45, 8359-8367.	4.6	110
3	Interactions between Perchlorate and Nitrate Reductions in the Biofilm of a Hydrogen-Based Membrane Biofilm Reactor. Environmental Science & Technology, 2011, 45, 10155-10162.	4.6	136
4	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
5	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. Science, 2011, 332, 970-974.	6.0	1,712
6	Barcoded Primers Used in Multiplex Amplicon Pyrosequencing Bias Amplification. Applied and Environmental Microbiology, 2011, 77, 7846-7849.	1.4	514
7	Metagenomic biomarker discovery and explanation. Genome Biology, 2011, 12, R60.	13.9	11,192
8	NLRP6 Inflammasome Regulates Colonic Microbial Ecology and Risk for Colitis. Cell, 2011, 145, 745-757.	13.5	1,716
9	Hydrogen-isotopic variability in fatty acids from Yellowstone National Park hot spring microbial communities. Geochimica Et Cosmochimica Acta, 2011, 75, 4830-4845.	1.6	66
10	Tidying Up International Nucleotide Sequence Databases: Ecological, Geographical and Sequence Quality Annotation of ITS Sequences of Mycorrhizal Fungi. PLoS ONE, 2011, 6, e24940.	1.1	51
11	Application of Two-Part Statistics for Comparison of Sequence Variant Counts. PLoS ONE, 2011, 6, e20296.	1.1	55
12	Pyrosequencing for Mini-Barcoding of Fresh and Old Museum Specimens. PLoS ONE, 2011, 6, e21252.	1.1	66
13	Removing Noise From Pyrosequenced Amplicons. BMC Bioinformatics, 2011, 12, 38.	1.2	1,320
14	Comparative analysis of hydrogen-producing bacterial biofilms and granular sludge formed in continuous cultures of fermentative bacteria. Bioresource Technology, 2011, 102, 10057-10064.	4.8	72
15	Caspase deficiency alters the murine gut microbiome. Cell Death and Disease, 2011, 2, e220-e220.	2.7	61
16	Bayesian community-wide culture-independent microbial source tracking. Nature Methods, 2011, 8, 761-763.	9.0	1,284
17	Enteral Tube Feeding Alters the Oral Indigenous Microbiota in Elderly Adults. Applied and Environmental Microbiology, 2011, 77, 6739-6745.	1.4	37
18	Incorporating 16S Gene Copy Number Information Improves Estimates of Microbial Diversity and Abundance. PLoS Computational Biology, 2012, 8, e1002743.	1.5	400

#	Article	IF	CITATIONS
19	Bioinformatics for the Human Microbiome Project. PLoS Computational Biology, 2012, 8, e1002779.	1.5	73
20	Inferring Correlation Networks from Genomic Survey Data. PLoS Computational Biology, 2012, 8, e1002687.	1.5	1,874
21	PCR Biases Distort Bacterial and Archaeal Community Structure in Pyrosequencing Datasets. PLoS ONE, 2012, 7, e43093.	1.1	366
22	Bayesian estimation of bacterial community composition from 454 sequencing data. Nucleic Acids Research, 2012, 40, 5240-5249.	6.5	27
23	Grinder: a versatile amplicon and shotgun sequence simulator. Nucleic Acids Research, 2012, 40, e94-e94.	6.5	180
24	Biodiversity in Oscypek, a Traditional Polish Cheese, Determined by Culture-Dependent and -Independent Approaches. Applied and Environmental Microbiology, 2012, 78, 1890-1898.	1.4	120
25	Abundance, Distribution, and Activity of Fe(II)-Oxidizing and Fe(III)-Reducing Microorganisms in Hypersaline Sediments of Lake Kasin, Southern Russia. Applied and Environmental Microbiology, 2012, 78, 4386-4399.	1.4	86
26	Diversity patterns and activity of uncultured marine heterotrophic flagellates unveiled with pyrosequencing. ISME Journal, 2012, 6, 1823-1833.	4.4	114
27	DECIPHER, a Search-Based Approach to Chimera Identification for 16S rRNA Sequences. Applied and Environmental Microbiology, 2012, 78, 717-725.	1.4	589
28	The Adult Cystic Fibrosis Airway Microbiota Is Stable over Time and Infection Type, and Highly Resilient to Antibiotic Treatment of Exacerbations. PLoS ONE, 2012, 7, e45001.	1.1	320
29	Distance-Decay Relationships Partially Determine Diversity Patterns of Phyllosphere Bacteria on Tamrix Trees across the Sonoran Desert. Applied and Environmental Microbiology, 2012, 78, 6187-6193.	1.4	92
30	Activated fluid transport regulates bacterial-epithelial interactions and significantly shifts the murine colonic microbiome. Gut Microbes, 2012, 3, 250-260.	4.3	49
31	454 Pyrosequencing reveals bacterial diversity of activated sludge from 14 sewage treatment plants. ISME Journal, 2012, 6, 1137-1147.	4.4	957
32	Low Evolutionary Diversification in a Widespread and Abundant Uncultured Protist (MAST-4). Molecular Biology and Evolution, 2012, 29, 1393-1406.	3.5	42
33	Genomic analysis identifies association of <i>Fusobacterium</i> with colorectal carcinoma. Genome Research, 2012, 22, 292-298.	2.4	1,587
34	Abiotic Factors Shape Microbial Diversity in Sonoran Desert Soils. Applied and Environmental Microbiology, 2012, 78, 7527-7537.	1.4	195
35	Barcoded Primers Used in Multiplex Amplicon Pyrosequencing Bias Amplification. Applied and Environmental Microbiology, 2012, 78, 612-612.	1.4	146
36	Sample richness and genetic diversity as drivers of chimera formation in nSSU metagenetic analyses. Nucleic Acids Research, 2012, 40, e66-e66.	6.5	74

#	Article	IF	CITATIONS
37	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. ISME Journal, 2012, 6, 94-103.	4.4	537
38	Novel High-Rank Phylogenetic Lineages within a Sulfur Spring (Zodletone Spring, Oklahoma), Revealed Using a Combined Pyrosequencing-Sanger Approach. Applied and Environmental Microbiology, 2012, 78, 2677-2688.	1.4	40
39	Recruitment of Members from the Rare Biosphere of Marine Bacterioplankton Communities after an Environmental Disturbance. Applied and Environmental Microbiology, 2012, 78, 1361-1369.	1.4	102
40	Increased rectal microbial richness is associated with the presence of colorectal adenomas in humans. ISME Journal, 2012, 6, 1858-1868.	4.4	195
41	A Crypt-Specific Core Microbiota Resides in the Mouse Colon. MBio, 2012, 3, .	1.8	172
42	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
43	Discrimination of the oral microbiota associated with high hydrogen sulfide and methyl mercaptan production. Scientific Reports, 2012, 2, 215.	1.6	68
44	Pyrosequence Read Length of 16S rRNA Gene Affects Phylogenetic Assignment of Plant-associated Bacteria. Microbes and Environments, 2012, 27, 204-208.	0.7	19
46	Role of the intestinal microbiome in health and disease: from correlation to causation. Nutrition Reviews, 2012, 70, S45-S56.	2.6	333
47	Comparing clustering and pre-processing in taxonomy analysis. Bioinformatics, 2012, 28, 2891-2897.	1.8	76
48	Comparative faecal microbiota of dogs with and without calcium oxalate stones. Journal of Applied Microbiology, 2012, 113, 745-756.	1.4	18
49	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
50	Upper Respiratory Tract Microbial Communities, Acute Otitis Media Pathogens, and Antibiotic Use in Healthy and Sick Children. Applied and Environmental Microbiology, 2012, 78, 6262-6270.	1.4	172
51	Metagenomics: microbial diversity through a scratched lens. Current Opinion in Microbiology, 2012, 15, 605-612.	2.3	106
52	Familial transmission rather than defective innate immunity shapes the distinct intestinal microbiota of TLR-deficient mice. Journal of Experimental Medicine, 2012, 209, 1445-1456.	4.2	295
53	Genomic approaches to studying the human microbiota. Nature, 2012, 489, 250-256.	13.7	429
54	Microbiome dynamics of human epidermis following skin barrier disruption. Genome Biology, 2012, 13, R101.	13.9	201
55	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. Genome Biology, 2012, 13, R79.	13.9	2,258

#	ARTICLE	IF	CITATIONS
56	Evaluation of the environmental specificity of Fluorescence In Situ Hybridization (FISH) using Fluorescence-Activated Cell Sorting (FACS) of probe (PSE1284)-positive cells extracted from rhizosphere soil. Systematic and Applied Microbiology, 2012, 35, 533-540.	1.2	10
57	Next-generation Sequencing Approaches to Understanding the Oral Microbiome. Advances in Dental Research, 2012, 24, 81-85.	3.6	62
58	Evidence for a bacterial mechanism for group-specific social odors among hyenas. Scientific Reports, 2012, 2, 615.	1.6	107
59	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
60	Transcriptome-wide discovery of circular RNAs in Archaea. Nucleic Acids Research, 2012, 40, 3131-3142.	6.5	482
61	Profiling bulking and foaming bacteria in activated sludge by high throughput sequencing. Water Research, 2012, 46, 2772-2782.	5.3	172
62	Lung-enriched Organisms and Aberrant Bacterial and Fungal Respiratory Microbiota after Lung Transplant. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 536-545.	2.5	275
63	Prevention of Virus-Induced Type 1 Diabetes with Antibiotic Therapy. Journal of Immunology, 2012, 189, 3805-3814.	0.4	97
64	Reference databases for taxonomic assignment in metagenomics. Briefings in Bioinformatics, 2012, 13, 682-695.	3.2	82
65	Archaea of the Miscellaneous Crenarchaeotal Group are abundant, diverse and widespread in marine sediments. ISME Journal, 2012, 6, 1949-1965.	4.4	281
66	Improved detection of microbial risk of releasing genetically modified bacteria in soil by using massive sequencing and antibiotic resistance selection. Journal of Hazardous Materials, 2012, 227-228, 172-178.	6.5	11
67	Detection of diverse aquatic microbes in blood and organs of drowning victims: First metagenomic approach using high-throughput 454-pyrosequencing. Forensic Science International, 2012, 220, 135-146.	1.3	52
68	Sequencing our way towards understanding global eukaryotic biodiversity. Trends in Ecology and Evolution, 2012, 27, 233-243.	4.2	395
69	Periodontal disease and the oral microbiota in newâ€onset rheumatoid arthritis. Arthritis and Rheumatism, 2012, 64, 3083-3094.	6.7	399
70	Integrated next-generation sequencing of 16S rDNA and metaproteomics differentiate the healthy urine microbiome from asymptomatic bacteriuria in neuropathic bladder associated with spinal cord injury. Journal of Translational Medicine, 2012, 10, 174.	1.8	388
71	Dryland biological soil crust cyanobacteria show unexpected decreases in abundance under longâ€ŧerm elevated <scp>CO₂</scp> . Environmental Microbiology, 2012, 14, 3247-3258.	1.8	61
72	Millimeter-scale patterns of phylogenetic and trait diversity in a salt marsh microbial mat. Frontiers in Microbiology, 2012, 3, 293.	1.5	52
73	Metagenomic investigation of microbes and viruses in patients with jaw osteonecrosis associated with bisphosphonate therapy. Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology, 2012, 114, 764-770.	0.2	29

#	ARTICLE	IF	CITATIONS
74	Environmental microbiology through the lens of high-throughput DNA sequencing: Synopsis of current platforms and bioinformatics approaches. Journal of Microbiological Methods, 2012, 91, 106-113.	0.7	115
75	Reconstruction of Ribosomal RNA Genes from Metagenomic Data. PLoS ONE, 2012, 7, e39948.	1.1	59
76	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
77	Metaproteome Analysis and Molecular Genetics of Rat Intestinal Microbiota Reveals Section and Localization Resolved Species Distribution and Enzymatic Functionalities. Journal of Proteome Research, 2012, 11, 5406-5417.	1.8	63
78	The Genboree Microbiome Toolset and the analysis of 16S rRNA microbial sequences. BMC Bioinformatics, 2012, 13, S11.	1.2	44
79	Inflammatory Bowel Diseases Phenotype, C. difficile and NOD2 Genotype Are Associated with Shifts in Human Ileum Associated Microbial Composition. PLoS ONE, 2012, 7, e26284.	1.1	207
80	Host Genes Related to Paneth Cells and Xenobiotic Metabolism Are Associated with Shifts in Human Ileum-Associated Microbial Composition. PLoS ONE, 2012, 7, e30044.	1.1	28
81	Deep Sequencing Analyses of Low Density Microbial Communities: Working at the Boundary of Accurate Microbiota Detection. PLoS ONE, 2012, 7, e32942.	1.1	160
82	Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. PLoS ONE, 2012, 7, e36427.	1.1	48
83	Determining the Repertoire of Immunodominant Proteins via Whole-Genome Amplification of Intracellular Pathogens. PLoS ONE, 2012, 7, e36456.	1.1	12
84	Bacterial Communities in the Sediments of Dianchi Lake, a Partitioned Eutrophic Waterbody in China. PLoS ONE, 2012, 7, e37796.	1.1	131
85	Fungal Diversity Associated with Hawaiian Drosophila Host Plants. PLoS ONE, 2012, 7, e40550.	1.1	22
86	Novel Device to Sample the Esophageal Microbiome—The Esophageal String Test. PLoS ONE, 2012, 7, e42938.	1.1	85
87	Characterization of the Active Microbiotas Associated with Honey Bees Reveals Healthier and Broader Communities when Colonies are Genetically Diverse. PLoS ONE, 2012, 7, e32962.	1.1	143
88	Non-Invasive Mapping of the Gastrointestinal Microbiota Identifies Children with Inflammatory Bowel Disease. PLoS ONE, 2012, 7, e39242.	1.1	252
89	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. PLoS ONE, 2012, 7, e47656.	1.1	208
90	Next Generation Sequencing to Define Prokaryotic and Fungal Diversity in the Bovine Rumen. PLoS ONE, 2012, 7, e48289.	1.1	234
91	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

#	Article	IF	CITATIONS
92	Characterization of Metabolically Active Bacterial Populations in Subseafloor Nankai Trough Sediments above, within, and below the Sulfate–Methane Transition Zone. Frontiers in Microbiology, 2012, 3, 113.	1.5	39
93	Detection of autotrophic verrucomicrobial methanotrophs in a geothermal environment using stable isotope probing. Frontiers in Microbiology, 2012, 3, 303.	1.5	55
94	Bacterial Biofilm Diversity in Contact Lens-Related Disease: Emerging Role of <i>Achromobacter</i> , <i>Stenotrophomonas</i> , and <i>Delftia</i> , 2012, 53, 3896.		100
95	Microbiological water quality monitoring in a resource-limited urban area: a study in Cameroon, Africa. Journal of Public Health in Africa, 2012, 3, 19.	0.2	4
96	CHANGES IN THE HUMAN SKIN MICROBIOME OVER ONE YEAR'S TIME. Current Research in Microbiology, 2012, 3, 18-30.	0.2	1
97	Spatial and temporal dynamics of the microbial community in the Hanford unconfined aquifer. ISME Journal, 2012, 6, 1665-1676.	4.4	109
98	Patterns in the distribution of soil bacterial 16S rRNA gene sequences from different regions of Antarctica. Geoderma, 2012, 181-182, 45-55.	2.3	50
99	Third-generation sequencing techniques and applications to drug discovery. Expert Opinion on Drug Discovery, 2012, 7, 231-243.	2.5	54
100	Human Microbiome and HIV/AIDS. Current HIV/AIDS Reports, 2012, 9, 44-51.	1.1	64
101	Quality-Score Refinement of SSU rRNA Gene Pyrosequencing Differs Across Gene Region for Environmental Samples. Microbial Ecology, 2012, 64, 499-508.	1.4	19
102	Biogeography of pelagic bacterioplankton across an antagonistic temperature–salinity gradient in the Red Sea. Molecular Ecology, 2012, 21, 388-405.	2.0	98
103	The genetic ghost of an invasion past: colonization and extinction revealed by historical hybridization in <i>Senecio</i> . Molecular Ecology, 2012, 21, 369-387.	2.0	34
104	Experimental and analytical tools for studying the human microbiome. Nature Reviews Genetics, 2012, 13, 47-58.	7.7	601
105	Comparison of microbial communities in marinated and unmarinated broiler meat by metagenomics. International Journal of Food Microbiology, 2012, 157, 142-149.	2.1	101
106	A fast, highly sensitive doubleâ€nested PCRâ€based method to screen fish immunobiomes. Molecular Ecology Resources, 2012, 12, 1027-1039.	2.2	11
107	Phylogenetic clustering increases with elevation for microbes. Environmental Microbiology Reports, 2012, 4, 217-226.	1.0	144
108	Molecular methods for pathogen and microbial community detection and characterization: Current and potential application in diagnostic microbiology. Infection, Genetics and Evolution, 2012, 12, 505-521.	1.0	123
109	Two decades of describing the unseen majority of aquatic microbial diversity. Molecular Ecology, 2012, 21, 1878-1896.	2.0	180

#	Article	IF	CITATIONS
110	Bioinformatic challenges for DNA metabarcoding of plants and animals. Molecular Ecology, 2012, 21, 1834-1847.	2.0	243
111	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
112	Cyanobacterial construction of hot spring siliceous stromatolites in Yellowstone National Park. Environmental Microbiology, 2012, 14, 1182-1197.	1.8	75
113	Analysis of 454 sequencing error rate, error sources, and artifact recombination for detection of Low-frequency drug resistance mutations in HIV-1 DNA. Retrovirology, 2013, 10, 18.	0.9	89
114	Inflammation-associated enterotypes, host genotype, cage and inter-individual effects drive gut microbiota variation in common laboratory mice. Genome Biology, 2013, 14, R4.	13.9	381
115	Biogeography of the ecosystems of the healthy human body. Genome Biology, 2013, 14, R1.	13.9	540
116	Diversified pattern of the human colorectal cancer microbiome. Gut Pathogens, 2013, 5, 2.	1.6	121
117	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
118	Fluorescent epibiotic microbial community on the carapace of a Bahamian ostracod. Archives of Microbiology, 2013, 195, 595-604.	1.0	3
119	Microbial Community Assembly and Succession on Lake Sturgeon Egg Surfaces as a Function of Simulated Spawning Stream Flow Rate. Microbial Ecology, 2013, 66, 500-511.	1.4	29
120	Microbial Communities Involved in Biological Ammonium Removal from Coal Combustion Wastewaters. Microbial Ecology, 2013, 66, 49-59.	1.4	17
121	Deep Sequencing of Myxilla (Ectyomyxilla) methanophila, an Epibiotic Sponge on Cold-Seep Tubeworms, Reveals Methylotrophic, Thiotrophic, and Putative Hydrocarbon-Degrading Microbial Associations. Microbial Ecology, 2013, 65, 450-461.	1.4	25
122	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
123	Pyrosequencing analysis of the human microbiota of healthy Chinese undergraduates. BMC Genomics, 2013, 14, 390.	1.2	105
124	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	9.4	8,049
125	Validation of the PLEX-IDTM mass spectrometry mitochondrial DNA assay. International Journal of Legal Medicine, 2013, 127, 277-286.	1.2	8
126	Anaerobic Metabolism in Tidal Freshwater Wetlands: II. Effects of Plant Removal on Archaeal Microbial Communities. Estuaries and Coasts, 2013, 36, 471-481.	1.0	8
127	UPARSE: highly accurate OTU sequences from microbial amplicon reads. Nature Methods, 2013, 10, 996-998.	9.0	13,193

#	Article	IF	Citations
128	Bacterial communities in different sections of a municipal wastewater treatment plant revealed by 16S rDNA 454 pyrosequencing. Applied Microbiology and Biotechnology, 2013, 97, 2681-2690.	1.7	253
129	Isolation of facultatively anaerobic soil bacteria from Ny-Ãlesund, Svalbard. Polar Biology, 2013, 36, 787-796.	0.5	14
130	Reductions in intestinal Clostridiales precede the development of nosocomial Clostridium difficile infection. Microbiome, 2013, 1, 18.	4.9	107
131	Investigation of coal-associated bacterial and archaeal populations from a diffusive microbial sampler (DMS). International Journal of Coal Geology, 2013, 115, 64-70.	1.9	70
132	Development of a Dual-Index Sequencing Strategy and Curation Pipeline for Analyzing Amplicon Sequence Data on the MiSeq Illumina Sequencing Platform. Applied and Environmental Microbiology, 2013, 79, 5112-5120.	1.4	5,923
133	Microbial Community Dynamics during Acetate Biostimulation of RDX-Contaminated Groundwater. Environmental Science & Technology, 2013, 47, 7672-7678.	4.6	32
134	SIV-Induced Instability of the Chimpanzee Gut Microbiome. Cell Host and Microbe, 2013, 14, 340-345.	5.1	75
135	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. Letters in Applied Microbiology, 2013, 57, 492-501.	1.0	90
136	Slowing PCR ramp speed reduces chimera formation from environmental samples. Journal of Microbiological Methods, 2013, 93, 203-205.	0.7	68
137	Temporal Bacterial Community Dynamics Vary Among Ulcerative Colitis Patients After Fecal Microbiota Transplantation. American Journal of Gastroenterology, 2013, 108, 1620-1630.	0.2	298
138	A Dried Yeast Fermentate Selectively Modulates both the Luminal and Mucosal Gut Microbiota and Protects against Inflammation, As Studied in an Integrated in Vitro Approach. Journal of Agricultural and Food Chemistry, 2013, 61, 9380-9392.	2.4	49
139	Ahead of the curve: next generation estimators of drug resistance in malaria infections. Trends in Parasitology, 2013, 29, 321-328.	1.5	21
140	Power production from different types of sewage sludge using microbial fuel cells:ÂA comparative study with energetic and microbiological perspectives. Journal of Power Sources, 2013, 235, 280-288.	4.0	54
141	Effects of Different Complementary Feeding Regimens on Iron Status and Enteric Microbiota in Breastfed Infants. Journal of Pediatrics, 2013, 163, 416-423.e4.	0.9	109
142	Human Gut Microbiome and Risk for Colorectal Cancer. Journal of the National Cancer Institute, 2013, 105, 1907-1911.	3.0	807
143	Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing. Bioinformatics, 2013, 29, 2096-2102.	1.8	39
144	Environmental bio-monitoring with high-throughput sequencing. Briefings in Bioinformatics, 2013, 14, 575-588.	3.2	26
145	Culture-Independent Analysis of Aerosol Microbiology in a Metropolitan Subway System. Applied and Environmental Microbiology, 2013, 79, 3485-3493.	1.4	109

#	Article	IF	CITATIONS
146	Comparison of microbial diversity determined with the same variable tag sequence extracted from two different PCR amplicons. BMC Microbiology, 2013, 13, 208.	1.3	55
147	Diversity of picoeukaryotes at an oligotrophic site off the Northeastern Red Sea Coast. Aquatic Biosystems, 2013, 9, 16.	1.8	29
148	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. BMC Genomics, 2013, 14, 530.	1.2	111
149	The murine lung microbiome in relation to the intestinal and vaginal bacterial communities. BMC Microbiology, 2013, 13, 303.	1.3	100
150	Community differentiation of the cutaneous microbiota in psoriasis. Microbiome, 2013, 1, 31.	4.9	353
151	Optimal operational conditions for biohydrogen production from sugar refinery wastewater in an ASBR. International Journal of Hydrogen Energy, 2013, 38, 13895-13906.	3.8	36
152	High throughput sequencing methods and analysis for microbiome research. Journal of Microbiological Methods, 2013, 95, 401-414.	0.7	210
153	Future-Generation Sequencing and Clinical Microbiology. Clinics in Laboratory Medicine, 2013, 33, 685-704.	0.7	3
154	Effect of probiotic bacteria on the intestinal microbiota in irritable bowel syndrome. Journal of Gastroenterology and Hepatology (Australia), 2013, 28, 1624-1631.	1.4	79
155	A meta-analysis of changes in bacterial and archaeal communities with time. ISME Journal, 2013, 7, 1493-1506.	4.4	322
156	Assembling Full-Length rRNA Genes from Short-Read Metagenomic Sequence Datasets Using EMIRGE. Methods in Enzymology, 2013, 531, 333-352.	0.4	9
157	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	0.4	553
158	Higher seasonal variation of actinobacterial communities than spatial heterogeneity in the surface sediments of Taihu Lake, China. Canadian Journal of Microbiology, 2013, 59, 353-358.	0.8	3
159	Sex Differences in the Gut Microbiome Drive Hormone-Dependent Regulation of Autoimmunity. Science, 2013, 339, 1084-1088.	6.0	1,565
160	Comparative metagenomic and <scp>rRNA</scp> microbial diversity characterization using archaeal and bacterial synthetic communities. Environmental Microbiology, 2013, 15, 1882-1899.	1.8	202
161	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
162	Correlating microbial community structure and composition with aeration intensity in submerged membrane bioreactors by 454 high-throughput pyrosequencing. Water Research, 2013, 47, 859-869.	5.3	218
163	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

#	Article	IF	CITATIONS
164	Biogeography of bacterial communities exposed to progressive long-term environmental change. ISME Journal, 2013, 7, 937-948.	4.4	330
165	Lineage-Specific Responses of Microbial Communities to Environmental Change. Applied and Environmental Microbiology, 2013, 79, 39-47.	1.4	20
166	Bacteria and diatom coâ€occurrence patterns in microbial mats from polar desert streams. Environmental Microbiology, 2013, 15, 1115-1131.	1.8	44
167	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
168	The Neuropathic Diabetic Foot Ulcer Microbiome Is Associated With Clinical Factors. Diabetes, 2013, 62, 923-930.	0.3	249
169	Effects of OTU Clustering and PCR Artifacts on Microbial Diversity Estimates. Microbial Ecology, 2013, 65, 709-719.	1.4	47
170	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
171	The effect of coal oxidation on methane production and microbial community structure in Powder River Basin coal. International Journal of Coal Geology, 2013, 115, 71-78.	1.9	55
172	The effect of coal bed dewatering and partial oxidation on biogenic methane potential. International Journal of Coal Geology, 2013, 115, 54-63.	1.9	47
173	Biowaste: A Lactobacillus habitat and lactic acid fermentation substrate. Bioresource Technology, 2013, 143, 647-652.	4.8	29
174	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
175	Microbial communities in an anaerobic dynamic membrane bioreactor (AnDMBR) for municipal wastewater treatment: Comparison of bulk sludge and cake layer. Process Biochemistry, 2013, 48, 510-516.	1.8	90
176	Bacterial census of poultry intestinal microbiome. Poultry Science, 2013, 92, 671-683.	1.5	375
177	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
178	Propionibacterium acnes Strain Populations in the Human Skin Microbiome Associated with Acne. Journal of Investigative Dermatology, 2013, 133, 2152-2160.	0.3	557
179	Estimation of metagenome size and structure in an experimental soil microbiota from low coverage next-generation sequence data. Journal of Applied Microbiology, 2013, 114, 141-151.	1.4	23
180	Exploring the bovine rumen bacterial community from birth to adulthood. ISME Journal, 2013, 7, 1069-1079.	4.4	799
181	Experimentally induced habitat filtering in marine bacterial communities. Marine Ecology - Progress Series, 2013, 477, 77-86.	0.9	18

ARTICLE IF CITATIONS # Evaluation of DNA extraction methods of rumen microbial populations. World Journal of 182 1.7 11 Microbiology and Biotechnology, 2013, 29, 301-307. Testing three pipelines for 18S rDNA-based metabarcoding of soil faunal diversity. Science China Life 2.3 24 Sciences, 2013, 56, 73-81. Phylogenetic analysis of nitrate- and sulfate-reducing bacteria in a hydrogen-fed biofilm. FEMS 184 1.3 43 Microbiology Ecology, 2013, 85, 158-167. Microbial communities in the subglacial waters of the Vatnajökull ice cap, Iceland. ISME Journal, 2013, 4.4 7, 427-437. Diversity of human small intestinal <i>Streptococcus </i>and <i>Veillonella </i>populations. FEMS 186 1.3 121 Microbiology Ecology, 2013, 85, 376-388. Screening and Expression of Genes from Metagenomes. Advances in Applied Microbiology, 2013, 83, 1-68. 1.3 Relative impacts of tillage, residue management and crop-rotation on soil bacterial communities in a 188 4.2 251 semi-arid agroecosystem. Soil Biology and Biochemistry, 2013, 65, 86-95. Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. ISME Journal, 2013, 7, 4.4 198 50-60. Quantitatively Different, yet Qualitatively Alike: A Meta-Analysis of the Mouse Core Gut Microbiome 190 1.1 182 with a View towards the Human Gut Microbiome. PLoS ONE, 2013, 8, e62578. Bacterial colonization of <i>Hydra</i>hatchlings follows a robust temporal pattern. ISME Journal, 4.4 2013, 7, 781-790. Association of gut microbiota with post-operative clinical course in Crohn's disease. BMC 192 0.8 95 Gastroenterology, 2013, 13, 131. Bacterial diversity of the rock-water interface in an East Antarctic freshwater ecosystem, Lake 1.8 Tawani(P)â€. Aquatic Biosystems, 2013, 9, 4. Robustness of Gut Microbiota of Healthy Adults in Response to Probiotic Intervention Revealed by 194 1.5 272 High-Throughput Pyrosequencing. DNA Research, 2013, 20, 241-253. Fungal community analysis by highâ€throughput sequencing of amplified markers – a user's guide. New Phytologist, 2013, 199, 288-299. 3.5 747 Micrometer-scale physical structure and microbial composition of soil macroaggregates. Soil Biology 196 4.2 54 and Biochemistry, 2013, 65, 60-68. Suppression of methanogenesis in cellulose-fed microbial fuel cells in relation to performance, 4.8 metabolite formation, and microbial population. Bioresource Technology, 2013, 129, 281-288. Symbiotic prokaryotic communities from different populations of the giant barrel sponge, 198 1.2 45 <i>Xestospongia muta</i>. MicrobiologyOpen, 2013, 2, 938-952. Outgrowth of the Bacterial Airway Microbiome after Rhinovirus Exacerbation of Chronic 199 Obstructive Pulmonary Disease. Ámerican Journal of Respiratory and Critical Care Medicine, 2013, 188, 329 1224-1231.

c		Repo	D.T.
		17 F D()	121
\sim			IX I

#	Article	IF	CITATIONS
200	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
201	More effective cell-based therapy through biofilm suppression. Journal of Wound Care, 2013, 22, 26-31.	0.5	12
202	Standard methods for research on <i>Apis mellifera</i> gut symbionts. Journal of Apicultural Research, 2013, 52, 1-24.	0.7	98
203	Microbiome in Human Health and Disease. Science Progress, 2013, 96, 153-170.	1.0	18
204	Fine Analysis of Genetic Diversity of the tpr Gene Family among Treponemal Species, Subspecies and Strains. PLoS Neglected Tropical Diseases, 2013, 7, e2222.	1.3	84
205	Dominant Fecal Microbiota in Newly Diagnosed Untreated Inflammatory Bowel Disease Patients. Gastroenterology Research and Practice, 2013, 2013, 1-13.	0.7	46
206	The individual-specific and diverse nature of the preterm infant microbiota. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2013, 98, F334-F340.	1.4	105
207	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
208	Abiotic and Microbiotic Factors Controlling Biofilm Formation by Thermophilic Sporeformers. Applied and Environmental Microbiology, 2013, 79, 5652-5660.	1.4	43
209	An rpoD gene sequence based evaluation of cultured Pseudomonas diversity on different growth media. Microbiology (United Kingdom), 2013, 159, 2097-2108.	0.7	24
210	Quantitation and Composition of Cutaneous Microbiota in Diabetic and Nondiabetic Men. Journal of Infectious Diseases, 2013, 207, 1105-1114.	1.9	90
211	Improved Inference of Taxonomic Richness from Environmental DNA. PLoS ONE, 2013, 8, e71974.	1.1	33
212	Intestinal Microbiota Containing Barnesiella Species Cures Vancomycin-Resistant Enterococcus faecium Colonization. Infection and Immunity, 2013, 81, 965-973.	1.0	391
213	Analytical Tools and Databases for Metagenomics in the Next-Generation Sequencing Era. Genomics and Informatics, 2013, 11, 102.	0.4	117
214	Rapid 16S rRNA Next-Generation Sequencing of Polymicrobial Clinical Samples for Diagnosis of Complex Bacterial Infections. PLoS ONE, 2013, 8, e65226.	1.1	186
215	Biased Diversity Metrics Revealed by Bacterial 16S Pyrotags Derived from Different Primer Sets. PLoS ONE, 2013, 8, e53649.	1.1	167
216	Accuracy of protist diversity assessments: morphology compared with cloning and direct pyrosequencing of 18S rRNA genes and ITS regions using the conspicuous tintinnid ciliates as a case study. ISME Journal, 2013, 7, 244-255.	4.4	159
217	Facility-Specific "House―Microbiome Drives Microbial Landscapes of Artisan Cheesemaking Plants. Applied and Environmental Microbiology, 2013, 79, 5214-5223.	1.4	232

#	Article	IF	CITATIONS
218	Land coverage influences the bacterial community composition in the critical zone of a sub-Arctic basaltic environment. FEMS Microbiology Ecology, 2013, 86, 381-393.	1.3	30
219	Effects of amoxicillin treatment on the salivary microbiota in children with acute otitis media. Clinical Microbiology and Infection, 2013, 19, e335-e342.	2.8	36
220	Benzene and sulfide removal from groundwater treated in a microbial fuel cell. Biotechnology and Bioengineering, 2013, 110, 3104-3113.	1.7	48
221	Microbial Succession and Metabolite Changes during Longâ€Term Storage of Kimchi. Journal of Food Science, 2013, 78, M763-9.	1.5	103
222	Analysis of the bacterial communities associated with two ant–plant symbioses. MicrobiologyOpen, 2013, 2, 276-283.	1.2	35
223	Wastewater Treatment Effluent Reduces the Abundance and Diversity of Benthic Bacterial Communities in Urban and Suburban Rivers. Applied and Environmental Microbiology, 2013, 79, 1897-1905.	1.4	284
224	Distinctive Microbial Community Structure in Highly Stratified Deep-Sea Brine Water Columns. Applied and Environmental Microbiology, 2013, 79, 3425-3437.	1.4	57
225	Distinct antimicrobial peptide expression determines host species-specific bacterial associations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3730-8.	3.3	312
226	Reduced diversity and changed bacterioplankton community composition do not affect utilization of dissolved organic matter in the Adriatic Sea. Aquatic Microbial Ecology, 2013, 71, 15-24.	0.9	13
227	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
228	Targeting the Microbiota to Address Diet-Induced Obesity: A Time Dependent Challenge. PLoS ONE, 2013, 8, e65790.	1.1	132
229	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
230	Stimulatory Effect of Xenobiotics on Oxidative Electron Transport of Chemolithotrophic Nitrifying Bacteria Used as Biosensing Element. PLoS ONE, 2013, 8, e53484.	1.1	5
231	Pyrosequencing Reveals High-Temperature Cellulolytic Microbial Consortia in Great Boiling Spring after In Situ Lignocellulose Enrichment. PLoS ONE, 2013, 8, e59927.	1.1	42
232	Assessing the Consequences of Denoising Marker-Based Metagenomic Data. PLoS ONE, 2013, 8, e60458.	1.1	51
233	Shedding Light on the Microbial Community of the Macropod Foregut Using 454-Amplicon Pyrosequencing. PLoS ONE, 2013, 8, e61463.	1.1	41
234	Impact of Colonoscopy Bowel Preparation on Intestinal Microbiota. PLoS ONE, 2013, 8, e62815.	1.1	85
235	Analyses of the Stability and Core Taxonomic Memberships of the Human Microbiome. PLoS ONE, 2013, 8, e63139.	1.1	184

#	ARTICLE	IF	Citations
236	Association of the Vaginal Microbiota with Human Papillomavirus Infection in a Korean Twin Cohort. PLoS ONE, 2013, 8, e63514.	1.1	254
237	Monitoring Seasonal Changes in Winery-Resident Microbiota. PLoS ONE, 2013, 8, e66437.	1.1	167
238	The Ecology of Microbial Communities Associated with Macrocystis pyrifera. PLoS ONE, 2013, 8, e67480.	1.1	100
239	Comparison of DNA Extraction Methods in Analysis of Salivary Bacterial Communities. PLoS ONE, 2013, 8, e67699.	1.1	76
240	Season, Irrigation, Leaf Age, and Escherichia coli Inoculation Influence the Bacterial Diversity in the Lettuce Phyllosphere. PLoS ONE, 2013, 8, e68642.	1.1	121
241	Prospecting Environmental Mycobacteria: Combined Molecular Approaches Reveal Unprecedented Diversity. PLoS ONE, 2013, 8, e68648.	1.1	34
242	Spaceflight Influences both Mucosal and Peripheral Cytokine Production in PTN-Tg and Wild Type Mice. PLoS ONE, 2013, 8, e68961.	1.1	10
243	Light Structures Phototroph, Bacterial and Fungal Communities at the Soil Surface. PLoS ONE, 2013, 8, e69048.	1.1	24
244	Quality Score Based Identification and Correction of Pyrosequencing Errors. PLoS ONE, 2013, 8, e73015.	1.1	9
245	Development of the Preterm Gut Microbiome in Twins at Risk of Necrotising Enterocolitis and Sepsis. PLoS ONE, 2013, 8, e73465.	1.1	114
246	The Impact of Helicobacter pylori Infection on the Gastric Microbiota of the Rhesus Macaque. PLoS ONE, 2013, 8, e76375.	1.1	46
247	Ultradeep 16S rRNA Sequencing Analysis of Geographically Similar but Diverse Unexplored Marine Samples Reveal Varied Bacterial Community Composition. PLoS ONE, 2013, 8, e76724.	1.1	56
248	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
249	Distinct Phyllosphere Bacterial Communities on Arabidopsis Wax Mutant Leaves. PLoS ONE, 2013, 8, e78613.	1.1	81
250	A Metagenomic Framework for the Study of Airborne Microbial Communities. PLoS ONE, 2013, 8, e81862.	1.1	127
251	Reduced Incidence of Prevotella and Other Fermenters in Intestinal Microflora of Autistic Children. PLoS ONE, 2013, 8, e68322.	1.1	709
252	Metagenomic evidence for sulfur lithotrophy by Epsilonproteobacteria as the major energy source for primary productivity in a sub-aerial arctic glacial deposit, Borup Fiord Pass. Frontiers in Microbiology, 2013, 4, 63.	1.5	42
253	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. Frontiers in Microbiology, 2013, 4, 115.	1.5	53

#	Article	IF	Citations
254	Archaeal and bacterial communities in three alkaline hot springs in Heart Lake Geyser Basin, Yellowstone National Park. Frontiers in Microbiology, 2013, 4, 330.	1.5	64
255	Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis. ELife, 2013, 2, e01202.	2.8	1,507
256	Potential Role of the Bovine Rumen Microbiome in Modulating Milk Composition and Feed Efficiency. PLoS ONE, 2014, 9, e85423.	1.1	417
257	In Vivo Pyro-SIP Assessing Active Gut Microbiota of the Cotton Leafworm, Spodoptera littoralis. PLoS ONE, 2014, 9, e85948.	1.1	86
258	Application of Microarray and Functional-Based Screening Methods for the Detection of Antimicrobial Resistance Genes in the Microbiomes of Healthy Humans. PLoS ONE, 2014, 9, e86428.	1.1	62
259	Toward Understanding the Dynamics of Microbial Communities in an Estuarine System. PLoS ONE, 2014, 9, e94449.	1.1	24
260	Identification of the Microbiota in Carious Dentin Lesions Using 16S rRNA Gene Sequencing. PLoS ONE, 2014, 9, e103712.	1.1	75
261	Microbial Community Structure of Relict Niter-Beds Previously Used for Saltpeter Production. PLoS ONE, 2014, 9, e104752.	1.1	4
262	Application of Ion Torrent Sequencing to the Assessment of the Effect of Alkali Ballast Water Treatment on Microbial Community Diversity. PLoS ONE, 2014, 9, e107534.	1.1	22
263	Specific Microbiome Changes in a Mouse Model of Parenteral Nutrition Associated Liver Injury and Intestinal Inflammation. PLoS ONE, 2014, 9, e110396.	1.1	64
264	Novosphingobium and Its Potential Role in Chronic Obstructive Pulmonary Diseases: Insights from Microbiome Studies. PLoS ONE, 2014, 9, e111150.	1.1	23
265	Deciphering the Prokaryotic Community and Metabolisms in South African Deep-Mine Biofilms through Antibody Microarrays and Graph Theory. PLoS ONE, 2014, 9, e114180.	1.1	23
266	Bacteria and Methanogens Differ along the Gastrointestinal Tract of Chinese Roe Deer (Capreolus) Tj ETQq0 0 0	rgBT /Over 1.1	lock 10 Tf 50
267	Investigation of bacterial diversity in the feces of cattle fed different diets1. Journal of Animal Science, 2014, 92, 683-694.	0.2	134
268	Two distinct microbial communities revealed in the sponge Cinachyrella. Frontiers in Microbiology, 2014, 5, 581.	1.5	42
269	Evaluation of Automated Ribosomal Intergenic Spacer Analysis for Bacterial Fingerprinting of Rumen Microbiome Compared to Pyrosequencing Technology. Pathogens, 2014, 3, 109-120.	1.2	31
270	MEAT SCIENCE AND MUSCLE BIOLOGY SYMPOSIUM:Escherichia coli O157:H7, diet, and fecal microbiome in beef cattle12. Journal of Animal Science, 2014, 92, 1345-1355.	0.2	19
271	T lymphocytes control microbial composition by regulating the abundance of Vibrio in the zebrafish gut. Gut Microbes, 2014, 5, 737-747.	4.3	51

#	Article	IF	CITATIONS
272	Diversity of Rickettsiales in the Microbiome of the Lone Star Tick, Amblyomma americanum. Applied and Environmental Microbiology, 2014, 80, 354-359.	1.4	82
273	Probiotics and virulent human rotavirus modulate the transplanted human gut microbiota in gnotobiotic pigs. Gut Pathogens, 2014, 6, 39.	1.6	49
274	Effects of Farmhouse Hotel and Paper Mill Effluents on Bacterial Community Structures in Sediment and Surface Water of Nanxi River, China. Microbial Ecology, 2014, 68, 773-784.	1.4	7
275	A comparative study of microbial communities in soils amended by manures from pigs fed with organic versus synthetic feeds. Toxicological and Environmental Chemistry, 2014, 96, 426-441.	0.6	1
276	The presence of nitrate dramatically changed the predominant microbial community in perchlorate degrading cultures under saline conditions. BMC Microbiology, 2014, 14, 225.	1.3	23
277	Gut microbiota influences low fermentable substrate diet efficacy in children with irritable bowel syndrome. Gut Microbes, 2014, 5, 165-175.	4.3	121
278	The conjunctival microbiome in health and trachomatous disease: a case control study. Genome Medicine, 2014, 6, 99.	3.6	144
279	A review of software for analyzing molecular sequences. BMC Research Notes, 2014, 7, 830.	0.6	63
280	Dominance of Methanosarcinales Phylotypes and Depth-Wise Distribution of Methanogenic Community in Fresh Water Sediments of Sitka Stream from Czech Republic. Current Microbiology, 2014, 69, 809-816.	1.0	12
281	LotuS: an efficient and user-friendly OTU processing pipeline. Microbiome, 2014, 2, 30.	4.9	233
282	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
283	Microbial cargo: do bacteria on symbiotic propagules reinforce the microbiome of lichens?. Environmental Microbiology, 2014, 16, 3743-3752.	1.8	78
284	Removal of Pharmaceuticals and Personal Care Products during Water Recycling: Microbial Community Structure and Effects of Substrate Concentration. Applied and Environmental Microbiology, 2014, 80, 2440-2450.	1.4	37
285	Intestinal Dysbiosis Associated with Systemic Lupus Erythematosus. MBio, 2014, 5, e01548-14.	1.8	500
286	Fermented Dairy Products Modulate Citrobacter rodentium–Induced Colonic Hyperplasia. Journal of Infectious Diseases, 2014, 210, 1029-1041.	1.9	31
287	Scabies Mites Alter the Skin Microbiome and Promote Growth of Opportunistic Pathogens in a Porcine Model. PLoS Neglected Tropical Diseases, 2014, 8, e2897.	1.3	67
288	Applications of Next-Generation Sequencing Technologies to the Study of the Human Microbiome. Comprehensive Analytical Chemistry, 2014, , 75-106.	0.7	0
289	A Comprehensive Insight into Tetracycline Resistant Bacteria and Antibiotic Resistance Genes in Activated Sludge Using Next-Generation Sequencing. International Journal of Molecular Sciences, 2014, 15, 10083-10100.	1.8	60

#	Article	IF	CITATIONS
290	Assessing the Accuracy of Quantitative Molecular Microbial Profiling. International Journal of Molecular Sciences, 2014, 15, 21476-21491.	1.8	17
291	A Compositional Look at the Human Gastrointestinal Microbiome and Immune Activation Parameters in HIV Infected Subjects. PLoS Pathogens, 2014, 10, e1003829.	2.1	343
292	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
293	The adult nasopharyngeal microbiome as a determinant of pneumococcal acquisition. Microbiome, 2014, 2, 44.	4.9	82
294	Development and Accuracy of Quantitative Real-Time Polymerase Chain Reaction Assays for Detection and Quantification of Enterotoxigenic Escherichia coli (ETEC) Heat Labile and Heat Stable Toxin Genes in Travelers' Diarrhea Samples. American Journal of Tropical Medicine and Hygiene, 2014, 90, 124-132.	0.6	22
295	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
296	Deodorization of pig slurry and characterization of bacterial diversity using 16S rDNA sequence analysis. Journal of Microbiology, 2014, 52, 918-929.	1.3	8
297	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. ISME Journal, 2014, 8, 1153-1165.	4.4	139
298	Distribution and diversity of <i>Prochlorococcus</i> ecotypes in the Red Sea. FEMS Microbiology Letters, 2014, 356, 118-126.	0.7	29
299	Spatial distribution of microbial communities associated with dune landform in the Gurbantunggut Desert, China. Journal of Microbiology, 2014, 52, 898-907.	1.3	16
300	The skin microbiome of caspaseâ€14â€deficient mice shows mild dysbiosis. Experimental Dermatology, 2014, 23, 561-567.	1.4	15
301	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
302	StreamingTrim 1.0: a Java software for dynamic trimming of 16S <scp>rRNA</scp> sequence data from metagenetic studies. Molecular Ecology Resources, 2014, 14, 426-434.	2.2	44
303	Changes in the Bacterial Community Structure in Stored Wormbed Leachate. Journal of Molecular Microbiology and Biotechnology, 2014, 24, 105-113.	1.0	10
304	Bacterial Diversity Assessment in Antarctic Terrestrial and Aquatic Microbial Mats: A Comparison between Bidirectional Pyrosequencing and Cultivation. PLoS ONE, 2014, 9, e97564.	1.1	60
305	Analysis of plant microbe interactions in the era of next generation sequencing technologies. Frontiers in Plant Science, 2014, 5, 216.	1.7	194
306	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
307	Protein Quality and the Protein to Carbohydrate Ratio within a High Fat Diet Influences Energy Balance and the Gut Microbiota In C57BL/6J Mice. PLoS ONE, 2014, 9, e88904.	1.1	77

\sim			n
C1	TAT	ION	Report

#	Article	IF	CITATIONS
308	Analysis, Optimization and Verification of Illumina-Generated 16S rRNA Gene Amplicon Surveys. PLoS ONE, 2014, 9, e94249.	1.1	287
309	Early life establishment of site-specific microbial communities in the gut. Gut Microbes, 2014, 5, 192-201.	4.3	55
310	The Use of DNA Methods to Characterize Biofilm Infection. Springer Series on Biofilms, 2014, , 15-30.	0.0	3
311	Effects of Elevated Carbon Dioxide and Salinity on the Microbial Diversity in Lithifying Microbial Mats. Minerals (Basel, Switzerland), 2014, 4, 145-169.	0.8	11
312	Genusâ€wide acid tolerance accounts for the biogeographical distribution of soil <i>Burkholderia</i> populations. Environmental Microbiology, 2014, 16, 1503-1512.	1.8	105
313	Phylogenetic and structural response of heterotrophic bacteria to dissolved organic matter of different chemical composition in a continuous culture study. Environmental Microbiology, 2014, 16, 1668-1681.	1.8	117
314	Metagenomic <scp>16S rDNA I</scp> llumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. Environmental Microbiology, 2014, 16, 2659-2671.	1.8	291
315	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
316	Patterns of Rare and Abundant Marine Microbial Eukaryotes. Current Biology, 2014, 24, 813-821.	1.8	450
317	Comparison of brush and biopsy sampling methods of the ileal pouch for assessment of mucosa-associated microbiota of human subjects. Microbiome, 2014, 2, 5.	4.9	95
318	Detecting the Nonviable and Heat-Tolerant Bacteria in Activated Sludge by Minimizing DNA from Dead Cells. Microbial Ecology, 2014, 67, 829-836.	1.4	22
319	Pyrosequencing Analysis of Oral Microbiota Shifting in Various Caries States in Childhood. Microbial Ecology, 2014, 67, 962-969.	1.4	126
320	Cost-efficient high-throughput HLA typing by MiSeq amplicon sequencing. BMC Genomics, 2014, 15, 63.	1.2	238
321	Characterization of Bacterial Communities in Sediments Receiving Various Wastewater Effluents with High-Throughput Sequencing Analysis. Microbial Ecology, 2014, 67, 612-623.	1.4	63
322	Respiratory Microbiota Dynamics following Streptococcus pneumoniae Acquisition in Young and Elderly Mice. Infection and Immunity, 2014, 82, 1725-1731.	1.0	26
323	Resilience of the Natural Phyllosphere Microbiota of the Grapevine to Chemical and Biological Pesticides. Applied and Environmental Microbiology, 2014, 80, 3585-3596.	1.4	144
324	Altered Fecal Microbiota Composition Associated with Food Allergy in Infants. Applied and Environmental Microbiology, 2014, 80, 2546-2554.	1.4	295
325	Mosquitoes rely on their gut microbiota for development. Molecular Ecology, 2014, 23, 2727-2739.	2.0	429

		CITATION RE	EPORT	
#	Article		IF	CITATIONS
326	The Placenta Harbors a Unique Microbiome. Science Translational Medicine, 2014, 6, 2	237ra65.	5.8	1,717
327	Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. N Ecology, 2014, 23, 1268-1283.	1olecular	2.0	276
328	Intestinal Microbiota Reduces Genotoxic Endpoints Induced By High-Energy Protons. R Research, 2014, 181, 45-53.	adiation	0.7	26
329	Spatial and temporal variations of microbial community in a mixed plugâ€flow loop read dairy manure. Microbial Biotechnology, 2014, 7, 332-346.	actor fed with	2.0	60
330	Humboldt's spa: microbial diversity is controlled by temperature in geothermal env Journal, 2014, 8, 1166-1174.	vironments. ISME	4.4	186
331	Specificity and transcriptional activity of microbiota associated with low and high micr abundance sponges from the Red Sea. Molecular Ecology, 2014, 23, 1348-1363.	obial	2.0	139
332	Bacterial communities in manures of piglets and adult pigs bred with different feeds re rDNA 454 pyrosequencing. Applied Microbiology and Biotechnology, 2014, 98, 2657-2		1.7	56
333	Metaâ€analysis of deepâ€sequenced fungal communities indicates limited taxon shari and the presence of biogeographic patterns. New Phytologist, 2014, 201, 623-635.	ng between studies	3.5	106
334	Mineral Microniches Control the Diversity of Subsurface Microbial Populations. Geomic Journal, 2014, 31, 246-261.	crobiology	1.0	68
335	Diet alters probiotic <scp><i>L</i></scp> <i>actobacillus</i> persistence and function Environmental Microbiology, 2014, 16, 2915-2926.	in the intestine.	1.8	51
336	SEK: sparsity exploiting k-mer-based estimation of bacterial community composition. E 2014, 30, 2423-2431.	ioinformatics,	1.8	11
337	Exopolysaccharide-Producing Probiotic Lactobacilli Reduce Serum Cholesterol and Mo Microbiota in ApoE-Deficient Mice. Journal of Nutrition, 2014, 144, 1956-1962.	dify Enteric	1.3	80
338	Biofouling and Microbial Communities in Membrane Distillation and Reverse Osmosis. Science & Technology, 2014, 48, 13155-13164.	Environmental	4.6	75
339	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. the National Academy of Sciences of the United States of America, 2014, 111, E139-4		3.3	791
340	Assessing the impact of water treatment on bacterial biofilms in drinking water distrib using high-throughput DNA sequencing. Chemosphere, 2014, 117, 185-192.	ution systems	4.2	35
341	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. Proceedings Academy of Sciences of the United States of America, 2014, 111, E5096-104.	of the National	3.3	98
342	Gastric microbiota is altered in oesophagitis and <scp>B</scp> arrett's oesophagus an modified by proton pump inhibitors. Environmental Microbiology, 2014, 16, 2905-291		1.8	150
343	Effects of river sediment addition to the beach microbial communities. Toxicological a Environmental Chemistry, 2014, 96, 68-83.	nd	0.6	2

#	Article	IF	CITATIONS
344	Routes of Acquisition of the Gut Microbiota of the Honey Bee Apis mellifera. Applied and Environmental Microbiology, 2014, 80, 7378-7387.	1.4	380
345	Psychrotrophic lactic acid bacteria associated with production batch recalls and sporadic cases of early spoilage in Belgium between 2010 and 2014. International Journal of Food Microbiology, 2014, 191, 157-163.	2.1	41
346	Multiplex sequencing of pooled mitochondrial genomes—a crucial step toward biodiversity analysis using mito-metagenomics. Nucleic Acids Research, 2014, 42, e166-e166.	6.5	230
347	Conducting a Microbiome Study. Cell, 2014, 158, 250-262.	13.5	625
348	Human Mitochondrial DNA and Endogenous Bacterial Surrogates for Risk Assessment of Graywater Reuse. Environmental Science & Technology, 2014, 48, 7993-8002.	4.6	20
349	Patterned progression of bacterial populations in the premature infant gut. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12522-12527.	3.3	449
350	Drivers shaping the diversity and biogeography of total and active bacterial communities in the South China Sea. Molecular Ecology, 2014, 23, 2260-2274.	2.0	194
351	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
352	Getting Started with Microbiome Analysis: Sample Acquisition to Bioinformatics. Current Protocols in Human Genetics, 2014, 82, 18.8.1-29.	3.5	111
354	Synchronous dynamics and correlations between bacteria and phytoplankton in a subtropical drinking water reservoir. FEMS Microbiology Ecology, 2014, 90, 126-138.	1.3	72
355	Exercise induction of gut microbiota modifications in obese, non-obese and hypertensive rats. BMC Genomics, 2014, 15, 511.	1.2	244
356	Assessing the hodgepodge of non-mapped reads in bacterial transcriptomes: real or artifactual RNA chimeras?. BMC Genomics, 2014, 15, 633.	1.2	4
357	Metataxonomic profiling and prediction of functional behaviour of wheat straw degrading microbial consortia. Biotechnology for Biofuels, 2014, 7, 92.	6.2	88
358	Pyrosequencing reveals transient cystic fibrosis lung microbiome changes with intravenous antibiotics. European Respiratory Journal, 2014, 44, 922-930.	3.1	71
359	A Hidden Pitfall in the Preparation of Agar Media Undermines Microorganism Cultivability. Applied and Environmental Microbiology, 2014, 80, 7659-7666.	1.4	192
360	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
361	Patterns of Bacterial Diversity Along a Long-Term Mercury-Contaminated Gradient in the Paddy Soils. Microbial Ecology, 2014, 68, 575-583.	1.4	72
362	Metabolic Characteristics of a Glycogen-Accumulating Organism in Defluviicoccus Cluster II Revealed by Comparative Genomics. Microbial Ecology, 2014, 68, 716-728.	1.4	22

#	Article	IF	CITATIONS
363	Diversity, abundance, and spatial distribution of riverine microbial communities response to effluents from swine farm versus farmhouse restaurant. Applied Microbiology and Biotechnology, 2014, 98, 7597-7608.	1.7	6
364	Bacterial colonization of a fumigated alkaline saline soil. Extremophiles, 2014, 18, 733-743.	0.9	4
365	Niche partitioning of bacterial communities in biological crusts and soils under grasses, shrubs and trees in the Kalahari. Biodiversity and Conservation, 2014, 23, 1709-1733.	1.2	47
366	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. Microbiome, 2014, 2, 11.	4.9	225
367	Exploration of bacterial community classes in major human habitats. Genome Biology, 2014, 15, R66.	13.9	109
368	Bacterial community structure in fumigated soil. Soil Biology and Biochemistry, 2014, 73, 122-129.	4.2	26
369	Exploring the uncultured microeukaryote majority in the oceans: reevaluation of ribogroups within stramenopiles. ISME Journal, 2014, 8, 854-866.	4.4	157
370	Influence of DNA Extraction Method, 16S rRNA Targeted Hypervariable Regions, and Sample Origin on Microbial Diversity Detected by 454 Pyrosequencing in Marine Chemosynthetic Ecosystems. Applied and Environmental Microbiology, 2014, 80, 4626-4639.	1.4	87
371	The unseen world: environmental microbial sequencing and identification methods for ecologists. Frontiers in Ecology and the Environment, 2014, 12, 224-231.	1.9	27
372	Regional effects on chimera formation in 454 pyrosequenced amplicons from a mock community. Journal of Microbiology, 2014, 52, 566-573.	1.3	10
373	Comparison of methods for fecal microbiome biospecimen collection. BMC Microbiology, 2014, 14, 103.	1.3	150
374	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
375	Targeted and Highly Multiplexed Detection of Microorganisms by Employing an Ensemble of Molecular Probes. Applied and Environmental Microbiology, 2014, 80, 4153-4161.	1.4	6
376	Neotropical Andes hot springs harbor diverse and distinct planktonic microbial communities. FEMS Microbiology Ecology, 2014, 89, 56-66.	1.3	21
377	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
378	Analyzing the Human Microbiome: A "How To―guide for Physicians. American Journal of Gastroenterology, 2014, 109, 983-993.	0.2	69
379	Characterization of biofouling in a lab-scale forward osmosis membrane bioreactor (FOMBR). Water Research, 2014, 58, 141-151.	5.3	91
380	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

#	Article	IF	CITATIONS
381	The source of inoculum plays a defining role in the development of MEC microbial consortia fed with acetic and propionic acid mixtures. Journal of Biotechnology, 2014, 182-183, 11-18.	1.9	52
382	Characterization of the gut microbiota in leptin deficient obese mice – Correlation to inflammatory and diabetic parameters. Research in Veterinary Science, 2014, 96, 241-250.	0.9	75
383	Exercise and associated dietary extremes impact on gut microbial diversity. Gut, 2014, 63, 1913-1920.	6.1	987
384	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. ISME Journal, 2014, 8, 1989-2001.	4.4	221
385	High-Resolution Melt Analysis for Rapid Comparison of Bacterial Community Compositions. Applied and Environmental Microbiology, 2014, 80, 3568-3575.	1.4	55
386	Abundance of Broad Bacterial Taxa in the Sargasso Sea Explained by Environmental Conditions but Not Water Mass. Applied and Environmental Microbiology, 2014, 80, 2786-2795.	1.4	36
387	Unraveling the outcome of 16S rDNA-based taxonomy analysis through mock data and simulations. Bioinformatics, 2014, 30, 1530-1538.	1.8	29
388	Bayesian clustering of DNA sequences using Markov chains and a stochastic partition model. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 105-21.	0.2	14
389	Active and diverse rainwater bacteria collected at an inland site in spring and summer 2011. Atmospheric Environment, 2014, 94, 409-416.	1.9	29
390	Novel Gut-Based Pharmacology of Metformin in Patients with Type 2 Diabetes Mellitus. PLoS ONE, 2014, 9, e100778.	1.1	218
391	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
392	The Bacterial Community Structure of Hydrocarbon-Polluted Marine Environments as the Basis for the Definition of an Ecological Index of Hydrocarbon Exposure. Microbes and Environments, 2014, 29, 269-276.	0.7	32
393	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
394	Characterization of Early Microbial Communities on Volcanic Deposits along a Vegetation Gradient on the Island of Miyake, Japan. Microbes and Environments, 2014, 29, 38-49.	0.7	26
395	PATTERNS OF UNCULTURED BACTERIA PHYLA IN DIFFERENT WASTEWATER TREATMENT SLUDGES. Journal of Japan Society of Civil Engineers Ser G (Environmental Research), 2014, 70, 42-52.	0.1	1
396	HIGH ORGANIC LOADING TREATMENT OF MOLASSES WASTEWATER BY COMBINED SYSTEM CONSISTED OF THERMOPHILIC MULTI-STAGED UASB REACTOR AND MESOPHILIC UASB REACTOR. Journal of Japan Society of Civil Engineers Ser G (Environmental Research), 2014, 70, III_151-III_158.	0.1	0
397	DNA metabarcoding of insects and allies: an evaluation of primers and pipelines. Bulletin of Entomological Research, 2015, 105, 717-727.	0.5	138
398	High diversity and distinctive community structure of bacteria on glaciers in China revealed by 454 pyrosequencing. Systematic and Applied Microbiology, 2015, 38, 578-585.	1.2	35

#	ARTICLE	IF	CITATIONS
399	Correlations of Gut Microbial Community Shift with Hepatic Damage and Growth Inhibition of <i>Carassius auratus</i> Induced by Pentachlorophenol Exposure. Environmental Science & amp; Technology, 2015, 49, 11894-11902.	4.6	107
400	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
401	Diversity Profile of Microbes Associated with Anaerobic Sulfur Oxidation in an Upflow Anaerobic Sludge Blanket Reactor Treating Municipal Sewage. Microbes and Environments, 2015, 30, 157-163.	0.7	13
402	Reduction of butyrate- and methane-producing microorganisms in patients with Irritable Bowel Syndrome. Scientific Reports, 2015, 5, 12693.	1.6	248
403	River bacterioplankton community responses to a high inflow event. Aquatic Microbial Ecology, 2015, 75, 187-205.	0.9	23
404	Application of density gradient for the isolation of the fecal microbial stool component and the potential use thereof. Scientific Reports, 2015, 5, 16807.	1.6	44
405	Annual periodicity in planktonic bacterial and archaeal community composition of eutrophic Lake Taihu. Scientific Reports, 2015, 5, 15488.	1.6	74
406	Microbial Community Analysis Using High-Throughput Amplicon Sequencing. , 2015, , 2.4.2-1-2.4.2-26.		4
407	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
408	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
409	Distinct composition of the oral indigenous microbiota in South Korean and Japanese adults. Scientific Reports, 2014, 4, 6990.	1.6	58
410	Micelle PCR reduces chimera formation in 16S rRNA profiling of complex microbial DNA mixtures. Scientific Reports, 2015, 5, 14181.	1.6	26
411	Cecum microbial communities from steers differing in feed efficiency1,2,3. Journal of Animal Science, 2015, 93, 5327-5340.	0.2	58
412	Spatial heterogeneity of gut microbiota reveals multiple bacterial communities with distinct characteristics. Scientific Reports, 2014, 4, 6185.	1.6	35
413	Robust species taxonomy assignment algorithm for 16S rRNA NGS reads: application to oral carcinoma samples. Journal of Oral Microbiology, 2015, 7, 28934.	1.2	101
414	The effect of dietary resistant starch type 2 on the microbiota and markers of gut inflammation in rural Malawi children. Microbiome, 2015, 3, 37.	4.9	53
415	Genetic associations and shared environmental effects on the skin microbiome of Korean twins. BMC Genomics, 2015, 16, 992.	1.2	61
416	The first microbial environment of infants born by C-section: the operating room microbes. Microbiome, 2015, 3, 59	4.9	110

	CITATION RE	PORT	
#	Article	IF	CITATIONS
417	SPINGO: a rapid species-classifier for microbial amplicon sequences. BMC Bioinformatics, 2015, 16, 324.	1.2	122
418	An accurate and efficient experimental approach for characterization of the complex oral microbiota. Microbiome, 2015, 3, 48.	4.9	95
419	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
420	Characterization of the relative importance of human- and infrastructure-associated bacteria in grey water: a case study. Journal of Applied Microbiology, 2015, 119, 289-301.	1.4	18
421	WASTEWATER TREATMENT CHARACTERISTIC OF LACTATE CONTAINING WASTEWATER BY A SINGLE CHAMBER MICROBIAL FUEL CELL. Journal of Japan Society of Civil Engineers Ser G (Environmental Research), 2015, 71, III_389-III_396.	0.1	0
422	Marine protist diversity in <scp>E</scp> uropean coastal waters and sediments as revealed by highâ€throughput sequencing. Environmental Microbiology, 2015, 17, 4035-4049.	1.8	384
423	Low dietary iron intake restrains the intestinal inflammatory response and pathology of enteric infection by foodâ€borne bacterial pathogens. European Journal of Immunology, 2015, 45, 2553-2567.	1.6	56
424	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
425	<scp>I</scp> nner <scp>M</scp> ongolian steppe arbuscular mycorrhizal fungal communities respond more strongly to water availability than to nitrogen fertilization. Environmental Microbiology, 2015, 17, 3051-3068.	1.8	62
426	The Quantification of Representative Sequences pipeline for amplicon sequencing: case study on withinâ€population <scp>ITS</scp> 1 sequence variation in a microparasite infecting <i><scp>D</scp>aphnia</i> . Molecular Ecology Resources, 2015, 15, 1385-1395.	2.2	7
427	Archaeal Communities in a Heterogeneous Hypersaline-Alkaline Soil. Archaea, 2015, 2015, 1-11.	2.3	24
428	A Comparison of Three Bioinformatics Pipelines for the Analysis of Preterm Gut Microbiota using 16S rRNA Gene Sequencing Data. Journal of Proteomics and Bioinformatics, 2015, 8, .	0.4	86
429	Long-Read, Single Molecule, Real-Time (SMRT) DNA Sequencing for Metagenomic Applications. , 2015, , 25-38.		2
430	Avoidance and Potential Remedy Solutions of Chimeras in Reconstructing the Phylogeny of Aphids Using the 16S rRNA Gene of Buchnera: A Case in Lachninae (Hemiptera). International Journal of Molecular Sciences, 2015, 16, 20152-20167.	1.8	5
431	Novel and Unexpected Microbial Diversity in Acid Mine Drainage in Svalbard (78° N), Revealed by Culture-Independent Approaches. Microorganisms, 2015, 3, 667-694.	1.6	44
432	riboFrame: An Improved Method for Microbial Taxonomy Profiling from Non-Targeted Metagenomics. Frontiers in Genetics, 2015, 6, 329.	1.1	15
433	Increased seawater temperature increases the abundance and alters the structure of natural Vibrio populations associated with the coral Pocillopora damicornis. Frontiers in Microbiology, 2015, 6, 432.	1.5	142
434	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

#	Article	IF	CITATIONS
435	Metagenome-based diversity analyses suggest a significant contribution of non-cyanobacterial lineages to carbonate precipitation in modern microbialites. Frontiers in Microbiology, 2015, 6, 797.	1.5	50
436	Anaerobic carboxydotrophic bacteria in geothermal springs identified using stable isotope probing. Frontiers in Microbiology, 2015, 6, 897.	1.5	27
437	Metagenomic analysis of the rumen microbial community following inhibition of methane formation by a halogenated methane analog. Frontiers in Microbiology, 2015, 6, 1087.	1.5	97
438	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
439	Resistance of Undisturbed Soil Microbiomes to Ceftriaxone Indicates Extended Spectrum β-Lactamase Activity. Frontiers in Microbiology, 2015, 6, 1233.	1.5	14
440	Weak Coherence in Abundance Patterns Between Bacterial Classes and Their Constituent OTUs Along a Regulated River. Frontiers in Microbiology, 2015, 6, 1293.	1.5	14
441	Transient Changes in Bacterioplankton Communities Induced by the Submarine Volcanic Eruption of El Hierro (Canary Islands). PLoS ONE, 2015, 10, e0118136.	1.1	22
442	Longitudinal Analysis of the Premature Infant Intestinal Microbiome Prior to Necrotizing Enterocolitis: A Case-Control Study. PLoS ONE, 2015, 10, e0118632.	1.1	146
443	Microbial Community Analysis of Anaerobic Reactors Treating Soft Drink Wastewater. PLoS ONE, 2015, 10, e0119131.	1.1	27
444	Response of the Rumen Microbiota of Sika Deer (Cervus nippon) Fed Different Concentrations of Tannin Rich Plants. PLoS ONE, 2015, 10, e0123481.	1.1	46
445	Effects of Vaccination with 10-Valent Pneumococcal Non-Typeable Haemophilus influenza Protein D Conjugate Vaccine (PHiD-CV) on the Nasopharyngeal Microbiome of Kenyan Toddlers. PLoS ONE, 2015, 10, e0128064.	1.1	26
446	Esophageal Microbiome in Eosinophilic Esophagitis. PLoS ONE, 2015, 10, e0128346.	1.1	134
447	Rumen Microbiome from Steers Differing in Feed Efficiency. PLoS ONE, 2015, 10, e0129174.	1.1	307
448	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
449	Bioinformatic Amplicon Read Processing Strategies Strongly Affect Eukaryotic Diversity and the Taxonomic Composition of Communities. PLoS ONE, 2015, 10, e0130035.	1.1	67
450	Litter Breakdown and Microbial Succession on Two Submerged Leaf Species in a Small Forested Stream. PLoS ONE, 2015, 10, e0130801.	1.1	21
451	Inter-Individual Differences in the Oral Bacteriome Are Greater than Intra-Day Fluctuations in Individuals. PLoS ONE, 2015, 10, e0131607.	1.1	47
452	Late-Onset Bloodstream Infection and Perturbed Maturation of the Gastrointestinal Microbiota in Premature Infants. PLoS ONE, 2015, 10, e0132923.	1.1	75

#	Article	IF	Citations
453	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
454	Design and Investigation of PolyFermS In Vitro Continuous Fermentation Models Inoculated with Immobilized Fecal Microbiota Mimicking the Elderly Colon. PLoS ONE, 2015, 10, e0142793.	1.1	59
455	Oral Microbiota and Risk for Esophageal Squamous Cell Carcinoma in a High-Risk Area of China. PLoS ONE, 2015, 10, e0143603.	1.1	146
456	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
457	Selective Spectrum Antibiotic Modulation of the Gut Microbiome in Obesity and Diabetes Rodent Models. PLoS ONE, 2015, 10, e0145499.	1.1	39
458	Temporal Relationships Exist Between Cecum, lleum, and Litter Bacterial Microbiomes in a Commercial Turkey Flock, and Subtherapeutic Penicillin Treatment Impacts lleum Bacterial Community Establishment. Frontiers in Veterinary Science, 2015, 2, 56.	0.9	48
459	Hypothesis: Artifacts, Including Spurious Chimeric RNAs with a Short Homologous Sequence, Caused by Consecutive Reverse Transcriptions and Endogenous Random Primers. Journal of Cancer, 2015, 6, 555-567.	1.2	32
460	Mapping microbial ecosystems and spoilage-gene flow in breweries highlights patterns of contamination and resistance. ELife, 2015, 4, .	2.8	71
461	Bioinformation and 'Omic Approaches for Characterization of Environmental Microorganisms. , 2015, , 483-505.		4
462	Metagenomic Analysis of Chicken Gut Microbiota for Improving Metabolism and Health of Chickens — A Review. Asian-Australasian Journal of Animal Sciences, 2015, 28, 1217-1225.	2.4	90
463	Navigating the labyrinth: a guide to sequenceâ€based, community ecology of arbuscular mycorrhizal fungi. New Phytologist, 2015, 207, 235-247.	3.5	106
464	Microbial biogeography of the transnational fermented milk matsoni. Food Microbiology, 2015, 50, 12-19.	2.1	47
465	Sex, Body Mass Index, and Dietary Fiber Intake Influence the Human Gut Microbiome. PLoS ONE, 2015, 10, e0124599.	1.1	330
466	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. MBio, 2015, 6, e00306-15.	1.8	380
467	Aerobic biodegradation of organic compounds in hydraulic fracturing fluids. Biodegradation, 2015, 26, 271-287.	1.5	83
468	Programming rumen bacterial communities in newborn Merino lambs. Small Ruminant Research, 2015, 129, 48-59.	0.6	39
469	Analysis of microbial community structure and composition in leachates from a young landfill by 454 pyrosequencing. Applied Microbiology and Biotechnology, 2015, 99, 5657-5668.	1.7	75
470	Study of the diversity and short-chain fatty acids production by the bacterial community in overweight and obese Mexican children. European Journal of Clinical Microbiology and Infectious Diseases, 2015, 34, 1337-1346.	1.3	114

ARTICLE IF CITATIONS # International interlaboratory study comparing single organism 16S rRNA gene sequencing data: 471 7.0 3 Beyond consensus sequence comparisons. Biomolecular Detection and Quantification, 2015, 3, 17-24. The truth about metagenomics: quantifying and counteracting bias in 16S rRNA studies. BMC 1.3 388 Microbiology, 2015, 15, 66. The Microbiome, Intestinal Function, and Arginine Metabolism of Healthy Indian Women Are Different 473 1.3 40 from Those of American and Jamaican Women. Journal of Nutrition, 2016, 146, 706-713. NGS-eval: NGS Error analysis and novel sequence VAriant detection tooL. Nucleic Acids Research, 2015, 474 43, W301-W305. Sources of PCR-induced distortions in high-throughput sequencing data sets. Nucleic Acids Research, 475 6.5 182 2015, 43, gkv717. Combined amendment of immobilizers and the plant growth-promoting strain Burkholderia phytofirmans PsJN favours plant growth and reduces heavy metal uptake. Soil Biology and 4.2 Biochemistry, 2015, 91, 140-150 Novel Mass Bio System (MBS) and its potential application in advanced treatment of coal gasification 477 1.7 25 wastewater. RSC Advances, 2015, 5, 88692-88702. Diet strongly influences the gut microbiota of surgeonfishes. Molecular Ecology, 2015, 24, 656-672. 194 Bacterial community structure in maize residue amended soil with contrasting management practices. 479 2.1 83 Applied Soil Ecologý, 2015, 90, 49-59. No difference in small bowel microbiota between patients with irritable bowel syndrome and healthy 1.6 controls. Scientific Reports, 2015, 5, 8508. The nexus of syntrophyâ€associated microbiota in anaerobic digestion revealed by longâ€term enrichment 481 149 1.8 and community survey. Environmental Microbiology, 2015, 17, 1707-1720. Dental plaque development on a hydroxyapatite disk in young adults observed by using a barcoded 1.6 pyrosequencing approach. Scientific Reports, 2015, 5, 8136. Potential applications of soil microbial ecology and next-generation sequencing in criminal 483 2.1 34 investigations. Applied Soil Ecology, 2015, 88, 69-78. Studying Genome Heterogeneity within the Arbuscular Mycorrhizal Fungal Cytoplasm. Genome Biology and Evolution, 2015, 7, 505-521. 484 1.1 Depth shapes $\hat{I} \pm \hat{a} \in \hat{I}$ and $\hat{I}^2 \hat{a} \in \hat{I}$ diversities of microbial eukaryotes in surficial sediments of coastal ecosystems. 485 98 1.8 Environmental Microbiology, 2015, 17, 3722-3737. Distinct composition signatures of archaeal and bacterial phylotypes in the Wanda Glacier forefield, 486 Antarctic Peninsula. FEMS Microbiology Ecology, 2015, 91, 1-10. Microbial Community Composition and Ultrastructure of Granules from a Full-Scale Anammox 487 1.4 115 Reactor. Microbial Ecology, 2015, 70, 118-131. Comparison of the microbial communities in solid-state anaerobic digestion (SS-AD) reactors operated 488 at mesophilic and thermophilic temperatures. Applied Microbiology and Biotechnology, 2015, 99, 104 969-980

#	Article	IF	CITATIONS
489	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
490	The shared microbiota of humans and companion animals as evaluated from Staphylococcus carriage sites. Microbiome, 2015, 3, 2.	4.9	95
491	Biological support media influence the bacterial biofouling community in reverse osmosis water reclamation demonstration plants. Biofouling, 2015, 31, 173-180.	0.8	9
492	Temporal variation in community structure and lipid composition of Thaumarchaeota from subtropical soil: Insight into proposing a new soil pH proxy. Organic Geochemistry, 2015, 83-84, 54-64.	0.9	22
493	Stable microbial community composition on the Greenland Ice Sheet. Frontiers in Microbiology, 2015, 6, 193.	1.5	56
494	Polar front associated variation in prokaryotic community structure in Arctic shelf seafloor. Frontiers in Microbiology, 2015, 6, 17.	1.5	34
495	Successive bioanode regenerations to maintain efficient current production from biowaste. Bioelectrochemistry, 2015, 106, 133-140.	2.4	20
496	Roots Shaping Their Microbiome: Global Hotspots for Microbial Activity. Annual Review of Phytopathology, 2015, 53, 403-424.	3.5	595
497	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
498	Production attributes of Merino sheep genetically divergent for wool growth are reflected in differing rumen microbiotas. Livestock Science, 2015, 178, 119-129.	0.6	5
499	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
500	Distribution of ether lipids and composition of the archaeal community in terrestrial geothermal springs: impact of environmental variables. Environmental Microbiology, 2015, 17, 1600-1614.	1.8	29
501	Diversity and functions of bacterial community in drinking water biofilms revealed by high-throughput sequencing. Scientific Reports, 2015, 5, 10044.	1.6	71
502	Hologenome theory supported by cooccurrence networks of species-specific bacterial communities in siphonous algae (<i>Caulerpa</i>). FEMS Microbiology Ecology, 2015, 91, fiv067.	1.3	55
503	Using Amplicon Sequencing To Characterize and Monitor Bacterial Diversity in Drinking Water Distribution Systems. Applied and Environmental Microbiology, 2015, 81, 6463-6473.	1.4	63
504	Assay for estimating total bacterial load: relative qPCR normalisation of bacterial load with associated clinical implications. Diagnostic Microbiology and Infectious Disease, 2015, 83, 1-6.	0.8	22
505	Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. Science, 2015, 349, 860-864.	6.0	957
506	Genomic Applications in the Clinical Management of Infectious Diseases. , 2015, , 581-604.		О

#	Article	IF	CITATIONS
507	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
508	Error filtering, pair assembly and error correction for next-generation sequencing reads. Bioinformatics, 2015, 31, 3476-3482.	1.8	1,102
509	RNA shotgun metagenomic sequencing of northern California (USA) mosquitoes uncovers viruses, bacteria, and fungi. Frontiers in Microbiology, 2015, 06, 185.	1.5	124
510	Enterolignan-Producing Phenotypes Are Associated with Increased Gut Microbial Diversity and Altered Composition in Premenopausal Women in the United States. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 546-554.	1.1	55
511	The preterm placental microbiome varies in association with excess maternal gestational weight gain. American Journal of Obstetrics and Gynecology, 2015, 212, 653.e1-653.e16.	0.7	173
512	The pig gut microbial diversity: Understanding the pig gut microbial ecology through the next generation high throughput sequencing. Veterinary Microbiology, 2015, 177, 242-251.	0.8	218
513	Systems Biology Tools for Methylotrophs. Springer Protocols, 2015, , 97-118.	0.1	4
514	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
515	Metagenomic analysis of the bacterial microbiota linked to the traditional Algerian date product "Btana― Annals of Microbiology, 2015, 65, 2415-2424.	1.1	1
516	A novel sub-phylum method discriminates better the impact of crop management on soil microbial community. Agronomy for Sustainable Development, 2015, 35, 1157-1166.	2.2	27
517	NoDe: a fast error-correction algorithm for pyrosequencing amplicon reads. BMC Bioinformatics, 2015, 16, 88.	1.2	13
518	High-throughput sequencing for the detection of the bacterial and fungal diversity in Mongolian naturally fermented cow's milk in Russia. BMC Microbiology, 2015, 15, 45.	1.3	67
519	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
520	Changes in soil aggregation and microbial community structure control carbon sequestration after afforestation of semiarid shrublands. Soil Biology and Biochemistry, 2015, 87, 110-121.	4.2	98
521	Mongolians core gut microbiota and its correlation with seasonal dietary changes. Scientific Reports, 2014, 4, 5001.	1.6	126
522	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. Microbial Ecology, 2015, 69, 333-345.	1.4	20
523	Two decades of warming increases diversity of a potentially lignolytic bacterial community. Frontiers in Microbiology, 2015, 6, 480.	1.5	73
524	Changes in northern Gulf of Mexico sediment bacterial and archaeal communities exposed to hypoxia. Geobiology, 2015, 13, 478-493.	1.1	16

#	Article	IF	CITATIONS
525	Associations between Gut Microbial Colonization in Early Life and Respiratory Outcomes in Cystic Fibrosis. Journal of Pediatrics, 2015, 167, 138-147.e3.	0.9	131
526	Elements of metacommunity structure and communityâ€environment relationships in stream organisms. Freshwater Biology, 2015, 60, 973-988.	1.2	58
527	16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. Applied Microbiology and Biotechnology, 2015, 99, 4119-4129.	1.7	79
528	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
529	Next-Generation Sequencing for Infectious Disease Diagnosis and Management. Journal of Molecular Diagnostics, 2015, 17, 623-634.	1.2	151
530	Microbial community profiles of the colon from steers differing in feed efficiency. SpringerPlus, 2015, 4, 454.	1.2	52
531	Clone Libraries of Ribosomal RNA Gene Sequences for Characterization of Microbial Communities. Springer Protocols, 2015, , 127-154.	0.1	2
532	Subchronic Exposure of Mice to Cadmium Perturbs Their Hepatic Energy Metabolism and Gut Microbiome. Chemical Research in Toxicology, 2015, 28, 2000-2009.	1.7	174
534	Microbiology and Molecular Biology Tools for Biogas Process Analysis, Diagnosis and Control. Advances in Biochemical Engineering/Biotechnology, 2015, 151, 1-40.	0.6	9
535	Nitrogen recovery from pig slurry in a two-chambered bioelectrochemical system. Bioresource Technology, 2015, 194, 373-382.	4.8	62
536	Nitrogen removal and water microbiota in grass carp culture following supplementation with Bacillus licheniformis BSK-4. World Journal of Microbiology and Biotechnology, 2015, 31, 1711-1718.	1.7	29
537	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
538	Randomised clinical trial: gut microbiome biomarkers are associated with clinical response to a low <scp>FODMAP</scp> diet in children with the irritable bowel syndrome. Alimentary Pharmacology and Therapeutics, 2015, 42, 418-427.	1.9	353
539	Structure and function of the healthy pre-adolescent pediatric gut microbiome. Microbiome, 2015, 3, 36.	4.9	283
540	Stool Bacteriomic Profiling in Patients with Metastatic Renal Cell Carcinoma Receiving Vascular Endothelial Growth Factor–Tyrosine Kinase Inhibitors. Clinical Cancer Research, 2015, 21, 5286-5293.	3.2	52
541	Detailed investigation of the microbial community in foaming activated sludge reveals novel foam formers. Scientific Reports, 2015, 5, 7637.	1.6	44
542	Earlyâ€ i ife establishment of the swine gut microbiome and impact on host phenotypes. Environmental Microbiology Reports, 2015, 7, 554-569.	1.0	320
543	Effect of organic loading on the microbiota in a temperature-phased anaerobic digestion (TPAD) system co-digesting dairy manure and waste whey. Applied Microbiology and Biotechnology, 2015, 99, 8777-8792.	1.7	9

#	Article	IF	CITATIONS
544	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
545	Fecal microbiota analysis: an overview of sample collection methods and sequencing strategies. Future Microbiology, 2015, 10, 1485-1504.	1.0	90
546	The activated sludge bulking filament Eikelboom morphotype 0803 embraces more than one member of theChloroflexi. FEMS Microbiology Ecology, 2015, 91, fiv100.	1.3	22
547	Gut Microbiome Composition in Young Nicaraguan Children During Diarrhea Episodes and Recovery. American Journal of Tropical Medicine and Hygiene, 2015, 93, 1187-1193.	0.6	30
548	Metagenomics study of endophytic bacteria in Aloe vera using next-generation technology. Genomics Data, 2015, 6, 159-163.	1.3	136
549	The African buffalo parasite Theileria. sp. (buffalo) can infect and immortalize cattle leukocytes and encodes divergent orthologues ofÂTheileria parva antigen genes. International Journal for Parasitology: Parasites and Wildlife, 2015, 4, 333-342.	0.6	32
550	Early life microbial colonization of the gut and intestinal development differ between genetically divergent broiler lines. BMC Genomics, 2015, 16, 418.	1.2	107
551	Evaluation of microbial diversity in the pilot-scale beer brewing process by culture-dependent and culture-independent method. Journal of Applied Microbiology, 2015, 118, 454-469.	1.4	14
552	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
553	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
554	CATCh, an Ensemble Classifier for Chimera Detection in 16S rRNA Sequencing Studies. Applied and Environmental Microbiology, 2015, 81, 1573-1584.	1.4	58
555	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
556	Vegetation-soil system controls soil mechanisms for nitrogen transformations in an oligotrophic Mexican desert. Journal of Arid Environments, 2015, 114, 62-69.	1.2	22
557	Changes in bacterial community metabolism and composition during the degradation of dissolved organic matter from the jellyfish Aurelia aurita in a Mediterranean coastal lagoon. Environmental Science and Pollution Research, 2015, 22, 13638-13653.	2.7	41
558	Microbial diversity and dynamics of a groundwater and a still bottled natural mineral water. Environmental Microbiology, 2015, 17, 577-593.	1.8	40
559	In-depth diversity analysis of the bacterial community resident in the camel rumen. Systematic and Applied Microbiology, 2015, 38, 67-76.	1.2	92
560	Dysbiosis Anticipating Necrotizing Enterocolitis in Very Premature Infants. Clinical Infectious Diseases, 2015, 60, 389-397.	2.9	168
561	Streptozotocin-induced type-1-diabetes disease onset in Sprague–Dawley rats is associated with an altered intestinal microbiota composition and decreased diversity. Microbiology (United Kingdom), 2015. 161. 182-193.	0.7	70

#	Article	IF	CITATIONS
562	Community Composition of Known and Uncultured Archaeal Lineages in Anaerobic or Anoxic Wastewater Treatment Sludge. Microbial Ecology, 2015, 69, 586-596.	1.4	59
563	Bacterial Community Composition and Fermentation Patterns in the Rumen of Sika Deer (Cervus) Tj ETQq1 1 0.7	784314 rg 1.4	BT/Qverloc
564	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
565	Microbial communities associated with human decomposition and their potential use as postmortem clocks. International Journal of Legal Medicine, 2015, 129, 623-632.	1.2	77
566	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
567	Phylogenetics and the Human Microbiome. Systematic Biology, 2015, 64, e26-e41.	2.7	36
568	Reduced dependence of rhizosphere microbiome on plant-derived carbon in 32-year long-term inorganic and organic fertilized soils. Soil Biology and Biochemistry, 2015, 80, 70-78.	4.2	176
569	Interpreting 16S metagenomic data without clustering to achieve sub-OTU resolution. ISME Journal, 2015, 9, 68-80.	4.4	184
570	Next-Generation Sequencing: A Review of Technologies and Tools for Wound Microbiome Research. Advances in Wound Care, 2015, 4, 50-58.	2.6	109
571	Catchment-scale biogeography of riverine bacterioplankton. ISME Journal, 2015, 9, 516-526.	4.4	202
572	Enrichment of Fusobacteria in Sea Surface Oil Slicks from the Deepwater Horizon Oil Spill. Microorganisms, 2016, 4, 24.	1.6	23
573	Exploring the Shift in Structure and Function of Microbial Communities Performing Biological Phosphorus Removal. PLoS ONE, 2016, 11, e0161506.	1.1	9
574	Altered expression pattern of circular RNAs in primary and metastatic sites of epithelial ovarian carcinoma. Oncotarget, 2016, 7, 36366-36381.	0.8	148
575	Technological advancements and their importance for nematode identification. Soil, 2016, 2, 257-270.	2.2	11
576	Archaea and Bacteria Acclimate to High Total Ammonia in a Methanogenic Reactor Treating Swine Waste. Archaea, 2016, 2016, 1-10.	2.3	26
577	The Bacteriomes of Ileal Mucosa and Cecal Content of Broiler Chickens and Turkeys as Revealed by Metagenomic Analysis. International Journal of Microbiology, 2016, 2016, 1-12.	0.9	14
578	Microbial community profiles of the jejunum from steers differing in feed efficiency1,2,3. Journal of Animal Science, 2016, 94, 327-338.	0.2	62
579	Analysis of the Vaginal Microbiome by Next-Generation Sequencing and Evaluation of its Performance as a Clinical Diagnostic Tool in Vaginitis. Annals of Laboratory Medicine, 2016, 36, 441-449.	1.2	35

		PORT	
# 580	ARTICLE The A, C, G, and T of Genome Assembly. BioMed Research International, 2016, 2016, 1-10.	IF 0.9	CITATIONS
581	Benchmarking DNA Metabarcoding for Biodiversity-Based Monitoring and Assessment. Frontiers in Marine Science, 2016, 3, .	1.2	157
582	Implementing and Innovating Marine Monitoring Approaches for Assessing Marine Environmental Status. Frontiers in Marine Science, 2016, 3, .	1.2	163
583	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
584	Bacterioplankton Dynamics within a Large Anthropogenically Impacted Urban Estuary. Frontiers in Microbiology, 2015, 6, 1438.	1.5	98
585	A Lipid-Accumulating Alga Maintains Growth in Outdoor, Alkaliphilic Raceway Pond with Mixed Microbial Communities. Frontiers in Microbiology, 2015, 6, 1480.	1.5	30
586	New Insights into the Microbiota of the Svalbard Reindeer Rangifer tarandus platyrhynchus. Frontiers in Microbiology, 2016, 7, 170.	1.5	14
587	Spatial-Temporal Changes of Bacterioplankton Community along an Exhorheic River. Frontiers in Microbiology, 2016, 7, 250.	1.5	32
588	Species Specificity of Bacteria Associated to the Brown Seaweeds Lobophora (Dictyotales,) Tj ETQq0 0 0 rgBT /O Frontiers in Microbiology, 2016, 7, 316.	verlock 10 1.5	D Tf 50 427 1 53
589	Comparison of Fermentation and Wines Produced by Inoculation of Hanseniaspora vineae and Saccharomyces cerevisiae. Frontiers in Microbiology, 2016, 7, 338.	1.5	91
590	Spatiotemporal Dynamics of Vibrio spp. within the Sydney Harbour Estuary. Frontiers in Microbiology, 2016, 7, 460.	1.5	69
591	Host and Environmental Specificity in Bacterial Communities Associated to Two Highly Invasive Marine Species (Genus Asparagopsis). Frontiers in Microbiology, 2016, 7, 559.	1.5	72
592	Experimental Evolution on a Wild Mammal Species Results in Modifications of Gut Microbial Communities. Frontiers in Microbiology, 2016, 7, 634.	1.5	27
593	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. Frontiers in Microbiology, 2016, 7, 987.	1.5	61
594	Insights into Abundant Rumen Ureolytic Bacterial Community Using Rumen Simulation System. Frontiers in Microbiology, 2016, 7, 1006.	1.5	52
595	Microbial Diversity in Sediment Ecosystems (Evaporites Domes, Microbial Mats, and Crusts) of Hypersaline Laguna Tebenquiche, Salar de Atacama, Chile. Frontiers in Microbiology, 2016, 7, 1284.	1.5	79
596	The Arctic Soil Bacterial Communities in the Vicinity of a Little Auk Colony. Frontiers in Microbiology, 2016, 7, 1298.	1.5	4
597	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

#	Article	IF	CITATIONS
598	Evaluation of the Microbial Diversity in Amyotrophic Lateral Sclerosis Using High-Throughput Sequencing. Frontiers in Microbiology, 2016, 7, 1479.	1.5	145
599	Polycyclic Aromatic Hydrocarbon-Induced Changes in Bacterial Community Structure under Anoxic Nitrate Reducing Conditions. Frontiers in Microbiology, 2016, 7, 1775.	1.5	29
600	The Microbiota of Recreational Freshwaters and the Implications for Environmental and Public Health. Frontiers in Microbiology, 2016, 7, 1826.	1.5	70
601	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. Frontiers in Nutrition, 2016, 3, 26.	1.6	40
602	Metabarcoding of Bacteria Associated with the Acute Oak Decline Syndrome in England. Forests, 2016, 7, 95.	0.9	32
603	Machine Learning Meta-analysis of Large Metagenomic Datasets: Tools and Biological Insights. PLoS Computational Biology, 2016, 12, e1004977.	1.5	434
604	Actinorhizal Alder Phytostabilization Alters Microbial Community Dynamics in Gold Mine Waste Rock from Northern Quebec: A Greenhouse Study. PLoS ONE, 2016, 11, e0150181.	1.1	42
605	Soil Respiration and Bacterial Structure and Function after 17 Years of a Reciprocal Soil Transplant Experiment. PLoS ONE, 2016, 11, e0150599.	1.1	60
606	Age-Related Differences in the Gastrointestinal Microbiota of Chinstrap Penguins (Pygoscelis) Tj ETQq0 0 0 rgBT	/Oyerlock	10Jf 50 422
607	A Novel Analysis Method for Paired-Sample Microbial Ecology Experiments. PLoS ONE, 2016, 11, e0154804.	1.1	9
608	Key Microbiota Identification Using Functional Gene Analysis during Pepper (Piper nigrum L.) Peeling. PLoS ONE, 2016, 11, e0165206.	1.1	0
609	Distribution of Root-Associated Bacterial Communities Along a Salt-Marsh Primary Succession. Frontiers in Plant Science, 2015, 6, 1188.	1.7	27
610	Leaf Treatments with a Protein-Based Resistance Inducer Partially Modify Phyllosphere Microbial Communities of Grapevine. Frontiers in Plant Science, 2016, 7, 1053.	1.7	20
611	Exploring the cockatiel (<i>Nymphicus hollandicus</i>) fecal microbiome, bacterial inhabitants of a worldwide pet. PeerJ, 2016, 4, e2837.	0.9	22
612	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
613	Saharan dust nutrients promote <i>Vibrio</i> bloom formation in marine surface waters. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5964-5969.	3.3	90
614	On the use of highâ€ŧhroughput sequencing for the study of cyanobacterial diversity in Antarctic aquatic mats. Journal of Phycology, 2016, 52, 356-368.	1.0	36
	Microbial <scp>F</scp> e(<scp>III</scp>) oxide reduction potential in <scp>C</scp> hocolate		

#	Article	IF	CITATIONS
616	Structural Change in Microbiota by a Probiotic Cocktail Enhances the Gut Barrier and Reduces Cancer via TLR2 Signaling in a Rat Model of Colon Cancer. Digestive Diseases and Sciences, 2016, 61, 2908-2920.	1.1	121
617	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
618	Metagenomic analysis provides insights into functional capacity in a hyperarid desert soil niche community. Environmental Microbiology, 2016, 18, 1875-1888.	1.8	96
619	Cultivating microbial dark matter in benzeneâ€degrading methanogenic consortia. Environmental Microbiology, 2016, 18, 2923-2936.	1.8	54
620	Nextâ€Generation Sequencing of the Bacterial 16S <scp>rRNA</scp> Gene for Forensic Soil Comparison: A Feasibility Study. Journal of Forensic Sciences, 2016, 61, 607-617.	0.9	47
621	Bacterial indicator taxa in soils under different long-term agricultural management. Journal of Applied Microbiology, 2016, 120, 921-933.	1.4	56
622	An Effective Approach for Cloud-Based Microbial Metagenomics Analysis. , 2016, , .		0
623	The gut microbiota in conventional and serrated precursors of colorectal cancer. Microbiome, 2016, 4, 69.	4.9	206
624	Surfactant-associated bacteria in the near-surface layer of the ocean. Scientific Reports, 2016, 6, 19123.	1.6	53
625	Large-scale benchmarking reveals false discoveries and count transformation sensitivity in 16S rRNA gene amplicon data analysis methods used in microbiome studies. Microbiome, 2016, 4, 62.	4.9	138
626	Population Dynamics of Bulking and Foaming Bacteria in a Full-scale Wastewater Treatment Plant over Five Years. Scientific Reports, 2016, 6, 24180.	1.6	30
627	Effect of short-term room temperature storage on the microbial community in infant fecal samples. Scientific Reports, 2016, 6, 26648.	1.6	39
628	Impact of aluminum chloride on process performance and microbial community structure of granular sludge in an upflow anaerobic sludge blanket reactor for natural rubber processing wastewater treatment. Water Science and Technology, 2016, 74, 500-507.	1.2	10
629	Profiling bacterial communities associated with sediment-based aquaculture bioremediation systems under contrasting redox regimes. Scientific Reports, 2016, 6, 38850.	1.6	38
630	The developing hypopharyngeal microbiota in early life. Microbiome, 2016, 4, 70.	4.9	46
631	The Denture-Associated Oral Microbiome in Health and Stomatitis. MSphere, 2016, 1, .	1.3	44
632	Silicon content of individual cells of Synechococcus from the North Atlantic Ocean. Marine Chemistry, 2016, 187, 16-24.	0.9	24
633	Influence of maternal breast milk ingestion on acquisition of the intestinal microbiome in preterm infants. Microbiome, 2016, 4, 68.	4.9	155

ARTICLE IF CITATIONS # Pitfalls of haplotype phasing from amplicon-based long-read sequencing. Scientific Reports, 2016, 6, 634 1.6 62 21746. Seasonal Changes in Bacterial Communities Cause Foaming in a Wastewater Treatment Plant. 1.4 Microbial Ecology, 2016, 71, 660-671. Metagenomic Profiling, Interaction of Genomics with Meta-genomics. Translational Bioinformatics, 636 0.0 0 2016, , 241-267. Shifts of live bacterial community in secondary effluent by chlorine disinfection revealed by Miseq high-throughput sequencing combined with propidium monoazide treatment. Applied Microbiology and Biotechnology, 2016, 100, 6435-6446. Illumina-based analysis of core actinobacteriome in roots, stems, and grains of rice. Microbiological 638 2.5 34 Research, 2016, 190, 12-18. BMPOS: a Flexible and User-Friendly Tool Sets for Microbiome Studies. Microbial Ecology, 2016, 72, 639 1.4 443-447. Composition and function of the pediatric colonic mucosal microbiome in untreated patients with 640 4.3 84 ulcerative colitis. Gut Microbes, 2016, 7, 384-396. Intricacies of assessing the human microbiome in epidemiologic studies. Annals of Epidemiology, 2016, 641 46 26, 311-321. Microbial community dynamics in continuous microbial fuel cells fed with synthetic wastewater and 642 2.4 42 pig slurry. Bioelectrochémistry, 2016, 111, 70-82. Performance assessment and microbial diversity of two pilot scale multi-stage sub-surface flow 643 3.2 constructed wetland systems. Journal of Environmental Sciences, 2016, 46, 38-46. Exploring the Bacterial Diversity of Belgian Steak Tartare Using Metagenetics and Quantitative 644 0.8 24 Real-Time PCR Analysis. Journal of Food Protection, 2016, 79, 220-229. Fecal bacterial microbiome diversity in chronic HIV-infected patients in China. Emerging Microbes and 3.0 Infections, 2016, 5, 1-7. Mineralogy and Microbial Diversity of the Microbialites in the Hypersaline Storr's Lake, the Bahamas. 646 1.5 23 Astrobiology, 2016, 16, 282-300. 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. 647 1.3 46 Analysis of microbial diversity and dynamics during wine fermentation of Grenache grape variety by 648 2.5107 high-throughput barcoding sequencing. LWT - Food Science and Technology, 2016, 72, 317-321. A chronic rhinosinusitis–derived isolate of <i>Pseudomonas aeruginosa</i> induces acute and pervasive effects on the murine upper airway microbiome and host immune response. International 649 Forum of Allergy and Rhinology, 2016, 6, 1229-1237. Detailed comparison of bacterial communities during seasonal sludge bulking in a municipal 650 5.396 wastewater treatment plant. Water Research, 2016, 105, 157-166. Bacterial microbiota associated with flower pollen is influenced by pollination type, and shows a 1.8 high degree of diversity and speciesâ€specificity. Environmental Microbiology, 2016, 18, 5161-5174.

#	Article	IF	CITATIONS
652	Efficiency of different solarization-based ecological soil treatments on the control of Fusarium wilt and their impacts on the soil microbial community. Applied Soil Ecology, 2016, 108, 341-351.	2.1	26
653	Effect of dietary interventions on the intestinal microbiota of Mongolian hosts. Science Bulletin, 2016, 61, 1605-1614.	4.3	16
654	Unique hyper-thermal composting process in Kagoshima City forms distinct bacterial community structures. Journal of Bioscience and Bioengineering, 2016, 122, 606-612.	1.1	24
655	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
656	Bacterial microbiota compositions of naturally fermented milk are shaped by both geographic origin and sample type. Journal of Dairy Science, 2016, 99, 7832-7841.	1.4	69
657	Testing life history and trait-based predictions of AM fungal community assembly. Pedobiologia, 2016, 59, 203-213.	0.5	16
658	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
659	From the Cover: Exposure to Oral Antibiotics Induces Gut Microbiota Dysbiosis Associated with Lipid Metabolism Dysfunction and Low-Grade Inflammation in Mice. Toxicological Sciences, 2016, 154, 140-152.	1.4	70
660	High-Level Culturability of Epiphytic Bacteria and Frequency of Biosurfactant Producers on Leaves. Applied and Environmental Microbiology, 2016, 82, 5997-6009.	1.4	32
661	Metagenomic and near full-length 16S rRNA sequence data in support of the phylogenetic analysis of the rumen bacterial community in steers. Data in Brief, 2016, 8, 1048-1053.	0.5	12
662	Metabarcoding Marine Sediments: Preparation of Amplicon Libraries. Methods in Molecular Biology, 2016, 1452, 183-196.	0.4	33
663	Effects of heat shocks on microbial community structure and microbial activity of a methanogenic enrichment degrading benzoate. Letters in Applied Microbiology, 2016, 63, 356-362.	1.0	40
664	Effect of Wild and Cultivated Rice Genotypes on Rhizosphere Bacterial Community Composition. Rice, 2016, 9, 42.	1.7	75
665	Morphine Promotes Colonization of Anastomotic Tissues with Collagenase - Producing Enterococcus faecalis and Causes Leak. Journal of Gastrointestinal Surgery, 2016, 20, 1744-1751.	0.9	43
666	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
667	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
668	Coupling among Microbial Communities, Biogeochemistry and Mineralogy across Biogeochemical Facies. Scientific Reports, 2016, 6, 30553.	1.6	26
669	Chronic Repression of mTOR Complex 2 Induces Changes in the Gut Microbiota of Diet-induced Obese Mice. Scientific Reports, 2016, 6, 30887.	1.6	142

#	Article	IF	CITATIONS
670	Pipeline for amplifying and analyzing amplicons of the V1–V3 region of the 16S rRNA gene. BMC Research Notes, 2016, 9, 380.	0.6	61
671	Metagenomics and Bioinformatics in Microbial Ecology: Current Status and Beyond. Microbes and Environments, 2016, 31, 204-212.	0.7	76
672	Longitudinal Survey of Microbiota in Hospitalized Preterm Very‣owâ€Birthâ€Weight Infants. Journal of Pediatric Gastroenterology and Nutrition, 2016, 62, 292-303.	0.9	58
673	Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies. Nature Biotechnology, 2016, 34, 942-949.	9.4	623
674	Antibiotics, birth mode, and diet shape microbiome maturation during early life. Science Translational Medicine, 2016, 8, 343ra82.	5.8	1,012
675	Barcoding lichen-forming fungi using 454 pyrosequencing is challenged by artifactual and biological sequence variation. Genome, 2016, 59, 685-704.	0.9	32
676	Bacterial community composition and structure in an Urban River impacted by different pollutant sources. Science of the Total Environment, 2016, 566-567, 1176-1185.	3.9	149
677	Glial-cell-derived neuroregulators control type 3 innate lymphoid cells and gut defence. Nature, 2016, 535, 440-443.	13.7	272
678	Quality assessment of ice-stored tropical yellowfin tuna (Thunnus albacares) and influence of vacuum and modified atmosphere packaging. Food Microbiology, 2016, 60, 62-72.	2.1	47
679	Variations of rhizosphere bacterial communities in tea (<i>Camellia sinensis</i> L.) continuous cropping soil by high-throughput pyrosequencing approach. Journal of Applied Microbiology, 2016, 121, 787-799.	1.4	95
680	Human CODIS STR loci profiling from HTS data. , 2016, , .		4
681	Gut dysbiosis impairs recovery after spinal cord injury. Journal of Experimental Medicine, 2016, 213, 2603-2620.	4.2	236
682	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. MSphere, 2016, 1, .	1.3	28
683	Emerging diagnostic and therapeutic options for treating mucormycosis. Expert Opinion on Orphan Drugs, 2016, 4, 1253-1261.	0.5	4
684	Composition of gut microbiota in infants in China and global comparison. Scientific Reports, 2016, 6, 36666.	1.6	63
685	Bacterial and archaeal communities in the deep-sea sediments of inactive hydrothermal vents in the Southwest India Ridge. Scientific Reports, 2016, 6, 25982.	1.6	52
686	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
687	Bacterial diversity in saliva and oral health-related conditions: the Hisayama Study. Scientific Reports, 2016, 6, 22164.	1.6	221

#	Article	IF	CITATIONS
688	Planktonic protistan communities in lakes along a large-scale environmental gradient. FEMS Microbiology Ecology, 2017, 93, fiw231.	1.3	28
689	A key genetic factor for fucosyllactose utilization affects infant gut microbiota development. Nature Communications, 2016, 7, 11939.	5.8	284
690	MetaTrans: an open-source pipeline for metatranscriptomics. Scientific Reports, 2016, 6, 26447.	1.6	87
691	Colonic transit time is related to bacterial metabolism and mucosal turnover in the gut. Nature Microbiology, 2016, 1, 16093.	5.9	321
692	Alterations in the Fecal Microbiota of Patients with HIV-1 Infection: An Observational Study in A Chinese Population. Scientific Reports, 2016, 6, 30673.	1.6	153
693	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. Genome Biology, 2016, 17, 217.	3.8	128
694	Next generation sequencing data of a defined microbial mock community. Scientific Data, 2016, 3, 160081.	2.4	90
695	EFFECT OF VARIATION IN ORGANIC ACID COMPOSITION ON PERFORMANCE OF MICROBIAL FUEL CELL. Journal of Japan Society of Civil Engineers Ser G (Environmental Research), 2016, 72, III_145-III_152.	0.1	0
696	Species-level core oral bacteriome identified by 16S rRNA pyrosequencing in a healthy young Arab population. Journal of Oral Microbiology, 2016, 8, 31444.	1.2	14
697	High purity galacto-oligosaccharides enhance specific Bifidobacterium species and their metabolic activity in the mouse gut microbiome. Beneficial Microbes, 2016, 7, 247-264.	1.0	85
698	RiboTagger: fast and unbiased 16S/18S profiling using whole community shotgun metagenomic or metatranscriptome surveys. BMC Bioinformatics, 2016, 17, 508.	1.2	22
699	Improved assembly procedure of viral RNA genomes amplified with Phi29 polymerase from new generation sequencing data. Biological Research, 2016, 49, 39.	1.5	10
700	Effect of pH on soil bacterial diversity. Journal of Ecology and Environment, 2016, 40, .	1.6	50
701	Response of bacterial colonization in <scp><i>N</i></scp> <i>ematostella vectensis</i> to development, environment and biogeography. Environmental Microbiology, 2016, 18, 1764-1781.	1.8	109
702	The effects of host age and spatial location on bacterial community composition in the English Oak tree (<i>Quercus robur</i>). Environmental Microbiology Reports, 2016, 8, 649-658.	1.0	33
703	Targeted DNA Region Re-sequencing. , 2016, , 43-68.		9
704	Benthic protists: the under-charted majority. FEMS Microbiology Ecology, 2016, 92, fiw120.	1.3	94
705	Evaluation of 16S rRNA amplicon sequencing using two next-generation sequencing technologies for phylogenetic analysis of the rumen bacterial community in steers. Journal of Microbiological Methods, 2016, 127, 132-140.	0.7	79

#	Article	IF	CITATIONS
706	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. MBio, 2016, 7, .	1.8	325
707	Diversity at low abundance: The phenomenon of the rare bacterial biosphere. Microbiology, 2016, 85, 272-282.	0.5	18
708	Metagenomic analysis of bacterial community composition and antibiotic resistance genes in a wastewater treatment plant and its receiving surface water. Ecotoxicology and Environmental Safety, 2016, 132, 260-269.	2.9	123
709	Investigation of bacterial and archaeal communities: novel protocols using modern sequencing by Illumina MiSeq and traditional DGCE-cloning. Extremophiles, 2016, 20, 795-808.	0.9	17
710	Identification of abiotic and biotic reductive dechlorination in a chlorinated ethene plume after thermal source remediation by means of isotopic and molecular biology tools. Journal of Contaminant Hydrology, 2016, 192, 1-19.	1.6	42
711	A comparison of tools for the simulation of genomic next-generation sequencing data. Nature Reviews Genetics, 2016, 17, 459-469.	7.7	163
712	Lotic bacterioplankton and phytoplankton community changes under dissolved organic-carbon amendment: evidence for competition for nutrients. Marine and Freshwater Research, 2016, 67, 1362.	0.7	11
713	Limited genetic and antigenic diversity within parasite isolates used in a live vaccine against Theileria parva. International Journal for Parasitology, 2016, 46, 495-506.	1.3	41
714	Endophytic bacterial and fungal microbiota in sprouts, roots and stems of rice (Oryza sativa L.). Microbiological Research, 2016, 188-189, 1-8.	2.5	102
715	Environmental Sequencing Provides Reasonable Estimates of the Relative Abundance of Specific Picoeukaryotes. Applied and Environmental Microbiology, 2016, 82, 4757-4766.	1.4	118
716	Bacterial community in Haemaphysalis ticks of domesticated animals from the Orang Asli communities in Malaysia. Ticks and Tick-borne Diseases, 2016, 7, 929-937.	1.1	62
717	Challenges for case-control studies with microbiome data. Annals of Epidemiology, 2016, 26, 336-341.e1.	0.9	28
718	Hydrogeochemistry and coal-associated bacterial populations from a methanogenic coal bed. International Journal of Coal Geology, 2016, 162, 14-26.	1.9	56
719	Biogeochemical gradients above a coal tar DNAPL. Science of the Total Environment, 2016, 563-564, 741-754.	3.9	6
720	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
721	Long-Term Field Study of Microbial Community and Dechlorinating Activity Following Carboxymethyl Cellulose-Stabilized Nanoscale Zero-Valent Iron Injection. Environmental Science & Technology, 2016, 50, 7658-7670.	4.6	97
722	Characterization of the microbial community composition and the distribution of Fe-metabolizing bacteria in a creek contaminated by acid mine drainage. Applied Microbiology and Biotechnology, 2016, 100, 8523-8535.	1.7	40
723	Novel nitrifiers and comammox in a full-scale hybrid biofilm and activated sludge reactor revealed by metagenomic approach. Applied Microbiology and Biotechnology, 2016, 100, 8225-8237.	1.7	90

#	Article	IF	CITATIONS
724	16S rRNA gene sequencing of mock microbial populations- impact of DNA extraction method, primer choice and sequencing platform. BMC Microbiology, 2016, 16, 123.	1.3	241
725	Response of the bacterial community associated with a cosmopolitan marine diatom to crude oil shows a preference for the biodegradation of aromatic hydrocarbons. Environmental Microbiology, 2016, 18, 1817-1833.	1.8	68
726	The Fecal Microbiome in Pediatric Patients With Short Bowel Syndrome. Journal of Parenteral and Enteral Nutrition, 2016, 40, 1106-1113.	1.3	57
727	The microbiome of diabetic foot osteomyelitis. European Journal of Clinical Microbiology and Infectious Diseases, 2016, 35, 293-298.	1.3	80
728	Supraglacial bacterial community structures vary across the Greenland ice sheet. FEMS Microbiology Ecology, 2016, 92, fiv164.	1.3	48
729	Evaluation of microbial population and functional genes during the bioremediation of petroleum-contaminated soil as an effective monitoring approach. Ecotoxicology and Environmental Safety, 2016, 125, 153-160.	2.9	85
730	Aerobic biofilm reactor for treating a commercial formulation of the herbicides 2,4-D and dicamba: Biodegradation kinetics and biofilm bacterial diversity. International Biodeterioration and Biodegradation, 2016, 107, 123-131.	1.9	36
731	Inhibitory effects of laminaran and alginate on production of putrefactive compounds from soy protein by intestinal microbiota in vitro and in rats. Carbohydrate Polymers, 2016, 143, 61-69.	5.1	51
732	Exploring potential bacterial and fungal biocontrol agents transmitted from seeds to sprouts of wheat. Biological Control, 2016, 98, 27-33.	1.4	119
733	Genome-Based Microbial Taxonomy Coming of Age. Cold Spring Harbor Perspectives in Biology, 2016, 8, a018085.	2.3	69
734	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
735	Cigarette smoking and the oral microbiome in a large study of American adults. ISME Journal, 2016, 10, 2435-2446.	4.4	445
736	Inâ€solution hybridization for mammalian mitogenome enrichment: pros, cons and challenges associated with multiplexing degraded DNA. Molecular Ecology Resources, 2016, 16, 1173-1188.	2.2	50
737	Skin Microbiome Surveys Are Strongly Influenced by Experimental Design. Journal of Investigative Dermatology, 2016, 136, 947-956.	0.3	249
738	Archaeal ammonium oxidation coupled with bacterial nitrite oxidation in a simulated drinking water premise plumbing system. Environmental Science: Water Research and Technology, 2016, 2, 658-669.	1.2	3
739	Interactions between hydrology and water chemistry shape bacterioplankton biogeography across boreal freshwater networks. ISME Journal, 2016, 10, 1755-1766.	4.4	183
740	Profiling microbial community in a watershed heavily contaminated by an active antimony (Sb) mine in Southwest China. Science of the Total Environment, 2016, 550, 297-308.	3.9	104
741	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
742	A novel conceptual approach to read-filtering in high-throughput amplicon sequencing studies. Nucleic Acids Research, 2016, 44, e40-e40.	6.5	35
743	Structural variation detection using next-generation sequencing data. Methods, 2016, 102, 36-49.	1.9	129
744	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
745	Comparison of biogas sludge and raw crop material as source of hydrolytic cultures for anaerobic digestion. Bioresource Technology, 2016, 207, 244-251.	4.8	27
746	Airborne Bacterial Diversity from the Low Atmosphere of Greater Mexico City. Microbial Ecology, 2016, 72, 70-84.	1.4	31
747	Self-decontaminating photocatalytic zinc oxide nanorod coatings for prevention of marine microfouling: a mesocosm study. Biofouling, 2016, 32, 383-395.	0.8	38
748	bioOTU: An Improved Method for Simultaneous Taxonomic Assignments and Operational Taxonomic Units Clustering of 16s rRNA Gene Sequences. Journal of Computational Biology, 2016, 23, 229-238.	0.8	11
749	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
750	Responses of anaerobic microorganisms to different culture conditions and corresponding effects on biogas production and solid digestate quality. Biomass and Bioenergy, 2016, 85, 84-93.	2.9	29
751	Temporal–spatial variation of bacterial diversity in estuary sediments in the south of Zhejiang Province, China. Applied Microbiology and Biotechnology, 2016, 100, 2817-2828.	1.7	31
752	Microbial community in a pilot-scale bioreactor promoting anaerobic digestion and sulfur-driven denitrification for domestic sewage treatment. Bioprocess and Biosystems Engineering, 2016, 39, 341-352.	1.7	50
753	Microbial Signatures of Cadaver Gravesoil During Decomposition. Microbial Ecology, 2016, 71, 524-529.	1.4	81
754	Prokaryotic Community Structure Driven by Salinity and Ionic Concentrations in Plateau Lakes of the Tibetan Plateau. Applied and Environmental Microbiology, 2016, 82, 1846-1858.	1.4	81
755	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
756	Bacterial community dynamics in surface flow constructed wetlands for the treatment of swine waste. Science of the Total Environment, 2016, 544, 68-76.	3.9	45
757	Tools for the Microbiome: Nano and Beyond. ACS Nano, 2016, 10, 6-37.	7.3	137
758	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
759	Lactulose Challenge Determines Visceral Sensitivity and Severity of Symptoms in Patients With Irritable Bowel Syndrome. Clinical Gastroenterology and Hepatology, 2016, 14, 226-233.e3.	2.4	38

#	Article	IF	CITATIONS
760	Long-Term Enrichment on Cellulose or Xylan Causes Functional and Taxonomic Convergence of Microbial Communities from Anaerobic Digesters. Applied and Environmental Microbiology, 2016, 82, 1519-1529.	1.4	28
761	Impact of different ratios of feedstock to liquid anaerobic digestion effluent on the performance and microbiome of solid-state anaerobic digesters digesting corn stover. Bioresource Technology, 2016, 200, 744-752.	4.8	47
762	Development of a BR–UASB–DHS system for natural rubber processing wastewater treatment. Environmental Technology (United Kingdom), 2016, 37, 459-465.	1.2	21
763	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
764	Massively parallel sequencing-based survey of eukaryotic community structures in Hiroshima Bay and Ishigaki Island. Gene, 2016, 576, 681-689.	1.0	17
765	Microbiote shift in the Medicago sativa rhizosphere in response to cyanotoxins extract exposure. Science of the Total Environment, 2016, 539, 135-142.	3.9	37
766	Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. ISME Journal, 2016, 10, 582-595.	4.4	91
767	Activity and community structures of sulfate-reducing microorganisms in polar, temperate and tropical marine sediments. ISME Journal, 2016, 10, 796-809.	4.4	85
768	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. Applied and Environmental Microbiology, 2016, 82, 157-166.	1.4	73
769	When riverine dissolved organic matter (DOM) meets labile DOM in coastal waters: changes in bacterial community activity and composition. Aquatic Sciences, 2017, 79, 27-43.	0.6	44
770	Psyllium Fiber Reduces Abdominal Pain in Children With Irritable Bowel Syndrome in a Randomized, Double-Blind Trial. Clinical Gastroenterology and Hepatology, 2017, 15, 712-719.e4.	2.4	77
771	Ecological succession of the microbial communities of an air-conditioning cooling coil in the tropics. Indoor Air, 2017, 27, 345-353.	2.0	22
772	Maturation of the infant microbiome community structure and function across multiple body sites and in relation to mode of delivery. Nature Medicine, 2017, 23, 314-326.	15.2	751
773	Performing Skin Microbiome Research: A Method to the Madness. Journal of Investigative Dermatology, 2017, 137, 561-568.	0.3	164
774	Bovine milk oligosaccharides decrease gut permeability and improve inflammation and microbial dysbiosis in diet-induced obese mice. Journal of Dairy Science, 2017, 100, 2471-2481.	1.4	64
775	Impact of elevated CO2 concentrations on carbonate mineral precipitation ability of sulfate-reducing bacteria and implications forÂCO2 sequestration. Applied Geochemistry, 2017, 78, 250-271.	1.4	20
776	Optimisation of methods for bacterial skin microbiome investigation: primer selection and comparison of the 454 versus MiSeq platform. BMC Microbiology, 2017, 17, 23.	1.3	133
777	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

#	Article	IF	CITATIONS
778	Long-term performance of sediment microbial fuel cells with multiple anodes. Bioresource Technology, 2017, 237, 178-185.	4.8	39
779	Development and evaluation of a trickle bed bioreactor for enhanced mass transfer and methanol production from biogas. Biochemical Engineering Journal, 2017, 122, 103-114.	1.8	31
780	Prebiotic milk oligosaccharides prevent development of obese phenotype, impairment of gut permeability, and microbial dysbiosis in high fat-fed mice. American Journal of Physiology - Renal Physiology, 2017, 312, G474-G487.	1.6	58
781	Metabolic in Vivo Labeling Highlights Differences of Metabolically Active Microbes from the Mucosal Gastrointestinal Microbiome between High-Fat and Normal Chow Diet. Journal of Proteome Research, 2017, 16, 1593-1604.	1.8	26
782	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
783	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
784	Effect of advanced oxidation on N-nitrosodimethylamine (NDMA) formation and microbial ecology during pilot-scale biological activated carbon filtration. Water Research, 2017, 113, 160-170.	5.3	27
785	Tumour-associated and non-tumour-associated microbiota in colorectal cancer. Gut, 2017, 66, 633-643.	6.1	623
786	Association of oral microbiome with type 2 diabetes risk. Journal of Periodontal Research, 2017, 52, 636-643.	1.4	150
787	Quantification of Chloroflexi Eikelboom morphotype 1851 for prediction and control of bulking events in municipal activated sludge plants in Japan. Applied Microbiology and Biotechnology, 2017, 101, 3861-3869.	1.7	25
788	Glycomacropeptide Sustains Microbiota Diversity and Promotes Specific Taxa in an Artificial Colon Model of Elderly Gut Microbiota. Journal of Agricultural and Food Chemistry, 2017, 65, 1836-1846.	2.4	35
789	Experimental fossilization of matâ€forming cyanobacteria in coarseâ€grained siliciclastic sediments. Geobiology, 2017, 15, 484-498.	1.1	24
790	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
792	Effect of inoculum pretreatment on the microbial community structure and its performance during dark fermentation using anaerobic fluidized-bed reactors. International Journal of Hydrogen Energy, 2017, 42, 9589-9599.	3.8	15
793	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
794	Microbial Community Structure in a Serpentine-Hosted Abiotic Gas Seepage at the Chimaera Ophiolite, Turkey. Applied and Environmental Microbiology, 2017, 83, .	1.4	37
795	Sediment anoxia limits microbial-driven seagrass carbon remineralization under warming conditions. FEMS Microbiology Ecology, 2017, 93, .	1.3	82
796	Liver microbiome of Peromyscus leucopus , a key reservoir host species for emerging infectious diseases in North America. Infection, Genetics and Evolution, 2017, 52, 10-18.	1.0	14

ARTICLE IF CITATIONS A signature of tree health? Shifts in the microbiome and the ecological drivers of horse chestnut 797 3.5 61 bleeding canker disease. New Phytologist, 2017, 215, 737-746. pH-Mediated Microbial and Metabolic Interactions in Fecal Enrichment Cultures. MSphere, 2017, 2, . 798 1.3 Effect of fumigation with chloropicrin on soil bacterial communities and genes encoding key enzymes 799 3.7 84 involved in nitrogen cycling. Environmental Pollution, 2017, 227, 534-542. 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. 800 3.9 DNA-based study of the diet of the marine calanoid copepod Calanus sinicus. Journal of Experimental 801 0.7 29 Marine Biology and Ecology, 2017, 494, 1-9. Differences in gut microbial composition correlate with regional brain volumes in irritable bowel 228 syndrome. Microbiome, 2017, 5, 49. Geographic distribution of cadmium and its interaction with the microbial community in the 803 1.6 18 Longjiang River: risk evaluation after a shocking pollution accident. Scientific Reports, 2017, 7, 227. Changes in rumen protozoal community by condensed tannin fractions of different molecular weights from a<i>Leucaena leucocephala</i>hybrid<i>inÂvitro</i>. Journal of Applied Microbiology, 804 1.4 9 2017, 123, 41-53. The role of microbiota, and probiotics and prebiotics in skin health. Archives of Dermatological 805 72 1.1 Research, 2017, 309, 411-421. Characterization of an autotrophic bioreactor microbial consortium degrading thiocyanate. Applied 1.7 Microbiology and Biotechnology, 2017, 101, 5889-5901. Diabetes-associated microbiota in fa/fa rats is modified by Roux-en-Y gastric bypass. ISME Journal, 2017, 807 4.4 52 11, 2035-2046. Effect of biochar on anaerobic degradation of pentabromodiphenyl ether (BDE-99) by archaea during natural groundwater recharge with treated municipal wastewater. International Biodeterioration and Biodegradation, 2017, 124, 119-127. 808 Topical Antimicrobial Treatments Can Elicit Shifts to Resident Skin Bacterial Communities and Reduce Colonization by Staphylococcus aureus Competitors. Antimicrobial Agents and Chemotherapy, 2017, 61, 809 1.4 48 Land use alters arbuscular mycorrhizal fungal communities and their potential role in carbon 1.6 39 sequestration on the Tibetan Plateau. Scientific Reports, 2017, 7, 3067. Optimizing methods and dodging pitfalls in microbiome research. Microbiome, 2017, 5, 52. 811 4.9 420 The response of archaeal species to seasonal variables in a subtropical aerated soil: insight into the low abundant methanogens. Applied Microbiology and Biotechnology, 2017, 101, 6505-6515. Bioaerosol sampling and detection methods based on molecular approaches: No pain no gain. Science 813 3.9 54 of the Total Environment, 2017, 599-600, 2095-2104. Body fluid prediction from microbial patterns for forensic application. Forensic Science 814 International: Genetics, 2017, 30, 10-17.

#	Article	IF	CITATIONS
815	Evaluation of method bias for determining bacterial populations in bacterial community analyses. Journal of Bioscience and Bioengineering, 2017, 124, 476-486.	1.1	9
816	The influence of rosuvastatin on the gastrointestinal microbiota and host gene expression profiles. American Journal of Physiology - Renal Physiology, 2017, 312, G488-G497.	1.6	43
817	Temporal dynamics of the gut microbiota in people sharing a confined environment, a 520-day ground-based space simulation, MARS500. Microbiome, 2017, 5, 39.	4.9	89
818	Large-scale 16S gene assembly using metagenomics shotgun sequences. Bioinformatics, 2017, 33, 1447-1456.	1.8	13
819	Protective effects of mannan oligosaccharides on turbot Scophthalmus maximus suffering from soy enteropathy. Aquaculture, 2017, 476, 141-151.	1.7	40
820	Methods for Microbiome Analysis. Translational Medicine Research, 2017, , 269-298.	0.0	1
821	The Dynamic Microbiota Profile During Pepper (Piper nigrum L.) Peeling by Solid-State Fermentation. Current Microbiology, 2017, 74, 739-746.	1.0	10
822	Novel 16S rDNA primers revealed the diversity and habitats-related community structure of sphingomonads in 10 different niches. Antonie Van Leeuwenhoek, 2017, 110, 877-889.	0.7	9
823	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
824	Integrating the microbiota of the respiratory tract with the unified airway model. Respiratory Medicine, 2017, 126, 68-74.	1.3	23
825	Human milk microbiome in urban and rural populations of India. Meta Gene, 2017, 13, 13-22.	0.3	25
826	Electricity and biomass production in a bacteria- Chlorella based microbial fuel cell treating wastewater. Journal of Power Sources, 2017, 356, 299-309.	4.0	66
827	Microbial community and metabolic pathway succession driven by changed nutrient inputs in tailings: effects of different nutrients on tailing remediation. Scientific Reports, 2017, 7, 474.	1.6	37
828	Community structure of the gut microbiota in sympatric species of wild <i>Drosophila</i> . Ecology Letters, 2017, 20, 629-639.	3.0	118
829	The lower airway microbiota in early cystic fibrosis lung disease: a longitudinal analysis. Thorax, 2017, 72, 1104-1112.	2.7	90
830	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
831	Enlightening discriminative network functional modules behind Principal Component Analysis separation in differential-omic science studies. Scientific Reports, 2017, 7, 43946.	1.6	45
832	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. Environmental Science & Technology, 2017, 51, 3609-3620.	4.6	22

#	Article	IF	CITATIONS
833	High throughput 16SrRNA gene sequencing reveals the correlation between Propionibacterium acnes and sarcoidosis. Respiratory Research, 2017, 18, 28.	1.4	27
834	Organism and Microbiome Analysis. Otolaryngologic Clinics of North America, 2017, 50, 521-532.	0.5	3
835	Metagenomics of Hyperthermophilic Environments: Biodiversity and Biotechnology. , 2017, , 103-135.		7
836	Diel-scale temporal dynamics recorded for bacterial groups in Namib Desert soil. Scientific Reports, 2017, 7, 40189.	1.6	42
837	Exploration of bacterial species associated with the salivary microbiome of individuals with a low susceptibility to dental caries. Clinical Oral Investigations, 2017, 21, 2399-2406.	1.4	17
838	Helminth burden and ecological factors associated with alterations in wild host gastrointestinal microbiota. ISME Journal, 2017, 11, 663-675.	4.4	30
839	Patterns of bacterial diversity in the marine planktonic particulate matter continuum. ISME Journal, 2017, 11, 999-1010.	4.4	128
840	Impact of short-chain galactooligosaccharides on the gut microbiome of lactose-intolerant individuals. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E367-E375.	3.3	193
841	Molecular methods resolve the bacterial composition of natural marine biofilms on galvanically coupled stainless steel cathodes. Journal of Industrial Microbiology and Biotechnology, 2017, 44, 167-180.	1.4	4
842	Tobacco bacterial wilt suppression with biochar soil addition associates to improved soil physiochemical properties and increased rhizosphere bacteria abundance. Applied Soil Ecology, 2017, 112, 90-96.	2.1	109
843	Environmental Enteric Dysfunction and the Fecal Microbiota in Malawian Children. American Journal of Tropical Medicine and Hygiene, 2017, 96, 473-476.	0.6	41
844	Haptophyte Diversity and Vertical Distribution Explored by 18S and 28S Ribosomal <scp>RNA</scp> Gene Metabarcoding and Scanning Electron Microscopy. Journal of Eukaryotic Microbiology, 2017, 64, 514-532.	0.8	35
845	Effects of microbe- and mussel-based diets on the gut microbiota in Arctic charr (Salvelinus alpinus). Aquaculture Reports, 2017, 5, 34-40.	0.7	50
846	Thiosulfate Conversion to Sulfide by a Haloalkaliphilic Microbial Community in a Bioreactor Fed with H ₂ Gas. Environmental Science & Technology, 2017, 51, 914-923.	4.6	8
847	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
848	Depth-resolved microbial community analyses in two contrasting soil cores contaminated by antimony and arsenic. Environmental Pollution, 2017, 221, 244-255.	3.7	60
849	<i>In Situ</i> Stimulation of Thiocyanate Biodegradation through Phosphate Amendment in Gold Mine Tailings Water. Environmental Science & amp; Technology, 2017, 51, 13353-13362.	4.6	20
850	Ammonia exposure alters the expression of immune-related and antioxidant enzymes-related genes and the gut microbial community of crucian carp (Carassius auratus). Fish and Shellfish Immunology, 2017, 70, 485-492.	1.6	88

#	Article	IF	CITATIONS
851	Exploring the Plant Microbiome Through Multi-omics Approaches. , 2017, , 233-268.		11
852	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
853	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
854	Community structure of denitrifying and total bacteria during nitrogen accumulation in an ammoniaâ€loaded biofilter. Journal of Applied Microbiology, 2017, 123, 1498-1511.	1.4	14
855	High reactivity of deep biota under anthropogenic CO2 injection into basalt. Nature Communications, 2017, 8, 1063.	5.8	55
856	Prokaryotic Community Distribution along an Ecological Gradient of Salinity in Surface and Subsurface Saline Soils. Scientific Reports, 2017, 7, 13332.	1.6	33
857	Host–microbiota interaction induces bi-phasic inflammation and glucose intolerance in mice. Molecular Metabolism, 2017, 6, 1371-1380.	3.0	30
858	Core fecal microbiota of domesticated herbivorous ruminant, hindgut fermenters, and monogastric animals. MicrobiologyOpen, 2017, 6, e00509.	1.2	83
859	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	1.9	84
860	Coupling Bioflocculation of <i>Dehalococcoides mccartyi</i> to High-Rate Reductive Dehalogenation of Chlorinated Ethenes. Environmental Science & amp; Technology, 2017, 51, 11297-11307.	4.6	18
861	Environmental <scp>DNA</scp> metabarcoding: Transforming how we survey animal and plant communities. Molecular Ecology, 2017, 26, 5872-5895.	2.0	1,210
862	Investigating sources and sinks of N2O expression from freshwater microbial communities in urban watershed sediments. Chemosphere, 2017, 188, 697-705.	4.2	26
863	Antibiotic treatment for Tuberculosis induces a profound dysbiosis of the microbiome that persists long after therapy is completed. Scientific Reports, 2017, 7, 10767.	1.6	148
864	Identifying the Active Microbiome Associated with Roots and Rhizosphere Soil of Oilseed Rape. Applied and Environmental Microbiology, 2017, 83, .	1.4	141
865	The saliva microbiome profiles are minimally affected by collection method or DNA extraction protocols. Scientific Reports, 2017, 7, 8523.	1.6	103
866	Bacterial diversity among four healthcare-associated institutes in Taiwan. Scientific Reports, 2017, 7, 8230.	1.6	18
867	Intestinal colonisation patterns in breastfed and formula-fed infants during the first 12 weeks of life reveal sequential microbiota signatures. Scientific Reports, 2017, 7, 8327.	1.6	115
868	Lineage overwhelms environmental conditions in determining rhizosphere bacterial community structure in a cosmopolitan invasive plant. Nature Communications, 2017, 8, 433.	5.8	99

#	Article	IF	CITATIONS
869	The dynamics of the bacterial communities developed in maize silage. Microbial Biotechnology, 2017, 10, 1663-1676.	2.0	77
870	Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. Water Research, 2017, 124, 77-84.	5.3	82
871	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
872	Monitoring of Toxigenic Cyanobacteria Using Next-Generation Sequencing Techniques. , 2017, , 277-299.		0
873	Analysis of large 16S <scp>rRNA</scp> Illumina data sets: Impact of singleton read filtering on microbial community description. Molecular Ecology Resources, 2017, 17, e122-e132.	2.2	55
874	Relationships between gastrointestinal microbiota and blood group antigens. Physiological Genomics, 2017, 49, 473-483.	1.0	34
875	Enhancing biodegradation of C16-alkyl quaternary ammonium compounds using an oxygen-based membrane biofilm reactor. Water Research, 2017, 123, 825-833.	5.3	57
876	Major phylumâ€level differences between porefluid and host rock bacterial communities in the terrestrial deep subsurface. Environmental Microbiology Reports, 2017, 9, 501-511.	1.0	46
877	PCR cycles above routine numbers do not compromise high-throughput DNA barcoding results. Genome, 2017, 60, 868-873.	0.9	26
878	Association Between Gut Microbiota and Bone Health: Potential Mechanisms and Prospective. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 3635-3646.	1.8	103
879	Bioinspired nanocoatings for biofouling prevention by photocatalytic redox reactions. Scientific Reports, 2017, 7, 3624.	1.6	63
880	Microbiome analysis and confocal microscopy of used kitchen sponges reveal massive colonization by Acinetobacter, Moraxella and Chryseobacterium species. Scientific Reports, 2017, 7, 5791.	1.6	41
881	Insights into Butyrate Production in a Controlled Fermentation System via Gene Predictions. MSystems, 2017, 2, .	1.7	169
882	A clinician's guide to microbiome analysis. Nature Reviews Gastroenterology and Hepatology, 2017, 14, 585-595.	8.2	124
883	Photosynthetic carbon uptake induces autoflocculation of the marine microalga Nannochloropsis oculata. Algal Research, 2017, 26, 302-311.	2.4	42
884	Metabolic pathway analysis based on high-throughput sequencing in a batch biogas production process. Energy, 2017, 139, 571-579.	4.5	30
885	Modeling time-series data from microbial communities. ISME Journal, 2017, 11, 2526-2537.	4.4	52
886	Microbial Diversity of Genital Ulcers of HSV-2 Seropositive Women. Scientific Reports, 2017, 7, 15475.	1.6	8

#	Article	IF	CITATIONS
887	An intact gut microbiota may be required for lactoferrin-driven immunomodulation in rats. Journal of Functional Foods, 2017, 39, 268-278.	1.6	13
888	Effect of cytomegalovirus and Epstein–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
889	Application of the entomogenous fungus, Metarhizium anisopliae, for leafroller (Cnaphalocrocis) Tj ETQq0 0 0 rg Biotechnology, 2017, 101, 6793-6807.	BT /Overlo 1.7	ock 10 Tf 50 (26
890	Response of Soil Microbial Communities to Elevated Antimony and Arsenic Contamination Indicates the Relationship between the Innate Microbiota and Contaminant Fractions. Environmental Science & Technology, 2017, 51, 9165-9175.	4.6	133
891	Bacterial profile in human atherosclerotic plaques. Atherosclerosis, 2017, 263, 177-183.	0.4	49
892	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
893	Development of a genus-specific next generation sequencing approach for sensitive and quantitative determination of the Legionella microbiome in freshwater systems. BMC Microbiology, 2017, 17, 79.	1.3	32
894	Aberrant intestinal microbiota due to IL-1 receptor antagonist deficiency promotes IL-17- and TLR4-dependent arthritis. Microbiome, 2017, 5, 63.	4.9	73
895	Brain Structure and Response to Emotional Stimuli as Related to Gut Microbial Profiles in Healthy Women. Psychosomatic Medicine, 2017, 79, 905-913.	1.3	158
896	Optical properties of dissolved organic matter relate to different depth-specific patterns of archaeal and bacterial community structure in the North Atlantic Ocean. FEMS Microbiology Ecology, 2017, 93, fiw224.	1.3	39
897	Bacterial succession along a long-term chronosequence of paddy soil in the Yangtze River Delta, China. Soil Biology and Biochemistry, 2017, 104, 59-67.	4.2	70
898	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
899	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
900	Long-term fertilizer and crop-rotation treatments differentially affect soil bacterial community structure. Plant and Soil, 2017, 413, 145-159.	1.8	119
901	<scp>ITS</scp> all right mama: investigating the formation of chimeric sequences in the <scp>ITS</scp> 2 region by <scp>DNA</scp> metabarcoding analyses of fungal mock communities of different complexities. Molecular Ecology Resources, 2017, 17, 730-741.	2.2	52
902	Probiotics, gut microbiota, and their influence on host health and disease. Molecular Nutrition and Food Research, 2017, 61, 1600240.	1.5	678
903	The Bacterial Community Structure and Dynamics of Carbon and Nitrogen when Maize (Zea mays L.) and Its Neutral Detergent Fibre Were Added to Soil from Zimbabwe with Contrasting Management Practices. Microbial Ecology, 2017, 73, 135-152.	1.4	36
904	Seasonal variation in an acid mine drainage microbial community. Canadian Journal of Microbiology, 2017, 63, 137-152.	0.8	16

# 905	ARTICLE Microbial population analysis improves the evidential value of faecal traces in forensic investigations. International Journal of Legal Medicine, 2017, 131, 45-51.	IF 1.2	CITATIONS
906	Oral colostrum priming shortens hospitalization without changing the immunomicrobial milieu. Journal of Perinatology, 2017, 37, 36-41.	0.9	37
907	Distribution and Diversity of Microbial Eukaryotes in Bathypelagic Waters of the South China Sea. Journal of Eukaryotic Microbiology, 2017, 64, 370-382.	0.8	36
908	Anammox biofilm in activated sludge swine wastewater treatment plants. Chemosphere, 2017, 167, 300-307.	4.2	51
909	Gut microbiome and liver disease. Translational Research, 2017, 179, 49-59.	2.2	78
910	Molecular approaches for the detection and monitoring of microbial communities in bioaerosols: A review. Journal of Environmental Sciences, 2017, 51, 234-247.	3.2	113
911	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
912	Immune Response and Mortality Risk Relate to Distinct Lung Microbiomes in Patients with HIV and Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 104-114.	2.5	60
913	Abundant and rare picoeukaryotic subâ€communities present contrasting patterns in the epipelagic waters of marginal seas in the northwestern <scp>P</scp> acific <scp>O</scp> cean. Environmental Microbiology, 2017, 19, 287-300.	1.8	183
914	Experimental metagenomics and ribosomal profiling of the human skin microbiome. Experimental Dermatology, 2017, 26, 211-219.	1.4	34
915	Recruitment and establishment of the gut microbiome in arctic shorebirds. FEMS Microbiology Ecology, 2017, 93, .	1.3	64
916	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
917	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
918	Shift of hindgut microbiota and microbial short chain fatty acids profiles in dairy calves from birth to pre-weaning. FEMS Microbiology Ecology, 2018, 94, .	1.3	61
919	An attempt to semi-quantify potentially toxic diatoms of the genus <i>Pseudo-nitzschia</i> in Tokyo Bay, Japan by using massively parallel sequencing technology. Plankton and Benthos Research, 2017, 12, 248-258.	0.2	15
920	Sediment Remediation by Microbial Fuel Cells and Effect of Vertical Position of Anode Buried in Sediment. Journal of Japan Society on Water Environment, 2017, 40, 51-57.	0.1	4
921	Microbial Community Structure and Enumeration of <i>Bacillus</i> species in Activated Sludge. Journal of Water and Environment Technology, 2017, 15, 233-240.	0.3	18
922	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
923	From reads to operational taxonomic units: an ensemble processing pipeline for MiSeq amplicon sequencing data. GigaScience, 2017, 6, 1-10.	3.3	47
924	A comparison of sequencing platforms and bioinformatics pipelines for compositional analysis of the gut microbiome. BMC Microbiology, 2017, 17, 194.	1.3	196
925	Towards a balanced view of the bacterial tree of life. Microbiome, 2017, 5, 140.	4.9	102
926	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
927	Comparative analysis of the intestinal flora in type 2 diabetes and nondiabetic mice. Experimental Animals, 2017, 66, 405-416.	0.7	94
928	Individual Signatures Define Canine Skin Microbiota Composition and Variability. Frontiers in Veterinary Science, 2017, 4, 6.	0.9	26
929	The Cause of Death of a Child in the 18th Century Solved by Bone Microbiome Typing Using Laser Microdissection and Next Generation Sequencing. International Journal of Molecular Sciences, 2017, 18, 109.	1.8	10
930	It Is Imperative to Establish a Pellucid Definition of Chimeric RNA and to Clear Up a Lot of Confusion in the Relevant Research. International Journal of Molecular Sciences, 2017, 18, 714.	1.8	15
931	Changes in Marine Prokaryote Composition with Season and Depth Over an Arctic Polar Year. Frontiers in Marine Science, 2017, 4, .	1.2	73
932	Characterization of Gut Microbiome Dynamics in Developing Pekin Ducks and Impact of Management System. Frontiers in Microbiology, 2016, 7, 2125.	1.5	46
933	Methane Production in Dairy Cows Correlates with Rumen Methanogenic and Bacterial Community Structure. Frontiers in Microbiology, 2017, 8, 226.	1.5	218
934	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
935	Structure and Function of the Fecal Microbiota in Diarrheic Neonatal Piglets. Frontiers in Microbiology, 2017, 8, 502.	1.5	103
936	Guar Gum Stimulates Biogenic Sulfide Production at Elevated Pressures: Implications for Shale Gas Extraction. Frontiers in Microbiology, 2017, 8, 679.	1.5	14
937	The Bacteriophage EF-P29 Efficiently Protects against Lethal Vancomycin-Resistant Enterococcus faecalis and Alleviates Gut Microbiota Imbalance in a Murine Bacteremia Model. Frontiers in Microbiology, 2017, 8, 837.	1.5	78
938	Bacterial Composition and Diversity in Breast Milk Samples from Mothers Living in Taiwan and Mainland China. Frontiers in Microbiology, 2017, 8, 965.	1.5	114
939	Zinc Oxide Nanoparticles Influence Microflora in Ileal Digesta and Correlate Well with Blood Metabolites. Frontiers in Microbiology, 2017, 8, 992.	1.5	44
940	The Arbuscular Mycorrhizal Fungus Funneliformis mosseae Alters Bacterial Communities in Subtropical Forest Soils during Litter Decomposition. Frontiers in Microbiology, 2017, 8, 1120.	1.5	36

ARTICLE IF CITATIONS The Cyanobacteria-Dominated Sponge Dactylospongia elegans in the South China Sea: Prokaryotic 941 1.5 15 Community and Metagenomic Insights. Frontiers in Microbiology, 2017, 8, 1387. Wood Ash Induced pH Changes Strongly Affect Soil Bacterial Numbers and Community Composition. Frontiers in Microbiology, 2017, 8, 1400. 942 1.5 74 Identification of Fungal Communities Associated with the Biodeterioration of Waterlogged 943 1.5 27 Archeological Wood in a Han Dynasty Tomb in China. Frontiers in Microbiology, 2017, 8, 1633. Illumina Sequencing Approach to Characterize Thiamine Metabolism Related Bacteria and the Impacts of Thiamine Supplementation on Ruminal Microbiota in Dairy Cows Fed High-Grain Diets. Frontiers in Microbiology, 2017, 8, 1818. 944 Seasonal Changes in a Maize-Based Polyculture of Central Mexico Reshape the Co-occurrence 945 1.5 36 Networks of Soil Bacterial Communities. Frontiers in Microbiology, 2017, 8, 2478. Invasion by Cordgrass Increases Microbial Diversity and Alters Community Composition in a Mangrove Nature Reserve. Frontiers in Microbiology, 2017, 8, 2503. 946 1.5 Independent Effects of a Herbivore's Bacterial Symbionts on Its Performance and Induced Plant 947 1.8 40 Defences. International Journal of Molecular Sciences, 2017, 18, 182. Tuber indicum shapes the microbial communities of ectomycorhizosphere soil and ectomycorrhizae of 948 1.1 an indigenous tree (Pinus armandii). PLoS ONE, 2017, 12, é0175720. Urinary catheter-associated microbiota change in accordance with treatment and infection status. 949 1.1 37 PLoS ÓNE, 2017, 12, e0177633. Endosphere microbiome comparison between symptomatic and asymptomatic roots of Brassica napus 1.1 infected with Plasmodiophora brassicae. PLoS ONE, 2017, 12, e0185907. Spatiotemporal analysis of microbial community dynamics during seasonal stratification events in a 951 1.1 47 freshwater lake (Grand Lake, OK, USA). PLoS ONE, 2017, 12, e0177488. Microbiomes associated with infective stages of root-knot and lesion nematodes in soil. PLoS ONE, 1.1 2017, 12, e0177145. A novel ultra high-throughput 16S rRNA gene amplicon sequencing library preparation method for the 953 4.9 93 Illumina HiSeq platform. Microbiome, 2017, 5, 68. Longitudinal profiling reveals a persistent intestinal dysbiosis triggered by conventional 954 anti-tuberculosis therapy. Microbiome, 2017, 5, 71. Characterization of the upper and lower respiratory tract microbiota in Piedmontese calves. 955 52 4.9 Microbiome, 2017, 5, 152. Endolysin LysEF-P10 shows potential as an alternative treatment strategy for multidrug-resistant 38 Enterococcus faecalis infections. Scientific Reports, 2017, 7, 10164. Evaluation of the accuracy and sensitivity of highâ€'throughput sequencing technology using known 957 1.1 11 microbiota. Molecular Médicine Reports, 2017, 17, 408-413. Functional Predictions of Microbial Communities in Soil as Affected by Longâ€term Tillage Practices. Agricultural and Environmental Letters, 2017, 2, 170031.

#	Article	IF	CITATIONS
959	Diverse bacterial communities exist on canine skin and are impacted by cohabitation and time. PeerJ, 2017, 5, e3075.	0.9	30
960	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
961	Nitrogen Cycling of Active Bacteria within Oligotrophic Sediment of the Mid-Atlantic Ridge Flank. Geomicrobiology Journal, 2018, 35, 468-483.	1.0	50
962	Comparison of the microbial community structure between inflamed and nonâ€inflamed sites in patients with ulcerative colitis. Journal of Gastroenterology and Hepatology (Australia), 2018, 33, 1590-1597.	1.4	87
963	Dietary lipid levels could improve growth and intestinal microbiota of juvenile swimming crab, Portunus trituberculatus. Aquaculture, 2018, 490, 208-216.	1.7	65
964	The influence of microbial communities for triadimefon enantiomerization in soils with different pH values. Chirality, 2018, 30, 293-301.	1.3	12
965	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
966	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
967	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. Nature Communications, 2018, 9, 1517.	5.8	256
968	A combination of Lactobacillus mali APS1 and dieting improved the efficacy of obesity treatment via manipulating gut microbiome in mice. Scientific Reports, 2018, 8, 6153.	1.6	31
969	Gut microbiome of Moroccan colorectal cancer patients. Medical Microbiology and Immunology, 2018, 207, 211-225.	2.6	68
970	Seagrass rhizosphere microenvironment alters plantâ€associated microbial community composition. Environmental Microbiology, 2018, 20, 2854-2864.	1.8	79
971	Diversity and community composition of pico- and nanoplanktonic protists in the Vistula River estuary (Gulf of Gdańsk, Baltic Sea). Estuarine, Coastal and Shelf Science, 2018, 207, 242-249.	0.9	22
972	HIV-exposure, early life feeding practices and delivery mode impacts on faecal bacterial profiles in a South African birth cohort. Scientific Reports, 2018, 8, 5078.	1.6	28
973	Long-term phosphorus application to a maize monoculture influences the soil microbial community and its feedback effects on maize seedling biomass. Applied Soil Ecology, 2018, 128, 12-22.	2.1	17
974	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
975	Antibioticâ€mediated bacteriome depletion in Apc ^{<i>Min/+</i>} mice is associated with reduction in mucusâ€producing goblet cells and increased colorectal cancer progression. Cancer Medicine, 2018, 7, 2003-2012.	1.3	36
976	A Consistent and Predictable Commercial Broiler Chicken Bacterial Microbiota in Antibiotic-Free Production Displays Strong Correlations with Performance. Applied and Environmental Microbiology, 2018, 84, .	1.4	122

#	Article	IF	CITATIONS
977	Gut-dependent microbial translocation induces inflammation and cardiovascular events after ST-elevation myocardial infarction. Microbiome, 2018, 6, 66.	4.9	185
978	Tidal Stage Changes in Structure and Diversity of Intertidal Benthic Diatom Assemblages: a Case Study from Two Contrasting Charleston Harbor Flats. Estuaries and Coasts, 2018, 41, 772-783.	1.0	10
979	Season structures prokaryotic partners but not algal symbionts in subtropical hard corals. Applied Microbiology and Biotechnology, 2018, 102, 4963-4973.	1.7	30
980	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
981	Microbiome profiling of commercial pigs from farrow to finish. Journal of Animal Science, 2018, 96, 1778-1794.	0.2	87
982	Stool and urine trefoil factor 3 levels: associations with symptoms, intestinal permeability, and microbial diversity in irritable bowel syndrome. Beneficial Microbes, 2018, 9, 345-355.	1.0	15
983	Direct comparison of culture-dependent and culture-independent molecular approaches reveal the diversity of fungal endophytic communities in stems of grapevine (Vitis vinifera). Fungal Diversity, 2018, 90, 85-107.	4.7	143
984	The Madness of Microbiome: Attempting To Find Consensus "Best Practice―for 16S Microbiome Studies. Applied and Environmental Microbiology, 2018, 84, .	1.4	422
985	The effect of temperature on the microbial communities of peak biogas production in batch biogas reactors. Renewable Energy, 2018, 123, 15-25.	4.3	56
986	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
987	Detecting anomalies in the Cytochrome C Oxidase I amplicon sequences using minimum scoring segments. ACM SIGAPP Applied Computing Review: A Publication of the Special Interest Group on Applied Computing, 2018, 17, 6-14.	0.5	3
988	Free-living bacteria and potential bacterial pathogens in sewage treatment plants. Applied Microbiology and Biotechnology, 2018, 102, 2455-2464.	1.7	47
989	Microbial community and short-chain fatty acid profile in gastrointestinal tract of goose. Poultry Science, 2018, 97, 1420-1428.	1.5	46
990	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
991	Taxonomy of anaerobic digestion microbiome reveals biases associated with the applied high throughput sequencing strategies. Scientific Reports, 2018, 8, 1926.	1.6	70
992	Diagnosis of Periprosthetic Joint Infection: The Potential of Next-Generation Sequencing. Journal of Bone and Joint Surgery - Series A, 2018, 100, 147-154.	1.4	218
993	Exploring coral microbiome assemblages in the South China Sea. Scientific Reports, 2018, 8, 2428.	1.6	31
994	Bacterial diversity and community structure in Chongqing radish paocai brines revealed using PacBio singleâ€molecule realâ€ŧime sequencing technology. Journal of the Science of Food and Agriculture, 2018, 98, 3234-3245.	1.7	43

	Сітат	ION REPORT	
#	Article	IF	CITATIONS
995	Ectomycorrhization of <i>Tricholoma matsutake</i> with <i>Quercus aquifolioides</i> affects the endophytic microbial community of host plant. Journal of Basic Microbiology, 2018, 58, 238-246.	1.8	5
996	Cultivation of seaweed <i>Gracilaria lemaneiformis</i> enhanced biodiversity in a eukaryotic plankton community as revealed via metagenomic analyses. Molecular Ecology, 2018, 27, 1081-1093.	2.0	35
997	Differences in fecal microbial metabolites and microbiota of children with autism spectrum disorders. Anaerobe, 2018, 49, 121-131.	1.0	249
998	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
999	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
1000	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. Nature Biotechnology, 2018, 36, 190-195.	9.4	165
1001	Scaling up: A guide to highâ€throughput genomic approaches for biodiversity analysis. Molecular Ecology, 2018, 27, 313-338.	2.0	248
1002	A novel membrane bioreactor inoculated with symbiotic sludge bacteria and algae: Performance and microbial community analysis. Bioresource Technology, 2018, 251, 311-319.	4.8	69
1003	Differential Engagement of Fermentative Taxa in Gut Contents of the Earthworm Lumbricus terrestris. Applied and Environmental Microbiology, 2018, 84, .	1.4	32
1004	Bifidobacteria or Fiber Protects against Diet-Induced Microbiota-Mediated Colonic Mucus Deterioration. Cell Host and Microbe, 2018, 23, 27-40.e7.	5.1	477
1005	Gamma-aminobutyric Acid Enriched Rice Bran Diet Attenuates Insulin Resistance and Balances Energy Expenditure via Modification of Gut Microbiota and Short-Chain Fatty Acids. Journal of Agricultural and Food Chemistry, 2018, 66, 881-890.	2.4	54
1006	Low amounts of dietary fibre increase in vitro production of short-chain fatty acids without changing human colonic microbiota structure. Scientific Reports, 2018, 8, 435.	1.6	75
1007	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
1008	FROGS: Find, Rapidly, OTUs with Galaxy Solution. Bioinformatics, 2018, 34, 1287-1294.	1.8	660
1009	Maturation of the gut microbiome and risk of asthma in childhood. Nature Communications, 2018, 9, 141.	5.8	380
1010	Beneficial changes in rumen bacterial community profile in sheep and dairy calves as a result of feeding the probiotic <i>Bacillus amyloliquefaciens</i> H57. Journal of Applied Microbiology, 2018, 124, 855-866.	1.4	34
1011	Association of Oral Microbiome With Risk for Incident Head and Neck Squamous Cell Cancer. JAMA Oncology, 2018, 4, 358.	3.4	218
1012	Fast acquisition of a polysaccharide fermenting gut microbiome by juvenile green turtles Chelonia mydas after settlement in coastal habitats. Microbiome, 2018, 6, 69.	4.9	51

	Ста	ATION REPORT	
#	Article	IF	CITATIONS
1013	Analysis of Theileria orientalis draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. BMC Genomics, 2018, 19, 298.	1.2	24
1014	Differential human gut microbiome assemblages during soil-transmitted helminth infections in Indonesia and Liberia. Microbiome, 2018, 6, 33.	4.9	102
1015	Microbial Community Composition in a Simultaneous Nitrification and Denitrification Bioreactor for Domestic Wastewater Treatment. IOP Conference Series: Earth and Environmental Science, 2018, 112, 012007.	0.2	4
1016	Organic loading rate and hydraulic retention time shape distinct ecological networks of anaerobic digestion related microbiome. Bioresource Technology, 2018, 262, 184-193.	4.8	104
1017	Influence of Bactrian camel milk on the gut microbiota. Journal of Dairy Science, 2018, 101, 5758-5769.	. 1.4	42
1018	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
1019	Allometry and Ecology of the Bilaterian Gut Microbiome. MBio, 2018, 9, .	1.8	29
1020	Chronic exposure to low concentrations of lead induces metabolic disorder and dysbiosis of the gut microbiota in mice. Science of the Total Environment, 2018, 631-632, 439-448.	3.9	123
1021	Effect of reclamation of abandoned salinized farmland on soil bacterial communities in arid northwest China. Science of the Total Environment, 2018, 630, 799-808.	3.9	40
1022	Biodiversity of fungi on Vitis vinifera L. revealed by traditional and high-resolution culture-independent approaches. Fungal Diversity, 2018, 90, 1-84.	4.7	101
1023	Changes in Larval Mosquito Microbiota Reveal Non-target Effects of Insecticide Treatments in Hurricane-Created Habitats. Microbial Ecology, 2018, 76, 719-728.	1.4	13
1024	SeekDeep: single-base resolution de novo clustering for amplicon deep sequencing. Nucleic Acids Research, 2018, 46, e21-e21.	6.5	134
1025	The Pancreatic Cancer Microbiome Promotes Oncogenesis by Induction of Innate and Adaptive Immune Suppression. Cancer Discovery, 2018, 8, 403-416.	2 7.7	834
1026	A Survey of Virus Recombination Uncovers Canonical Features of Artificial Chimeras Generated During Deep Sequencing Library Preparation. G3: Genes, Genomes, Genetics, 2018, 8, 1129-1138.	0.8	21
1027	A global comparison of the microbiome compositions of three gut locations in commercial pigs with extreme feed conversion ratios. Scientific Reports, 2018, 8, 4536.	1.6	121
1028	Ancient diversity and geographical sub-structuring in African buffalo Theileria parva populations revealed through metagenetic analysis of antigen-encoding loci. International Journal for Parasitology, 2018, 48, 287-296.	1.3	27
1029	Comparative Analysis of the Gut Bacterial Community of Four Anastrepha Fruit Flies (Diptera:) Tj ETQq0) 0 0 rgBT /Overlock 1.0	10 Tf 50 102
1030	Tissue Localization and Variation of Major Symbionts in Haemaphysalis longicornis, Rhipicephalus haemaphysaloides, and Dermacentor silvarum in China. Applied and Environmental Microbiology, 2018,	, 1.4	28

84,.

#	Article	IF	CITATIONS
1032	Human oral microbiome and prospective risk for pancreatic cancer: a population-based nested case-control study. Gut, 2018, 67, 120-127.	6.1	536
1033	Photoreactivity of riverine and phytoplanktonic dissolved organic matter and its effects on the dynamics of a bacterial community from the coastal Mediterranean Sea. Progress in Oceanography, 2018, 163, 82-93.	1.5	5
1034	A prospective microbiomeâ€wide association study of food sensitization and food allergy in early childhood. Allergy: European Journal of Allergy and Clinical Immunology, 2018, 73, 145-152.	2.7	163
1035	Microeukaryote community in a partial nitritation reactor prior to anammox and an insight into the potential of ciliates as performance bioindicators. New Biotechnology, 2018, 43, 3-12.	2.4	5
1036	Opportunities and challenges in metabarcoding approaches for helminth community identification in wild mammals. Parasitology, 2018, 145, 608-621.	0.7	28
1037	A Combination of Stable Isotope Probing, Illumina Sequencing, and Co-occurrence Network to Investigate Thermophilic Acetate- and Lactate-Utilizing Bacteria. Microbial Ecology, 2018, 75, 113-122.	1.4	32
1038	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
1039	Impacts of water quality on the corrosion of cast iron pipes for water distribution and proposed source water switch strategy. Water Research, 2018, 129, 428-435.	5.3	85
1040	Brown Rot Syndrome and Changes in the Bacterial Сommunity of the Baikal Sponge Lubomirskia baicalensis. Microbial Ecology, 2018, 75, 1024-1034.	1.4	24
1041	Location-Specific Oral Microbiome Possesses Features Associated With CKD. Kidney International Reports, 2018, 3, 193-204.	0.4	24
1042	Effect of salinity on removal performance and activated sludge characteristics in sequencing batch reactors. Bioresource Technology, 2018, 249, 890-899.	4.8	181
1043	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
1044	Medium shapes the microbial community of water filters with implications for effluent quality. Water Research, 2018, 129, 499-508.	5.3	85
1045	The plant circadian clock influences rhizosphere community structure and function. ISME Journal, 2018, 12, 400-410.	4.4	106
1046	Diversity of bacterial communities in French chicken cuts stored under modified atmosphere packaging. Food Microbiology, 2018, 70, 7-16.	2.1	65
1047	PacBio metabarcoding of Fungi and other eukaryotes: errors, biases and perspectives. New Phytologist, 2018, 217, 1370-1385.	3.5	211
1048	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. ISME Journal, 2018, 12, 31-47.	4.4	59
1049	Rapid startup of thermophilic anaerobic digester to remove tetracycline and sulfonamides resistance genes from sewage sludge. Science of the Total Environment, 2018, 612, 788-798	3.9	90

#	Article	IF	CITATIONS
1050	Short communication: Does early-life administration of a Megasphaera elsdenii probiotic affect long-term establishment of the organism in the rumen and alter rumen metabolism in the dairy calf?. Journal of Dairy Science, 2018, 101, 1747-1751.	1.4	13
1051	Gut Microbiomeâ€Induced Shift of Acetate to Butyrate Positively Manages Dysbiosis in High Fat Diet. Molecular Nutrition and Food Research, 2018, 62, 1700670.	1.5	58
1052	An apparent Acanthamoeba genotype is the product of a chimeric 18S rDNA artifact. Parasitology Research, 2018, 117, 571-577.	0.6	8
1053	Effects of microbial diversity on nitrite concentration in pao cai , a naturally fermented cabbage product from China. Food Microbiology, 2018, 72, 185-192.	2.1	84
1054	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. Environmental Microbiology, 2018, 20, 734-754.	1.8	53
1055	Optical fiber-mediated photosynthesis for enhanced subsurface oxygen delivery. Chemosphere, 2018, 195, 742-748.	4.2	8
1056	Dynamic correlations between microbiota succession and flavor development involved in the ripening of Kazak artisanal cheese. Food Research International, 2018, 105, 733-742.	2.9	88
1057	Biohydrogen production at pH below 3.0: Is it possible?. Water Research, 2018, 128, 350-361.	5.3	58
1058	Fecal microbial dysbiosis in Chinese patients with inflammatory bowel disease. World Journal of Gastroenterology, 2018, 24, 1464-1477.	1.4	49
1059	Additives in Plasticised Polyvinyl Chloride Fuel Microbial Nitrate Reduction at High pH: Implications for Nuclear Waste Disposal. Frontiers in Environmental Science, 2018, 6, .	1.5	12
1060	Fungal loop transfer of nitrogen depends on biocrust constituents and nitrogen form. Biogeosciences, 2018, 15, 3831-3840.	1.3	18
1061	An intensive milk replacer feeding program benefits immune response and intestinal microbiota of lambs during weaning. BMC Veterinary Research, 2018, 14, 366.	0.7	18
1062	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
1063	Rapid analysis of metagenomic data using signature-based clustering. BMC Bioinformatics, 2018, 19, 509.	1.2	2
1064	Biodiversity Genomics: Monitoring Restoration Efforts Using DNA Barcoding and Environmental DNA. , 2018, , 395-417.		0
1065	Run-to-Run Sequencing Variation Can Introduce Taxon-Specific Bias in the Evaluation of Fungal Microbiomes. Phytobiomes Journal, 2018, 2, 165-170.	1.4	13
1067	The Effect of Hydrated Sodium Calcium Aluminosilicate on Fatty Liver and the Composition of the Intestinal Microbiota in Overfed Landes Geese. Brazilian Journal of Poultry Science, 2018, 20, 393-402.	0.3	2
1068	Evaluation of patient- versus provider-collected vaginal swabs for microbiome analysis during pregnancy. BMC Research Notes, 2018, 11, 706.	0.6	6

#	Article	IF	CITATIONS
1069	Gut microbiota of preterm infants supplemented with probiotics: sub-study of the ProPrems trial. BMC Microbiology, 2018, 18, 184.	1.3	50
1070	Composition Analysis and Feature Selection of the Oral Microbiota Associated with Periodontal Disease. BioMed Research International, 2018, 2018, 1-14.	0.9	67
1071	Geographical Distribution and Risk Assessment of Heavy Metals in Nearby River of Heap Bioleaching Plant: A Case Study At the Zijin Copper Mine, China. IOP Conference Series: Earth and Environmental Science, 2018, 182, 012005.	0.2	0
1072	Influence of Feeding Type and <i>Nosema ceranae</i> Infection on the Gut Microbiota of <i>Apis cerana</i> Workers. MSystems, 2018, 3, .	1.7	34
1073	Impact of DNA extraction method and targeted 16S-rRNA hypervariable region on oral microbiota profiling. Scientific Reports, 2018, 8, 16321.	1.6	126
1074	The Rootstock Regulates Microbiome Diversity in Root and Rhizosphere Compartments of Vitis vinifera Cultivar Lambrusco. Frontiers in Microbiology, 2018, 9, 2240.	1.5	54
1075	Studying safe storage time of orange peel (Citrus reticulata) using highâ€ŧhroughput sequencing and conventional pure culture. Food Science and Nutrition, 2018, 6, 2545-2552.	1.5	6
1076	Formal description of sequence-based voucherless Fungi: promises and pitfalls, and how to resolve them. IMA Fungus, 2018, 9, 143-165.	1.7	42
1077	Ecological Succession of Sulfur-Oxidizing Epsilon- and Gammaproteobacteria During Colonization of a Shallow-Water Gas Vent. Frontiers in Microbiology, 2018, 9, 2970.	1.5	25
1078	Stability and resilience of the intestinal microbiota in children in daycare – a 12 month cohort study. BMC Microbiology, 2018, 18, 223.	1.3	15
1079	Summer shifts of bacterial communities associated with the invasive brown seaweed Sargassum muticum are location and tissue dependent. PLoS ONE, 2018, 13, e0206734.	1.1	57
1080	Pre-obese children's dysbiotic gut microbiome and unhealthy diets may predict the development of obesity. Communications Biology, 2018, 1, 222.	2.0	65
1081	Lactobacillus reuteri HCM2 protects mice against Enterotoxigenic Escherichia coli through modulation of gut microbiota. Scientific Reports, 2018, 8, 17485.	1.6	38
1082	The effects of dietary astaxanthin on intestinal health of juvenile tiger puffer Takifugu rubripes in terms of antioxidative status, inflammatory response and microbiota. Aquaculture Nutrition, 2018, 25, 466.	1.1	2
1083	Identification of metabolite and protein explanatory variables governing microbiome establishment and re-establishment within a cellulose-degrading anaerobic bioreactor. PLoS ONE, 2018, 13, e0204831.	1.1	0
1084	Microbial Community Composition and Predicted Functional Attributes of Antarctic Lithobionts Using Targeted Next-Generation Sequencing and Bioinformatics Tools. Methods in Microbiology, 2018, , 243-290.	0.4	3
1085	Rhizosphere Microbial Response to Multiple Metal(loid)s in Different Contaminated Arable Soils Indicates Crop-Specific Metal-Microbe Interactions. Applied and Environmental Microbiology, 2018, 84,	1.4	47
1086	Chinese Black Truffle (Tuber indicum) Alters the Ectomycorrhizosphere and Endoectomycosphere Microbiome and Metabolic Profiles of the Host Tree Quercus aliena. Frontiers in Microbiology, 2018, 9, 2202	1.5	38

		CITATION RE	EPORT	
#	Article		IF	CITATIONS
1087	Organic matter removal associated with forest harvest leads to decade scale alteratior fungal communities and functional guilds. Soil Biology and Biochemistry, 2018, 127, 1		4.2	17
1088	Variation of bacterial community associated with Phaeodactylum tricornutum in respo different inorganic nitrogen concentrations. Acta Oceanologica Sinica, 2018, 37, 118-	nse to 128.	0.4	4
1089	Tong-Xie-Yao-Fang Regulates 5-HT Level in Diarrhea Predominant Irritable Bowel Syndr Gut Microbiota Modulation. Frontiers in Pharmacology, 2018, 9, 1110.	ome Through	1.6	41
1090	Soil amendment with sewage sludge affects soil prokaryotic community composition, resistome. FEMS Microbiology Ecology, 2019, 95, .	mobilome and	1.3	12
1091	Biases in Prokaryotic Community Amplicon Sequencing Affected by DNA Extraction Me Saline and Non-saline Soil. Frontiers in Microbiology, 2018, 9, 1796.	ethods in Both	1.5	12
1092	PCR-based quantification of taxa-specific abundances in microbial communities: Quantavoiding common pitfalls. Journal of Microbiological Methods, 2018, 153, 139-147.	Lifying and	0.7	79
1093	A Natural History of Actinic Keratosis and Cutaneous Squamous Cell Carcinoma Micro 2018, 9, .	biomes. MBio,	1.8	37
1094	Intestinal toxicity of deoxynivalenol is limited by supplementation with Lactobacillus p and consequentially altered gut microbiota in broiler chickens. Journal of Animal Science Biotechnology, 2018, 9, 74.	lantarum JM113 ce and	2.1	65
1095	Functional profiling of the gut microbiomes in two different populations of the brown Nilaparvata lugens. Journal of Asia-Pacific Entomology, 2018, 21, 1309-1314.	planthopper,	0.4	15
1096	Composition and Genetic Diversity of the Nicotiana tabacum Microbiome in Different Areas and Growth Periods. International Journal of Molecular Sciences, 2018, 19, 3421		1.8	15
1097	Association of dietary fibre intake and gut microbiota in adults. British Journal of Nutrit 1014-1022.	tion, 2018, 120,	1.2	63
1098	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dy alteration of community structure. Microbiome, 2018, 6, 180.	sbiosis and	4.9	23
1099	Community profiling of the urinary microbiota: considerations for low-biomass sample Reviews Urology, 2018, 15, 735-749.	s. Nature	1.9	87
1100	Response of bentonite microbial communities to stresses relevant to geodisposal of rawaste. Chemical Geology, 2018, 501, 58-67.	dioactive	1.4	22
1101	Deciphering the bacterial composition in the rhizosphere of Baphicacanthus cusia (Neo Scientific Reports, 2018, 8, 15831.	2S) Bremek.	1.6	15
1102	The gastric mucosal-associated microbiome in patients with gastric polyposis. Scientifi 8, 13817.	c Reports, 2018,	1.6	30
1103	Disentangling protist communities identified from <scp>DNA</scp> and <scp>RNAPearl River–South China Sea Continuum during the wet and dry seasons. Molecular 4627-4640.</scp>	cp> surveys in the Ecology, 2018, 27,	2.0	24
1104	HmmUFOtu: An HMM and phylogenetic placement based ultra-fast taxonomic assignr picking tool for microbiome amplicon sequencing studies. Genome Biology, 2018, 19,	nent and OTU 82.	3.8	32

#	Article	IF	CITATIONS
1105	Effect of tillage and static abiotic soil properties on microbial diversity. Applied Soil Ecology, 2018, 132, 135-145.	2.1	101
1106	Yeast Probiotics Shape the Gut Microbiome and Improve the Health of Early-Weaned Piglets. Frontiers in Microbiology, 2018, 9, 2011.	1.5	50
1107	Alteration of the cutaneous microbiome in psoriasis and potential role in Th17 polarization. Microbiome, 2018, 6, 154.	4.9	190
1108	Bacterial communities under long-term conventional and transgenic cotton farming systems using V3-V5 and V5-V9 of 16s rDNA. Ecotoxicology and Environmental Safety, 2018, 164, 618-628.	2.9	5
1109	Exposures Related to House Dust Microbiota in a U.S. Farming Population. Environmental Health Perspectives, 2018, 126, 067001.	2.8	23
1110	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
1111	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
1112	Diet during Pregnancy and Infancy and the Infant Intestinal Microbiome. Journal of Pediatrics, 2018, 203, 47-54.e4.	0.9	66
1113	Influence of cigarette smoking on the human duodenal mucosa-associated microbiota. Microbiome, 2018, 6, 150.	4.9	72
1114	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
1115	Effects of limestone inclusion on growth performance, intestinal microbiota, and the jejunal transcriptomic profile when fed to weaning pigs. Animal Feed Science and Technology, 2018, 242, 8-20.	1.1	5
1116	Differential metabolic effects of oral butyrate treatment in lean versus metabolic syndrome subjects. Clinical and Translational Gastroenterology, 2018, 9, e155.	1.3	123
1117	Supplementation of fructooligosaccharides to suckling piglets affects intestinal microbiota colonization and immune development1. Journal of Animal Science, 2018, 96, 2139-2153.	0.2	49
1118	Inhalational exposure to particulate matter air pollution alters the composition of the gut microbiome. Environmental Pollution, 2018, 240, 817-830.	3.7	181
1119	A Newly Designed Primer Revealed High Phylogenetic Diversity of <i>Endozoicomonas</i> in Coral Reefs. Microbes and Environments, 2018, 33, 172-185.	0.7	10
1120	Early Salmonella Typhimurium infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa. Scientific Reports, 2018, 8, 7788.	1.6	61
1121	Molecular profiling of mucosal tissue associated microbiota in patients manifesting acute exacerbations and remission stage of ulcerative colitis. World Journal of Microbiology and Biotechnology, 2018, 34, 76.	1.7	53
1122	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

#	Article	IF	CITATIONS
1123	Treatment of acidic sulfate-containing wastewater using revolving algae biofilm reactors: Sulfur removal performance and microbial community characterization. Bioresource Technology, 2018, 264, 24-34.	4.8	67
1124	Analysis of the bacterial communities in the waterlogged wooden cultural relics of the <i>Xiaobaijiao No. 1</i> shipwreck via high-throughput sequencing technology. Holzforschung, 2018, 72, 609-619.	0.9	14
1125	Intestinal microbial-derived sphingolipids are inversely associated with childhood food allergy. Journal of Allergy and Clinical Immunology, 2018, 142, 335-338.e9.	1.5	37
1126	AnalyticÂMethods in Microbiome Studies. , 2018, , 29-42.		0
1127	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
1128	Influence of Bacillus subtilis B068150 on cucumber rhizosphere microbial composition as a plant protective agent. Plant and Soil, 2018, 429, 519-531.	1.8	18
1129	Alterations in the gut bacterial microbiome in fungal Keratitis patients. PLoS ONE, 2018, 13, e0199640.	1.1	65
1130	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
1131	Exploiting the real wastewater potential for resource recovery – <i>n</i> -caproate production from acid whey. Green Chemistry, 2018, 20, 3790-3803.	4.6	93
1132	Specificities and Efficiencies of Primers Targeting Candidatus Phylum Saccharibacteria in Activated Sludge. Materials, 2018, 11, 1129.	1.3	22
1133	Bacterial interactions during sequential degradation of cyanobacterial necromass in a sulfidic arctic marine sediment. Environmental Microbiology, 2018, 20, 2927-2940.	1.8	50
1134	Structure and function of high Arctic pelagic, particleâ€associated and benthic bacterial communities. Environmental Microbiology, 2018, 20, 2941-2954.	1.8	31
1135	Optimizing body fluid recognition from microbial taxonomic profiles. Forensic Science International: Genetics, 2018, 37, 13-20.	1.6	23
1136	<i>Papio</i> spp. Colon microbiome and its link to obesity in pregnancy. Journal of Medical Primatology, 2018, 47, 393-401.	0.3	3
1137	Microbial community changes during a toxic cyanobacterial bloom in an alkaline Hungarian lake. Antonie Van Leeuwenhoek, 2018, 111, 2425-2440.	0.7	12
1138	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
1139	Genetic Markers Are Associated with the Ruminal Microbiome and Metabolome in Grain and Sugar Challenged Dairy Heifers. Frontiers in Genetics, 2018, 9, 62.	1.1	24
1140	Respiratory Disease following Viral Lung Infection Alters the Murine Gut Microbiota. Frontiers in Immunology, 2018, 9, 182.	2.2	178

#	Article	IF	CITATIONS
1141	Bacteriome from Pinus arizonica and P. durangensis: Diversity, Comparison of Assemblages, and Overlapping Degree with the Gut Bacterial Community of a Bark Beetle That Kills Pines. Frontiers in Microbiology, 2018, 9, 77.	1.5	16
1142	The Effect of DNA Extraction Methods on Observed Microbial Communities from Fibrous and Liquid Rumen Fractions of Dairy Cows. Frontiers in Microbiology, 2018, 9, 92.	1.5	46
1143	Variance Component Selection With Applications to Microbiome Taxonomic Data. Frontiers in Microbiology, 2018, 9, 509.	1.5	10
1144	Gut Microbiome Associates With Lipid-Lowering Effect of Rosuvastatin in Vivo. Frontiers in Microbiology, 2018, 9, 530.	1.5	86
1145	Direct and Indirect Effects of Penguin Feces on Microbiomes in Antarctic Ornithogenic Soils. Frontiers in Microbiology, 2018, 9, 552.	1.5	20
1146	Comparative Analysis of the Microbiota Between Sheep Rumen and Rabbit Cecum Provides New Insight Into Their Differential Methane Production. Frontiers in Microbiology, 2018, 9, 575.	1.5	42
1147	Stem Cell Transcription Factor FoxO Controls Microbiome Resilience in Hydra. Frontiers in Microbiology, 2018, 9, 629.	1.5	24
1148	Predicted Bacterial Interactions Affect in Vivo Microbial Colonization Dynamics in Nematostella. Frontiers in Microbiology, 2018, 9, 728.	1.5	36
1149	Killing Effects of an Isolated Serratia marcescens KH-001 on Diaphorina citri via Lowering the Endosymbiont Numbers. Frontiers in Microbiology, 2018, 9, 860.	1.5	7
1150	Impact of Microbial Composition of Cambodian Traditional Dried Starters (Dombea) on Flavor Compounds of Rice Wine: Combining Amplicon Sequencing With HP-SPME-GCMS. Frontiers in Microbiology, 2018, 9, 894.	1.5	37
1151	A Mosaic of Geothermal and Marine Features Shapes Microbial Community Structure on Deception Island Volcano, Antarctica. Frontiers in Microbiology, 2018, 9, 899.	1.5	30
1152	Clean Low-Biomass Procedures and Their Application to Ancient Ice Core Microorganisms. Frontiers in Microbiology, 2018, 9, 1094.	1.5	24
1153	Comparison of Database Search Methods for the Detection of Legionella pneumophila in Water Samples Using Metagenomic Analysis. Frontiers in Microbiology, 2018, 9, 1272.	1.5	13
1154	Diversity of Fungal Communities in Heshang Cave of Central China Revealed by Mycobiome-Sequencing. Frontiers in Microbiology, 2018, 9, 1400.	1.5	23
1155	Agulhas Current properties shape microbial community diversity and potential functionality. Scientific Reports, 2018, 8, 10542.	1.6	12
1156	Exposure to Formaldehyde Perturbs the Mouse Gut Microbiome. Genes, 2018, 9, 192.	1.0	11
1157	A Long-Standing Complex Tropical Dipole Shapes Marine Microbial Biogeography. Applied and Environmental Microbiology, 2018, 84, .	1.4	6
1158	Taxon Disappearance from Microbiome Analysis Reinforces the Value of Mock Communities as a Standard in Every Sequencing Run. MSystems, 2018, 3, .	1.7	62

#	Article	IF	CITATIONS
1159	Can we use environmental DNA as holotypes?. Fungal Diversity, 2018, 92, 1-30.	4.7	54
1160	Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. Biotechnology for Biofuels, 2018, 11, 200.	6.2	99
1161	Resource Availability Drives Responses of Soil Microbial Communities to Short-term Precipitation and Nitrogen Addition in a Desert Shrubland. Frontiers in Microbiology, 2018, 9, 186.	1.5	82
1162	Considerations and consequences of allowing DNA sequence data as types of fungal taxa. IMA Fungus, 2018, 9, 167-175.	1.7	45
1163	Analysis of microbial abundance and community composition in esophagus and intestinal tract of wild veined rapa whelk (<i>Rapana venosa</i>) by 16S rRNA gene sequencing. Journal of General and Applied Microbiology, 2018, 64, 158-166.	0.4	18
1164	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
1165	Combining 16S rRNA gene variable regions enables high-resolution microbial community profiling. Microbiome, 2018, 6, 17.	4.9	171
1166	In-feed bambermycin medication induces anti-inflammatory effects and prevents parietal cell loss without influencing Helicobacter suis colonization in the stomach of mice. Veterinary Research, 2018, 49, 35.	1.1	12
1167	DNA-SIP Reveals the Diversity of Chemolithoautotrophic Bacteria Inhabiting Three Different Soil Types in Typical Karst Rocky Desertification Ecosystems in Southwest China. Microbial Ecology, 2018, 76, 976-990.	1.4	16
1168	Microbial diversity and ecotoxicity of sediments 3Âyears after the Jiaozhou Bay oil spill. AMB Express, 2018, 8, 79.	1.4	19
1169	Concentration and Community of Airborne Bacteria in Response to Cyclical Haze Events During the Fall and Midwinter in Beijing, China. Frontiers in Microbiology, 2018, 9, 1741.	1.5	35
1170	Diversity of Bacterial Communities in the Intestinal Tracts of Two Geographically Distant Populations of Bactrocera dorsalis (Diptera: Tephritidae). Journal of Economic Entomology, 2018, 111, 2861-2868.	0.8	20
1171	Coâ€occurrence network analysis reveals thermodynamicsâ€driven microbial interactions in methanogenic bioreactors. Environmental Microbiology Reports, 2018, 10, 673-685.	1.0	22
1172	Marchantia liverworts as a proxy to plants' basal microbiomes. Scientific Reports, 2018, 8, 12712.	1.6	46
1173	Sulfated polysaccharide from sea cucumber modulates the gut microbiota and its metabolites in normal mice. International Journal of Biological Macromolecules, 2018, 120, 502-512.	3.6	57
1174	Variation in animal performance explained by the rumen microbiome or by diet composition1. Journal of Animal Science, 2018, 96, 4658-4673.	0.2	12
1175	Substrate-Induced Response in Biogas Process Performance and Microbial Community Relates Back to Inoculum Source. Microorganisms, 2018, 6, 80.	1.6	21
1176	Determinants of the Nasal Microbiome: Pilot Study of Effects of Intranasal Medication Use. Allergy and Rhinology, 2018, 9, 215265671878951.	0.7	21

#	Article	IF	CITATIONS
1177	Taxonomy of Oral Bacteria. Methods in Microbiology, 2018, , 171-201.	0.4	3
1178	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
1179	Transcriptional-Readthrough RNAs Reflect the Phenomenon of "A Gene Contains Gene(s)―or "Gene(s) within a Gene―in the Human Genome, and Thus Are Not Chimeric RNAs. Genes, 2018, 9, 40.	1.0	45
1180	Long-term in situ permafrost thaw effects on bacterial communities and potential aerobic respiration. ISME Journal, 2018, 12, 2129-2141.	4.4	73
1181	Analyzing High-Throughput Microbial Amplicon Sequence Data Using Multiple Markers. , 2018, , 121-138.		2
1182	Combined oral and topical antimicrobial therapy for male partners of women with bacterial vaginosis: Acceptability, tolerability and impact on the genital microbiota of couples - A pilot study. PLoS ONE, 2018, 13, e0190199.	1.1	55
1183	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
1184	What's the risk? Identifying potential human pathogens within grey-headed flying foxes faeces. PLoS ONE, 2018, 13, e0191301.	1.1	16
1185	Co-occurrence Network Reveals the Higher Fragmentation of the Bacterial Community in Kaidu River Than Its Tributaries in Northwestern China. Microbes and Environments, 2018, 33, 127-134.	0.7	22
1186	The biogeochemical fate of nickel during microbial ISA degradation; implications for nuclear waste disposal. Scientific Reports, 2018, 8, 8753.	1.6	15
1187	Environmental legacy contributes to the resilience of methane consumption in a laboratory microcosm system. Scientific Reports, 2018, 8, 8862.	1.6	12
1188	Early colonisation and temporal dynamics of the gut microbial ecosystem in Standardbred foals. Equine Veterinary Journal, 2019, 51, 231-237.	0.9	44
1189	Profiling the Gut Microbiome: Practice and Potential. , 2019, , 200-217.		0
1190	Loss of HDAC6 alters gut microbiota and worsens obesity. FASEB Journal, 2019, 33, 1098-1109.	0.2	36
1191	Methanogenic Archaea dominate mature heartwood habitats of Eastern Cottonwood (<i>Populus) Tj ETQq0 0 0</i>	rg <u>BT</u> /Over	'lo <u>၄</u> န 10 Tf 5(
1192	Longitudinal Comparison of Bacterial Diversity and Antibiotic Resistance Genes in New York City Sewage. MSystems, 2019, 4, .	1.7	19
1193	Metagenomic insights into the diversity and functions of microbial assemblages in lakes. , 2019, , 175-223.		3
1194	The Potential of Highâ€Throughput DNA Sequencing of the Paranasal Sinus Microbiome in Diagnosing Odontogenic Sinusitis. Otolaryngology - Head and Neck Surgery, 2019, 161, 1043-1047.	1.1	11

#	Article	IF	Citations
1195	Modification of the equine gastrointestinal microbiota by Jerusalem artichoke meal supplementation. PLoS ONE, 2019, 14, e0220553.	1.1	11
1196	Gut microbiome response to a modern Paleolithic diet in a Western lifestyle context. PLoS ONE, 2019, 14, e0220619.	1.1	62
1197	Spatial variations of microbial communities in abyssal and hadal sediments across the Challenger Deep. PeerJ, 2019, 7, e6961.	0.9	48
1198	Effect of coffee on the compositional shift of oral indigenous microbiota cultured <i>in vitro </i> . Journal of Oral Science, 2019, 61, 418-424.	0.7	4
1199	Long-read amplicon denoising. Nucleic Acids Research, 2019, 47, e104-e104.	6.5	31
1200	Dysbiosis of gut microbiota by dietary exposure of three graphene-family materials in zebrafish (Danio) Tj ETQq1	9.78431	4 rgBT /Over
1201	Characteristics of the Salivary Microbiota in Patients With Various Digestive Tract Cancers. Frontiers in Microbiology, 2019, 10, 1780.	1.5	57
1202	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
1203	Optimized PCR conditions minimizing the formation of chimeric DNA molecules from MPRA plasmid libraries. BMC Genomics, 2019, 20, 536.	1.2	24
1204	Altered diversity and composition of the gut microbiome in patients with cervical cancer. AMB Express, 2019, 9, 40.	1.4	55
1205	Supplementation of diet with non-digestible oligosaccharides alters the intestinal microbiota, but not arthritis development, in IL-1 receptor antagonist deficient mice. PLoS ONE, 2019, 14, e0219366.	1.1	9
1206	Incense Burning is Associated with Human Oral Microbiota Composition. Scientific Reports, 2019, 9, 10039.	1.6	12
1207	Microbial Community of Saline, Alkaline Lakes in the Nebraska Sandhills Based on 16S rRNA Gene Amplicon Sequence Data. Microbiology Resource Announcements, 2019, 8, .	0.3	3
1208	Comparison of gut microbiota diversity between wild and captive bharals (Pseudois nayaur). BMC Veterinary Research, 2019, 15, 243.	0.7	29
1209	Variation in rhizosphere microbiota correlates with edaphic factor in an abandoned antimony tailing dump. Environmental Pollution, 2019, 253, 141-151.	3.7	56
1210	Differences in soil microbial response to anthropogenic disturbances in Sanjiang and Momoge Wetlands, China. FEMS Microbiology Ecology, 2019, 95, .	1.3	18
1211	Gut Microbiota Differs Between Parkinson's Disease Patients and Healthy Controls in Northeast China. Frontiers in Molecular Neuroscience, 2019, 12, 171.	1.4	100
1212	Comparison of the gut microbiotas of laboratory and wild Asian house shrews (<i>Suncus) Tj ETQq1 1 0.784</i>	·314 rgBT 0.7	/Qyerlock 1(

#	Article	IF	CITATIONS
1213	Development of a Humanized Murine Model for the Study of Oxalobacter formigenes Intestinal Colonization. Journal of Infectious Diseases, 2019, 220, 1848-1858.	1.9	9
1214	The spatial distribution and drivers of soil microbial richness and diversity in a karst broadleaf forest. Forest Ecology and Management, 2019, 449, 117241.	1.4	25
1215	Response of gastrointestinal fermentative activity and colonic microbiota to protected sodium butyrate and protected sodium heptanoate in weaned piglets challenged with ETEC F4 ⁺ . Archives of Animal Nutrition, 2019, 73, 339-359.	0.9	9
1216	Amish (Rural) vs. non-Amish (Urban) Infant Fecal Microbiotas Are Highly Diverse and Their Transplantation Lead to Differences in Mucosal Immune Maturation in a Humanized Germfree Piglet Model. Frontiers in Immunology, 2019, 10, 1509.	2.2	31
1217	Lactobacillus plantarum PS128 ameliorates 2,5-Dimethoxy-4-iodoamphetamine-induced tic-like behaviors via its influences on the microbiota–gut-brain-axis. Brain Research Bulletin, 2019, 153, 59-73.	1.4	36
1218	Establishment of Coral-Bacteria Symbioses Reveal Changes in the Core Bacterial Community With Host Ontogeny. Frontiers in Microbiology, 2019, 10, 1529.	1.5	50
1219	Hotspots of Sequence Variability in Gut Microbial Genes Encoding Pro-Inflammatory Factors Revealed by Oligotyping. Frontiers in Genetics, 2019, 10, 631.	1.1	0
1220	Characterization and comparison of gut microbiomes in nine species of parrots in captivity. Symbiosis, 2019, 78, 241-250.	1.2	15
1221	Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. GigaScience, 2019, 8, .	3.3	132
1222	Consumption of post-fermented Jing-Wei Fuzhuan brick tea alleviates liver dysfunction and intestinal microbiota dysbiosis in high fructose diet-fed mice. RSC Advances, 2019, 9, 17501-17513.	1.7	19
1223	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
1224	Fitness and evolution of insecticide resistance associated with gut symbionts in metaflumizone-resistant Plutella xylostella. Crop Protection, 2019, 124, 104869.	1.0	12
1225	Determining the Reliability of Measuring Mercury Cycling Gene Abundance with Correlations with Mercury and Methylmercury Concentrations. Environmental Science & Technology, 2019, 53, 8649-8663.	4.6	99
1226	iMAP: an integrated bioinformatics and visualization pipeline for microbiome data analysis. BMC Bioinformatics, 2019, 20, 374.	1.2	34
1227	Phylogenetic Techniques in Geomicrobiology. , 2019, , 360-404.		0
1228	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
1229	Effects of Warming and Nitrogen Addition on the Soil Bacterial Community in a Subtropical Chinese Fir Plantation. Forests, 2019, 10, 861.	0.9	12
1230	Characteristics of Gut Microbiota in Patients with Hypertension and/or Hyperlipidemia: A Cross-Sectional Study on Rural Residents in Xinxiang County, Henan Province. Microorganisms, 2019, 7, 399.	1.6	36

#	Article	IF	CITATIONS
1231	Microbial reduction of Fe(III) coupled to the biodegradation of isosaccharinic acid (ISA). Applied Geochemistry, 2019, 109, 104399.	1.4	11
1232	Fluoride contributes to the shaping of microbial community in high fluoride groundwater in Qiji County, Yuncheng City, China. Scientific Reports, 2019, 9, 14488.	1.6	20
1233	Regulation of dietary astragalus polysaccharide (APS) supplementation on the non-specific immune response and intestinal microbiota of sea cucumber Apostichopus japonicus. Fish and Shellfish Immunology, 2019, 94, 517-524.	1.6	37
1234	Effects of Tropilaelaps mercedesae on midgut bacterial diversity of Apis mellifera. Experimental and Applied Acarology, 2019, 79, 169-186.	0.7	9
1236	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
1237	Mucosal Exposure to Cigarette Components Induces Intestinal Inflammation and Alters Antimicrobial Response in Mice. Frontiers in Immunology, 2019, 10, 2289.	2.2	29
1238	Preliminary Study on the Effect of <i>Bacillus amyloliquefaciens</i> TL on Cecal Bacterial Community Structure of Broiler Chickens. BioMed Research International, 2019, 2019, 1-11.	0.9	26
1239	Effect of <i>Rhodopseudomonas sphaeroides</i> –Treated Wastewater on Yield, Digestive Enzymes, Antioxidants, Nonspecific Immunity, and Intestinal Microbiota of Common Carp. North American Journal of Aquaculture, 2019, 81, 385-398.	0.7	6
1240	A collection of rumen bacteriome data from 334 mid-lactation dairy cows. Scientific Data, 2019, 6, 180301.	2.4	13
1241	Distinct Gut Microbiota Induced by Different Fat-to-Sugar-Ratio High-Energy Diets Share Similar Pro-obesity Genetic and Metabolite Profiles in Prediabetic Mice. MSystems, 2019, 4, .	1.7	18
1242	Illumina-based Analysis of Endophytic Bacterial Diversity of four Allium species. Scientific Reports, 2019, 9, 15271.	1.6	19
1243	Exploring possible associations of the intestine bacterial microbiome with the pre-weaned weight gaining performance of piglets in intensive pig production. Scientific Reports, 2019, 9, 15534.	1.6	27
1244	Infant airway microbiota and topical immune perturbations in the origins of childhood asthma. Nature Communications, 2019, 10, 5001.	5.8	92
1245	Microbial communities and soil chemical features associated with commercial production of the medicinal mushroom Ganoderma lingzhi in soil. Scientific Reports, 2019, 9, 15839.	1.6	8
1246	The Effect of Organic Carbon on Soil Bacterial Diversity in an Antarctic Lake Region. Journal of Ocean University of China, 2019, 18, 1402-1410.	0.6	1
1247	Effects of 2,2-dichloroacetamide (DCAcAm), an emerging disinfection by-product in drinking water, on the intestinal microbiota of adult zebrafish. Journal of Water and Health, 2019, 17, 683-690.	1.1	14
1248	Longitudinal development of the gut microbiota in healthy and diarrheic piglets induced by ageâ€related dietary changes. MicrobiologyOpen, 2019, 8, e923.	1.2	44
1249	Effect of Fermented Corn-Soybean Meal on Serum Immunity, the Expression of Genes Related to Gut Immunity, Gut Microbiota, and Bacterial Metabolites in Grower-Finisher Pigs. Frontiers in Microbiology, 2019, 10, 2620.	1.5	36

#	Article	IF	CITATIONS
1250	Exact variance component tests for longitudinal microbiome studies. Genetic Epidemiology, 2019, 43, 250-262.	0.6	5
1251	Effect of carbon and nitrogen ratio control on Artemia growth, water quality, biofloc microbial diversity under high salinity and zero-water exchange culture condition. Journal of Oceanology and Limnology, 2019, 37, 1768-1776.	0.6	3
1252	Soil acidification in continuously cropped tobacco alters bacterial community structure and diversity via the accumulation of phenolic acids. Scientific Reports, 2019, 9, 12499.	1.6	49
1253	Humic Acid Fertilizer Improved Soil Properties and Soil Microbial Diversity of Continuous Cropping Peanut: A Three-Year Experiment. Scientific Reports, 2019, 9, 12014.	1.6	110
1254	The effects of milk replacer allowance and weaning age on the performance, nutrients digestibility, and ruminal microbiota communities of lambs. Animal Feed Science and Technology, 2019, 257, 114263.	1.1	16
1255	Comparative effects of dietary supplementations with sodium butyrate, medium-chain fatty acids, and n-3 polyunsaturated fatty acids in late pregnancy and lactation on the reproductive performance of sows and growth performance of suckling piglets. Journal of Animal Science, 2019, 97, 4256-4267.	0.2	37
1257	Soil bacterial communities in the Brazilian Cerrado: Response to vegetation type and management. Acta Oecologica, 2019, 100, 103463.	0.5	16
1258	An orally administered magnoloside A ameliorates functional dyspepsia by modulating brain-gut peptides and gut microbiota. Life Sciences, 2019, 233, 116749.	2.0	22
1259	Comparative analysis of the fecal microbiota from different species of domesticated and wild suids. Scientific Reports, 2019, 9, 13616.	1.6	30
1260	Succession of oral microbiota community as a tool to estimate postmortem interval. Scientific Reports, 2019, 9, 13063.	1.6	29
1261	Analysis of Sinonasal Microbiota in Exacerbations of Chronic Rhinosinusitis Subgroups. OTO Open, 2019, 3, 2473974X1987510.	0.6	10
1262	Does duckweed ponds used for wastewater treatment emit or sequester greenhouse gases?. Science of the Total Environment, 2019, 691, 1043-1050.	3.9	23
1263	Characteristics and Evolution of sill-driven off-axis hydrothermalism in Guaymas Basin – the Ringvent site. Scientific Reports, 2019, 9, 13847.	1.6	33
1264	Water stress affects the frequency of Firmicutes, Clostridiales and Lysobacter in rhizosphere soils of greenhouse grape. Agricultural Water Management, 2019, 226, 105776.	2.4	35
1265	Urban beaches are environmental hotspots for antibiotic resistance following rainfall. Water Research, 2019, 167, 115081.	5.3	37
1266	Composition and Drivers of Gut Microbial Communities in Arctic-Breeding Shorebirds. Frontiers in Microbiology, 2019, 10, 2258.	1.5	49
1267	The Effects of Dietary Pattern during Intensified Training on Stool Microbiota of Elite Race Walkers. Nutrients, 2019, 11, 261.	1.7	62
1268	Isolation and characterization of Aspergillus niger NBC001 underlying suppression against Heterodera glycines. Scientific Reports, 2019, 9, 591.	1.6	11

# 1269	ARTICLE Microbial community and fermentation characteristic of Italian ryegrass silage prepared with corn stover and lactic acid bacteria. Bioresource Technology, 2019, 279, 166-173.	IF 4.8	CITATIONS
1270	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
1271	Exploring the Fecal Microbial Composition and Metagenomic Functional Capacities Associated With Feed Efficiency in Commercial DLY Pigs. Frontiers in Microbiology, 2019, 10, 52.	1.5	77
1272	Changes in rhizosphere bacterial and fungal community composition with vegetation restoration in planted forests. Land Degradation and Development, 2019, 30, 1147-1157.	1.8	63
1273	Ovotransferrin ameliorates the dysbiosis of immunomodulatory function and intestinal microbiota induced by cyclophosphamide. Food and Function, 2019, 10, 1109-1122.	2.1	50
1274	Lactobacillus plantarum PFM 105 Promotes Intestinal Development Through Modulation of Gut Microbiota in Weaning Piglets. Frontiers in Microbiology, 2019, 10, 90.	1.5	82
1275	Bacterial Community Diversity in Particulate Matter (PM2.5 and PM10) Within Broiler Houses in Different Broiler Growth Stages Under Intensive Rearing Conditions in Summer. Journal of Applied Poultry Research, 2019, 28, 479-489.	0.6	8
1276	Streptomyces pactum Act12 controls tomato yellow leaf curl virus disease and alters rhizosphere microbial communities. Biology and Fertility of Soils, 2019, 55, 149-169.	2.3	25
1277	The Impact of DNA Polymerase and Number of Rounds of Amplification in PCR on 16S rRNA Gene Sequence Data. MSphere, 2019, 4, .	1.3	91
1278	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
1279	Effect of bioaugmentation on biochemical characterisation and microbial communities in <i>Daqu</i> using <i>Bacillus</i> , <i> Saccharomycopsis</i> and <i>Absidia</i> . International Journal of Food Science and Technology, 2019, 54, 2639-2651.	1.3	29
1280	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
1281	Microbiota data from low biomass milk samples is markedly affected by laboratory and reagent contamination. PLoS ONE, 2019, 14, e0218257.	1.1	36
1282	Protist diversity and community assembly in surface sediments of the South China Sea. MicrobiologyOpen, 2019, 8, e891.	1.2	24
1283	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
1284	Vegetation biomass and soil moisture coregulate bacterial community succession under altered precipitation regimes in a desert steppe in northwestern China. Soil Biology and Biochemistry, 2019, 136, 107520.	4.2	82
1285	Changes in endophytic bacterial communities during different growth stages of cucumber (Cucumis) Tj ETQq0 0	0 ₁₉ BT /O	verlock 10 Tf 12

1286	Characterization of the non-glandular gastric region microbiota in Helicobacter suis-infected versus non-infected pigs identifies a potential role for Fusobacterium gastrosuis in gastric ulceration. Veterinary Research, 2019, 50, 39.	1.1	15	
------	---	-----	----	--

#	Article	IF	CITATIONS
1287	A specific synbiotic-containing amino acid-based formula restores gut microbiota in non-IgE mediated cow's milk allergic infants: a randomized controlled trial. Clinical and Translational Allergy, 2019, 9, 27.	1.4	24
1288	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
1289	Protective role of dryland rearing on netting floors against mortality through gut microbiota-associated immune performance in Shaoxing ducks. Poultry Science, 2019, 98, 4530-4538.	1.5	13
1290	Isolation of phytase-producing yeasts from rice seedlings for prospective probiotic applications. 3 Biotech, 2019, 9, 216.	1.1	8
1291	Microbiota and Antibiotic Resistome of Lettuce Leaves and Radishes Grown in Soils Receiving Manure-Based Amendments Derived From Antibiotic-Treated Cows. Frontiers in Sustainable Food Systems, 2019, 3, .	1.8	22
1292	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
1293	High-throughput sequencing analysis of bacterial community composition and quality characteristics in refrigerated pork during storage. Food Microbiology, 2019, 83, 86-94.	2.1	87
1294	Antimicrobial removal on piglets promotes health and higher bacterial diversity in the nasal microbiota. Scientific Reports, 2019, 9, 6545.	1.6	30
1295	A Link Between Plasma Microbial Translocation, Microbiome, and Autoantibody Development in Firstâ€Degree Relatives of Systemic Lupus Erythematosus Patients. Arthritis and Rheumatology, 2019, 71, 1858-1868.	2.9	71
1296	Archaeal communities in the deep-sea sediments of the South China Sea revealed by Illumina high-throughput sequencing. Annals of Microbiology, 2019, 69, 839-848.	1.1	15
1297	Evolution of the gut microbiome following acute HIV-1 infection. Microbiome, 2019, 7, 73.	4.9	69
1298	Engineering banana endosphere microbiome to improve Fusarium wilt resistance in banana. Microbiome, 2019, 7, 74.	4.9	70
1299	Co-occurrence analysis reveal that biotic and abiotic factors influence soil fungistasis against Fusarium graminearum. FEMS Microbiology Ecology, 2019, 95, .	1.3	15
1300	Gamma Irradiation Influences the Survival and Regrowth of Antibiotic-Resistant Bacteria and Antibiotic-Resistance Genes on Romaine Lettuce. Frontiers in Microbiology, 2019, 10, 710.	1.5	11
1301	Absence of evidence is not evidence of absence: Nanopore sequencing and complete assembly of the European lobster (Homarus gammarus) mitogenome uncovers the missing nad2 and a new major gene cluster duplication. BMC Genomics, 2019, 20, 335.	1.2	20
1302	Correlation of the rumen fluid microbiome and the average daily gain with a dietary supplementation of Allium mongolicum Regel extracts in sheep1. Journal of Animal Science, 2019, 97, 2865-2877.	0.2	20
1303	Effects of Various Carbon Nanotubes on Soil Bacterial Community Composition and Structure. Environmental Science & Technology, 2019, 53, 5707-5716.	4.6	41
1304	Structure and stability of the coral microbiome in space and time. Scientific Reports, 2019, 9, 6785.	1.6	74

#	Article	IF	CITATIONS
1305	Influence of the Intestinal Microbiota on Colonization Resistance to <i>Salmonella</i> and the Shedding Pattern of Naturally Exposed Pigs. MSystems, 2019, 4, .	1.7	40
1306	The effects of the supplementation of multiâ€strain probiotics on intestinal microbiota, metabolites and inflammation of young <scp>SPF</scp> chickens challenged with <i>Salmonella enterica</i> subsp. <i>enterica</i> . Animal Science Journal, 2019, 90, 737-746.	0.6	13
1307	Effect of longâ€ŧerm organic and mineral fertilization strategies on rhizosphere microbiota assemblage and performance of lettuce. Environmental Microbiology, 2019, 21, 2426-2439.	1.8	42
1308	Comparison of microbial community and metabolites in spontaneous fermentation of two types Daqu starter for traditional Chinese vinegar production. Journal of Bioscience and Bioengineering, 2019, 128, 307-315.	1.1	22
1309	Metagenomic analysis of composition, function and cycling processes of microbial community in water, sediment and effluent of Litopenaeus vannamei farming environments under different culture modes. Aquaculture, 2019, 506, 280-293.	1.7	56
1310	Insights gained into activated sludge nitrification through structural and functional profiling of microbial community response to starvation stress. Environmental Science: Water Research and Technology, 2019, 5, 884-896.	1.2	13
1311	Immunosuppression-induced alterations in fish gut microbiota may increase the susceptibility to pathogens. Fish and Shellfish Immunology, 2019, 88, 540-545.	1.6	31
1312	Alterations of the Mice Gut Microbiome via Schistosoma japonicum Ova-Induced Granuloma. Frontiers in Microbiology, 2019, 10, 352.	1.5	63
1313	Understanding and overcoming the pitfalls and biases of next-generation sequencing (NGS) methods for use in the routine clinical microbiological diagnostic laboratory. European Journal of Clinical Microbiology and Infectious Diseases, 2019, 38, 1059-1070.	1.3	154
1314	Sanguinarine and resveratrol affected rumen fermentation parameters and bacterial community in calves. Animal Feed Science and Technology, 2019, 251, 64-75.	1.1	14
1315	Exposure to Titanium Dioxide Nanoparticles During Pregnancy Changed Maternal Gut Microbiota and Increased Blood Glucose of Rat. Nanoscale Research Letters, 2019, 14, 26.	3.1	43
1316	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
1317	COD/sulfate ratio does not affect the methane yield and microbial diversity in anaerobic digesters. Water Research, 2019, 155, 444-454.	5.3	44
1318	Amplicon sequencing reveals different microbial communities in living poplar wetwood and sapwood. Trees - Structure and Function, 2019, 33, 851-865.	0.9	5
1319	Characterization of the gut microbiota of invasive Agrilus mali Matsumara (Coleoptera: Buprestidae) using high-throughput sequencing: uncovering plant cell-wall degrading bacteria. Scientific Reports, 2019, 9, 4923.	1.6	29
1320	Effects of Bacillus subtilis on the growth, colony maintenance, and attached bacterial community composition of colonial cyanobacteria. Environmental Science and Pollution Research, 2019, 26, 14977-14987.	2.7	10
1321	Phylogenetic analyses and characteristics of the microbiomes from five mealybugs (Hemiptera:) Tj ETQq0 0 0 r	gBT /Oyerlc	ock 10 Tf 50 1

1322	Fitness and microbial networks of the common wasp, <i>Vespula vulgaris</i> (Hymenoptera: Vespidae), in its native and introduced ranges. Ecological Entomology, 2019, 44, 512-523.	1.1	11	
------	---	-----	----	--

#	Article	IF	CITATIONS
1323	Fungal community analysis in seawater of the Mariana Trench as estimated by Illumina HiSeq. RSC Advances, 2019, 9, 6956-6964.	1.7	22
1324	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
1325	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
1326	Diversity and environmental distribution of the cosmopolitan endosymbiont "Candidatus Megaira― Scientific Reports, 2019, 9, 1179.	1.6	46
1327	Rhizobacterial Community Assembly Patterns Vary Between Crop Species. Frontiers in Microbiology, 2019, 10, 581.	1.5	42
1328	Seasonal succession and spatial distribution of bacterial community structure in a eutrophic freshwater Lake, Lake Taihu. Science of the Total Environment, 2019, 669, 29-40.	3.9	103
1329	Undernutrition Shapes the Gut Microbiota and Bile Acid Profile in Association with Altered Gut-Liver FXR Signaling in Weaning Pigs. Journal of Agricultural and Food Chemistry, 2019, 67, 3691-3701.	2.4	36
1330	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. MSphere, 2019, 4, .	1.3	14
1331	Differential composition of gut microbiota among healthy volunteers, morbidly obese patients and postâ€'bariatric surgery patients. Experimental and Therapeutic Medicine, 2019, 17, 2268-2278.	0.8	23
1332	Potential Functions of the Gastrointestinal Microbiome Inhabiting the Length of the Rat Digest Tract. International Journal of Molecular Sciences, 2019, 20, 1232.	1.8	4
1333	Analysis of the Effects of Dietary Pattern on the Oral Microbiome of Elite Endurance Athletes. Nutrients, 2019, 11, 614.	1.7	54
1334	Associations of Gut Microbiota With Heat Stress-Induced Changes of Growth, Fat Deposition, Intestinal Morphology, and Antioxidant Capacity in Ducks. Frontiers in Microbiology, 2019, 10, 903.	1.5	59
1335	External carbon addition for enhancing denitrification modifies bacterial community composition and affects CH4 and N2O production in sub-arctic mining pond sediments. Water Research, 2019, 158, 22-33.	5.3	32
1336	<i>APOE</i> genotype influences the gut microbiome structure and function in humans and mice: relevance for Alzheimer's disease pathophysiology. FASEB Journal, 2019, 33, 8221-8231.	0.2	124
1337	Assessing Microbial Community Patterns During Incipient Soil Formation From Basalt. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 941-958.	1.3	16
1338	Microbial taxonomic, nitrogen cycling and phosphorus recycling community composition during long-term organic greenhouse farming. FEMS Microbiology Ecology, 2019, 95, .	1.3	40
1339	Direct and indirect effects of zinc oxide and titanium dioxide nanoparticles on the decomposition of leaf litter in streams. Ecotoxicology, 2019, 28, 435-448.	1.1	5
1340	<i>In Vitro</i> and <i>In Vivo</i> Activities of Zinc Linolenate, a Selective Antibacterial Agent against Helicobacter pylori. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	29

#	Article	IF	CITATIONS
1341	Oral Administration of Compound Probiotics Improved Canine Feed Intake, Weight Gain, Immunity and Intestinal Microbiota. Frontiers in Immunology, 2019, 10, 666.	2.2	53
1342	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
1343	Enrichment of phosphate solubilizing bacteria during late developmental stages of eggplant (<i>Solanum melongena</i> L.). FEMS Microbiology Ecology, 2019, 95, .	1.3	27
1344	Biochemical but not compositional recovery of skin mucosal microbiome communities after disruption. Infection and Drug Resistance, 2019, Volume 12, 399-416.	1.1	5
1345	Electronâ€acceptor loadings affect chloroform dechlorination in a hydrogenâ€based membrane biofilm reactor. Biotechnology and Bioengineering, 2019, 116, 1439-1448.	1.7	13
1346	Root-Associated Endophytic Bacterial Community Composition of Pennisetum sinese from Four Representative Provinces in China. Microorganisms, 2019, 7, 47.	1.6	13
1347	Impact of Nitrogen Fertilizer on the Mycorrhizal Inoculating Potential and Fungal Community Structure in Rhizosphere of Medicinal PlantCurcuma longaL Geomicrobiology Journal, 2019, 36, 385-395.	1.0	3
1348	Rapid detection of macroalgal seed bank on cobbles: application of DNA metabarcoding using next-generation sequencing. Journal of Applied Phycology, 2019, 31, 2743-2753.	1.5	12
1349	Bacterial community analysis for investigating bacterial transfer from tonsils to the pig carcass. International Journal of Food Microbiology, 2019, 295, 8-18.	2.1	12
1350	Combined Metabarcoding and Co-occurrence Network Analysis to Profile the Bacterial, Fungal and Fusarium Communities and Their Interactions in Maize Stalks. Frontiers in Microbiology, 2019, 10, 261.	1.5	51
1351	Microbiomes of China's Space Station During Assembly, Integration, and Test Operations. Microbial Ecology, 2019, 78, 631-650.	1.4	13
1352	Gut Microbiota Dysbiosis Is Not Independently Associated With Neurocognitive Impairment in People Living With HIV. Frontiers in Microbiology, 2018, 9, 3352.	1.5	19
1353	Nasopharyngeal Microbiota in Children With Invasive Pneumococcal Disease: Identification of Bacteria With Potential Disease-Promoting and Protective Effects. Frontiers in Microbiology, 2019, 10, 11.	1.5	33
1354	Contrasting histories of microcystin-producing cyanobacteria in two temperate lakes as inferred from quantitative sediment DNA analyses. Lake and Reservoir Management, 2019, 35, 102-117.	0.4	19
1355	Identification and evaluation of the microbiome in the female and male reproductive tracts. Human Reproduction Update, 2019, 25, 298-325.	5.2	115
1356	Bifidogenic and butyrogenic effects of young barely leaf extract in an in vitro human colonic microbiota model. AMB Express, 2019, 9, 182.	1.4	8
1357	Prebiotic oligosaccharides in early life alter gut microbiome development in male mice while supporting influenza vaccination responses. Beneficial Microbes, 2019, 10, 279-291.	1.0	16
1358	Enfoque metagenómico para la caracterización del microbioma de aves corral. Revisión. Revista Colombiana De BiotecnologÃa, 2019, 21, 77-97.	0.5	0

#	Article	IF	CITATIONS
1359	Low Temperature (15 °C) Reduces Bacterial Diversity and Prolongs the Preservation Time of Volvariella volvacea. Microorganisms, 2019, 7, 475.	1.6	7
1360	Efficacy of medium-chain fatty acid salts distilled from coconut oil against two enteric pathogen challenges in weanling piglets. Journal of Animal Science and Biotechnology, 2019, 10, 89.	2.1	23
1361	Group I alkenones and Isochrysidales in the world's largest maar lakes and their potential paleoclimate applications. Organic Geochemistry, 2019, 138, 103924.	0.9	7
1362	Dynamic Changes in the Microbiome and Mucosal Immune Microenvironment of the Lower Respiratory Tract by Influenza Virus Infection. Frontiers in Microbiology, 2019, 10, 2491.	1.5	36
1363	Patterns of PCR Amplification Artifacts of the Fungal Barcode Marker in a Hybrid Mushroom. Frontiers in Microbiology, 2019, 10, 2686.	1.5	9
1364	Water-soluble phosphorus contributes significantly to shaping the community structure of rhizospheric bacteria in rocky desertification areas. Scientific Reports, 2019, 9, 18408.	1.6	11
1365	Dynamics and stabilization of the rumen microbiome in yearling Tibetan sheep. Scientific Reports, 2019, 9, 19620.	1.6	35
1366	Improved utilization of soybean meal through fermentation with commensal Shewanella sp. MR-7 in turbot (Scophthalmus maximus L.). Microbial Cell Factories, 2019, 18, 214.	1.9	33
1367	Exploring Actinobacteria Associated With Rhizosphere and Endosphere of the Native Alpine Medicinal Plant Leontopodium nivale Subspecies alpinum. Frontiers in Microbiology, 2019, 10, 2531.	1.5	28
1368	Changes of Root Endophytic Bacterial Community Along a Chronosequence of Intensively Managed Lei Bamboo (Phyllostachys praecox) Forests in Subtropical China. Microorganisms, 2019, 7, 616.	1.6	10
1369	Early life nutrition influences susceptibility to chronic inflammatory colitis in later life. Scientific Reports, 2019, 9, 18111.	1.6	12
1370	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
1371	Bacteriophage targeting of gut bacterium attenuates alcoholic liver disease. Nature, 2019, 575, 505-511.	13.7	493
1372	The Response of Microbiota Community to Streptococcus agalactiae Infection in Zebrafish Intestine. Frontiers in Microbiology, 2019, 10, 2848.	1.5	25
1373	Diet and irradiation effects on the bacterial community composition and structure in the gut of domesticated teneral and mature Queensland fruit fly, Bactrocera tryoni (Diptera: Tephritidae). BMC Microbiology, 2019, 19, 281.	1.3	26
1374	Microbial Communities Associated with Sustained Anaerobic Reductive Dechlorination of α-, β-, γ-, and Î-Hexachlorocyclohexane Isomers to Monochlorobenzene and Benzene. Environmental Science & Technology, 2020, 54, 255-265.	4.6	32
1375	Effect of Short-Term Dietary Intervention and Probiotic Mix Supplementation on the Gut Microbiota of Elderly Obese Women. Nutrients, 2019, 11, 3011.	1.7	47
1376	Microbial diversity within the digestive tract contents of Dezhou donkeys. PLoS ONE, 2019, 14, e0226186.	1.1	26

#	Article	IF	CITATIONS
1377	The Effect of Increasing Inclusion Levels of a Fucoidan-Rich Extract Derived from Ascophyllum nodosum on Growth Performance and Aspects of Intestinal Health of Pigs Post-Weaning. Marine Drugs, 2019, 17, 680.	2.2	10
1378	Impact of Tilapia hepcidin 2-3 dietary supplementation on the gut microbiota profile and immunomodulation in the grouper (Epinephelus lanceolatus). Scientific Reports, 2019, 9, 19047.	1.6	23
1379	Ecological and microbiological diversity of chigger mites, including vectors of scrub typhus, on small mammals across stratified habitats in Thailand. Animal Microbiome, 2019, 1, 18.	1.5	21
1380	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
1381	Metagenomic insights into the structure and function of intestinal microbiota of the farmed Pacific white shrimp (Litopenaeus vannamei). Aquaculture, 2019, 499, 109-118.	1.7	69
1382	Effect of Resistant Starch on the Gut Microbiota and Its Metabolites in Patients with Coronary Artery Disease. Journal of Atherosclerosis and Thrombosis, 2019, 26, 705-719.	0.9	24
1383	Influences of dietary selenomethionine exposure on tissue accumulation, blood biochemical profiles, gene expression and intestinal microbiota of Carassius auratus. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2019, 218, 21-29.	1.3	23
1384	Bacterial complexes of Bacillus subtilis and Pseudomonas stutzeri alter the microbial composition in grass carp water. Aquaculture International, 2019, 27, 303-312.	1.1	8
1385	Air pollution during the winter period and respiratory tract microbial imbalance in a healthy young population in Northeastern China. Environmental Pollution, 2019, 246, 972-979.	3.7	38
1386	Inulin Ameliorates Alcoholic Liver Disease via Suppressing <scp>LPS</scp> â€ <scp>TLR</scp> 4â€M <i>Ï^/i> Axis and Modulating Gut Microbiota in Mice. Alcoholism: Clinical and Experimental Research, 2019, 43, 411-424.</i>	1.4	65
1387	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
1388	Gut microbiota dysbiosis correlates with a low-dose PCB126-induced dyslipidemia and non-alcoholic fatty liver disease. Science of the Total Environment, 2019, 653, 274-282.	3.9	65
1389	GenCoF: a graphical user interface to rapidly remove human genome contaminants from metagenomic datasets. Bioinformatics, 2019, 35, 2318-2319.	1.8	28
1390	Unusual 18S rDNA of Acanthamoeba containing intron turned out to be a T5/T4 chimera. Parasitology Research, 2019, 118, 657-662.	0.6	3
1391	Hydra as Model to Determine the Role of FOXO in Longevity. Methods in Molecular Biology, 2019, 1890, 231-238.	0.4	2
1392	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
1393	Community structural differences shape microbial responses to high molecular weight organic matter. Environmental Microbiology, 2019, 21, 557-571.	1.8	40
1394	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

	Сіт	ATION REPORT	
#	Article	IF	CITATIONS
1395	Effect of post-harvest interventions on surficial carrot bacterial community dynamics, pathogen survival, and antibiotic resistance. International Journal of Food Microbiology, 2019, 291, 25-34.	2.1	8
1396	Understanding antimicrobial discovery and resistance from a metagenomic and metatranscriptomic perspective: advances and applications. Environmental Microbiology Reports, 2019, 11, 62-86.	1.0	34
1397	Insight into the correlation between biochar amendment and shifts in bacterial community 4 years after a single incorporation in soybean- and maize-planted soils in northeastern China. Canadian Journal of Microbiology, 2019, 65, 353-364.	0.8	8
1398	Linking Exoproteome Function and Structure to Anammox Biofilm Development. Environmental Science & Technology, 2019, 53, 1490-1500.	4.6	77
1399	Delayed differentiation of vaginal and uterine microbiomes in dairy cows developing postpartum endometritis. PLoS ONE, 2019, 14, e0200974.	1.1	57
1400	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
1401	Shaping microbial consortia in coupling glycerol fermentation and carboxylate chain elongation for Co-production of 1,3-propanediol and caproate: Pathways and mechanisms. Water Research, 2019, 14 281-291.	18, 5.3	30
1402	Highâ€ŧhroughput identification and diagnostics of pathogens and pests: Overview and practical recommendations. Molecular Ecology Resources, 2019, 19, 47-76.	2.2	91
1403	Effect of temperature on the microflora community composition in the digestive tract of the veined rapa whelk (Rapana venosa) revealed by 16S rRNA gene sequencing. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 145-153.	0.4	7
1404	Comparison of long-term ceramic membrane bioreactors without and with in-situ ozonation in wastewater treatment: Membrane fouling, effluent quality and microbial community. Science of the Total Environment, 2019, 652, 788-799.	3.9	47
1405	Structure and Diversity of the Bacterial Communities in the Acid and Thermophilic Crater-Lake of the Volcano "El ChichA³nâ€, Mexico. Geomicrobiology Journal, 2019, 36, 97-109.	1.0	14
1406	Altered host-gut microbes symbiosis in severely malnourished anorexia nervosa (AN) patients undergoing enteral nutrition: An explicative factor of functional intestinal disorders?. Clinical Nutrition, 2019, 38, 2304-2310.	2.3	62
1407	The role of gut microbiome and its interaction with arsenic exposure in carotid intima-media thickness in a Bangladesh population. Environment International, 2019, 123, 104-113.	4.8	30
1408	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
1409	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
1410	Using Partial Nitrification and Anammox To Remove Nitrogen from Low-Strength Wastewater by Co-immobilizing Biofilm inside a Moving Bed Bioreactor. ACS Sustainable Chemistry and Engineering, 2019, 7, 1353-1361.	3.2	35
1411	Effects of dietary crude protein and tannic acid on rumen fermentation, rumen microbiota and nutrient digestion in beef cattle. Archives of Animal Nutrition, 2019, 73, 30-43.	0.9	21
1412	Positron emission tomography to visualise in-situ microbial metabolism in natural sediments. Applied Radiation and Isotopes, 2019, 144, 104-110.	0.7	7

#	Article	IF	CITATIONS
1413	Dietary sanguinarine affected immune response, digestive enzyme activity and intestinal microbiota of Koi carp (cryprinus carpiod). Aquaculture, 2019, 502, 72-79.	1.7	31
1414	Changes in microbial communities and associated water and gas geochemistry across a sulfate gradient in coal beds: Powder River Basin, USA. Geochimica Et Cosmochimica Acta, 2019, 245, 495-513.	1.6	39
1415	Effect of Different Soil Phosphate Sources on the Active Bacterial Microbiota Is Greater in the Rhizosphere than in the Endorhiza of Barley (Hordeum vulgare L.). Microbial Ecology, 2019, 77, 689-700.	1.4	14
1416	The Effect of Leanâ€Seafood and Nonâ€Seafood Diets on Fecal Metabolites and Gut Microbiome: Results from a Randomized Crossover Intervention Study. Molecular Nutrition and Food Research, 2019, 63, e1700976.	1.5	30
1417	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. Briefings in Bioinformatics, 2019, 20, 1032-1056.	3.2	10
1418	Computational profiling of the gut–brain axis: microflora dysbiosis insights to neurological disorders. Briefings in Bioinformatics, 2019, 20, 825-841.	3.2	27
1419	OBSOLETE: Bioinformatic Platforms for Metagenomics. , 2020, , .		0
1420	Biocontrol of Root Diseases and Growth Promotion of the Tuberous Plant Aconitum carmichaelii Induced by Actinomycetes Are Related to Shifts in the Rhizosphere Microbiota. Microbial Ecology, 2020, 79, 134-147.	1.4	30
1421	Arabinoxylans and gelled arabinoxylans used as anti-obesogenic agents could protect the stability of intestinal microbiota of rats consuming high-fat diets. International Journal of Food Sciences and Nutrition, 2020, 71, 74-83.	1.3	12
1422	The association between gut microbiome and anthropometric measurements in Bangladesh. Gut Microbes, 2020, 11, 63-76.	4.3	31
1423	Antibiotic exposure perturbs the bacterial community in the small brown planthopper <i>Laodelphax striatellus</i> . Insect Science, 2020, 27, 895-907.	1.5	28
1424	Supplementation of dietary non-digestible oligosaccharides from birth onwards improve social and reduce anxiety-like behaviour in male BALB/c mice. Nutritional Neuroscience, 2020, 23, 896-910.	1.5	27
1426	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
1427	Diversity, Tissue Localization, and Infection Pattern of Bacterial Symbionts of the White-Backed Planthopper, Sogatella furcifera (Hemiptera: Delphacidae). Microbial Ecology, 2020, 79, 720-730.	1.4	22
1428	Differentiation of symbiotic bacteria is a new evidence for two genetic clades of <i>Aphelinus mali</i> (Hymenoptera: Aphelinidae) in China. Oriental Insects, 2020, 54, 447-464.	0.1	1
1429	Trimethylamine But Not Trimethylamine Oxide Increases With Age in Rat Plasma and Affects Smooth Muscle Cells Viability. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 1276-1283.	1.7	37
1430	Sharp contrasts between freshwater and marine microbial enzymatic capabilities, community composition, and DOM pools in a NE Greenland fjord. Limnology and Oceanography, 2020, 65, 77-95.	1.6	17
1431	Different milk replacers alter growth performance and rumen bacterial diversity of dairy bull calves. Livestock Science, 2020, 231, 103862.	0.6	5

ARTICLE IF CITATIONS Exploring the accuracy of ampliconâ€based internal transcribed spacer markers for a fungal 1432 2.2 49 community. Molecular Ecology Resources, 2020, 20, 170-184. Bacterial succession and the dynamics of flavor compounds in the Huangjiu fermented from corn. 1433 1.0 Archives of Microbiology, 202Ó, 202, 299-308. Comparison of microbial communities and physiochemical characteristics of two traditionally 1434 2.9 70 fermented vegetables. Food Research International, 2020, 128, 108755. Geographical distribution and risk assessment of heavy metals: a case study of mine tailings pond. 1435 Chemistry and Ecology, 2020, 36, 1-15. Prediction of nutrient digestibility in growerâ€finisher pigs based on faecal microbiota composition. 1436 0.8 12 Journal of Animal Breeding and Genetics, 2020, 137, 23-35. Bacteriome and Mycobiome in <i>Nicotiana tabacum</i> Fields Affected by Black Shank Disease. Plant Disease, 2020, 104, 315-319. Effects of dietary calcium pyruvate on gastrointestinal tract development, intestinal health and growth performance of newly weaned piglets fed lowâ€protein diets. Journal of Applied Microbiology, 2020, 128, 355-365. 1438 1.4 14 Increased loading stress leads to convergence of microbial communities and high methane yields in 5.3 adapted anaerobic co-digesters. Water Research, 2020, 169, 115155. Vertical changes in bacterial community composition down to a depth of 20 m on the degraded Loess 1440 20 1.8 Plateau in China. Land Degradation and Development, 2020, 31, 1300-1313. Systematic Analysis of Impact of Sampling Regions and Storage Methods on Fecal Gut Microbiome and 1441 1.3 Metabolome Profiles. MSphere, 2020, 5, . Analysis of Myoglobin Stability and Bacterial Community Diversity in Mutton Chop Rolls During Cold 1442 1.0 6 Preservation. Current Microbiology, 2020, 77, 826-835. <i>Cutibacterium acnes</i> is less commonly identified by next-generation sequencing than culture in primary shoulder surgery. Shoulder and Elbow, 2020, 12, 170-177. 1443 Purified plant cell walls with adsorbed polyphenols alter porcine faecal bacterial communities 1444 2.1 15 during <i>in vitro</i> fermentation. Food and Function, 2020, 11, 834-845. The impact of food additives, artificial sweeteners and domestic hygiene products on the human gut 1445 1.8 microbiome and its fibre fermentation capacity. European Journal of Nutrition, 2020, 59, 3213-3230. 1446 Soil microbial succession with soil development since costal reclamation. Catena, 2020, 187, 104393. 2.2 29 Heavy metals, antibiotics and nutrients affect the bacterial community and resistance genes in chicken 1447 96 manure composting and fertilized soil. Journal of Environmental Management, 2020, 257, 109980. Interactions between elevated CO2 levels and floating aquatic plants on the alteration of bacterial 1448 function in carbon assimilation and decomposition in eutrophic waters. Water Research, 2020, 171, 5.330 115398. Highly heterogeneous temporal dynamics in the abundance and diversity of the emerging pathogens 1449 5.3 Arcobacter at an urban beach. Water Research, 2020, 171, 115405.

#	Article	IF	CITATIONS
1450	Disordered cutaneous microbiota in systemic lupus erythematosus. Journal of Autoimmunity, 2020, 108, 102391.	3.0	35
1451	Effects of application rates of poly-γ-glutamic acid on vegetable growth and soil bacterial community structure. Applied Soil Ecology, 2020, 147, 103405.	2.1	21
1452	Biochar addition to forest plantation soil enhances phosphorus availability and soil bacterial community diversity. Forest Ecology and Management, 2020, 455, 117635.	1.4	66
1453	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
1454	Artificial light at night erases positive interactions across trophic levels. Functional Ecology, 2020, 34, 694-706.	1.7	28
1455	Geographically isolated Colorado potato beetle mediating distinct defense responses in potato is associated with the alteration of gut microbiota. Journal of Pest Science, 2020, 93, 379-390.	1.9	11
1456	Pichia kudriavzevii retards fungal decay by influencing the fungal community succession during cherry tomato fruit storage. Food Microbiology, 2020, 88, 103404.	2.1	35
1457	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
1458	The Association Between Smoking and Gut Microbiome in Bangladesh. Nicotine and Tobacco Research, 2020, 22, 1339-1346.	1.4	39
1459	Effects of 10-valent pneumococcal conjugate (PCV10) vaccination on the nasopharyngeal microbiome. Vaccine, 2020, 38, 1436-1443.	1.7	7
1460	Bacterial communities in Haemaphysalis, Dermacentor and Amblyomma ticks collected from wild boar of an Orang Asli Community in Malaysia. Ticks and Tick-borne Diseases, 2020, 11, 101352.	1.1	19
1461	Seasonal Variability of Conditionally Rare Taxa in the Water Column Bacterioplankton Community of Subtropical Reservoirs in China. Microbial Ecology, 2020, 80, 14-26.	1.4	54
1462	Diversity and flexibility of the bacterial communities on Cancer pagurus at different temperatures. Journal of Sea Research, 2020, 156, 101827.	0.6	8
1463	Evaluation of seven chemical pesticides by mixed microbial culture (PCS-1): Degradation ability, microbial community, and Medicago sativa phytotoxicity. Journal of Hazardous Materials, 2020, 389, 121834.	6.5	39
1464	Manganese and cobalt redox cycling in laterites; Biogeochemical and bioprocessing implications. Chemical Geology, 2020, 531, 119330.	1.4	22
1465	Harmful algal blooms significantly reduce the resource use efficiency in a coastal plankton community. Science of the Total Environment, 2020, 704, 135381.	3.9	31
1466	Effects of thiosulfate addition on ammonia and nitrogen removal in biofilters packed with Oyaishi (pumice tuff). Animal Science Journal, 2020, 91, e13313.	0.6	3
1467	Funneliformis mosseae alters soil fungal community dynamics and composition during litter decomposition. Fungal Ecology, 2020, 43, 100864.	0.7	11

#	Article	IF	CITATIONS
1468	Changes in intestinal microflora in digestive tract diseases during pregnancy. Archives of Gynecology and Obstetrics, 2020, 301, 243-249.	0.8	21
1469	<i>Paenibacillus</i> infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. Science Translational Medicine, 2020, 12, .	5.8	39
1470	An Improved hgcAB Primer Set and Direct High-Throughput Sequencing Expand Hg-Methylator Diversity in Nature. Frontiers in Microbiology, 2020, 11, 541554.	1.5	33
1471	Longitudinal analysis of fecal microbiome and metabolome during renal fibrotic progression in a unilateral ureteral obstruction animal model. European Journal of Pharmacology, 2020, 886, 173555.	1.7	12
1472	Are marine benthic microeukaryotes different from macrobenthos in terms of regional geographical distribution? New insights revealed by RNA metabarcoding. Continental Shelf Research, 2020, 209, 104255.	0.9	3
1473	Study on the Intervention Effect of Qi Gong Wan Prescription on Patients with Phlegm-Dampness Syndrome of Polycystic Ovary Syndrome Based on Intestinal Flora. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-18.	0.5	4
1474	Changes in Gut Microorganism in Patients with Positive Immune Antibody-Associated Recurrent Abortion. BioMed Research International, 2020, 2020, 1-15.	0.9	6
1475	Core Mycobiome and Their Ecological Relevance in the Gut of Five Ips Bark Beetles (Coleoptera:) Tj ETQq1 1 0.784	1314 rgBT 1.5	/94erlock 1
1476	Identification of bacteria and fungi inhabiting fruiting bodies of Burgundy truffle (Tuber aestivum) Tj ETQq0 0 0 rg	BT /Overlo	ock 10 Tf 50
1477	Effects of phytosterols supplementation on growth performance and intestinal microflora of yellow-feather broilers. Poultry Science, 2020, 99, 6022-6030.	1.5	15
1477 1478		1.5	15 9
	yellow-feather broilers. Poultry Science, 2020, 99, 6022-6030. Associations of sodium and potassium consumption with the gut microbiota and host metabolites in a		
1478	yellow-feather broilers. Poultry Science, 2020, 99, 6022-6030. Associations of sodium and potassium consumption with the gut microbiota and host metabolites in a population-based study in Chinese adults. American Journal of Clinical Nutrition, 2020, 112, 1599-1612. Alterations of Gut Microbiota in Type 2 Diabetes Individuals and the Confounding Effect of	2.2	9
1478 1479	yellow-feather broilers. Poultry Science, 2020, 99, 6022-6030. Associations of sodium and potassium consumption with the gut microbiota and host metabolites in a population-based study in Chinese adults. American Journal of Clinical Nutrition, 2020, 112, 1599-1612. Alterations of Gut Microbiota in Type 2 Diabetes Individuals and the Confounding Effect of Antidiabetic Agents. Journal of Diabetes Research, 2020, 2020, 1-14. Exploring microbial determinants of apple replant disease (ARD): a microhabitat approach under	2.2	9 23
1478 1479 1480	 yellow-feather broilers. Poultry Science, 2020, 99, 6022-6030. Associations of sodium and potassium consumption with the gut microbiota and host metabolites in a population-based study in Chinese adults. American Journal of Clinical Nutrition, 2020, 112, 1599-1612. Alterations of Gut Microbiota in Type 2 Diabetes Individuals and the Confounding Effect of Antidiabetic Agents. Journal of Diabetes Research, 2020, 2020, 1-14. Exploring microbial determinants of apple replant disease (ARD): a microhabitat approach under split-root design. FEMS Microbiology Ecology, 2020, 96, . Soil microbial interactions modulate the effect of Artemisia ordosica on herbaceous species in a 	2.2 1.0 1.3	9 23 19
1478 1479 1480 1481	 yellow-feather broilers. Poultry Science, 2020, 99, 6022-6030. Associations of sodium and potassium consumption with the gut microbiota and host metabolites in a population-based study in Chinese adults. American Journal of Clinical Nutrition, 2020, 112, 1599-1612. Alterations of Gut Microbiota in Type 2 Diabetes Individuals and the Confounding Effect of Antidiabetic Agents. Journal of Diabetes Research, 2020, 2020, 1-14. Exploring microbial determinants of apple replant disease (ARD): a microhabitat approach under split-root design. FEMS Microbiology Ecology, 2020, 96, . Soil microbial interactions modulate the effect of Artemisia ordosica on herbaceous species in a desert ecosystem, northern China. Soil Biology and Biochemistry, 2020, 150, 108013. Food Resource Sharing of Alder Leaf Beetle Specialists (Coleoptera: Chrysomelidae) as Potential Insectâ€"Plant Interface for Horizontal Transmission of Endosymbionts. Environmental Entomology, 	 2.2 1.0 1.3 4.2 	9 23 19 17
1478 1479 1480 1481 1482	 yellow-feather broilers. Poultry Science, 2020, 99, 6022-6030. Associations of sodium and potassium consumption with the gut microbiota and host metabolites in a population-based study in Chinese adults. American Journal of Clinical Nutrition, 2020, 112, 1599-1612. Alterations of Gut Microbiota in Type 2 Diabetes Individuals and the Confounding Effect of Antidiabetic Agents. Journal of Diabetes Research, 2020, 2020, 1-14. Exploring microbial determinants of apple replant disease (ARD): a microhabitat approach under split-root design. FEMS Microbiology Ecology, 2020, 96, . Soil microbial interactions modulate the effect of Artemisia ordosica on herbaceous species in a desert ecosystem, northern China. Soil Biology and Biochemistry, 2020, 150, 108013. Food Resource Sharing of Alder Leaf Beetle Specialists (Coleoptera: Chrysomelidae) as Potential Insect–Plant Interface for Horizontal Transmission of Endosymbionts. Environmental Entomology, 2020, 49, 1402-1414. The intestine of artificially bred larval turbot (Scophthalmus maximus) contains a stable core group 	 2.2 1.0 1.3 4.2 0.7 	9 23 19 17 10

#	Article	IF	CITATIONS
1486	Population dynamics of microbial species under high and low ammonia nitrogen in the alternate layer bioreactor landfill (ALBL) approach. Bioresource Technology, 2020, 315, 123787.	4.8	14
1487	Metagenomic data on bacterial diversity profiling of high-microbial-abundance tropical marine sponges Aaptos aaptos and Xestospongia muta from waters off terengganu, South China Sea. Data in Brief, 2020, 31, 105971.	0.5	4
1488	Vertical zonation of bacterial assemblages attributed to physical stratification during the summer relaxation of the coastal upwelling off Galicia (NW Spain). Estuarine, Coastal and Shelf Science, 2020, 245, 106791.	0.9	7
1489	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
1490	Viral control of biomass and diversity of bacterioplankton in the deep sea. Communications Biology, 2020, 3, 256.	2.0	18
1491	Mucosal dysbiosis in patients with gastrointestinal follicular lymphoma. Hematological Oncology, 2020, 38, 181-188.	0.8	11
1492	Diversity and specificity of the bacterial community in Chinese horse milk cheese. MicrobiologyOpen, 2020, 9, e1066.	1.2	7
1493	Effect of Menopausal Hormone Therapy on the Vaginal Microbiota and Genitourinary Syndrome of Menopause in Chinese Menopausal Women. Frontiers in Microbiology, 2020, 11, 590877.	1.5	9
1494	Oral microbial community analysis of the patients in the progression of liver cancer. Microbial Pathogenesis, 2020, 149, 104479.	1.3	28
1495	The Impact of Air Pollution on Intestinal Microbiome of Asthmatic Children: A Panel Study. BioMed Research International, 2020, 2020, 1-13.	0.9	20
1496	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
1497	Does geographical variation confound the relationship between host factors and the human gut microbiota: a population-based study in China. BMJ Open, 2020, 10, e038163.	0.8	20
1498	Carbon and nitrogen cycling in Yedoma permafrost controlled by microbial functional limitations. Nature Geoscience, 2020, 13, 794-798.	5.4	45
1499	Effects of Chemical and Solar Soil-Disinfection Methods on Soil Bacterial Communities. Sustainability, 2020, 12, 9833.	1.6	3
1500	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
1501	Delivery mode and gut microbial changes correlate with an increased risk of childhood asthma. Science Translational Medicine, 2020, 12, .	5.8	92
1502	Nitrate Removal and Dynamics of Microbial Community of A Hydrogen-Based Membrane Biofilm Reactor at Diverse Nitrate Loadings and Distances from Hydrogen Supply End. Water (Switzerland), 2020, 12, 3196.	1.2	9
1503	Efficient COI barcoding using high throughput single-end 400 bp sequencing. BMC Genomics, 2020, 21, 862.	1.2	19

#	Article	IF	CITATIONS
1505	Composition of gut and oropharynx bacterial communities in Rattus norvegicus and Suncus murinus in China. BMC Veterinary Research, 2020, 16, 413.	0.7	9
1506	<i>Rhodopseudomonas palustris</i> in effluent enhances the disease resistance, TOR and NFâ€₽̂B signalling pathway, intestinal microbiota and aquaculture water quality of <i>Pelteobagrus vachelli</i> . Aquaculture Research, 2020, 51, 3959-3971.	0.9	5
1507	Effects of reducing dietary crude protein concentration and supplementation with laminarin or zinc oxide on the faecal scores and colonic microbiota in newly weaned pigs. Journal of Animal Physiology and Animal Nutrition, 2020, 104, 1471-1483.	1.0	8
1508	Intestinal Inflammation Induced by Soybean Meal Ingestion Increases Intestinal Permeability and Neutrophil Turnover Independently of Microbiota in Zebrafish. Frontiers in Immunology, 2020, 11, 1330.	2.2	16
1509	Agricultural Utilization of Unused Resources: Liquid Food Waste Material as a New Source of Plant Growth-Promoting Microbes. Agronomy, 2020, 10, 954.	1.3	8
1510	Seasonal Variation of Bacterial Diversity Along the Marine Particulate Matter Continuum. Frontiers in Microbiology, 2020, 11, 1590.	1.5	42
1511	Characterization of two MHC II genes (DOB, DRB) in white-tailed deer (Odocoileus virginianus). BMC Genetics, 2020, 21, 83.	2.7	4
1512	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
1513	Archaea Haloferax supplementation improves Artemia biomass production in hypersaline conditions. Aquaculture, 2020, 528, 735540.	1.7	6
1514	Glycosidic Linkage Structures Influence Dietary Fiber Fermentability and Propionate Production by Human Colonic Microbiota In Vitro. Biotechnology Journal, 2020, 15, 1900523.	1.8	7
1515	Letrozole and the Traditional Chinese Medicine, Shaofu Zhuyu Decoction, Reduce Endometriotic Disease Progression in Rats: A Potential Role for Gut Microbiota. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-14.	0.5	17
1516	Effects of fermented feeds and ginseng polysaccharides on the intestinal morphology and microbiota composition of Xuefeng black-bone chicken. PLoS ONE, 2020, 15, e0237357.	1.1	16
1517	In-situ remediation of acid mine drainage from abandoned coal mine by filed pilot-scale passive treatment system: Performance and response of microbial communities to low pH and elevated Fe. Bioresource Technology, 2020, 317, 123985.	4.8	33
1518	Biogas Production and Microbial Communities in the Anaerobic Digestion of Sewage Sludge Under Hydrothermal Pretreatment with Air and a Catalyst. Bioenergy Research, 2020, 14, 828.	2.2	3
1519	The Rumen Specific Bacteriome in Dry Dairy Cows and Its Possible Relationship with Phenotypes. Animals, 2020, 10, 1791.	1.0	9
1520	Compositional and Functional Comparisons of the Microbiota in the Colostrum and Mature Milk of Dairy Goats. Animals, 2020, 10, 1955.	1.0	9
1521	Are all faecal bacteria detected with equal efficiency? A study using next-generation sequencing and quantitative culture of infants' faecal samples. Journal of Microbiological Methods, 2020, 177, 106018.	0.7	5
1522	Inoculation of Ensifer fredii strain LP2/20 immobilized in agar results in growth promotion and alteration of bacterial community structure of Chinese kale planted soil. Scientific Reports, 2020, 10, 15857.	1.6	17

#	Article	IF	CITATIONS
1523	Characterization of bacterial communities associated with the exotic and heavy metal tolerant wetland plant Spartina alterniflora. Scientific Reports, 2020, 10, 17985.	1.6	11
1524	Variation of rhizosphere bacterial community diversity in the desert ephemeral plant Ferula sinkiangensis across environmental gradients. Scientific Reports, 2020, 10, 18442.	1.6	3
1525	Enhancement of microbial redox cycling of iron in zero-valent iron oxidation coupling with deca-brominated diphenyl ether removal. Science of the Total Environment, 2020, 748, 141328.	3.9	8
1526	Baicalin-Copper Complex Modulates Gut Microbiota, Inflammatory Responses, and Hormone Secretion in DON-Challenged Piglets. Animals, 2020, 10, 1535.	1.0	13
1527	Microbiome of the larvae of <i>Spodoptera frugiperda</i> (J.E. Smith) (Lepidoptera: Noctuidae) from maize plants. Journal of Applied Entomology, 2020, 144, 764-776.	0.8	20
1528	Decrease of oral microbial diversity might correlate with radiation esophagitis in patients with esophageal cancer undergoing chemoradiation: A pilot study. Precision Radiation Oncology, 2020, 4, 81-88.	0.4	4
1529	Fungal diversity in deep-sea sediments from the Magellan seamounts as revealed by a metabarcoding approach targeting the ITS2 regions. Mycology, 2020, 11, 214-229.	2.0	16
1530	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
1531	First record of a tandem-repeat region within the mitochondrial genome of Clonorchis sinensis using a long-read sequencing approach. PLoS Neglected Tropical Diseases, 2020, 14, e0008552.	1.3	18
1532	Colonic Mucosal Microbiota and Association of Bacterial Taxa with the Expression of Host Antimicrobial Peptides in Pediatric Ulcerative Colitis. International Journal of Molecular Sciences, 2020, 21, 6044.	1.8	20
1533	Gene expression concerning fatty acid and amino acid metabolism in Chlorella vulgaris cultured with antibiotics. Applied Microbiology and Biotechnology, 2020, 104, 8025-8036.	1.7	9
1534	Intestinal Tract Microbe Communities Associated with Horseshoe Crabs from Beibu Gulf, China. Current Microbiology, 2020, 77, 3330-3338.	1.0	12
1535	Bacterial Diversity in the Rhizosphere of Anabasis aphylla in the Gurbantunggut Desert, China. Current Microbiology, 2020, 77, 3750-3759.	1.0	7
1536	Integration of molecular profiles in a longitudinal wellness profiling cohort. Nature Communications, 2020, 11, 4487.	5.8	66
1537	Effects of Rearing Conditions and Sex on Cecal Microbiota in Ducks. Frontiers in Microbiology, 2020, 11, 565367.	1.5	14
1538	Effects of graphene oxide on PCR amplification for microbial community survey. BMC Microbiology, 2020, 20, 278.	1.3	4
1539	Metagenomics approach to the intestinal microbiome structure and function in high fat diet-induced obesity in mice fed with conjugated linoleic acid (CLA). Food and Function, 2020, 11, 9729-9739.	2.1	18
1540	An unusual microbiome characterises a spatially-aggressive crustose alga rapidly overgrowing shallow Caribbean reefs. Scientific Reports, 2020, 10, 20949.	1.6	8

#	Article	IF	CITATIONS
1541	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
1542	Compositional Shift of Oral Microbiota Following Surgical Resection of Tongue Cancer. Frontiers in Cellular and Infection Microbiology, 2020, 10, 600884.	1.8	13
1543	Probiotic Lactobacillus rhamnosus GG Promotes Mouse Gut Microbiota Diversity and T Cell Differentiation. Frontiers in Microbiology, 2020, 11, 607735.	1.5	34
1544	Effects of Soil Tillage, Management Practices, and Mulching Film Application on Soil Health and Peanut Yield in a Continuous Cropping System. Frontiers in Microbiology, 2020, 11, 570924.	1.5	14
1545	Investigational Assay for Haplotype Phasing of the Huntingtin Gene. Molecular Therapy - Methods and Clinical Development, 2020, 19, 162-173.	1.8	9
1546	The effects of taxonomy, diet, and ecology on the microbiota of riverine macroinvertebrates. Ecology and Evolution, 2020, 10, 14000-14019.	0.8	5
1547	The Composition and Predictive Function of the Fecal Microbiota Differ Between Young and Adult Donkeys. Frontiers in Microbiology, 2020, 11, 596394.	1.5	6
1548	Liver-specific knockdown of ANGPTL8 alters the structure of the gut microbiota in mice. Annals of Microbiology, 2020, 70, .	1.1	0
1549	A Novel Corn-Expressed Phytase Improves Daily Weight Gain, Protein Efficiency Ratio and Nutrients Digestibility and Alters Fecal Microbiota in Pigs Fed with Very Low Protein Diets. Animals, 2020, 10, 1926.	1.0	14
1550	Oral Microbial Species and Virulence Factors Associated with Oral Squamous Cell Carcinoma. Microbial Ecology, 2021, 82, 1030-1046.	1.4	29
1551	Mild heat stress changes the microbiota diversity in the respiratory tract and the cecum of layer-type pullets. Poultry Science, 2020, 99, 7015-7026.	1.5	19
1552	The Association of Fecal Microbiota in Ankylosing Spondylitis Cases with C-Reactive Protein and Erythrocyte Sedimentation Rate. Mediators of Inflammation, 2020, 2020, 1-8.	1.4	12
1553	Microbiota Analysis of Eggshells in Different Areas and During Different Storage Time by Non-cultural Methods. Current Microbiology, 2020, 77, 3842-3850.	1.0	5
1554	BIOCOM-PIPE: a new user-friendly metabarcoding pipeline for the characterization of microbial diversity from 16S, 18S and 23S rRNA gene amplicons. BMC Bioinformatics, 2020, 21, 492.	1.2	16
1555	Correlations Between Prokaryotic Microbes and Stress-Resistant Algae in Different Corals Subjected to Environmental Stress in Hong Kong. Frontiers in Microbiology, 2020, 11, 686.	1.5	12
1556	Biogeography of microbiome and short-chain fatty acids in the gastrointestinal tract of duck. Poultry Science, 2020, 99, 4016-4027.	1.5	21
1557	<i>Lycium barbarum</i> Polysaccharide Extracted from <i>Lycium barbarum</i> Leaves Ameliorates Asthma in Mice by Reducing Inflammation and Modulating Gut Microbiota. Journal of Medicinal Food, 2020, 23, 699-710.	0.8	35
1558	Analysis of microbiota in Hainan Yucha during fermentation by 16S rRNA gene highâ€ŧhroughput sequencing. Journal of Food Processing and Preservation, 2020, 44, e14523.	0.9	12

ARTICLE

1559 Correlation between gut microbial diversity and flatulence of silver pomfret (<i>Pampus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf $\frac{50}{5}$ 742 Td (

1560	Ecological succession in the vaginal microbiota during pregnancy and birth. ISME Journal, 2020, 14, 2325-2335.	4.4	45
1561	Bamboo nutrients and microbiome affect gut microbiome of giant panda. Symbiosis, 2020, 80, 293-304.	1.2	12
1562	Effects of different types of zinc supplement on the growth, incidence of diarrhea, immune function, and rectal microbiota of newborn dairy calves. Journal of Dairy Science, 2020, 103, 6100-6113.	1.4	37
1563	Effects of Fermented Herbal Tea Residues on the Intestinal Microbiota Characteristics of Holstein Heifers Under Heat Stress. Frontiers in Microbiology, 2020, 11, 1014.	1.5	14
1564	Aggregation-Induced Electrochemiluminescence of the Dichlorobis(1,10-phenanthroline)ruthenium(II) (Ru(phen) ₂ Cl ₂)/Tri- <i>n</i> -propylamine (TPrA) System in H ₂ O–MeCN Mixtures for Identification of Nucleic Acids. Analytical Chemistry, 2020, 92, 9613-9619.	3.2	27
1565	Comparing diversity levels in environmental samples: DNA sequence capture and metabarcoding approaches using 18S and COI genes. Molecular Ecology Resources, 2020, 20, 1333-1345.	2.2	40
1566	Influence of gut microbiota on mucosal IgA antibody response to the polio vaccine. Npj Vaccines, 2020, 5, 47.	2.9	33
1567	Optimized metabarcoding with Pacific biosciences enables semiâ€quantitative analysis of fungal communities. New Phytologist, 2020, 228, 1149-1158.	3.5	59
1568	Bacterial community dissimilarity in soils is driven by longâ€term landâ€useÂpractices. , 2020, 3, e20031.		15
1569	Community structure and diversity of the microbiomes of two microhabitats at the root–soil interface: implications of meta-analysis of the root-zone soil and root endosphere microbial communities in Xiong'an New Area. Canadian Journal of Microbiology, 2020, 66, 605-622.	0.8	10
1570	A geophysical, geochemical and microbiological study of a newly discovered pockmark with active gas seepage and submarine groundwater discharge (MET1-BH, central Gulf of Gdańsk, southern Baltic Sea). Science of the Total Environment, 2020, 742, 140306.	3.9	21
1571	Changes of water, sediment, and intestinal bacterial communities in Penaeus japonicus cultivation and their impacts on shrimp physiological health. Aquaculture International, 2020, 28, 1847-1865.	1.1	10
1572	Dynamic microbial diversity and fermentation quality of the mixed silage of corn and soybean grown in strip intercropping system. Bioresource Technology, 2020, 313, 123655.	4.8	45
1573	Alterations in Circulating Fatty Acid Are Associated With Gut Microbiota Dysbiosis and Inflammation in Multiple Sclerosis. Frontiers in Immunology, 2020, 11, 1390.	2.2	101
1574	16S rRNA sequencing analysis of the correlation between the intestinal microbiota and body-mass of grass carp (Ctenopharyngodon idella). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 35, 100699.	0.4	8
1575	Protist diversity and function in the dark ocean – Challenging the paradigms of deep-sea ecology with special emphasis on foraminiferans and naked protists. European Journal of Protistology, 2020, 75, 125721.	0.5	40
1576	Bacterial community colonization on tire microplastics in typical urban water environments and associated impacting factors. Environmental Pollution, 2020, 265, 114922.	3.7	58

#	Article	IF	CITATIONS
1577	A prospective longitudinal study on the microbiota composition in amyotrophic lateral sclerosis. BMC Medicine, 2020, 18, 153.	2.3	78
1578	Long-Term Stochasticity Combines With Short-Term Variability in Assembly Processes to Underlie Rice Paddy Sustainability. Frontiers in Microbiology, 2020, 11, 873.	1.5	7
1579	Coupling Between Carbon and Nitrogen Metabolic Processes Mediated by Coastal Microbes in Synechococcus-Derived Organic Matter Addition Incubations. Frontiers in Microbiology, 2020, 11, 1041.	1.5	19
1580	Soil Sickness in Aged Tea Plantation Is Associated With a Shift in Microbial Communities as a Result of Plant Polyphenol Accumulation in the Tea Gardens. Frontiers in Plant Science, 2020, 11, 601.	1.7	54
1581	Rumen Microbiota Distribution Analyzed by High-Throughput Sequencing After Oral Doxycycline Administration in Beef Cattle. Frontiers in Veterinary Science, 2020, 7, 251.	0.9	7
1582	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
1583	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
1584	Effect of dietary gossypol supplement on fermentation characteristics and bacterial diversity in the rumen of sheep. PLoS ONE, 2020, 15, e0234378.	1.1	7
1585	Nutrient loading diminishes the dissolved organic carbon drawdown capacity of seagrass ecosystems. Science of the Total Environment, 2020, 740, 140185.	3.9	28
1586	Effect of a Laminarin Rich Macroalgal Extract on the Caecal and Colonic Microbiota in the Post-Weaned Pig. Marine Drugs, 2020, 18, 157.	2.2	29
1587	Data on community structure and diversity of the intestinal bacteria in elver and fingerling stages of wild Indonesian shortfin eel (Anguilla bicolor bicolor). Data in Brief, 2020, 29, 105299.	0.5	2
1588	Characterization of antibiotic resistance and host-microbiome interactions in the human upper respiratory tract during influenza infection. Microbiome, 2020, 8, 39.	4.9	41
1589	Response of Bacterial and Fungal Soil Communities to Chinese Fir (Cunninghamia lanceolate) Long-Term Monoculture Plantations. Frontiers in Microbiology, 2020, 11, 181.	1.5	49
1590	Identification of Persistent Sulfidogenic Bacteria in Shale Gas Produced Waters. Frontiers in Microbiology, 2020, 11, 286.	1.5	15
1591	Sequence-Based Characterization of Intratumoral Bacteria—A Guide to Best Practice. Frontiers in Oncology, 2020, 10, 179.	1.3	37
1592	Characterization and comparison of the bacterial microbiota in different gastrointestinal tract compartments of Mongolian horses. MicrobiologyOpen, 2020, 9, 1085-1101.	1.2	23
1593	Thermophilic Anaerobic Digestion of Arundo donax cv. Lvzhou No. 1 for Biogas Production: Structure and Functional Analysis of Microbial Communities. Bioenergy Research, 2020, 13, 866-877.	2.2	6
1594	Experimental quantification of pollen with DNA metabarcoding using ITS1 and trnL. Scientific Reports, 2020, 10, 4202.	1.6	55

# 1595	ARTICLE 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,	IF 1.2	CITATIONS
1596	Dynamic interactions within the host-associated microbiota cause tumor formation in the basal metazoan Hydra. PLoS Pathogens, 2020, 16, e1008375.	2.1	28
1597	Colonic microbiota is associated with inflammation and host epigenomic alterations in inflammatory bowel disease. Nature Communications, 2020, 11, 1512.	5.8	167
1598	Probiotic-directed modulation of gut microbiota is basal microbiome dependent. Gut Microbes, 2020, 12, 1736974.	4.3	69
1599	The effects of daily fasting hours on shaping gut microbiota in mice. BMC Microbiology, 2020, 20, 65.	1.3	43
1600	Traditional Chinese Medicine Formula Kang Shuai Lao Pian Improves Obesity, Gut Dysbiosis, and Fecal Metabolic Disorders in High-Fat Diet-Fed Mice. Frontiers in Pharmacology, 2020, 11, 297.	1.6	46
1601	Effects of dietary raw or Enterococcus faecium fermented soybean meal on growth, antioxidant status, intestinal microbiota, morphology, and inflammatory responses in turbot (Scophthalmus) Tj ETQq0 0 0 rg	BTL/Overlo	oc ls £10 Tf 50
1602	Fungal communities differentially respond to warming and drought in tropical grassland soil. Molecular Ecology, 2020, 29, 1550-1559.	2.0	41
1603	Effects of a Diet Supplemented with Exogenous Catalase from Penicillium notatum on Intestinal Development and Microbiota in Weaned Piglets. Microorganisms, 2020, 8, 391.	1.6	14
1604	A rapid approach to profiling diverse fungal communities using the MinIONâ,,¢ nanopore sequencer. BioTechniques, 2020, 68, 72-78.	0.8	25
1605	Soil Functional Responses to Natural Ecosystem Restoration of a Pine Forest Peucedano-Pinetum after a Fire. Forests, 2020, 11, 286.	0.9	18
1606	Seasonal changes in the bacterial community structure of three eutrophicated urban lakes in Mexico city, with emphasis on Microcystis spp Toxicon, 2020, 179, 8-20.	0.8	16
1607	Changes in Symbiotic Microbiota and Immune Responses in Early Development Stages of Rapana venosa (Valenciennes, 1846) Provide Insights Into Immune System Development in Gastropods. Frontiers in Microbiology, 2020, 11, 1265.	1.5	6
1608	Evaluation of groundwater bacterial community composition to inform waterborne pathogen vulnerability assessments. Science of the Total Environment, 2020, 743, 140472.	3.9	10
1609	Water Microbiota in Greenhouses With Soilless Cultures of Tomato by Metabarcoding and Culture-Dependent Approaches. Frontiers in Microbiology, 2020, 11, 1354.	1.5	3
1610	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
1611	Colonic microbiome profiles for improved feed efficiency can be identified despite major effects of farm of origin and contemporary group in pigs. Animal, 2020, 14, 2472-2480.	1.3	14
1612	Effect of wet sea buckthorn pomace utilized as an additive on silage fermentation profile and bacterial community composition of alfalfa. Bioresource Technology, 2020, 314, 123773.	4.8	32

#	Article	IF	CITATIONS
1613	Dynamic distribution of gut microbiota during embryonic development in chicken. Poultry Science, 2020, 99, 5079-5090.	1.5	28
1614	Rhodopseudomonas sphaeroidesÂtreating mesosulfuron-methyl waste-water. Environmental Pollution, 2020, 262, 114166.	3.7	6
1615	Seasonal Variation and Sexual Dimorphism of the Microbiota in Wild Blue Sheep (Pseudois nayaur). Frontiers in Microbiology, 2020, 11, 1260.	1.5	15
1616	Applicability of an Unmedicated Feeding Program Aimed to Reduce the Use of Antimicrobials in Nursery Piglets: Impact on Performance and Fecal Microbiota. Animals, 2020, 10, 242.	1.0	2
1617	Analysis of microbial diversity and composition in small intestine during different development times in ducks. Poultry Science, 2020, 99, 1096-1106.	1.5	13
1618	Culture dependent and independent analyses suggest a low level of sharing of endospore-forming species between mothers and their children. Scientific Reports, 2020, 10, 1832.	1.6	12
1619	Nicotiana tabacum seed endophytic communities share a common core structure and genotype-specific signatures in diverging cultivars. Computational and Structural Biotechnology Journal, 2020, 18, 287-295.	1.9	35
1620	Effects of ozone concentration on the postharvest quality and microbial diversity of Muscat Hamburg grapes. RSC Advances, 2020, 10, 9037-9045.	1.7	12
1621	Impact of in-feed sodium butyrate or sodium heptanoate protected with medium-chain fatty acids on gut health in weaned piglets challenged with Escherichia coli F4+. Archives of Animal Nutrition, 2020, 74, 271-295.	0.9	9
1622	Analogous wheat root rhizosphere microbial successions in field and greenhouse trials in the presence of biocontrol agents <i>Paenibacillus peoriae</i> SP9 and <i>Streptomyces fulvissimus</i> FU14. Molecular Plant Pathology, 2020, 21, 622-635.	2.0	29
1623	The function of Apostichopus japonicas catalase in sea cucumber intestinal immunity. Aquaculture, 2020, 521, 735103.	1.7	10
1624	Gut microbial taxa as potential predictive biomarkers for acute coronary syndrome and post-STEMI cardiovascular events. Scientific Reports, 2020, 10, 2639.	1.6	48
1625	The effects of dietary sodium butyrate supplementation on the growth performance, carcass traits and intestinal microbiota of growingâ€finishing pigs. Journal of Applied Microbiology, 2020, 128, 1613-1623.	1.4	18
1626	Gut Microbiota Plasticity Influences the Adaptability of Wild and Domestic Animals in Co-inhabited Areas. Frontiers in Microbiology, 2020, 11, 125.	1.5	23
1627	Community Structures and Antifungal Activity of Root-Associated Endophytic Actinobacteria in Healthy and Diseased Cucumber Plants and Streptomyces sp. HAAG3-15 as a Promising Biocontrol Agent. Microorganisms, 2020, 8, 236.	1.6	31
1628	Linkages between changes in plant and mycorrhizal fungal community composition at high versus low elevation in alpine ecosystems. Environmental Microbiology Reports, 2020, 12, 229-240.	1.0	10
1629	Modulation of inflammatory response and gut microbiota in ankylosing spondylitis mouse model by bioactive peptide IQW. Journal of Applied Microbiology, 2020, 128, 1669-1677.	1.4	11
1630	Prenatal dietary supplements influence the infant airway microbiota in a randomized factorial clinical trial. Nature Communications, 2020, 11, 426.	5.8	25

#	Article	IF	CITATIONS
1631	Carbon Amendments Influence Composition and Functional Capacities of Indigenous Soil Microbiomes. Frontiers in Molecular Biosciences, 2019, 6, 151.	1.6	5
1632	Klebsiella michiganensis transmission enhances resistance to Enterobacteriaceae gut invasion by nutrition competition. Nature Microbiology, 2020, 5, 630-641.	5.9	67
1633	Biotic and Abiotic Imprints on Mg-Rich Stromatolites: Lessons from Lake Salda, SW Turkey. Geomicrobiology Journal, 2020, 37, 401-425.	1.0	19
1634	Endogenous FGF21-signaling controls paradoxical obesity resistance of UCP1-deficient mice. Nature Communications, 2020, 11, 624.	5.8	60
1635	Study on indoor and outdoor permeability coefficients and bacterial components, sources of fine particles in severe cold region of China. Sustainable Cities and Society, 2020, 55, 102020.	5.1	5
1636	Biodiversity of organisms inhabiting the water supply network of Wroclaw. Detection of pathogenic organisms constituting a threat for drinking water recipients. Science of the Total Environment, 2020, 715, 136732.	3.9	13
1637	Co-cultured non-marine ostracods from a temporary wetland harbor host-specific microbiota of different metabolic profiles. Hydrobiologia, 2020, 847, 2503-2519.	1.0	4
1638	Effects of di-n-butyl phthalate and di-2-ethylhexyl phthalate on pollutant removal and microbial community during wastewater treatment. Ecotoxicology and Environmental Safety, 2020, 198, 110665.	2.9	24
1639	Biochar Application Alleviated Negative Plant-Soil Feedback by Modifying Soil Microbiome. Frontiers in Microbiology, 2020, 11, 799.	1.5	48
1640	Variation of near surface atmosphere microbial communities at an urban and a suburban site in Philadelphia, PA, USA. Science of the Total Environment, 2020, 724, 138353.	3.9	23
1641	The effect of Lactobacillus plantarum administration on the intestinal microbiota of whiteleg shrimp Penaeus vannamei. Aquaculture, 2020, 526, 735331.	1.7	50
1642	Microbial bloom formation in a high pH spent nuclear fuel pond. Science of the Total Environment, 2020, 720, 137515.	3.9	24
1643	Reintroducing mothur: 10 Years Later. Applied and Environmental Microbiology, 2020, 86, .	1.4	160
1644	Improving Characterization of Understudied Human Microbiomes Using Targeted Phylogenetics. MSystems, 2020, 5, .	1.7	2
1645	A Novel "Microbial Bait―Technique for Capturing Fe(III)-Reducing Bacteria. Frontiers in Microbiology, 2020, 11, 330.	1.5	4
1646	Radiation Tolerance of Pseudanabaena catenata, a Cyanobacterium Relevant to the First Generation Magnox Storage Pond. Frontiers in Microbiology, 2020, 11, 515.	1.5	13
1647	Influence of Lactobacillus kefiri on Intestinal Microbiota and Fecal IgA Content of Healthy Dogs. Frontiers in Veterinary Science, 2020, 7, 146.	0.9	11
1648	Microbial colonization of metal sulfide minerals at a diffuseâ€flow deepâ€sea hydrothermal vent at 9°50′N on the East Pacific Rise. Geobiology, 2020, 18, 594-605.	1.1	3

#	Article	IF	CITATIONS
1649	Improvement of Cecal Commensal Microbiome Following the Insect Additive into Chicken Diet. Animals, 2020, 10, 577.	1.0	32
1650	Predicting postmortem interval based on microbial community sequences and machine learning algorithms. Environmental Microbiology, 2020, 22, 2273-2291.	1.8	39
1651	Intestinal microbial profiling of grass carp (Ctenopharyngodon idellus) challenged with Aeromonas hydrophila. Aquaculture, 2020, 524, 735292.	1.7	22
1652	Capsulized faecal microbiota transplantation ameliorates post-weaning diarrhoea by modulating the gut microbiota in piglets. Veterinary Research, 2020, 51, 55.	1.1	27
1653	Characterisation of the gut microbial community of rhesus macaques in high-altitude environments. BMC Microbiology, 2020, 20, 68.	1.3	25
1654	A combination of monosodium glutamate and high-fat and high-fructose diets increases the risk of kidney injury, gut dysbiosis and host-microbial co-metabolism. PLoS ONE, 2020, 15, e0231237.	1.1	18
1655	<p>Phocea, Pseudoflavonifractor and Lactobacillus intestinalis: Three Potential Biomarkers of Gut Microbiota That Affect Progression and Complications of Obesity-Induced Type 2 Diabetes Mellitus</p> . Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 2020, Volume 13, 835-850.	1,1	35
1656	Complementary DNA sequencing (cDNA): an effective approach for assessing the diversity and distribution of marine benthic ciliates along hydrographic gradients. Journal of Oceanology and Limnology, 2021, 39, 208-222.	0.6	4
1657	Partial function prediction of sulfate-reducing bacterial community from the rhizospheres of two typical coastal wetland plants in China. Journal of Oceanology and Limnology, 2021, 39, 185-197.	0.6	2
1658	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
1659	Characterizing Microbial Signatures on Sculptures and Paintings of Similar Provenance. Microbial Ecology, 2021, 81, 1098-1105.	1.4	6
1660	Root microbiome assembly of Asâ€hyperaccumulator <scp> <i>Pteris vittata</i> </scp> and its efficacy in arsenic requisition. Environmental Microbiology, 2021, 23, 1959-1971.	1.8	25
1661	Application of down-flow hanging sponge – Upflow sludge blanket system for nitrogen removal in Epinephelus bruneus closed recirculating aquaculture system. Aquaculture, 2021, 532, 735997.	1.7	13
1662	Profiling the differences of gut microbial structure between schizophrenia patients with and without violent behaviors based on 16S rRNA gene sequencing. International Journal of Legal Medicine, 2021, 135, 131-141.	1.2	18
1663	High-throughput sequencing-based characterization of the predominant microbial community associated with characteristic flavor formation in Jinhua Ham. Food Microbiology, 2021, 94, 103643.	2.1	41
1664	Pinewood Nematode Alters the Endophytic and Rhizospheric Microbial Communities of Pinus massoniana. Microbial Ecology, 2021, 81, 807-817.	1.4	16
1665	Determination of microbial diversities and aroma characteristics of Beitang shrimp paste. Food Chemistry, 2021, 344, 128695.	4.2	25
1666	Influence of the flooded time on the performance of a tidal flow constructed wetland treating urban stream water. Science of the Total Environment, 2021, 758, 143652.	3.9	14

#	Article	IF	CITATIONS
1667	Plant-microbial feedback in secondary succession of semiarid grasslands. Science of the Total Environment, 2021, 760, 143389.	3.9	10
1668	Differential responses of soil bacteria and fungi to altered precipitation in a meadow steppe. Geoderma, 2021, 384, 114812.	2.3	45
1669	Optimizing the quality of clinical studies on oral microbiome: A practical guide for planning, performing, and reporting. Periodontology 2000, 2021, 85, 210-236.	6.3	51
1670	A preliminary study of gut microbiome variation and HPA axis reactivity in healthy infants. Psychoneuroendocrinology, 2021, 124, 105046.	1.3	21
1671	Inter-trophic Interaction of Gut Microbiota in a Tripartite System. Microbial Ecology, 2021, 81, 1075-1087.	1.4	5
1672	Performance and microbial community dynamics in anaerobic continuously stirred tank reactor and sequencing batch reactor (CSTR-SBR) coupled with magnesium-ammonium-phosphate (MAP)-precipitation for treating swine wastewater. Bioresource Technology, 2021, 320, 124336.	4.8	21
1673	First report on the microbial communities of the wild and planted raspberry rhizosphere – A statement on the taxa, processes and a new indicator of functional diversity. Ecological Indicators, 2021, 121, 107117.	2.6	10
1674	Stronger impacts of long-term relative to short-term exposure to carbon nanomaterials on soil bacterial communities. Journal of Hazardous Materials, 2021, 410, 124550.	6.5	15
1675	Cathodes of membrane and packed manganese dioxide/titanium dioxide/graphitic carbon nitride/granular activated carbon promoted treatment of coking wastewater in microbial fuel cell. Bioresource Technology, 2021, 321, 124442.	4.8	19
1676	Dietary supplementation with berberine improves growth performance and modulates the composition and function of cecal microbiota in yellow-feathered broilers. Poultry Science, 2021, 100, 1034-1048.	1.5	26
1677	Soil prokaryotic community shows no response to 2 years of simulated nitrogen deposition in an arid ecosystem in northwestern China. Environmental Microbiology, 2021, 23, 1222-1237.	1.8	15
1678	Gut Microbiota and Host Plasma Metabolites in Association with Blood Pressure in Chinese Adults. Hypertension, 2021, 77, 706-717.	1.3	18
1679	Accumulation of antibiotic resistance genes in full-scale drinking water biological activated carbon (BAC) filters during backwash cycles. Water Research, 2021, 190, 116744.	5.3	28
1680	Thallium shifts the bacterial and fungal community structures in thallium mine waste rocks. Environmental Pollution, 2021, 268, 115834.	3.7	19
1681	A combined method for the source apportionment of sediment organic carbon in rivers. Science of the Total Environment, 2021, 752, 141840.	3.9	11
1682	Bacteria and Archaea Communities in Cerrado Natural Pond Sediments. Microbial Ecology, 2021, 81, 563-578.	1.4	11
1683	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
1684	Depth-Dependent Variables Shape Community Structure and Functionality in the Prince Edward Islands. Microbial Ecology, 2021, 81, 396-409.	1.4	5

#	Article	IF	CITATIONS
1685	Bacterial and archaeal communities in deep sea waters near the Ninetyeast Ridge in Indian Ocean. Journal of Oceanology and Limnology, 2021, 39, 582-597.	0.6	9
1686	Cantharellales Gäm. , 2021, , 320-328.		0
1687	Patterns and Dynamics of the Soil Microbial Community with Gradual Vegetation Succession in the Yellow River Delta, China. Wetlands, 2021, 41, 1.	0.7	13
1688	Potential use of molecular and structural characterization of the gut bacterial community for postmortem interval estimation in Sprague Dawley rats. Scientific Reports, 2021, 11, 225.	1.6	10
1689	Ginsenoside Rh4 alleviates antibiotic-induced intestinal inflammation by regulating the TLR4-MyD88-MAPK pathway and gut microbiota composition. Food and Function, 2021, 12, 2874-2885.	2.1	26
1690	Converting croplands to orchards changes soil microbial community composition and coâ€occurrence patterns. Land Degradation and Development, 2021, 32, 2509-2519.	1.8	7
1691	Effect of aquaculture water eutrophication on color development in Biolog EcoPlates. Aquaculture International, 2021, 29, 373-386.	1.1	5
1692	Investigating the microbiota of fermented fish products (Pla-ra) from different communities of northeastern Thailand. PLoS ONE, 2021, 16, e0245227.	1.1	21
1693	Effect of EOR Chemical Flooding on Local Microbial Ecological Characteristics in Oilfield Mining Area. IOP Conference Series: Earth and Environmental Science, 0, 647, 012166.	0.2	0
1694	Next-Generation Sequencing in Environmental Mycology. A Useful Tool?. , 2021, , 73-83.		3
1695	Effects of Mesobiliverdin IXα-Enriched Microalgae Feed on Gut Health and Microbiota of Broilers. Frontiers in Veterinary Science, 2020, 7, 586813.	0.9	7
1696	Relationship between Soil Fungi and Seedling Density in the Vicinity of Adult Conspecifics in an Arid Desert Forest. Forests, 2021, 12, 92.	0.9	4
1697	The Alteration of Intestinal Microbiota Profile and Immune Response in Epinephelus coioides during Pathogen Infection. Life, 2021, 11, 99.	1.1	16
1698	Comparison of Blood Bacterial Communities in Periodontal Health and Periodontal Disease. Frontiers in Cellular and Infection Microbiology, 2020, 10, 577485.	1.8	36
1699	Ecogenomics Reveals Microbial Metabolic Networks in a Psychrophilic Methanogenic Bioreactor Treating Soy Sauce Production Wastewater. Microbes and Environments, 2021, 36, n/a.	0.7	9
1700	Bioinformatic Platforms for Metagenomics. , 2021, , 91-112.		0
1702	Distinctive gut microbial dysbiosis between chronic alcoholic fatty liver disease and metabolic‑associated fatty liver disease in mice. Experimental and Therapeutic Medicine, 2021, 21, 418.	0.8	19
1703	Faecal bacterial composition in horses with and without free faecal liquid: a case control study. Scientific Reports, 2021, 11, 4745.	1.6	4

#	Article	IF	CITATIONS
1704	Green Manure Crops Affected Soil Chemical Properties and Fungal Diversity and Community of Apple Orchard in the Loess Plateau of China. Journal of Soil Science and Plant Nutrition, 2021, 21, 1089-1102.	1.7	24
1705	Using Bioinformatics to Quantify the Variability and Diversity of the Microbial Community Structure in Pond Ecosystems of a Subtropical Catchment. Current Bioinformatics, 2021, 15, 1178-1186.	0.7	6
1706	Fecal Microbiota Transplantation Shows Marked Shifts in the Multi-Omic Profiles of Porcine Post-weaning Diarrhea. Frontiers in Microbiology, 2021, 12, 619460.	1.5	11
1707	The Dynamics of the Bacterial Community of the Photobioreactor-Cultivated Green Microalga Haematococcus lacustris during Stress-Induced Astaxanthin Accumulation. Biology, 2021, 10, 115.	1.3	10
1708	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
1709	Complex microbial communities inhabiting natural Cordyceps militaris and the habitat soil and their predicted functions. Antonie Van Leeuwenhoek, 2021, 114, 465-477.	0.7	10
1710	Effects of Antibiotic Treatment and Probiotics on the Gut Microbiome of 40 Infants Delivered Before Term by Cesarean Section Analysed by Using 16S rRNA Quantitative Polymerase Chain Reaction Sequencing. Medical Science Monitor, 2021, 27, e928467.	0.5	10
1712	Efficiency of high rate treatment of low-strength municipality sewage by a pilot-scale combination system of a sedimentation tank and a down-flow hanging sponge reactor. Environmental Technology (United Kingdom), 2022, 43, 2457-2466.	1.2	6
1713	Protecting Intestinal Microenvironment Alleviates Acute Graft-Versus-Host Disease. Frontiers in Physiology, 2020, 11, 608279.	1.3	6
1714	Differences in the endophytic fungal community and effective ingredients in root of three <i>Glycyrrhiza</i> species in Xinjiang, China. PeerJ, 2021, 9, e11047.	0.9	13
1715	European eel (Anguilla anguilla) GI tract conserves a unique metagenomics profile in the recirculation aquaculture system (RAS). Aquaculture International, 2021, 29, 1529-1544.	1.1	5
1716	Effects of dietary hydrolyzable tannins on growth performance, antioxidant capacity, intestinal microï¬,ora and resistance against Vibrio parahaemolyticus of juvenile Paciff white shrimp, Litopenaeus vannamei (Boone, 1931). Aquaculture Reports, 2021, 19, 100601.	0.7	10
1717	Integrated Application of Rapeseed Cake and Green Manure Enhances Soil Nutrients and Microbial Communities in Tea Garden Soil. Sustainability, 2021, 13, 2967.	1.6	21
1718	Fermented traditional Chinese medicine alters the intestinal microbiota composition of broiler chickens. Research in Veterinary Science, 2021, 135, 8-14.	0.9	18
1719	Comparison of Microbial Communities in Colorado Potato Beetles (Leptinotarsa decemlineata Say) Collected From Different Sources in China. Frontiers in Microbiology, 2021, 12, 639913.	1.5	8
1720	Soil bacterial characteristics between surface and subsurface soils along a precipitation gradient in the Alxa Desert, China. Journal of Arid Land, 2021, 13, 257-273.	0.9	3
1721	Changes in Rumen Microbiota Affect Metabolites, Immune Responses and Antioxidant Enzyme Activities of Sheep under Cold Stimulation. Animals, 2021, 11, 712.	1.0	18
1722	p300 Serine 89: A Critical Signaling Integrator and Its Effects on Intestinal Homeostasis and Repair. Cancers, 2021, 13, 1288.	1.7	8

#	Article	IF	CITATIONS
1723	Effects of Exogenous Microbial Agents on Soil Nutrient and Microbial Community Composition in Greenhouse-Derived Vegetable Straw Composts. Sustainability, 2021, 13, 2925.	1.6	15
1724	Geographic Variation of Bacterial Communities Associated with Cotton Fleahopper, Pseudatomoscelis seriatus1. Southwestern Entomologist, 2021, 46, .	0.1	1
1725	Lacticaseibacillus paracasei PS23 Effectively Modulates Gut Microbiota Composition and Improves Gastrointestinal Function in Aged SAMP8 Mice. Nutrients, 2021, 13, 1116.	1.7	16
1726	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
1727	Soil Microbiome Structure and Function in Ecopiles Used to Remediate Petroleum-Contaminated Soil. Frontiers in Environmental Science, 2021, 9, .	1.5	11
1728	Novel disease resistance gene paralogs created by CRISPR/Cas9 in soy. Plant Cell Reports, 2021, 40, 1047-1058.	2.8	20
1729	Metabarcoding analysis and fermentation performance of the dominant fungal microbiota associated with the Algerian traditional date product "Btana― International Microbiology, 2021, 24, 351-361.	1.1	1
1730	Characterization of the first cultured free-living representative of <i>Candidatus</i> Izemoplasma uncovers its unique biology. ISME Journal, 2021, 15, 2676-2691.	4.4	32
1731	The effect of flue-curing procedure on the dynamic change of microbial diversity of tobaccos. Scientific Reports, 2021, 11, 5354.	1.6	13
1732	Multi-marker DNA metabarcoding reflects tardigrade diversity in different habitats. Genome, 2021, 64, 217-231.	0.9	9
1733	Effect of Supplementing Seaweed Extracts to Pigs until d35 Post-Weaning on Performance and Aspects of Intestinal Health. Marine Drugs, 2021, 19, 183.	2.2	16
1734	Nonlinear machine learning pattern recognition and bacteria-metabolite multilayer network analysis of perturbed gastric microbiome. Nature Communications, 2021, 12, 1926.	5.8	22
1735	Application of DNA barcoding and metabarcoding for species identification in salmon products. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2021, 38, 754-768.	1.1	11
1736	Spatiotemporal variation of bacterial communities in three cascade reservoirs in a southern city of China. Water Science and Technology: Water Supply, 2021, 21, 2532-2542.	1.0	1
1737	Alvis: a tool for contig and read ALignment VISualisation and chimera detection. BMC Bioinformatics, 2021, 22, 124.	1.2	14
1738	Effects of plastic mulch film residues on soil-microbe-plant systems under different soil pH conditions. Chemosphere, 2021, 267, 128901.	4.2	72
1739	Effects of monobutyrin supplementation on egg production, biochemical indexes, and gut microbiota of broiler breeders. Poultry Science, 2021, 100, 100907.	1.5	3
1740	Gut microbiome associations with outcome following co-infection with porcine reproductive and respiratory syndrome virus (PRRSV) and porcine circovirus type 2 (PCV2) in pigs immunized with a PRRS modified live virus vaccine. Veterinary Microbiology, 2021, 254, 109018.	0.8	5

#	Article	IF	CITATIONS
1741	The Airway Microbiota Modulates Effect of Azithromycin Treatment for Episodes of Recurrent Asthma-like Symptoms in Preschool Children: A Randomized Clinical Trial. American Journal of Respiratory and Critical Care Medicine, 2021, 204, 149-158.	2.5	27
1742	The gut microbiome composition and degradation enzymes activity of black Amur bream (<i>Megalobrama terminalis</i>) in response to breeding migratory behavior. Ecology and Evolution, 2021, 11, 5150-5163.	0.8	11
1743	Fecal Microbiome Transplantation from Children with Autism Spectrum Disorder Modulates Tryptophan and Serotonergic Synapse Metabolism and Induces Altered Behaviors in Germ-Free Mice. MSystems, 2021, 6, .	1.7	49
1744	High-throughput sequencing clarifies the spatial structures of microbial communities in cadmium-polluted rice soils. Environmental Science and Pollution Research, 2021, 28, 47086-47098.	2.7	13
1745	Plant flavones enrich rhizosphere Oxalobacteraceae to improve maize performance under nitrogen deprivation. Nature Plants, 2021, 7, 481-499.	4.7	247
1746	Genetically determined hypertensive phenotype affects gut microbiota composition, but not vice versa. Journal of Hypertension, 2021, 39, 1790-1799.	0.3	7
1748	Bacterial Diversity in Rhipicephalus sanguineus (Acari: Ixodidae) from Two States in Nigeria. Journal of Entomological Science, 2021, 56, 256-271.	0.2	1
1749	Illumina Sequencing and Metabolomics Analysis Reveal Thiamine Modulation of Ruminal Microbiota and Metabolome Characteristics in Goats Fed a High-Concentrate Diet. Frontiers in Microbiology, 2021, 12, 653283.	1.5	16
1750	Mosquito Identification From Bulk Samples Using DNA Metabarcoding: a Protocol to Support Mosquito-Borne Disease Surveillance in Canada. Journal of Medical Entomology, 2021, 58, 1686-1700.	0.9	8
1751	Gut dysbiosis and clinical phases of pancolitis in patients with ulcerative colitis. MicrobiologyOpen, 2021, 10, e1181.	1.2	13
1752	The Effects of Microbial Inoculants on Bacterial Communities of the Rhizosphere Soil of Maize. Agriculture (Switzerland), 2021, 11, 389.	1.4	4
1753	Alteration of the Immune Response and the Microbiota of the Skin during a Natural Infection by Vibrio harveyi in European Seabass (Dicentrarchus labrax). Microorganisms, 2021, 9, 964.	1.6	21
1754	Manure-Based Amendments Influence Surface-Associated Bacteria and Markers of Antibiotic Resistance on Radishes Grown in Soils with Different Textures. Applied and Environmental Microbiology, 2021, 87, .	1.4	6
1755	Oral Microbiota Changes in Elderly Patients, an Indicator of Alzheimer's Disease. International Journal of Environmental Research and Public Health, 2021, 18, 4211.	1.2	33
1756	BACTERIAL ESTABLISHMENT DURING THE FIRST YEAR OF OPERATION OF AN UNSATURATED AND A PARTIALLY SATURATED VERTICAL FLOW CONSTRUCTED WETLANDS. Revista AIDIS De IngenierÃa Y Ciencias Ambientales InvestigaciÃ ³ n Desarrollo Y Práctica, 2021, 14, 441.	0.0	0
1757	Aspergillus oryzae and Aspergillus niger Co-Cultivation Extract Affects In Vitro Degradation, Fermentation Characteristics, and Bacterial Composition in a Diet-Specific Manner. Animals, 2021, 11, 1248.	1.0	12
1758	Dietary Fiber Ameliorates Lipopolysaccharide-Induced Intestinal Barrier Function Damage in Piglets by Modulation of Intestinal Microbiome. MSystems, 2021, 6, .	1.7	26
1759	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

ARTICLE IF CITATIONS Effect of mangrove restoration on sediment properties and bacterial community. Ecotoxicology, 2021, 1760 1.1 14 30, 1672-1679. Developmental trajectory of the healthy human gut microbiota during the first 5 years of life. Cell 1762 5.1 208 Host and Microbe, 2021, 29, 765-776.e3. Effects of a Bioprocessed Soybean Meal Ingredient on the Intestinal Microbiota of Hybrid Striped Bass, 1763 1.6 8 Morone chrysops x M. saxatilis. Microorganisms, 2021, 9, 1032. The Lifestyle-Dependent Microbial Interactions Vary Between Upstream and Downstream of the Three 1764 1.1 Gorges Dám. Frontiers in Ecology and Evolution, 2021, 9, . 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, 1765 13 1.8 2021, 9, 678190. Soil microbial community dynamics indicate disruption of nitrogen cycling by pollution in vegetation buffer zones. Pedobiologia, 2021, 85-86, 150722. Spatial and seasonal variations in biofilm formation on microplastics in coastal waters. Science of 1767 3.9 71 the Total Environment, 2021, 770, 145303. Diversity, Relative Abundance, and Functional Genes of Intestinal Microbiota of Tiger Grouper (Epinephelus fuscoguttatus) and Asian Seabass (Lates calcarifer) Reared in A Semi-Closed Hatchery in 1768 0.1 Dry and Wet Seasons. Pertanika Journal of Science and Technology, 2021, 44, . Exploring microbial community structure and metabolic gene clusters during silage fermentation of paper mulberry, a high-protein woody plant. Animal Feed Science and Technology, 2021, 275, 114766. 1769 1.1 63 Bacterial Communities Associated With Four Blooming Scyphozoan Jellyfish: Potential Species-Specific 1770 1.5 Consequences for Marine Organisms and Humans Health. Frontiers in Microbiology, 2021, 12, 647089. Effects of Starch Level and a Mixture of Sunflower and Fish Oils on Nutrient Intake and Digestibility, 1771 4 1.0 Rumen Fermentation, and Ruminal Methane Emissions in Dairy Cows. Animals, 2021, 11, 1310. 1772 Identifying biases and their potential solutions in human microbiome studies. Microbiome, 2021, 9, 113. The use of PacBio SMRT technology to explore the microbial network and fermentation characteristics of woody silage prepared with exogenous carbohydrate additives. Journal of Applied Microbiology, 2021, 131, 2193-2211. 1773 1.4 25 Profile of microbial community of organic and conventional rice field using metagenomic analysis. Biogenesis Jurnal Ilmiah Biologi, 2021, 9, 1. 1774 Gut Microbiota Signature Among Asian Post-gestational Diabetes Women Linked to Macronutrient 1775 1.5 13 Intakes and Metabolic Phenotypes. Frontiers in Microbiology, 2021, 12, 680622. Influence of Maize Residues in Shaping Soil Microbiota and Fusarium spp. Communities. Microbial 1776 1.4 Ecology, 2022, 83, 702-713. Correlations Between Intestinal Microbial Community and Hematological Profile in Native Tibetans 1777 1.58 and Han Immigrants. Frontiers in Microbiology, 2021, 12, 615416. Mediterranean Diet to Prevent the Development of Colon Diseases: A Meta-Analysis of Gut Microbiota 1778 Studies. Nutrients, 2021, 13, 2234.

#	Article	IF	CITATIONS
" 1779	Effect of co-application of Trichoderma spp. with organic composts on plant growth enhancement, soil enzymes and fungal community in soil. Archives of Microbiology, 2021, 203, 4281-4291.	1.0	21
1780	The influence of exercise training volume alterations on the gut microbiome in highlyâ€ŧrained middleâ€distance runners. European Journal of Sport Science, 2022, 22, 1222-1230.	1.4	16
1781	Defining human-animal chimeras and hybrids: A comparison of legal systems and natural sciences. Ethics and Bioethics (in Central Europe), 2021, 11, 101-114.	0.1	0
1782	Bacterial Communities in Alkaline Saline Soils Amended with Young Maize Plants or Its (Hemi)Cellulose Fraction. Microorganisms, 2021, 9, 1297.	1.6	1
1783	Structural and Functional Impacts of Microbiota on Pyropia yezoensis and Surrounding Seawater in Cultivation Farms along Coastal Areas of the Yellow Sea. Microorganisms, 2021, 9, 1291.	1.6	9
1784	Dynamics of Diversity and Abundance of Sulfonamide Resistant Bacteria in a Silt Loam Soil Fertilized by Compost. Antibiotics, 2021, 10, 699.	1.5	6
1785	Genomics as a potential tool to unravel the rhizosphere microbiome interactions on plant health. Journal of Microbiological Methods, 2021, 185, 106215.	0.7	16
1786	Microbial community responses to land-use types and its ecological roles in mining area. Science of the Total Environment, 2021, 775, 145753.	3.9	20
1787	Intestinal Microbiota Mediates High-Fructose and High-Fat Diets to Induce Chronic Intestinal Inflammation. Frontiers in Cellular and Infection Microbiology, 2021, 11, 654074.	1.8	39
1788	Use of High-Throughput Sequencing to Identify Fungal Communities on the Surface of Citri Reticulatae Pericarpium During the 3-Year Aging Process. Current Microbiology, 2021, 78, 3142-3151.	1.0	12
1789	Microbial communities of biofilms developed in a chlorinated drinking water distribution system: A field study of antibiotic resistance and biodiversity. Science of the Total Environment, 2021, 774, 145113.	3.9	19
1790	Comparative Analyses of the Gut Microbiome of Two Fox Species, the Red Fox (Vulpes Vulpes) and Corsac Fox (Vulpes Corsac), that Occupy Different Ecological Niches. Microbial Ecology, 2022, 83, 753-765.	1.4	15
1791	Changes in Digestive Microbiota, Rumen Fermentations and Oxidative Stress around Parturition Are Alleviated by Live Yeast Feed Supplementation to Gestating Ewes. Journal of Fungi (Basel, Switzerland), 2021, 7, 447.	1.5	8
1792	Impact of specimen type on findings for bacterial composition within the intestinal tract of dogs and cats with and without chronic enteropathy. American Journal of Veterinary Research, 2021, 82, 494-501.	0.3	0
1793	Key Technologies for Progressing Discovery of Microbiome-Based Medicines. Frontiers in Microbiology, 2021, 12, 685935.	1.5	13
1794	Untapped Potential of Moving Bed Biofilm Reactors with Different Biocarrier Types for Bilge Water Treatment: A Laboratory-Scale Study. Water (Switzerland), 2021, 13, 1810.	1.2	11
1795	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
1796	MinION technology for microbiome sequencing applications for the conservation of cultural heritage. Microbiological Research, 2021, 247, 126727.	2.5	13

#	Article	IF	CITATIONS
1797	Anaerobic degradation of high-concentration polycyclic aromatic hydrocarbons (PAHs) in seawater sediments. Marine Pollution Bulletin, 2021, 167, 112294.	2.3	13
1798	Effects of Delayed Harvest and Additives on Fermentation Quality and Bacterial Community of Corn Stalk Silage. Frontiers in Microbiology, 2021, 12, 687481.	1.5	14
1799	Prokaryotic Communities in the Thalassohaline Tuz Lake, Deep Zone, and Kayacik, Kaldirim and Yavsan Salterns (Turkey) Assessed by 16S rRNA Amplicon Sequencing. Microorganisms, 2021, 9, 1525.	1.6	9
1800	Assessment of total bacterial diversity in whiteleg shrimps and its aquaculture environment in Pangkajene and Banyuwangi, Indonesia. Asia-Pacific Journal of Molecular Biology and Biotechnology, 0, , 26-37.	0.2	0
1801	Investigations of soil autotrophic ammonia oxidizers in farmlands through genetics and big data analysis. Science of the Total Environment, 2021, 777, 146091.	3.9	12
1802	Glacier ice archives nearly 15,000-year-old microbes and phages. Microbiome, 2021, 9, 160.	4.9	59
1803	Study on Microbial Community Succession and Protein Hydrolysis of Donkey Meat during Refrigerated Storage Based on Illumina NOVA Sequencing Technology. Food Science of Animal Resources, 2021, 41, 701-714.	1.7	4
1804	Deep-Sea Carbonates Are a Reservoir of Fossil Microbes Previously Inhabiting Cold Seeps. Frontiers in Marine Science, 2021, 8, .	1.2	1
1805	PacBio sequencing revealed variation in the microbiota diversity, species richness and composition between milk collected from healthy and mastitis cows. Microbiology (United Kingdom), 2021, 167, .	0.7	6
1807	Effects of varying dietary black garlic supplementation on the growth, immune response, digestive and antioxidant activities, intestinal microbiota of <i>Litopenaeus vannamei</i> and its resistance to <i>Vibrio parahaemolyticus</i> infection. Aquaculture Nutrition, 2021, 27, 1699-1720.	1.1	3
1808	Longâ€ŧerm stability of soil bacterial and fungal community structures revealed in their abundant and rare fractions. Molecular Ecology, 2021, 30, 4305-4320.	2.0	19
1809	Effects of three probiotic strains (Bacillus coagulans, B. licheniformis and Paenibacillus polymyxa) on growth, immune response, gut morphology and microbiota, and resistance against Vibrio harveyi of northern whitings, Sillago sihama ForsskÅil (1775). Animal Feed Science and Technology, 2021, 277, 114958.	1.1	16
1810	Dynamic Alterations of the Distal Intestinal Microbiota, Transcriptome, and Metabolome of Hybrid Grouper by β -Conglycinin With Reconciliations by Sodium Butyrate in Feed. Frontiers in Marine Science, 2021, 8, .	1.2	3
1811	Antimetastatic Effects of Ganoderma lucidum Polysaccharide Peptide on B16-F10-luc-G5 Melanoma Mice With Sleep Fragmentation. Frontiers in Pharmacology, 2021, 12, 650216.	1.6	14
1812	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
1813	The Response of Soil Nutrients and Microbial Community Structures in Long-Term Tea Plantations and Diverse Agroforestry Intercropping Systems. Sustainability, 2021, 13, 7799.	1.6	14
1814	Shifts in pond water bacterial communities are associated with the health status of sea bass (Lateolabrax maculatus). Ecological Indicators, 2021, 127, 107775.	2.6	3
1815	Effects of Human, Caprine, and Bovine Milk Fat Globules on Microbiota Adhesion and Gut Microecology. Journal of Agricultural and Food Chemistry, 2021, 69, 9778-9787.	2.4	4

#	Article	IF	CITATIONS
1816	The Novel Interplay between Commensal Gut Bacteria and Metabolites in Diet-Induced Hyperlipidemic Rats Treated with Simvastatin. Journal of Proteome Research, 2021, , .	1.8	5
1817	Ginsenoside Rk3 alleviates gut microbiota dysbiosis and colonic inflammation in antibiotic-treated mice. Food Research International, 2021, 146, 110465.	2.9	29
1818	The effects of smoking and drinking on the oral and esophageal microbiota of healthy people. Annals of Translational Medicine, 2021, 9, 1244-1244.	0.7	6
1819	Dairy Processing Affects the Gut Digestion and Microecology by Changing the Structure and Composition of Milk Fat Globules. Journal of Agricultural and Food Chemistry, 2021, 69, 10194-10205.	2.4	4
1820	Succession of Fungal Communities at Different Developmental Stages of Cabernet Sauvignon Grapes From an Organic Vineyard in Xinjiang. Frontiers in Microbiology, 2021, 12, 718261.	1.5	18
1821	Rumen Fermentation, Digestive Enzyme Activity, and Bacteria Composition between Pre-Weaning and Post-Weaning Dairy Calves. Animals, 2021, 11, 2527.	1.0	14
1822	Benchmarking laboratory processes to characterise low-biomass respiratory microbiota. Scientific Reports, 2021, 11, 17148.	1.6	10
1823	Microbial Diversity and Non-volatile Metabolites Profile of Low-Temperature Sausage Stored at Room Temperature. Frontiers in Microbiology, 2021, 12, 711963.	1.5	4
1824	Irrigation has a higher impact on soil bacterial abundance, diversity and composition than nitrogen fertilization. Scientific Reports, 2021, 11, 16901.	1.6	26
1825	DNA sequence and community structure diversity of multi-year soil fungi in Grape of Xinjiang. Scientific Reports, 2021, 11, 16367.	1.6	3
1826	Infection Heterogeneity and Microbiota Differences in Chicks Infected by Salmonella enteritidis. Microorganisms, 2021, 9, 1705.	1.6	8
1827	Effects of Age, Diet CP, NDF, EE, and Starch on the Rumen Bacteria Community and Function in Dairy Cattle. Microorganisms, 2021, 9, 1788.	1.6	9
1828	Response of the yellow mealworm (Tenebrio molitor) gut microbiome to diet shifts during polystyrene and polyethylene biodegradation. Journal of Hazardous Materials, 2021, 416, 126222.	6.5	54
1829	Nasopharyngeal microbiome reveals the prevalence of opportunistic pathogens in SARS-CoV-2 infected individuals and their association with host types. Microbes and Infection, 2022, 24, 104880.	1.0	31
1830	Bacterial Diversity and Community in Regional Water Microbiota between Different Towns in World's Longevity Township Jiaoling, China. Diversity, 2021, 13, 361.	0.7	2
1831	Changes in the Fecal Microbiota Associated with a Broad-Spectrum Antimicrobial Administration in Hospitalized Neonatal Foals with Probiotics Supplementation. Animals, 2021, 11, 2283.	1.0	2
1832	Green Fluorescent Protein-Tagged Bacillus axarquiensis TUBP1 Reduced Cotton Verticillium Wilt Incidence by Altering Soil Rhizosphere Microbial Communities. Current Microbiology, 2021, 78, 3562-3576.	1.0	3
1834	Low Crude Protein Diet Affects the Intestinal Microbiome and Metabolome Differently in Barrows and Gilts. Frontiers in Microbiology, 2021, 12, 717727.	1.5	3

#	Article	IF	CITATIONS
1835	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
1836	Microbial eukaryote assemblages and potential novel diversity in four tropical East African Great Lakes. FEMS Microbiology Ecology, 2021, 97, .	1.3	7
1837	Forming Consensus To Advance Urobiome Research. MSystems, 2021, 6, e0137120.	1.7	42
1838	Gut microbial biomarkers for the treatment response in first-episode, drug-naÃ⁻ve schizophrenia: a 24-week follow-up study. Translational Psychiatry, 2021, 11, 422.	2.4	25
1839	Response of Methanogen Communities to the Elevation of Cathode Potentials in Bioelectrochemical Reactors Amended with Magnetite. Applied and Environmental Microbiology, 2021, 87, e0148821.	1.4	1
1840	A Soybean Resistant Protein-Containing Diet Increased the Production of Reg3Î ³ Through the Regulation of the Gut Microbiota and Enhanced the Intestinal Barrier Function in Mice. Frontiers in Nutrition, 2021, 8, 701466.	1.6	5
1841	Diversity, Composition, Taxa Biomarkers, and Functional Genes of Fish Gut Microbes in Peat Swamp Forests and its Converted Areas in North Selangor, Malaysia. Pertanika Journal of Science and Technology, 2021, 44, .	0.1	0
1842	High throughput sequencing-based analysis of the soil bacterial community structure and functions of Tamarix shrubs in the lower reaches of the Tarim River. PeerJ, 2021, 9, e12105.	0.9	7
1843	Composition of the microbial communities at different body sites in women with preterm birth and their newborns. Medicine in Microecology, 2021, 9, 100046.	0.7	3
1844	Gut Bacterial Communities of Lymantria xylina and Their Associations with Host Development and Diet. Microorganisms, 2021, 9, 1860.	1.6	11
1845	Unraveling the bacterial diversity of Cangar Hot Spring, Indonesia by Next Generation Sequencing of 16S rRNA gene. Biodiversitas, 2021, 22, .	0.2	0
1846	Acute oral colchicine caused gastric mucosal injury and disturbance of associated microbiota in mice. Toxicology, 2021, 461, 152908.	2.0	11
1847	Sediment microbiota in polyculture of shrimp and fish pattern is distinctive from those in monoculture intensive shrimp or fish ponds. Science of the Total Environment, 2021, 787, 147594.	3.9	16
1848	The unusual microbiota of the traditional Bulgarian dairy product Krokmach – A pilot metagenomics study. International Journal of Dairy Technology, 2022, 75, 139-149.	1.3	8
1849	Spatial dynamics of bacterial community in chlorinated drinking water distribution systems supplied with two treatment plants: An integral study of free-living and particle-associated bacteria. Environment International, 2021, 154, 106552.	4.8	14
1850	Community Structure and Function of Epiphytic Bacteria Associated With Myriophyllum spicatum in Baiyangdian Lake, China. Frontiers in Microbiology, 2021, 12, 705509.	1.5	14
1851	Morchella importuna Flavones Improve Intestinal Integrity in Dextran Sulfate Sodium-Challenged Mice. Frontiers in Microbiology, 2021, 12, 742033.	1.5	5
1852	Sugarcane-Legume Intercropping Can Enrich the Soil Microbiome and Plant Growth. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	12

#	Article	IF	CITATIONS
1853	Diversity of microbiota, microbial functions, and flavor in different types of low-temperature Daqu. Food Research International, 2021, 150, 110734.	2.9	54
1854	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
1855	Strategies for sample labelling and library preparation in DNA metabarcoding studies. Molecular Ecology Resources, 2022, 22, 1231-1246.	2.2	40
1856	A novel organic carbon accumulation mechanism in croplands in the Yellow River Delta, China. Science of the Total Environment, 2022, 806, 150629.	3.9	6
1857	A critical perspective on interpreting amplicon sequencing data in soil ecological research. Soil Biology and Biochemistry, 2021, 160, 108357.	4.2	36
1858	Improved highâ€throughput MHC typing for nonâ€model species using longâ€read sequencing. Molecular Ecology Resources, 2022, 22, 862-876.	2.2	7
1859	The Fecal Microbiota of Dogs Switching to a Raw Diet Only Partially Converges to That of Wolves. Frontiers in Microbiology, 2021, 12, 701439.	1.5	8
1860	Effect of an algal amendment on the microbial conversion of coal to methane at different sulfate concentrations from the Powder River Basin, USA. International Journal of Coal Geology, 2021, 248, 103860.	1.9	8
1861	The Bacterial Diversity of Spontaneously Fermented Dairy Products Collected in Northeast Asia. Foods, 2021, 10, 2321.	1.9	14
1862	Efficient anaerobic bioremediation of high-concentration benzo[a]pyrene in marine environments. Environmental Pollution, 2021, 284, 117210.	3.7	13
1863	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
1864	The potential correlations between the fungal communities and volatile compounds of traditional dry sausages from Northeast China. Food Microbiology, 2021, 98, 103787.	2.1	23
1865	Plant legacies and soil microbial community dynamics control soil respiration. Soil Biology and Biochemistry, 2021, 160, 108350.	4.2	10
1866	Tailor-made microbial consortium for Kombucha fermentation: Microbiota-induced biochemical changes and biofilm formation. Food Research International, 2021, 147, 110549.	2.9	28
1867	Effects of Dietary Energy Levels on Rumen Fermentation, Gastrointestinal Tract Histology, and Bacterial Community Diversity in Fattening Male Hu Lambs. Frontiers in Microbiology, 2021, 12, 695445.	1.5	15
1868	A fucoidan from Sargassum fusiforme with novel structure and its regulatory effects on intestinal microbiota in high-fat diet-fed mice. Food Chemistry, 2021, 358, 129908.	4.2	26
1869	Fungal community succession and volatile compound dynamics in Harbin dry sausage during fermentation. Food Microbiology, 2021, 99, 103764.	2.1	17
1870	Role of Bacillus inoculation in rice straw composting and bacterial community stability after inoculation: Unite resistance or individual collapse. Bioresource Technology, 2021, 337, 125464.	4.8	44

#	Article	IF	CITATIONS
1871	Dominant plants affect litter decomposition mainly through modifications of the soil microbial community. Soil Biology and Biochemistry, 2021, 161, 108399.	4.2	37
1872	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
1873	A water-soluble Î ² -glucan improves growth performance by altering gut microbiome and health in weaned pigs. Animal Nutrition, 2021, 7, 1345-1351.	2.1	9
1874	Alien invasive plant Amaranthus spinosus mainly altered the community structure instead of the $\hat{I}\pm$ diversity of soil N-fixing bacteria under drought. Acta Oecologica, 2021, 113, 103788.	0.5	6
1875	Modification of total and phosphorus mineralizing bacterial communities associated with Zea mays L. through plant development and fertilization regimes. Journal of Integrative Agriculture, 2021, 20, 3026-3038.	1.7	4
1876	NGS-Based Metagenomic Study of Four Traditional Bulgarian Green Cheeses from Tcherni Vit. LWT - Food Science and Technology, 2021, 152, 112278.	2.5	9
1877	Lycium barbarum L. (goji berry) monocropping causes microbial diversity loss and induces Fusarium spp. enrichment at distinct soil layers. Applied Soil Ecology, 2021, 168, 104107.	2.1	17
1878	Analysis of bacterial community functional diversity in late-stage shrimp (Litopenaeus vannamei) ponds using Biolog EcoPlates and PICRUSt2. Aquaculture, 2022, 546, 737288.	1.7	14
1879	Recovery patterns of soil bacterial and fungal communities in Chinese boreal forests along a fire chronosequence. Science of the Total Environment, 2022, 805, 150372.	3.9	15
1880	A unique microbiome in a highly polluted and alkalic lake in a seasonally frozen area. Environmental Research, 2022, 204, 112056.	3.7	3
1881	Microbial investigations of new hydrogel-biochar composites as soil amendments for simultaneous nitrogen-use improvement and heavy metal immobilization. Journal of Hazardous Materials, 2022, 424, 127154.	6.5	11
1882	Insight to bacteria community response of organic management in apple orchard-bagasse fertilizer combined with biochar. Chemosphere, 2022, 286, 131693.	4.2	20
1884	Application of Omics Tools for Microbial Community Structure and Function Analysis. , 2021, , 433-456.		1
1885	Fecal microbiome and metabolome differ in healthy and food-allergic twins. Journal of Clinical Investigation, 2021, 131, .	3.9	69
1886	Recovery of microbial community profile information hidden in chimeric sequence reads. Computational and Structural Biotechnology Journal, 2021, 19, 5126-5139.	1.9	1
1887	Arbuscular mycorrhizal fungal colonization and soil pH induced by nitrogen and phosphorus additions affects leaf C:N:P stoichiometry in Chinese fir (Cunninghamia lanceolata) forests. Plant and Soil, 2021, 461, 421-440.	1.8	28
1888	Innate gut microbiota predisposes to high alcohol consumption. Addiction Biology, 2021, 26, e13018.	1.4	19
1889	Influence of soil microorganisms and physicochemical properties on plant diversity in an arid desert of Western China. Journal of Forestry Research, 2021, 32, 2645-2659.	1.7	15

#	Article	IF	CITATIONS
1890	Morphological and physiological properties of hybrid rice seeds with top-gray chalkiness. Bragantia, 0, 80, .	1.3	1
1891	DOCAâ€salt hypertension and the role of the OVLTâ€sympatheticâ€gut microbiome axis. Clinical and Experimental Pharmacology and Physiology, 2021, 48, 490-497.	0.9	0
1892	Gut Microbiome Changes in Captive Plateau Zokors (Eospalax baileyi). Evolutionary Bioinformatics, 2021, 17, 117693432199635.	0.6	4
1893	Unraveling Mechanisms and Impact of Microbial Recruitment on Oilseed Rape (Brassica napus L.) and the Rhizosphere Mediated by Plant Growth-Promoting Rhizobacteria. Microorganisms, 2021, 9, 161.	1.6	28
1894	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
1896	Mock Community Analysis. , 2014, , 1-7.		5
1897	Culture Independent Diversity Analysis of Soil Microbial Community and their Significance. Sustainable Development and Biodiversity, 2014, , 305-340.	1.4	2
1898	Eukaryotic Community in UASB Reactor Treating Domestic Sewage Based on 18S rRNA Gene Sequencing. Lecture Notes in Civil Engineering, 2017, , 218-224.	0.3	3
1899	Diversity and composition of microbiota during fermentation of traditional Nuodeng ham. Journal of Microbiology, 2021, 59, 20-28.	1.3	9
1900	Administration of commensal Shewanella sp. MR-7 ameliorates lipopolysaccharide-induced intestine dysfunction in turbot (Scophthalmus maximus L.). Fish and Shellfish Immunology, 2020, 102, 460-468.	1.6	10
1901	Occurrence of potentially pathogenic bacteria on shared bicycles. International Journal of Hygiene and Environmental Health, 2020, 224, 113442.	2.1	5
1902	Sclerotia of a phytopathogenic fungus restrict microbial diversity and improve soil health by suppressing other pathogens and enriching beneficial microorganisms. Journal of Environmental Management, 2020, 259, 109857.	3.8	16
1903	Modern urbanization has reshaped the bacterial microbiome profiles of house dust in domestic environments. World Allergy Organization Journal, 2020, 13, 100452.	1.6	13
1904	Surface Stability in Drylands Is Influenced by Dispersal Strategy of Soil Bacteria. Journal of Geophysical Research C: Biogeosciences, 2019, 124, 3403-3418.	1.3	16
1905	In vitro human colonic microbiota utilises D-β-hydroxybutyrate to increase butyrogenesis. Scientific Reports, 2020, 10, 8516.	1.6	21
1906	Changes in bacterial diversity and composition in the faeces and colon of weaned piglets after feeding fermented soybean meal. Journal of Medical Microbiology, 2018, 67, 1181-1190.	0.7	21
1907	Characterization of pelvic and cervical microbiotas from patients with pelvic inflammatory disease. Journal of Medical Microbiology, 2018, 67, 1519-1526.	0.7	22
1929	Dual epithelial and immune cell function of Dvl1 regulates gut microbiota composition and intestinal homeostasis. JCI Insight, 2016, 1, .	2.3	11

#	Article	IF	CITATIONS
1930	Fbxw7 increases CCL2/7 in CX3CR1hi macrophages to promote intestinal inflammation. Journal of Clinical Investigation, 2019, 129, 3877-3893.	3.9	79
1931	Marine bacterial communities in the upper gulf of Thailand assessed by Illumina next-generation sequencing platform. BMC Microbiology, 2020, 20, 19.	1.3	28
1932	Structure and diversity of native bacterial communities in soils contaminated with polychlorinated biphenyls. AMB Express, 2020, 10, 124.	1.4	10
1933	The Effects of High-Salt Gastric Intake on the Composition of the Intestinal Microbiota in Wistar Rats. Medical Science Monitor, 2020, 26, e922160.	0.5	10
1934	Breaking point: the genesis and impact of structural variation in tumours. F1000Research, 2018, 7, 1814.	0.8	7
1935	Exploited Application of Pyrosequencing in Microbial Diversity of Activated Sludge System of Common Effluent Treatment Plants. American Journal of Microbiological Research, 2014, 2, 157-165.	0.2	2
1936	Metagenomic analysis of microbial community in over-fermented tempeh. Biodiversitas, 2019, 20, 1106-1114.	0.2	15
1937	Molecular Identification of Bacteria in Tracheal Aspirate Fluid from Mechanically Ventilated Preterm Infants. PLoS ONE, 2011, 6, e25959.	1.1	69
1938	Reducing the Effects of PCR Amplification and Sequencing Artifacts on 16S rRNA-Based Studies. PLoS ONE, 2011, 6, e27310.	1.1	1,891
1939	Composition and Similarity of Bovine Rumen Microbiota across Individual Animals. PLoS ONE, 2012, 7, e33306.	1.1	508
1940	Novel Bacterial Taxa in the Human Microbiome. PLoS ONE, 2012, 7, e35294.	1.1	86
1941	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. PLoS ONE, 2012, 7, e36466.	1.1	572
1942	Metagenomics of the Svalbard Reindeer Rumen Microbiome Reveals Abundance of Polysaccharide Utilization Loci. PLoS ONE, 2012, 7, e38571.	1.1	190
1943	Evaluation of 16S rDNA-Based Community Profiling for Human Microbiome Research. PLoS ONE, 2012, 7, e39315.	1.1	240
1944	The "Most Wanted―Taxa from the Human Microbiome for Whole Genome Sequencing. PLoS ONE, 2012, 7, e41294.	1.1	104
1945	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
1946	Compositional Stability of a Salivary Bacterial Population against Supragingival Microbiota Shift following Periodontal Therapy. PLoS ONE, 2012, 7, e42806.	1.1	66
1947	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

#	Article	IF	CITATIONS
1948	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
1949	Characterization of the Fecal Microbiota Using High-Throughput Sequencing Reveals a Stable Microbial Community during Storage. PLoS ONE, 2012, 7, e46953.	1.1	190
1950	Metagenomic Analyses of Alcohol Induced Pathogenic Alterations in the Intestinal Microbiome and the Effect of Lactobacillus rhamnosus GG Treatment. PLoS ONE, 2013, 8, e53028.	1,1	439
1951	Cellulose Supplementation Early in Life Ameliorates Colitis in Adult Mice. PLoS ONE, 2013, 8, e56685.	1.1	55
1952	The Dental Plaque Microbiome in Health and Disease. PLoS ONE, 2013, 8, e58487.	1.1	174
1953	Control of Temperature on Microbial Community Structure in Hot Springs of the Tibetan Plateau. PLoS ONE, 2013, 8, e62901.	1.1	157
1954	Inflammation and Airway Microbiota during Cystic Fibrosis Pulmonary Exacerbations. PLoS ONE, 2013, 8, e62917.	1.1	155
1955	Role of Bacterial Exopolysaccharides (EPS) in the Fate of the Oil Released during the Deepwater Horizon Oil Spill. PLoS ONE, 2013, 8, e67717.	1.1	135
1956	Taxonomic Precision of Different Hypervariable Regions of 16S rRNA Gene and Annotation Methods for Functional Bacterial Groups in Biological Wastewater Treatment. PLoS ONE, 2013, 8, e76185.	1.1	84
1957	Potential Human Pathogenic Bacteria in a Mixed Urban Watershed as Revealed by Pyrosequencing. PLoS ONE, 2013, 8, e79490.	1.1	65
1958	Next Generation Sequencing Reveals the Hidden Diversity of Zooplankton Assemblages. PLoS ONE, 2013, 8, e81327.	1.1	188
1959	Allelic Differences within and among Sister Spores of the Arbuscular Mycorrhizal Fungus Glomus etunicatum Suggest Segregation at Sporulation. PLoS ONE, 2013, 8, e83301.	1.1	19
1960	MetaMetaDB: A Database and Analytic System for Investigating Microbial Habitability. PLoS ONE, 2014, 9, e87126.	1.1	22
1961	Evidence of a Putative Deep Sea Specific Microbiome in Marine Sponges. PLoS ONE, 2014, 9, e91092.	1.1	79
1962	Mycoplasma salivarium as a Dominant Coloniser of Fanconi Anaemia Associated Oral Carcinoma. PLoS ONE, 2014, 9, e92297.	1.1	32
1963	Bacterial Profile of Dentine Caries and the Impact of pH on Bacterial Population Diversity. PLoS ONE, 2014, 9, e92940.	1.1	119
1964	Comparison and Validation of Some ITS Primer Pairs Useful for Fungal Metabarcoding Studies. PLoS ONE, 2014, 9, e97629.	1.1	336
1965	Stepwise Threshold Clustering: A New Method for Genotyping MHC Loci Using Next-Generation Sequencing Technology. PLoS ONE, 2014, 9, e100587.	1.1	38

ARTICLE IF CITATIONS Extensive Recombination Due to Heteroduplexes Generates Large Amounts of Artificial Gene 1966 1.1 23 Fragments during PCR. PLoS ONE, 2014, 9, e106658. High Genetic Diversity and Novelty in Eukaryotic Plankton Assemblages Inhabiting Saline Lakes in the 1.1 Qaidam Basin. PLoS ÓNE, 2014, 9, e112812. Pesticide Side Effects in an Agricultural Soil Ecosystem as Measured by amoA Expression 1968 1.1 82 Quantification and Bacterial Diversity Changes. PLoS ONE, 2015, 10, e0126080. Gut Microbial Dysbiosis May Predict Diarrhea and Fatigue in Patients Undergoing Pelvic Cancer 1969 1.1 149 Radiotherapy: A Pilot Study. PLoS ONE, 2015, 10, e0126312. AmpliconDuo: A Split-Sample Filtering Protocol for High-Throughput Amplicon Sequencing of 1970 1.1 53 Microbial Communities. PLoS ONE, 2015, 10, e0141590. Linking the Composition of Bacterial and Archaeal Communities to Characteristics of Soil and Flora Composition in the Atlantic Rainforest. PLoS ONE, 2016, 11, e0146566. 1971 1.1 Allergic Patients with Long-Term Asthma Display Low Levels of Bifidobacterium adolescentis. PLoS 1972 1.1 90 ONE, 2016, 11, e0147809. Development of an Analysis Pipeline Characterizing Multiple Hypervariable Regions of 16S rRNA Using 1.1 Mock Samples. PLoS ONE, 2016, 11, e0148047. Microbial Community Profile and Water Quality in a Protected Area of the Caatinga Biome. PLoS ONE, 1974 1.1 20 2016, 11, e0148296. CLUSTOM-CLOUD: In-Memory Data Grid-Based Software for Clustering 16S rRNA Sequence Data in the 1.1 Cloud Environment. PLoS ONÉ, 2016, 11, e0151064. Variability of Bacterial Communities in the Moth Heliothis virescens Indicates Transient Association 1976 1.1 89 with the Host. PLoS ONE, 2016, 11, e0154514. Seasonality and Locality Affect the Diversity of Anopheles gambiae and Anopheles coluzzii Midgut 1977 1.1 58 Microbiotá from Ghana. PLoS ONE, 2016, 11, e0157529. Changes in the Bacterial Community Structure of Remediated Anthracene-Contaminated Soils. PLoS 1978 1.1 21 ONE, 2016, 11, e0160991. Transient and Prolonged Response of Chicken Cecum Mucosa to Colonization with Different Gut Microbiota. PLoS ONE, 2016, 11, e0163932. 1979 1.1 A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge 1980 1.1 46 Blanket Reactor. PLoS ONE, 2016, 11, e0167788. Distinctive Feature of Microbial Communities and Bacterial Functional Profiles in Tricholoma 39 matsutake Dominant Soil. PLoS ONE, 2016, 11, e0168573. Profiling Living Bacteria Informs Preparation of Fecal Microbiota Transplantations. PLoS ONE, 2017, 12, 1982 1.1 68 e0170922. Archaeal and bacterial communities in deep-sea hydrogenetic ferromanganese crusts on old 1983 1.1 seamounts of the northwestern Pacific. PLoS ONÉ, 2017, 12, e0173071.

#	Article	IF	CITATIONS
1984	Structure and dynamics of the gut bacterial microbiota of the bark beetle, Dendroctonus rhizophagus (Curculionidae: Scolytinae) across their life stages. PLoS ONE, 2017, 12, e0175470.	1.1	54
1985	Microscale spatial analysis provides evidence for adhesive monopolization of dietary nutrients by specific intestinal bacteria. PLoS ONE, 2017, 12, e0175497.	1.1	25
1986	Contrasting bacterial communities in two indigenous Chionochloa (Poaceae) grassland soils in New Zealand. PLoS ONE, 2017, 12, e0179652.	1.1	15
1987	Exploring the salivary microbiome of children stratified by the oral hygiene index. PLoS ONE, 2017, 12, e0185274.	1.1	59
1988	Differences in the intestinal microbiota between uninfected piglets and piglets infected with porcine epidemic diarrhea virus. PLoS ONE, 2018, 13, e0192992.	1.1	37
1989	Parallel ClickSeq and Nanopore sequencing elucidates the rapid evolution of defective-interfering RNAs in Flock House virus. PLoS Pathogens, 2017, 13, e1006365.	2.1	61
1990	Longitudinal analysis reveals characteristically high proportions of bacterial vaginosis-associated bacteria and temporal variability of vaginal microbiota in northern pig-tailed macaques (Macaca) Tj ETQq0 0 0 rgl	3Tø@verlo	ck610 Tf 50 4
1991	Effects of respiratory disease on Kele piglets lung microbiome, assessed through 16S rRNA sequencing. Veterinary World, 2020, 13, 1970-1981.	0.7	3
1992	Comparing Bacterial Diversity in Two Full-Scale Enhanced Biological Phosphate Removal Reactors Using 16S Amplicon Pyrosequencing. Polish Journal of Environmental Studies, 2018, 27, 709-745.	0.6	4
1993	Illumina Based Analysis of Bacterial and Fungal Flora in Foreguts and Hindguts of Crucian Carp (Carassius Aumtus) in Retail Markets. Open Journal of Bacteriology, 2017, 1, 001-006.	0.3	1
1994	Variations in gut microbial profiles in ankylosing spondylitis: disease phenotype-related dysbiosis. Annals of Translational Medicine, 2019, 7, 571-571.	0.7	29
1995	is Isolated from Air Swabs: Time to Doubt the Value of Traditional Cultures in Shoulder Surgery?. Archives of Bone and Joint Surgery, 2020, 8, 506-510.	0.1	8
1996	Interlake variation and environmental controls of denitrification across different geographical scales. Aquatic Microbial Ecology, 2013, 69, 1-16.	0.9	34
1997	Biogeography of globally distributed bacteria in temperate and boreal Québec lakes as revealed by tag pyrosequencing of 16S rRNA genes. Aquatic Microbial Ecology, 2015, 76, 175-188.	0.9	4
1998	Spatio-temporal variability in Mediterranean rocky shore microphytobenthos. Marine Ecology - Progress Series, 2017, 575, 17-29.	0.9	18
1999	Genomic Characterization of a Novel Gut Symbiont From the Hadal Snailfish. Frontiers in Microbiology, 2019, 10, 2978.	1.5	29
2000	Combination of Bacillus licheniformis and Salinomycin: Effect on the Growth Performance and GIT Microbial Populations of Broiler Chickens. Animals, 2020, 10, 889.	1.0	16
2001	Cloning of ribosomal ITS PCR products creates frequent, non-random chimeric sequences – a test involving heterozygotes between Gymnopus dichrous taxa I and II. MycoKeys, 0, 10, 45-56.	0.8	15

#	Article	lF	CITATIONS
2002	Correlation between invasive microbiota in margin-surrounding mucosa and anastomotic healing in patients with colorectal cancer. World Journal of Gastrointestinal Oncology, 2019, 11, 717-728.	0.8	12
2003	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
2004	Succession of microbial community in anaerobic digestion of dairy manure induced by manure-derived biochar. Environmental Engineering Research, 2021, 26, .	1.5	8
2005	Effects of Soybean Stover-Derived Biochar on Microbial Community and Structure in Loess Soil. Nature Environment and Pollution Technology, 2020, 19, 703-710.	0.2	4
2006	The impact of short-term acute heat stress on the rumen microbiome of Hanwoo steers. Journal of Animal Science and Technology, 2020, 62, 208-217.	0.8	22
2008	High-Throughput Sequencing Analysis of Endophytic Bacteria Diversity in Fruits of White and Red Pitayas from Three Different Origins. Polish Journal of Microbiology, 2018, 67, 27-35.	0.6	12
2009	— Invited Review — Metagenomic investigation of gastrointestinal microbiome in cattle. Asian-Australasian Journal of Animal Sciences, 2017, 30, 1515-1528.	2.4	41
2010	Microorganismos asociados a la rizosfera de jitomate en un agroecosistema del valle de Guasave, Sinaloa, México. Revista Mexicana De Biodiversidad, 2012, 83, .	0.4	7
2011	Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. ELife, 2018, 7, .	2.8	70
2012	The lost world of Cuatro Ciénegas Basin, a relictual bacterial niche in a desert oasis. ELife, 2018, 7, .	2.8	51
2013	Comparison of three clustering approaches for detecting novel environmental microbial diversity. Peerl, 2016, 4, e1692.	0.9	26
2014	Sequencing 16S rRNA gene fragments using the PacBio SMRT DNA sequencing system. PeerJ, 2016, 4, e1869.	0.9	200
2015	Agricultural land-use change in a Mexican oligotrophic desert depletes ecosystem stability. PeerJ, 2016, 4, e2365.	0.9	13
2016	A method for high precision sequencing of near full-length 16S rRNA genes on an Illumina MiSeq. PeerJ, 2016, 4, e2492.	0.9	59
2017	Accuracy of microbial community diversity estimated by closed- and open-reference OTUs. PeerJ, 2017, 5, e3889.	0.9	138
2018	Microbial secondary succession in soil microcosms of a desert oasis in the Cuatro Cienegas Basin, Mexico. PeerJ, 2013, 1, e47.	0.9	50
2019	The bacterial communities of <i>Drosophila suzukii</i> collected from undamaged cherries. PeerJ, 2014, 2, e474.	0.9	62
2020	Effects of wine-cap <i>Stropharia</i> cultivation on soil nutrients and bacterial communities in forestlands of northern China. PeerJ, 2018, 6, e5741.	0.9	20

#	Article	IF	CITATIONS
2021	An experimental comparison of composite and grab sampling of stream water for metagenetic analysis of environmental DNA. PeerJ, 2018, 6, e5871.	0.9	18
2022	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
2023	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
2024	Biodegradation of thiocyanate by a native groundwater microbial consortium. PeerJ, 2019, 7, e6498.	0.9	10
2025	The Koala (<i>Phascolarctos cinereus</i>) faecal microbiome differs with diet in a wild population. PeerJ, 2019, 7, e6534.	0.9	46
2026	Comparison of the fecal microbiota of two free-ranging Chinese subspecies of the leopard (<i>Panthera pardus</i>) using high-throughput sequencing. PeerJ, 2019, 7, e6684.	0.9	18
2027	Seasonal dynamics of microbial diversity in the rhizosphere of <i>Ulmus pumila</i> L. var. <i>sabulosa</i> in a steppe desert area of Northern China. PeerJ, 2019, 7, e7526.	0.9	15
2028	Host dietary specialization and neutral assembly shape gut bacterial communities of wild dragonflies. PeerJ, 2019, 7, e8058.	0.9	19
2029	Rhizosphere bacterial and fungal communities during the growth of <i>Angelica sinensis</i> seedlings cultivated in an Alpine uncultivated meadow soil. PeerJ, 2020, 8, e8541.	0.9	13
2030	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
2031	Variation of soil nutrients and bacterial community diversity of different land utilization types in Yangtze River Basin, Chongqing Municipality. PeerJ, 2020, 8, e9386.	0.9	9
2032	Gut microbiota of obese and diabetic Thai subjects and interplay with dietary habits and blood profiles. PeerJ, 2020, 8, e9622.	0.9	7
2033	Flaxseed Powder Attenuates Non-Alcoholic Steatohepatitis via Modulation of Gut Microbiota and Bile Acid Metabolism through Gut–Liver Axis. International Journal of Molecular Sciences, 2021, 22, 10858.	1.8	15
2034	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
2035	A Snapshot Picture of the Fungal Composition of Bee Bread in Four Locations in Bulgaria, Differing in Anthropogenic Influence. Journal of Fungi (Basel, Switzerland), 2021, 7, 845.	1.5	2
2036	lleal mucosa-associated microbiota overgrowth associated with pathogenesis of primary biliary cholangitis. Scientific Reports, 2021, 11, 19705.	1.6	8
2037	Lactobacillus reuteri Alleviates Gastrointestinal Toxicity of Rituximab by Regulating the Proinflammatory T Cells in vivo. Frontiers in Microbiology, 2021, 12, 645500.	1.5	5
2038	Effect of the administration of probiotics on the fecal microbiota of adult individuals. Food Science and Nutrition, 2021, 9, 6471-6479.	1.5	4

#	Article	IF	CITATIONS
2039	Largely invariant communities of bacterial endophytes in the nonphotosynthetic mycoheterotrophic plant <i>Pterospora andromedea</i> . American Journal of Botany, 2021, 108, 2208-2219.	0.8	0
2040	Effects of Dietary Glucose Oxidase Supplementation on the Performance, Apparent Ileal Amino Acids Digestibility, and Ileal Microbiota of Broiler Chickens. Animals, 2021, 11, 2909.	1.0	4
2041	The gut microbiota and microbial metabolites are associated with tail biting in pigs. Scientific Reports, 2021, 11, 20547.	1.6	14
2042	Analysis of Cow-Calf Microbiome Transfer Routes and Microbiome Diversity in the Newborn Holstein Dairy Calf Hindgut. Frontiers in Nutrition, 2021, 8, 736270.	1.6	16
2043	Mixture of Five Fermented Herbs (Zhihuasi Tk) Alters the Intestinal Microbiota and Promotes the Growth Performance in Piglets. Frontiers in Microbiology, 2021, 12, 725196.	1.5	10
2044	Metagenomics analysis of the fecal microbiota in Ring-necked pheasants (Phasianus colchicus) and Green pheasants (Phasianus versicolor) using next generation sequencing. Saudi Journal of Biological Sciences, 2022, 29, 1781-1788.	1.8	5
2046	Novel Gut Microbiota Patterns Involved in the Attenuation of Dextran Sodium Sulfate-Induced Mouse Colitis Mediated by Glycerol Monolaurate via Inducing Anti-inflammatory Responses. MBio, 2021, 12, e0214821.	1.8	23
2047	Effect of Aspergillus niger NBC001 on the soybean rhizosphere microbial community in a soybean cyst nematode-infested field. Journal of Integrative Agriculture, 2021, 20, 3230-3239.	1.7	9
2049	Application of Amplicon Pyrosequencing in Soil Microbial Ecology. Han'guk T'oyang Piryo Hakhoe Chi Han'guk T'oyang Piryo Hakhoe, 2012, 45, 1073-1085.	0.1	0
2050	Technical solutions. Journal of Wound Care, 2013, 22, S26-S30.	0.5	8
2052	The faecal flora: a source of healthcare-associated infections and antibiotic resistance. , 2013, , .		0
2053	Wastewater, wheat and table wipes: adventures in culture-independent microbiology. Microbiology Australia, 2014, 35, 188.	0.1	0
2055	Bacterial Communities in Different Sections of a Municipal Wastewater Treatment Plant Revealed by 16S rDNA 454 Pyrosequencing. , 2015, , 3-23.		0
2056	Taxonomic Precision of Different Hypervariable Regions of 16S rRNA Gene and Annotation Methods for Functional Bacterial Groups in Biological Wastewater Treatment. , 2015, , 25-53.		0
2062	A profile-based probabilistic approach for the detection of anomalies in the cytochrome C oxidase I amplicon sequences. , 2017, , .		0
2065	MOLECULAR ANALYSIS OF LOTUS PRODUCTION SOIL CAUSING REPLANT PROBLEM AND EVALUATION OF FERTILIZATION EFFECT OF BACILLUS AND NON-PARASITIC NEMATODES PREDOMINATED COMPOST. Journal of Japan Society of Civil Engineers Ser G (Environmental Research), 2018, 74, III_255-III_264.	0.1	1
2072	Response of active picoeukaryotes to the deposition of Saharan dust and European aerosols in the eastern Mediterranean Sea. Aquatic Microbial Ecology, 2018, 82, 31-42.	0.9	2
2075	Genomic Applications in theÂClinical Management of Infectious Diseases. , 2019, , 583-594.		0

#	Article	IF	CITATIONS
2077	Metagenomic Analysis Reveals Correlation Between Microbiome Structure and Leonardite Characteristics from Kazakhstan Coal Deposits. Eurasian Chemico-Technological Journal, 2019, 21, 135.	0.3	5
2080	High-throughput sequence analysis reveals variation in the relative abundance of components of the bacterial and fungal microbiota in the rhizosphere of <i>Ginkgo biloba</i> . PeerJ, 2019, 7, e8051.	0.9	2
2082	Gut microbiota of the scimitar-horned oryx, Oryx dammah. Folia Zoologica, 2019, 68, 269.	0.9	1
2085	Changes in the Intestinal Microbiota in Patients with Stage 5 Chronic Kidney Disease on a Low-Protein Diet and the Effects of Human to Rat Fecal Microbiota Transplantation. Medical Science Monitor, 2020, 26, e921557.	0.5	8
2086	Effects of supplementary feeding on the rumen morphology and bacterial diversity in lambs. PeerJ, 2020, 8, e9353.	0.9	16
2090	Rhizobacterial community structure in grafted tomato plants infected by Ralstonia solanacearum. Biodiversitas, 2020, 21, .	0.2	7
2091	Metabolomics Analyses Reveal Metabolites Affected by Plant Growth-Promoting Endophytic Bacteria in Roots of the Halophyte Mesembryanthemum crystallinum. International Journal of Molecular Sciences, 2021, 22, 11813.	1.8	13
2092	Observation of the Gut Microbiota Profile in C57BL/6 Mice Induced by Plasmodium berghei ANKA Infection. Frontiers in Cellular and Infection Microbiology, 2021, 11, 680383.	1.8	10
2093	Investigating the Reciprocal Interrelationships among the Ruminal Microbiota, Metabolome, and Mastitis in Early Lactating Holstein Dairy Cows. Animals, 2021, 11, 3108.	1.0	9
2094	Gut Microbiota in Canine Idiopathic Epilepsy: Effects of Disease and Treatment. Animals, 2021, 11, 3121.	1.0	11
2095	Degradation characteristics and soil remediation of thifensulfuron-methyl by immobilized Serratia marcecens N80 beads. Environmental Technology and Innovation, 2021, 24, 102059.	3.0	14
2096	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
2097	Metagenomic Analysis of Rhizosphere Bacteria in Desert Plant <i>Calotropis procera</i> . Geomicrobiology Journal, 2021, 38, 375-383.	1.0	7
2099	Trichoderma biofertilizer facilitating Leymus chinensis production in different growth stages is strongly linked to dynamically altered soil microbiomes. Agriculture, Ecosystems and Environment, 2022, 324, 107706.	2.5	9
2100	Impact of imidacloprid exposure on the biochemical responses, transcriptome, gut microbiota and growth performance of the Pacific white shrimp Litopenaeus vannamei. Journal of Hazardous Materials, 2022, 424, 127513.	6.5	40
2104	Microbial Ecology of French Dry Fermented Sausages and Mycotoxin Risk Evaluation During Storage. Frontiers in Microbiology, 2021, 12, 737140.	1.5	7
2105	Succession of Microbial Communities of Corn Silage Inoculated with Heterofermentative Lactic Acid Bacteria from Ensiling to Aerobic Exposure. Fermentation, 2021, 7, 258.	1.4	15
2106	Sequential Extraction, Characterization, and Analysis of Pumpkin Polysaccharides for Their Hypoglycemic Activities and Effects on Gut Microbiota in Mice. Frontiers in Nutrition, 2021, 8, 769181.	1.6	19

~			~	
C	ΙΤΛΤΙ	ON	Repc	DT
\sim	плп		NLFC	<u> </u>

#	Article	IF	CITATIONS
2107	Effect of Long-Term and Short-Term Imbalanced Zn Manipulation on Gut Microbiota and Screening for Microbial Markers Sensitive to Zinc Status. Microbiology Spectrum, 2021, 9, e0048321.	1.2	17
2112	Soil fungal networks are more sensitive to grazing exclusion than bacterial networks. PeerJ, 2020, 8, e9986.	0.9	10
2113	The nature and frequency of chimeras in eukaryotic metagenetic samples. Journal of Nematology, 2012, 44, 18-25.	0.4	7
2114	Alterations of fecal bacterial communities in patients with lung cancer. American Journal of Translational Research (discontinued), 2018, 10, 3171-3185.	0.0	38
2115	Dietary gamma-aminobutyric acid ameliorates growth impairment and intestinal dysfunction in turbot (<i>Scophthalmus maximus</i> L.) fed a high soybean meal diet. Food and Function, 2022, 13, 290-303.	2.1	8
2116	Consistent responses of soil bacterial communities to bioavailable silicon deficiency in croplands. Geoderma, 2022, 408, 115587.	2.3	5
2117	Effects of dietary xylooligosaccharide on growth, digestive enzymes activity, intestinal morphology, and the expression of inflammatory cytokines and tight junctions genes in triploid Oncorhynchus mykiss fed a low fishmeal diet. Aquaculture Reports, 2022, 22, 100941.	0.7	7
2118	Fecal microbiota changes in NZB/W F1 mice after induction of lupus disease. Scientific Reports, 2021, 11, 22953.	1.6	7
2119	The antiâ€fatigue activity of corn peptides and their effect on gut bacteria. Journal of the Science of Food and Agriculture, 2022, 102, 3456-3466.	1.7	5
2120	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
2121	Ancient Oriental Wisdom still Works: Removing ARGs in Drinking Water by Boiling as compared to Chlorination. Water Research, 2022, 209, 117902.	5.3	20
2123	Oral Mycobiome Differences in Various Spatial Niches With and Without Severe Early Childhood Caries. Frontiers in Pediatrics, 2021, 9, 748656.	0.9	7
2124	Influence of timing of maternal antibiotic administration during caesarean section on infant microbial colonisation: a randomised controlled trial. Gut, 2022, 71, 1803-1811.	6.1	19
2125	A Pilot Study: Composition and Diversity of 16S rRNA Based Skin Bacterial Microbiome in Indonesian Atopic Dermatitis Population. Clinical, Cosmetic and Investigational Dermatology, 2021, Volume 14, 1737-1744.	0.8	5
2126	Decreasing molecular diversity of soil dissolved organic matter related to microbial community along an alpine elevation gradient. Science of the Total Environment, 2022, 818, 151823.	3.9	19
2127	Regionally divergent patterns of grass carp relative abundance, feeding habits and trophic niches in the subtropical Pearl River basin. Aquatic Ecology, 2022, 56, 525-541.	0.7	3
2128	Emodin Improves Intestinal Health and Immunity through Modulation of Gut Microbiota in Mice Infected by Pathogenic Escherichia coli O1. Animals, 2021, 11, 3314.	1.0	6
2129	Effects of symbiotic population impairment on microbiome composition and longevity of Bactrocera dorsalis. Royal Society Open Science, 2021, 8, 211104.	1.1	2

#	Article	IF	CITATIONS
2130	Microbial regulation of hexokinase 2 links mitochondrial metabolism and cell death in colitis. Cell Metabolism, 2021, 33, 2355-2366.e8.	7.2	40
2131	Relevance of the microbial community to Sb and As biogeochemical cycling in natural wetlands. Science of the Total Environment, 2022, 818, 151826.	3.9	11
2132	Clostridium butyricum Alleviates Enterotoxigenic Escherichia coli K88-Induced Oxidative Damage Through Regulating the p62-Keap1-Nrf2 Signaling Pathway and Remodeling the Cecal Microbial Community. Frontiers in Immunology, 2021, 12, 771826.	2.2	23
2133	Analysis of Postmortem Intestinal Microbiota Successional Patterns with Application in Postmortem Interval Estimation. Microbial Ecology, 2022, 84, 1087-1102.	1.4	17
2134	Effects of Glutathione on Growth, Intestinal Antioxidant Capacity, Histology, Gene Expression, and Microbiota of Juvenile Triploid Oncorhynchus mykiss. Frontiers in Physiology, 2021, 12, 784852.	1.3	8
2135	Lupus gut microbiota transplants cause autoimmunity and inflammation. Clinical Immunology, 2021, 233, 108892.	1.4	25
2136	Dietary supplementation of montmorillonite promotes growth and intestinal health in turbot (Scophthalmus maximus). Animal Feed Science and Technology, 2022, 283, 115176.	1.1	7
2137	Biodiversity and degradation potential of oil-degrading bacteria isolated from sediments of hydrothermal and non-hydrothermal areas of the Southwest Mid-Indian Ocean Ridge. Environmental Science and Pollution Research, 2021, , 1.	2.7	1
2138	The Fungal Communities and Flavor Profiles in Different Types of High-Temperature Daqu as Revealed by High-Throughput Sequencing and Electronic Senses. Frontiers in Microbiology, 2021, 12, 784651.	1.5	16
2140	Incubation Habitats and Aging States Affect the Formation of Biofilms on Microplastics. SSRN Electronic Journal, 0, , .	0.4	0
2141	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
2142	Duodenal microbiota makes an important impact in functional dyspepsia. Microbial Pathogenesis, 2022, 162, 105297.	1.3	5
2143	Hepatic stellate cell activation and senescence induced by intrahepatic microbiota disturbances drive progression of liver cirrhosis toward hepatocellular carcinoma. , 2022, 10, e003069.		32
2144	The Depth-Depended Fungal Diversity and Non-depth-Depended Aroma Profiles of Pit Mud for Strong-Flavor Baijiu. Frontiers in Microbiology, 2021, 12, 789845.	1.5	18
2145	Integrated microbiology and metabolomics analysis reveal responses of soil microorganisms and metabolic functions to phosphorus fertilizer on semiarid farm. Science of the Total Environment, 2022, 817, 152878.	3.9	40
2146	Analysis of gut microbiota in patients with epilepsy treated with valproate: Results from a three months observational prospective cohort study. Microbial Pathogenesis, 2022, 162, 105340.	1.3	7
2147	Au-quantum dot nanocluster electrochemiluminescence coupled with cycling-amplification for sensitive microRNA detection. Analytical Biochemistry, 2022, 639, 114530.	1.1	3
2148	Denitrifying halophilic archaea derived from salt dominate the degradation of nitrite in salted radish during pickling. Food Research International, 2022, 152, 110906.	2.9	14

# 2149	ARTICLE Deyeuxia angustifolia Kom. encroachment changes soil physicochemical properties and microbial community in the alpine tundra under climate change. Science of the Total Environment, 2022, 813, 152615.	IF 3.9	CITATIONS 5
2150	Evaluation of the anti-oomycete bioactivity of rhizosphere soil-borne isolates and the biocontrol of soybean root rot caused by Phytophthora sojae. Biological Control, 2022, 166, 104818.	1.4	12
2151	Integrated omics analysis: the relationship between significantly increased Klebsiella post-hepatectomy and decreased hub-metabolite 3-methyl-2-oxobutanoic acid is associated with induced liver failure. Journal of Gastrointestinal Oncology, 2022, 13, 326-343.	0.6	4
2152	Dietary yeast culture facilitates the growth, immune response, digestive enzyme activity, intestinal microbiota and disease resistance against <i>Vibrio harveyi</i> of hybrid grouper (<i>Epinephelus) Tj ETQq1 1 0.</i>	7 8749 14 rg	gB4 /Overlock
2153	Unlocking the Changes of Phyllosphere Fungal Communities of Fishscale Bamboo (Phyllachora) Tj ETQq0 0 0 rgB	T /Oyerloc	k 10 Tf 50 58
2154	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
2155	Host fruits shape the changes in the gut microbiota and development of Bactrocera dorsalis (Diptera:) Tj ETQq0 (0.0 rgBT /0)verlock 10 T
2156	Calebin-A prevents HFD-induced obesity in mice by promoting thermogenesis and modulating gut microbiota. Journal of Traditional and Complementary Medicine, 2023, 13, 119-127.	1.5	10
2157	The microbiome of wild and mass-reared new world screwworm, Cochliomyia hominivorax. Scientific Reports, 2022, 12, 1042.	1.6	2
2158	Diversity of soil fungi in the vineyards of Changli region in China. Canadian Journal of Microbiology, 2022, 68, 341-352.	0.8	5
2159	Spatio-Temporal Dynamics in Physico-Chemical Properties, Phytoplankton and Bacterial Diversity as an Indication of the Bovan Reservoir Water Quality. Water (Switzerland), 2022, 14, 391.	1.2	7
2160	Effects of biochar and Trichoderma on bacterial community diversity in continuous cropping soil. Horticulture Environment and Biotechnology, 2022, 63, 1-12.	0.7	3
2161	The changes of microbial diversity and flavor compounds during the fermentation of millet Huangjiu, a traditional Chinese beverage. PLoS ONE, 2022, 17, e0262353.	1.1	16
2162	Rhizosphere analysis of field-grown Panax ginseng with different degrees of red skin provides the basis for preventing red skin syndrome. BMC Microbiology, 2022, 22, 12.	1.3	6
2163	Potato tillage method is associated with soil microbial communities, soil chemical properties, and potato yield. Journal of Microbiology, 2022, 60, 156-166.	1.3	7
2164	Fresh Rumen Liquid Inoculant Enhances the Rumen Microbial Community Establishment in Pre-weaned Dairy Calves. Frontiers in Microbiology, 2021, 12, 758395.	1.5	8
2165	Gallic Acid Alleviates Gut Dysfunction and Boosts Immune and Antioxidant Activities in Puppies Under Environmental Stress Based on Microbiome–Metabolomics Analysis. Frontiers in Immunology, 2021, 12, 813890.	2.2	27
2166	Immobilization of hexavalent chromium in contaminated soil by nano-sized layered double hydroxide intercalated with diethyldithiocarbamate: Fraction distribution, plant growth, and microbial evolution. Journal of Hazardous Materials, 2022, 430, 128382.	6.5	15

#	Article	IF	CITATIONS
2167	Metagenomic Analysis of Bacterial Communities and Antibiotic Resistance Genes in Penaeus monodon Biofloc-Based Aquaculture Environments. Frontiers in Marine Science, 2022, 8, .	1.2	6
2168	Regulatory Effects of Combined Dietary Supplementation With Essential Oils and Organic Acids on Microbial Communities of Cobb Broilers. Frontiers in Microbiology, 2021, 12, 814626.	1.5	6
2169	Microorganisms in Superficial Deposits on the Stone Monuments in Saint Petersburg. Microorganisms, 2022, 10, 316.	1.6	14
2170	Accumulation of Nylon Microplastics and Polybrominated Diphenyl Ethers and Effects on Gut Microbial Community OfÂChironomus Sancticaroli. SSRN Electronic Journal, 0, , .	0.4	0
2171	Alpine meadow degradation depresses soil nitrogen fixation by regulating plant functional groups and diazotrophic community composition. Plant and Soil, 2022, 473, 319-335.	1.8	17
2172	Variation in Bacterial Community Structure in Rhizosphere and Bulk Soils of Different Halophytes in the Yellow River Delta. Frontiers in Ecology and Evolution, 2022, 9, .	1.1	13
2173	Effects of Herbal Tea Residue on Growth Performance, Meat Quality, Muscle Metabolome, and Rumen Microbiota Characteristics in Finishing Steers. Frontiers in Microbiology, 2021, 12, 821293.	1.5	10
2174	Gastrointestinal Tract and Dietary Fiber Driven Alterations of Gut Microbiota and Metabolites in Durco × Bamei Crossbred Pigs. Frontiers in Nutrition, 2021, 8, 806646.	1.6	12
2175	Integrated Analysis of the Cecal Microbiome and Plasma Metabolomics to Explore NaoMaiTong and Its Potential Role in Changing the Intestinal Flora and Their Metabolites in Ischemic Stroke. Frontiers in Pharmacology, 2021, 12, 773722.	1.6	13
2176	Symbiotic microbiome and metabolism profiles reveal the effects of induction by oysters on the metamorphosis of the carnivorous gastropod Rapana venosa. Computational and Structural Biotechnology Journal, 2022, 20, 1-14.	1.9	7
2177	Response of bacterial communities in saline-alkali soil to different pesticide stresses. Environmental Science and Pollution Research, 2022, 29, 42709-42719.	2.7	4
2179	Exploring of seasonal dynamics of microbial community in multispecies fermentation of Shanxi mature vinegar. Journal of Bioscience and Bioengineering, 2022, 133, 375-381.	1.1	15
2180	Fracture-Associated Microbiome and Persistent Nonunion: Next-Generation Sequencing Reveals New Findings. Journal of Orthopaedic Trauma, 2022, 36, S40-S46.	0.7	5
2181	Use of Napier grass and rice straw hay as exogenous additive improves microbial community and fermentation quality of paper mulberry silage. Animal Feed Science and Technology, 2022, 285, 115219.	1.1	15
2182	Evaluating the flavor and divergent bacterial communities in corn-based zha-chili. Food Bioscience, 2022, 46, 101563.	2.0	8
2183	Are microbes and metabolites influencing the parental consumption of nestlings' faeces in grey-backed shrikes?. Environmental Epigenetics, 0, , .	0.9	1
2184	Diversity of site-specific microbes of occlusal and proximal lesions in severe- early childhood caries (S-ECC). Journal of Oral Microbiology, 2022, 14, 2037832.	1.2	7
2185	Structure and putative function of a soil microbial community impacted by the deposition of tailings and subsequent revegetation after the rupture of the Fundao Dam. Land Degradation and Development, 2022, 33, 1235-1248.	1.8	2

#	Article	IF	CITATIONS
2186	Immunomodulation and skin microbiota perturbations during an episode of chronic stress in gilthead seabream. Fish and Shellfish Immunology, 2022, 122, 234-245.	1.6	5
2187	Cervicovaginal Microbiota Predicts Neisseria gonorrhoeae Clinical Presentation. Frontiers in Microbiology, 2021, 12, 790531.	1.5	4
2188	A sustainable and economic strategy to reduce risk antibiotic resistance genes during poultry manure bioconversion by black soldier fly Hermetia illucens larvae: Larval density adjustment. Ecotoxicology and Environmental Safety, 2022, 232, 113294.	2.9	9
2189	Inhibition of gut microbial β-glucuronidase effectively prevents carcinogen-induced microbial dysbiosis and intestinal tumorigenesis. Pharmacological Research, 2022, 177, 106115.	3.1	10
2190	Green manure incorporation accelerates enzyme activity, plant growth, and changes in the fungal community of soil. Archives of Microbiology, 2022, 204, 7.	1.0	17
2191	Metabarcoding versus mapping unassembled shotgun reads for identification of prey consumed by arthropod epigeal predators. GigaScience, 2022, 11, .	3.3	7
2192	Oral microbiome research – A Beginner's glossary. Journal of Oral and Maxillofacial Pathology, 2022, 26, 87.	0.3	1
2193	Microbial Biofilms Along a Geochemical Gradient at the Shallow-Water Hydrothermal System of Vulcano Island, Mediterranean Sea. Frontiers in Microbiology, 2022, 13, 840205.	1.5	6
2194	Microbial communities of ascocarps and soils in a natural habitat of Tuber indicum. Archives of Microbiology, 2022, 204, 189.	1.0	2
2195	Gut microbiota and plasma cytokine levels in patients with attention-deficit/hyperactivity disorder. Translational Psychiatry, 2022, 12, 76.	2.4	12
2196	The Phylosymbiosis Pattern Between the Fig Wasps of the Same Genus and Their Associated Microbiota. Frontiers in Microbiology, 2021, 12, 800190.	1.5	1
2197	Distinct gut microbiota profiles of Asian honey bee (Apis cerana) foragers. Archives of Microbiology, 2022, 204, 187.	1.0	2
2198	Single-cell gene fusion detection by scFusion. Nature Communications, 2022, 13, 1084.	5.8	8
2199	Modulation of Gut Microbiota Combined with Upregulation of Intestinal Tight Junction Explains Anti-Inflammatory Effect of Corylin on Colitis-Associated Cancer in Mice. International Journal of Molecular Sciences, 2022, 23, 2667.	1.8	28
2200	Comparing PCR-generated artifacts of different polymerases for improved accuracy of DNA metabarcoding. Metabarcoding and Metagenomics, 0, 6, .	0.0	7
2201	A Parallel Tracking of Salivary and Gut Microbiota Profiles Can Reveal Maturation and Interplay of Early Life Microbial Communities in Healthy Infants. Microorganisms, 2022, 10, 468.	1.6	4
2202	Effect of Different Dietary Regimes on the Gut Microbiota and Fecal Metabolites of Père David's Deer. Animals, 2022, 12, 584.	1.0	6
2203	lsolation of rhizosheath and analysis of microbial community structure around roots of Stipa grandis. Scientific Reports, 2022, 12, 2707.	1.6	1

#	Article	IF	CITATIONS
2204	Transcriptome and Gut Microbiota Profiling Revealed the Protective Effect of Tibetan Tea on Ulcerative Colitis in Mice. Frontiers in Microbiology, 2021, 12, 748594.	1.5	10
2205	Correlation Analysis of Vaginal Microbiome Changes and Bacterial Vaginosis Plus Vulvovaginal Candidiasis Mixed Vaginitis Prognosis. Frontiers in Cellular and Infection Microbiology, 2022, 12, 860589.	1.8	8
2206	Fermented Wheat Bran Polysaccharides Intervention Alters Rumen Bacterial Community and Promotes Rumen Development and Growth Performance in Lambs. Frontiers in Veterinary Science, 2022, 9, 841406.	0.9	2
2207	A Comprehensive Network Integrating Signature Microbes and Crucial Soil Properties During Early Biological Soil Crust Formation on Tropical Reef Islands. Frontiers in Microbiology, 2022, 13, 831710.	1.5	3
2208	Plants with arbuscular mycorrhizal fungi efficiently acquire Nitrogen from substrate additions by shaping the decomposer community composition and their net plant carbon demand. Plant and Soil, 2022, 475, 473-490.	1.8	15
2209	Mycorrhizosphere Bacteria, Rahnella sp. HPDA25, Promotes the Growth of Armillaria gallica and Its Parasitic Host Gastrodia elata. Frontiers in Microbiology, 2022, 13, 842893.	1.5	7
2210	Contribution of Ruminal Bacteriome to the Individual Variation of Nitrogen Utilization Efficiency of Dairy Cows. Frontiers in Microbiology, 2022, 13, 815225.	1.5	5
2211	Comparative study of gut microbiota from decomposer fauna in household composter using metataxonomic approach. Archives of Microbiology, 2022, 204, 210.	1.0	6
2212	Observation of the Gut Microbiota Profile in BALB/c Mice Induced by Plasmodium yoelii 17XL Infection. Frontiers in Microbiology, 2022, 13, 858897.	1.5	6
2213	Characterization of the First Cultured Representative of " <i>Candidatus</i> Thermofonsia―Clade 2 within <i>Chloroflexi</i> Reveals Its Phototrophic Lifestyle. MBio, 2022, 13, e0028722.	1.8	8
2214	Effects of Growth Stage and Rearing Pattern on Pig Gut Microbiota. Current Microbiology, 2022, 79, 136.	1.0	8
2215	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
2216	Comparison of Cecal Microbiota and Performance Indices Between Lean-Type and Fatty-Type Pekin Ducks. Frontiers in Microbiology, 2022, 13, 820569.	1.5	6
2217	Deep sequencing reveals changes in prokaryotic taxonomy and functional diversity of pit muds in different distilleries of China. Annals of Microbiology, 2022, 72, .	1.1	5
2218	Effect of 6-Methoxybenzoxazolinone on the Cecal Microbiota of Adult Male Brandt's Vole. Frontiers in Microbiology, 2022, 13, 847073.	1.5	3
2219	Positive Effects of Neutrophil Elastase Inhibitor (Sivelestat) on Gut Microbiome and Metabolite Profiles of Septic Rats. Frontiers in Cellular and Infection Microbiology, 2022, 12, 818391.	1.8	5
2220	Insights into microbial diversity on plastisphere by multi-omics. Archives of Microbiology, 2022, 204, 216.	1.0	5
2222	Importance of substrate quality and clay content on microbial extracellular polymeric substances production and aggregate stability in soils. Biology and Fertility of Soils, 2022, 58, 435-457.	2.3	24

#	Article	IF	CITATIONS
2223	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
2224	Bioremediation of decabromodiphenyl ether or benzo(a)pyrene-contaminated rice-paddy soil. Journal of Soils and Sediments, 2022, 22, 1397-1417.	1.5	3
2225	Coupled magnetic nanoparticleâ€mediated isolation and singleâ€cell image recognition to detect <i>Bacillus</i> ' body size in soil. European Journal of Soil Science, 0, , .	1.8	1
2226	The microbial succession and their correlation with the dynamics of flavor compounds involved in the natural fermentation of suansun, a traditional Chinese fermented bamboo shoots. Food Research International, 2022, 157, 111216.	2.9	23
2227	Effects of Temperature and Nitrogen Application on Carbon and Nitrogen Accumulation and Bacterial Community Composition in Apple Rhizosphere Soil. Frontiers in Plant Science, 2022, 13, 859395.	1.7	9
2228	The combination of four main components in Xuebijing injection improved the preventive effects of Cyclosporin A in acute graft-versus-host disease mice by protecting intestinal microenvironment. Biomedicine and Pharmacotherapy, 2022, 148, 112675.	2.5	6
2229	16S rRNA gene sequencing analysis reveals an imbalance in the intestinal flora of Eriocheir sinensis with hepatopancreatic necrosis disease. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 42, 100988.	0.4	3
2230	Accumulation of nylon microplastics and polybrominated diphenyl ethers and effects on gut microbial community of Chironomus sancticaroli. Science of the Total Environment, 2022, 832, 155089.	3.9	17
2231	Gut Microbiome Analyses of Wild Migratory Freshwater Fish (Megalobrama terminalis) Through Geographic Isolation. Frontiers in Microbiology, 2022, 13, 858454.	1.5	6
2232	Biogeochemistry of three different shallow gas systems in continental shelf sediments of the South-Eastern Baltic Sea (Gulf of Gdańsk): Carbon cycling, origin of methane and microbial community composition. Chemical Geology, 2022, 597, 120799.	1.4	5
2233	Factors controlling soil organic carbon content in wetlands at multiple scales and assessment of the universality of estimation equations: A mega-data study. Science of the Total Environment, 2022, 827, 154380.	3.9	6
2234	Combined toxic effects of thiamethoxam on intestinal flora, transcriptome and physiology of Pacific white shrimp Litopenaeus vannamei. Science of the Total Environment, 2022, 830, 154799.	3.9	20
2235	Incubation habitats and aging treatments affect the formation of biofilms on polypropylene microplastics. Science of the Total Environment, 2022, 831, 154769.	3.9	22
2236	Effects of Tartary buckwheat on physicochemical properties and microbial community of low salt natural fermented soybean paste. Food Control, 2022, 138, 108953.	2.8	9
2237	MicroSEC filters sequence errors for formalin-fixed and paraffin-embedded samples. Communications Biology, 2021, 4, 1396.	2.0	2
2239	The Effects of Different Carbon Sources on the Production Environment and Breeding Parameters of Litopenaeus vannamei. Water (Switzerland), 2021, 13, 3584.	1.2	4
2240	Impact of ocean acidification on physiology and microbiota in hepatopancreas of Pacific oyster Crassostrea gigas. Journal of Oceanology and Limnology, 2022, 40, 620-633.	0.6	4
2241	Characteristics of the Cervicovaginal Microenvironment in Childbearing-Age Women with Different Degrees of Cervical Lesions and HR-HPV Positivity. Polish Journal of Microbiology, 2021, 70, 489-500.	0.6	5

#	Article	IF	CITATIONS
2242	The Archaeal Transcription Termination Factor aCPSF1 is a Robust Phylogenetic Marker for Archaeal Taxonomy. Microbiology Spectrum, 2021, 9, e0153921.	1.2	5
2243	Dual UMIs and Dual Barcodes With Minimal PCR Amplification Removes Artifacts and Acquires Accurate Antibody Repertoire. Frontiers in Immunology, 2021, 12, 778298.	2.2	2
2244	Lactoferrin modulates gut microbiota and Toll-like receptors (TLRs) in mice with dysbiosis induced by antibiotics. Food and Function, 2022, 13, 5854-5869.	2.1	14
2245	Temporal and Spatial Patterns of Sediment Microbial Communities and Driving Environment Variables in a Shallow Temperate Mountain River. Microorganisms, 2022, 10, 816.	1.6	8
2246	Community Assembly and Stability in the Root Microbiota During Early Plant Development. Frontiers in Microbiology, 2022, 13, 826521.	1.5	7
2247	Fungal Inhibition of Agricultural Soil Pathogen Stimulated by Nitrogen-Reducing Fertilization. Frontiers in Bioengineering and Biotechnology, 2022, 10, 866419.	2.0	4
2248	The responses of soil bacterial and archaeal communities to coastal embankments in three typical salt marshes of Eastern China. Plant and Soil, 0, , .	1.8	1
2249	Analysis of Gut Microbiota and Metabolites in Diannan Small Ear Sows at Diestrus and Metestrus. Frontiers in Microbiology, 2022, 13, 826881.	1.5	3
2250	Ecological impacts of sea-crossing bridge construction on local sediment microbiome in East China. Regional Studies in Marine Science, 2022, , 102363.	0.4	1
2251	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
2252	Cultivation and Functional Characterization of a Deep-Sea Lentisphaerae Representative Reveals Its Unique Physiology and Ecology. Frontiers in Marine Science, 2022, 9, .	1.2	1
2253	A dual treatment blocks alcohol binge-drinking relapse: Microbiota as a new player. Drug and Alcohol Dependence, 2022, 236, 109466.	1.6	7
2493	A cross-sectional analysis about bacterial vaginosis, high-risk human papillomavirus infection, and cervical intraepithelial neoplasia in Chinese women. Scientific Reports, 2022, 12, 6609.	1.6	10
2494	Bacterial DNA Detection in the Blood of Healthy Subjects Iranian Biomedical Journal, 2022, , .	0.4	0
2495	Konjac oligosaccharides attenuate DSS-induced ulcerative colitis in mice: mechanistic insights. Food and Function, 2022, 13, 5626-5639.	2.1	13
2496	Bacterial communities in soils as indicators of the potential of syenite as an agromineral. Pesquisa Agropecuaria Brasileira, 0, 57, .	0.9	1
2497	Composition and Diversity of Soil Microbial Community Associated With Land Use Types in the Agro–Pastoral Area in the Upper Yellow River Basin. Frontiers in Plant Science, 2022, 13, 819661.	1.7	6
2498	Gradual Enhancement of the Assemblage Stability of the Reed Rhizosphere Microbiome with Recovery Time. Microorganisms, 2022, 10, 937.	1.6	4

#	Article	IF	CITATIONS
2499	Suppressive Effect of Soil Microbiomes Associated with Tropical Fruit Trees on Meloidogyne enterolobii. Microorganisms, 2022, 10, 894.	1.6	2
2500	Gallnut Tannic Acid Exerts Anti-stress Effects on Stress-Induced Inflammatory Response, Dysbiotic Gut Microbiota, and Alterations of Serum Metabolic Profile in Beagle Dogs. Frontiers in Nutrition, 2022, 9, 847966.	1.6	8
2501	Factors driving the assembly of prokaryotic communities in bulk soil and rhizosphere of Torreya grandis along a 900-year age gradient. Science of the Total Environment, 2022, 837, 155573.	3.9	7
2502	Analysis of Phyllosphere Microorganisms and Potential Pathogens of Tobacco Leaves. Frontiers in Microbiology, 2022, 13, 843389.	1.5	7
2503	Xylitol-Containing Chewing Gum Reduces Cariogenic and Periodontopathic Bacteria in Dental Plaque—Microbiome Investigation. Frontiers in Nutrition, 2022, 9, .	1.6	4
2504	Supplementation with galacto-oligosaccharides in early life persistently facilitates the microbial colonization of the rumen and promotes growth of preweaning Holstein dairy calves. Animal Nutrition, 2022, 10, 223-233.	2.1	9
2505	Bacteria Community Inhabiting Heterobasidion Fruiting Body and Associated Wood of Different Decay Classes. Frontiers in Microbiology, 2022, 13, 864619.	1.5	2
2506	The Application of Mixed Organic and Inorganic Fertilizers Drives Soil Nutrient and Bacterial Community Changes in Teak Plantations. Microorganisms, 2022, 10, 958.	1.6	8
2507	Significant Differences in Gut Microbiota Between Irritable Bowel Syndrome with DiarrheaÂand Healthy ControlsÂin Southwest China. Digestive Diseases and Sciences, 2023, 68, 106-127.	1.1	5
2508	Composition and Potential Functions of Bacterial Communities Associated With Aurelia Polyps. Frontiers in Marine Science, 2022, 9, .	1.2	1
2509	Microbial and Nonvolatile Chemical Diversities of Chinese Dark Teas Are Differed by Latitude and Pile Fermentation. Journal of Agricultural and Food Chemistry, 2022, 70, 5701-5714.	2.4	11
2510	Land-Use Driven Changes in Soil Microbial Community Composition and Soil Fertility in the Dry-Hot Valley Region of Southwestern China. Microorganisms, 2022, 10, 956.	1.6	3
2511	Effects of microbial community structure and its co-occurrence on the dynamic changes of physicochemical properties and free amino acids in the Cantonese soy sauce fermentation process. Food Research International, 2022, 156, 111347.	2.9	16
2512	Paenibacillus sp. Strain OL15 Immobilized in Agar as a Potential Bioremediator for Waste Lubricating Oil-Contaminated Soils and Insights into Soil Bacterial Communities Affected by Inoculations of the Strain and Environmental Factors. Biology, 2022, 11, 727.	1.3	5
2513	Transformation of sulfidized nanoscale zero-valent iron particles and its effects on microbial communities in soil ecosystems. Environmental Pollution, 2022, 306, 119363.	3.7	12
2514	Correlations between dominant vegetation type and composition and diversity of soil bacterial communities in a subtropical forest. Soil Science Society of America Journal, 0, , .	1.2	2
2515	Synergy of Dietary Quercetin and Vitamin E Improves Cecal Microbiota and Its Metabolite Profile in Aged Breeder Hens. Frontiers in Microbiology, 2022, 13, .	1.5	1
2516	Distribution of Vaginal and Gut Microbiome in Advanced Maternal Age. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	1.8	3

#	Article	IF	CITATIONS
2517	Comparison of the performance of raw and Lactobacillus paracasei fermented soybean meal in diets for turbot (Scophthalmus maximus L.): Growth, intestinal morphology, apoptosis, tight junction, and microbiota. Aquaculture Reports, 2022, 24, 101184.	0.7	2
2518	Deep Metagenomic Sequencing for Endophthalmitis Pathogen Detection Using a Nanopore Platform. American Journal of Ophthalmology, 2022, 242, 243-251.	1.7	10
2519	The Bacterial Composition and Diversity in a Eucalyptus pellita Plantation in South Sumatra, Indonesia. Diversity, 2022, 14, 442.	0.7	0
2520	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
2521	Rhizosphere Soil Microbial Community Under Ice in a High-Latitude Wetland: Different Community Assembly Processes Shape Patterns of Rare and Abundant Microbes. Frontiers in Microbiology, 2022, 13, .	1.5	3
2522	Metagenomic Analysis Using Phylogenetic Placement—A Review of the First Decade. Frontiers in Bioinformatics, 2022, 2, .	1.0	17
2523	The relationships between health risk and special weather conditions according to fungal community characteristics. Aerobiologia, 0, , .	0.7	0
2524	High-throughput sequencing reveals rhizosphere fungal community composition and diversity at different growth stages of <i>Populus euphratica</i> in the lower reaches of the Tarim River. PeerJ, 0, 10, e13552.	0.9	2
2525	Probioticâ€fermented <i>Pueraria lobata</i> (Willd.) Ohwi alleviates alcoholic liver injury by enhancing antioxidant defense and modulating gut microbiota. Journal of the Science of Food and Agriculture, 2022, 102, 6877-6888.	1.7	11
2526	Polysaccharides from fermented wheat bran enhanced the growth performance of zebrafish (Danio) Tj ETQq1 1 (101188.).784314 i 0.7	rgBT /Overloc 5
2530	Bacterial DNA Detection in the Blood of Healthy Subjects. Iranian Biomedical Journal, 2022, 26, 230-239.	0.4	4
2531	A diversity profile of total bacteria (culturable and unculturable) as aquaculture marine water source of in central marine bio industry (BBIL) Mataram, Indonesia. IOP Conference Series: Earth and Environmental Science, 2022, 1033, 012005.	0.2	0
2532	Micrococcus luteus strain CGK112 isolated from cow dung demonstrated efficient biofilm-forming ability and degradation potential toward high-density polyethylene (HDPE). Archives of Microbiology, 2022, 204, .	1.0	11
2533	Evaluating Starter Feeding on Ruminal Function in Yak Calves: Combined 16S rRNA Sequencing and Metabolomics. Frontiers in Microbiology, 0, 13, .	1.5	5
2534	New compound probiotic beverage protects against antibiotic-associated diarrhea in mice by modulating the microbiota. Future Microbiology, 0, , .	1.0	2
2535	Effects of Fermented Herbal Tea Residue on Serum Indices and Fecal Microorganisms of Chuanzhong Black Goats. Microorganisms, 2022, 10, 1228.	1.6	2
2536	Influence of different irrigation methods on the alfalfa rhizosphere soil fungal communities in an arid region. PLoS ONE, 2022, 17, e0268175.	1.1	2
2537	Using PacBio SMRT Sequencing Technology and Metabolomics to Explore the Microbiota-Metabolome Interaction Related to Silage Fermentation of Woody Plant. Frontiers in Microbiology, 0, 13, .	1.5	4

#	Article	IF	CITATIONS
2538	Metagenomic profiles of the early life microbiome of Indonesian inpatient neonates and their influence on clinical characteristics. Scientific Reports, 2022, 12, .	1.6	3
2539	Symbiotic Algae of Hydra viridissima Play a Key Role in Maintaining Homeostatic Bacterial Colonization. Frontiers in Microbiology, 0, 13, .	1.5	5
2540	The Role of the Gut Microbiota in the Effects of Early-Life Stress and Dietary Fatty Acids on Later-Life Central and Metabolic Outcomes in Mice. MSystems, 2022, 7, .	1.7	4
2541	Patients with Infections of The Central Nervous System Have Lowered Gut Microbiota Alpha Diversity. Current Issues in Molecular Biology, 2022, 44, 2903-2914.	1.0	4
2542	The pig gut microbiota analysis techniques, a comparison. Archiva Zootehnica, 2022, 25, 90-115.	0.3	0
2543	Reno-Protective Effect of Low Protein Diet Supplemented With α-Ketoacid Through Gut Microbiota and Fecal Metabolism in 5/6 Nephrectomized Mice. Frontiers in Nutrition, 0, 9, .	1.6	5
2544	Bacterial community structure and diversity in the rhizospheric soil of Robinia pseudoacacia and Juniperus sabina planted in iron tailings matrix. Environmental Science and Pollution Research, 2022, 29, 83404-83416.	2.7	4
2545	Community composition, bacterial symbionts, antibacterial and antioxidant activities of honeybee-associated fungi. BMC Microbiology, 2022, 22, .	1.3	9
2546	Recombinant Muscovy Duck Parvovirus Led to Ileac Damage in Muscovy Ducklings. Viruses, 2022, 14, 1471.	1.5	1
2547	Comparison of the co-occurrence patterns of the gut microbial community between Bt-susceptible and Bt-resistant strains of the rice stem borer, Chilo suppressalis. Journal of Pest Science, 2023, 96, 299-315.	1.9	6
2548	Analysis of Microbiota Persistence in Quebec's Terroir Cheese Using a Metabarcoding Approach. Microorganisms, 2022, 10, 1381.	1.6	3
2549	A Mycorrhizal Bacteria Strain Isolated From Polyporus umbellatus Exhibits Broad-Spectrum Antifungal Activity. Frontiers in Plant Science, 0, 13, .	1.7	3
2550	Regulation of wheat bran feruloyl oligosaccharides in the intestinal antioxidative capacity of rats associated with the p38/ <scp>JNKâ€Nrf2</scp> signaling pathway and gut microbiota. Journal of the Science of Food and Agriculture, 2022, 102, 6992-7002.	1.7	5
2551	Characteristics of Gut Microbiota in Patients With Clear Cell Renal Cell Carcinoma. Frontiers in Microbiology, 0, 13, .	1.5	9
2552	Nisin and Nisin Probiotic Disrupt Oral Pathogenic Biofilms and Restore Their Microbiome Composition towards Healthy Control Levels in a Peri-Implantitis Setting. Microorganisms, 2022, 10, 1336.	1.6	9
2553	Effect of Doxycycline Use in the Early Broiler Production Cycle on the Microbiome. Frontiers in Microbiology, 0, 13, .	1.5	2
2554	Flavonoid-attracted <i>Aeromonas</i> sp. from the Arabidopsis root microbiome enhances plant dehydration resistance. ISME Journal, 2022, 16, 2622-2632.	4.4	44
2555	16S rRNA gene sequencing analysis on changes in the intestinal flora of Procambarus clarkii with "Black May―disease. Journal of Oceanology and Limnology, 0, , .	0.6	0

#	Article	IF	CITATIONS
2556	Acetic acid alters rhizosphere microbes and metabolic composition to improve willows drought resistance. Science of the Total Environment, 2022, 844, 157132.	3.9	15
2557	The effect of environment on intestinal microbial diversity of Panthera animals may exceed genetic relationship. Frontiers in Microbiology, 0, 13, .	1.5	3
2558	Effects of growing <i>Coptis chinensis</i> Franch in the natural understory <i>vs</i> . under a manmade scaffold on its growth, alkaloid contents, and rhizosphere soil microenvironment. PeerJ, O, 10, e13676.	0.9	2
2559	The impact of symbiotic population crash (or reduction) on microbiome structure and composition. International Journal of Pest Management, 0, , 1-12.	0.9	0
2560	Amplicon Sequencing Reveals Novel Fungal Species Responsible for a Controversial Tea Disease. Journal of Fungi (Basel, Switzerland), 2022, 8, 782.	1.5	4
2561	Jiedu-Yizhi Formula Alleviates Neuroinflammation in AD Rats by Modulating the Gut Microbiota. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-19.	0.5	5
2562	Dysfunction of histone demethylase IBM1 in <i>Arabidopsis</i> causes autoimmunity and reshapes the root microbiome. ISME Journal, 2022, 16, 2513-2524.	4.4	12
2563	Chemical fertilizer reduction combined with bio-organic fertilizers increases cauliflower yield via regulation of soil biochemical properties and bacterial communities in Northwest China. Frontiers in Microbiology, 0, 13, .	1.5	12
2564	Regulation of Dietary Protein Solubility Improves Ruminal Nitrogen Metabolism In Vitro: Role of Bacteria–Protozoa Interactions. Nutrients, 2022, 14, 2972.	1.7	6
2565	Environmental filtering drives the establishment of the distinctive rhizosphere, bulk, and root nodule bacterial communities of Sophora davidii in hilly and gully regions of the Loess Plateau of China. Frontiers in Microbiology, 0, 13, .	1.5	6
2566	Natural Environmental Variation Determines Microbial Diversity Patterns in Serofluid Dish, a Traditional Chinese Fermented Vegetable Food. Current Microbiology, 2022, 79, .	1.0	1
2567	Abdominal massage alleviates functional diarrhea in immature rats via modulation of intestinal microbiota and tight junction protein. Frontiers in Pediatrics, 0, 10, .	0.9	1
2569	Rhizosphere Microbial Communities and Geochemical Constraining Mechanism of Antimony Mine Waste-Adapted Plants in Southwestern China. Microorganisms, 2022, 10, 1507.	1.6	4
2570	Insight into bacterial community profiles of oil shale and sandstone in ordos basin by culture-dependent and culture-independent methods. Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering, 2022, 57, 723-735.	0.9	2
2571	Gastrointestinal Biogeography of Luminal Microbiota and Short-Chain Fatty Acids in Sika Deer (Cervus) Tj ETQqO	0.0 _{1.4} gBT /0	Dyerlock 10
2572	Differential richness inference for 16S rRNA marker gene surveys. Genome Biology, 2022, 23, .	3.8	5
2573	Overexpression of the rice gene Lsi1 (low silicon gene 1) enhances plant-microbe interactions that result in improved chilling tolerance. Plant Growth Regulation, 2022, 98, 525-538.	1.8	2
2574	Diversity of fungal assemblages in rhizosphere and endosphere of blueberry (<i>Vaccinium</i> spp.) under field conditions revealed by culturing and culture-independent molecular methods. Canadian Journal of Microbiology, 2022, 68, 622-632.	0.8	1

#	Article	IF	CITATIONS
2575	Microbial Diversity and Community Composition of Duodenum Microbiota of High and Low Egg-Yielding Taihang Chickens Identified Using 16S rRNA Amplicon Sequencing. Life, 2022, 12, 1262.	1.1	1
2576	Bacterial Community with Plant Growth-Promoting Potential Associated to Pioneer Plants from an Active Mexican Volcanic Complex. Microorganisms, 2022, 10, 1568.	1.6	6
2577	Gut microbiomes of cyprinid fish exhibit host-species symbiosis along gut trait and diet. Frontiers in Microbiology, 0, 13, .	1.5	3
2578	Estimation of the post-mortem interval by modelling the changes in oral bacterial diversity during decomposition. Journal of Applied Microbiology, 2022, 133, 3451-3464.	1.4	10
2579	Relationship between rumen microbial differences and traits among Hu sheep, Tan sheep, and Dorper sheep. Journal of Animal Science, 2022, 100, .	0.2	11
2580	Effects of scale worm parasitism on interactions between the symbiotic gill microbiome and gene regulation in deep sea mussel hosts. Frontiers in Microbiology, 0, 13, .	1.5	0
2581	Characterization of microbial communities in anaerobic acidification reactors fed with casein and/or lactose. Applied Microbiology and Biotechnology, 2022, 106, 6301-6316.	1.7	3
2582	Enrichment of bacteria involved in the nitrogen cycle and plant growth promotion in soil by sclerotia of rice sheath blight fungus. Stress Biology, 2022, 2, .	1.5	4
2583	In vitro and in vivo Studies of Soybean Peptides on Milk Production, Rumen Fermentation, Ruminal Bacterial Community, and Blood Parameters in Lactating Dairy Cows. Frontiers in Veterinary Science, 0, 9, .	0.9	0
2584	Characteristics of oral microbiota in plateau and plain youthâ€positive correlations between blood lipid level, metabolism and specific microflora in the plateau group. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	1
2585	An Investigation of the Effect of Water Additives on Broiler Growth and the Caecal Microbiota at Harvest. Pathogens, 2022, 11, 932.	1.2	1
2586	SCNIC: Sparse correlation network investigation for compositional data. Molecular Ecology Resources, 2023, 23, 312-325.	2.2	13
2587	Flavonoid extract of saffron byâ€product alleviates hyperuricemia via inhibiting xanthine oxidase and modulating gut microbiota. Phytotherapy Research, 2022, 36, 4604-4619.	2.8	4
2588	The Role of 4-Phenylbutyric Acid in Gut Microbial Dysbiosis in a Mouse Model of Simulated Microgravity. Life, 2022, 12, 1301.	1.1	6
2589	Deficiency of migration inhibitory factor influences the gut microbiota of C57BL/6 mice infected with Plasmodium berghei ANKA. Frontiers in Microbiology, 0, 13, .	1.5	2
2590	Effects of dietary vitamin C on growth, antioxidant enzyme activity and immuneâ€related gene expression of <i>Pampus argenteus</i> . Aquaculture Research, 0, , .	0.9	4
2591	Dynamic evolution of flavor substances and bacterial communities during fermentation of leaf mustard (Brassica juncea var. multiceps) and their correlation. LWT - Food Science and Technology, 2022, 167, 113796.	2.5	10
2592	Debaryomyces nepalensis reduces fungal decay by affecting the postharvest microbiome during jujube storage. International Journal of Food Microbiology, 2022, 379, 109866.	2.1	5

#	Article	IF	CITATIONS
2594	Uncovering the Fecal Bacterial Communities of Sympatric Sika Deer (Cervus nippon) and Wapiti (Cervus canadensis). Animals, 2022, 12, 2468.	1.0	1
2595	Effects of long-term application of organic manure and chemical fertilizer on soil properties and microbial communities in the agro-pastoral ecotone of North China. Frontiers in Environmental Science, 0, 10, .	1.5	5
2596	Enrichment of Methylosinus-dominant consortia from mangroves for polyhydroxybutyrate (PHB) production. Journal of Environmental Chemical Engineering, 2022, 10, 108490.	3.3	5
2597	Microbiome Changes during Regenerative Endodontic Treatment Using Different Methods of Disinfection. Journal of Endodontics, 2022, 48, 1273-1284.	1.4	16
2598	Long-Term Effective Remediation of Black-Odorous Water Via Calcium Nitrate Sustained-Release. SSRN Electronic Journal, 0, , .	0.4	0
2599	Toward global integration of biodiversity big data: a harmonized metabarcode data generation module for terrestrial arthropods. GigaScience, 2022, 11, .	3.3	12
2600	Addition of Organic Acids and Lactobacillus acidophilus to the Leguminous Forage Chamaecrista rotundifolia Improved the Quality and Decreased Harmful Bacteria of the Silage. Animals, 2022, 12, 2260.	1.0	6
2601	Effects of single- and mixed-bacterial inoculation on the colonization and assembly of endophytic communities in plant roots. Frontiers in Plant Science, 0, 13, .	1.7	3
2602	Root exudates and rhizosphere soil bacterial relationships of Nitraria tangutorum are linked to k-strategists bacterial community under salt stress. Frontiers in Plant Science, 0, 13, .	1.7	12
2603	Mechanism of hydrogen protection on high intensity sports injury in rats through antioxidation and its improvement of intestinal flora function. Science and Sports, 2023, 38, 161-173.	0.2	1
2604	The effects of fermented pineapple residue on growth performance, meat quality, and rumen microbiota of fattening Simmental bull. Frontiers in Microbiology, 0, 13, .	1.5	0
2605	Strongyloides stercoralis infection induces gut dysbiosis in chronic kidney disease patients. PLoS Neglected Tropical Diseases, 2022, 16, e0010302.	1.3	5
2606	Pyrolyzed or Composted Sewage Sludge Application Induces Short-Term Changes in the Terra Rossa Soil Bacterial and Fungal Communities. Sustainability, 2022, 14, 11382.	1.6	1
2607	Diversity, antibacterial activity and chemical analyses of gut-associated fungi isolated from the Crocothemis servilia. Frontiers in Microbiology, 0, 13, .	1.5	1
2608	The impact of pelvic floor electrical stimulation on vaginal microbiota and immunity. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	2
2609	Deoxycholic acid induces gastric intestinal metaplasia by activating STAT3 signaling and disturbing gastric bile acids metabolism and microbiota. Gut Microbes, 2022, 14, .	4.3	20
2610	Microbial Community Succession Associated with Poplar Wood Discoloration. Plants, 2022, 11, 2420.	1.6	3
2611	Short- and Long-Term Effects of a Prebiotic Intervention with Polyphenols Extracted from European Black Elderberry—Sustained Expansion of Akkermansia spp Journal of Personalized Medicine, 2022, 12, 1479.	1.1	7

#	Article	IF	CITATIONS
2612	A physicochemical double-cross-linked gelatin hydrogel with enhanced antibacterial and anti-inflammatory capabilities for improving wound healing. Journal of Nanobiotechnology, 2022, 20, .	4.2	22
2613	Determining why continuous cropping reduces the production of the morel Morchella sextelata. Frontiers in Microbiology, 0, 13, .	1.5	9
2614	Metabarcoding and Metabolome Analyses Reveal Mechanisms of Leymus chinensis Growth Promotion by Fairy Ring of Leucocalocybe mongolica. Journal of Fungi (Basel, Switzerland), 2022, 8, 944.	1.5	6
2615	Sterile Setup TableÂin the Operating Room Is Not So Sterile. Journal of Arthroplasty, 2023, 38, 562-566.e3.	1.5	3
2616	Metagenomic Analysis of Microbial Alliances for Efficient Degradation of PHE: Microbial Community Structure and Reconstruction of Metabolic Network. International Journal of Environmental Research and Public Health, 2022, 19, 12039.	1.2	4
2617	Oral and fecal microbiome of confiscated Bengal slow lorises in response to confinement duration. Frontiers in Microbiology, 0, 13, .	1.5	Ο
2618	Comparative Analysis of In Situ Eukaryotic Food Sources in Three Tropical Sea Cucumber Species by Metabarcoding. Animals, 2022, 12, 2303.	1.0	2
2619	Modulating effect of Xuanfei Baidu granule on host metabolism and gut microbiome in rats. Frontiers in Pharmacology, 0, 13, .	1.6	3
2620	Breast microbiome associations with breast tumor characteristics and neoadjuvant chemotherapy: A case-control study. Frontiers in Oncology, 0, 12, .	1.3	2
2621	Diversity of bacterial community in Jerusalem artichoke (Helianthus tuberosus L.) during storage is associated with the genotype and carbohydrates. Frontiers in Microbiology, 0, 13, .	1.5	3
2622	The diversity analysis and gene function prediction of intestinal bacteria in three equine species. Frontiers in Microbiology, 0, 13, .	1.5	0
2623	Supplementing the early diet of broilers with soy protein concentrate can improve intestinal development and enhance short-chain fatty acid-producing microbes and short-chain fatty acids, especially butyric acid. Journal of Animal Science and Biotechnology, 2022, 13, .	2.1	24
2624	Geochemistry and microbiology of tropical serpentine soils in the Santa Elena Ophiolite, a landscape-biogeographical approach. Geochemical Transactions, 2022, 23, .	1.8	0
2625	The Study of Soil Bacterial Diversity and the Influence of Soil Physicochemical Factors in Meltwater Region of Ny-Ãlesund, Arctic. Microorganisms, 2022, 10, 1913.	1.6	3
2626	Simulated seasonal diets alter yak rumen microbiota structure and metabolic function. Frontiers in Microbiology, 0, 13, .	1.5	4
2627	Dietary supplementation with Cyberlindnera jadinii improved growth performance, serum biochemical Indices, antioxidant status, and intestinal health in growing raccoon dogs (Nyctereutes) Tj ETQq1 1 0.784314 rg	3T1/©verlo	ck410 Tf 50 1
2628	Effect of Probiotic Lactobacillus plantarum Dad-13 on Metabolic Profiles and Gut Microbiota in Type 2 Diabetic Women: A Randomized Double-Blind Controlled Trial. Microorganisms, 2022, 10, 1806.	1.6	4
2629	Features of the oral microbiome in Japanese elderly people with 20 or more teeth and a non-severe periodontal condition during periodontal maintenance treatment: A cross-sectional study. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	1

#	Article	IF	CITATIONS
2630	Effective data filtering is prerequisite for robust microbial association network construction. Frontiers in Microbiology, 0, 13, .	1.5	1
2631	Altered gut microbiome diversity and function in patients with propionic acidemia. Molecular Genetics and Metabolism, 2022, 137, 308-322.	0.5	2
2632	The rhizosphere microbiome improves the adaptive capabilities of plants under high soil cadmium conditions. Frontiers in Plant Science, 0, 13, .	1.7	5
2633	Sustainable management of the potato cyst nematode, Globodera rostochiensis, with two microbial fermentation products. Frontiers in Plant Science, 0, 13, .	1.7	2
2634	Response of soil microbial communities to natural radionuclides along specific-activity gradients. Ecotoxicology and Environmental Safety, 2022, 246, 114156.	2.9	6
2635	Effects of Insect-Resistant Maize HGK60 on Community Diversity of Bacteria and Fungi in Rhizosphere Soil. Plants, 2022, 11, 2824.	1.6	2
2636	Nitrogen addition alters plant growth in China's Yellow River Delta coastal wetland through direct and indirect effects. Frontiers in Plant Science, 0, 13, .	1.7	1
2637	Effects of autochthonous strains mixture on gut microbiota and metabolic profile in cobia (Rachycentron canadum). Scientific Reports, 2022, 12, .	1.6	11
2638	Incubation determines favorable microbial communities in Chinese alligator nests. Frontiers in Microbiology, 0, 13, .	1.5	1
2639	A comparison of microbial composition under three tree ecosystems using the stochastic process and network complexity approaches. Frontiers in Microbiology, 0, 13, .	1.5	13
2640	Evolution of the PiauÃ-Laterite, Brazil: Mineralogical, Geochemical and Geomicrobiological Mechanisms for Cobalt and Nickel Enrichment. Minerals (Basel, Switzerland), 2022, 12, 1298.	0.8	3
2641	LotuS2: an ultrafast and highly accurate tool for amplicon sequencing analysis. Microbiome, 2022, 10,	4.9	22
2642	Microbial assemblages of Schisandraceae plants and the correlations between endophytic species and the accumulation of secondary metabolites. Plant and Soil, 2023, 483, 85-107.	1.8	4
2643	Association of body mass index and intestinal (faecal) Streptococcus in adults in Xining city, China P.R Beneficial Microbes, 2022, 13, 465-471.	1.0	5
2644	Analysis of biogenic amine in dry sausages collected from northeast China: From the perspective of free amino acid profile and bacterial community composition. Food Research International, 2022, 162, 112084.	2.9	6
2645	Hyperbaric oxygen improves depressionâ€like behaviors in chronic stress model mice by remodeling gut microbiota and regulating host metabolism. CNS Neuroscience and Therapeutics, 2023, 29, 239-255.	1.9	7
2646	The relationship between pelvic floor functions and vaginal microbiota in 6–8 weeks postpartum women. Frontiers in Microbiology, 0, 13, .	1.5	4
2647	Taxonomic dependency of beta diversity for bacteria, archaea, and fungi in a semi-arid lake. Frontiers in Microbiology, 0, 13, .	1.5	3

ARTICLE IF CITATIONS Atorvastatin Inhibits High-Fat Diet-Induced Lipid Metabolism Disorders in Rats by Inhibiting Bacteroides 2.0 2 2648 Reduction and Improving Metabolism. Drug Design, Development and Therapy, O, Volume 16, 3805-3816. Effects of ethanamizuril, sulfachlorpyridazine or their combination on cecum microbial community 2649 1.3 and metabolomics in chickens infected with Eimeria tenella. Microbial Pathogenesis, 2022, 173, 105823. Effects of different grains on bacterial diversity and enzyme activity associated with digestion of 2650 2 0.7 starch in the foal stomach. BMC Veterinary Research, 2022, 18, . Community distribution of rhizosphere and endophytic bacteria of ephemeral plants in desertâ€oasis 1.8 ecotone and analysis of environmental driving factors. Land Degradation and Development, 0, , . Dynamics of extracellular polymeric substances and soil organic carbon with mangrove zonation 2653 1.2 1 along a continuous tidal gradient. Frontiers in Marine Science, 0, 9, . Developmental stage variation in the gut microbiome of South China tigers. Frontiers in 2654 1.5 Microbiology, 0, 13, . Overcoming Anxiety Disorder by Probiotic Lactiplantibacillus plantarum LZU-J-TSL6 through 2655 1.9 6 Regulating Intestinal Homeostasis. Foods, 2022, 11, 3596. Washed microbiota transplantation improves patients with metabolic syndrome in South China. 1.8 9 Frontiers in Cellular and Infection Microbiology, 0, 12, . Effects of Softening Dry Food with Water on Stress Response, Intestinal Microbiome, and Metabolic 2657 2 1.3 Profile in Beagle Dogs. Metabolites, 2022, 12, 1124. A study on the correlation between intrauterine microbiota and uterine pyogenesis in dogs. Theriogenology, 2022, , . Variations in leaf phyllosphere microbial communities and development of tobacco brown spot before 2659 3 1.5 and after fungicide application. Frontiers in Microbiology, 0, 13, . Assessment of Bacterial Community Profile in the Rearing Pond Environment and the Intestinal Tract of Pacific White Shrimp Litopenaeus vannamei in Lampung Province, Indonesia using 16S rRNA Gene Amplicon Sequencing: A Short Research Investigation. Trends in Sciences, 2023, 20, 3418. 2660 Microbial diversity of milk ghee in southern Gansu and its effect on the formation of ghee flavor 2661 0.6 0 compounds. Open Life Sciences, 2022, 17, 1629-1640. Deciphering soil amendments and actinomycetes for remediation of cadmium (Cd) contaminated farmland. Ecotoxicology and Environmental Safety, 2023, 249, 114388. Quercetin inclusion complex gels ameliorate radiation-induced brain injury by regulating gut 2663 2.59 microbiota. Biomedicine and Pharmacotherapy, 2023, 158, 114142. Effects of molecular hydrogen intervention on the gut microbiome in methamphetamine abusers with mental disorder. Brain Research Bulletin, 2023, 193, 47-58. 2664 1.4 Elevated ozone enhances the network stability of rhizospheric bacteria rather than fungi. 2665 2.51 Agriculture, Ecosystems and Environment, 2023, 345, 108315. Pulsed light reduces postharvest losses of Chinese bayberries by affecting fungal microbiota during 2.8 cold storage. Food Control, 2023, 146, 109524.

#	Article	IF	CITATIONS
2667	Taxonomic and functional metagenomic profiling of microbial communities in urine sample. AIP Conference Proceedings, 2022, , .	0.3	0
2668	Effects of Acremonium cellulase and heat-resistant lactic acid bacteria on lignocellulose degradation, fermentation quality, and microbial community structure of hybrid elephant grass silage in humid and hot areas. Frontiers in Microbiology, 0, 13, .	1.5	1
2669	Variations in the substrate composition and microbial community structure in the anaerobic fermentation process using the green algae Enteromorpha prolifera. Food Production Processing and Nutrition, 2022, 4, .	1.1	3
2670	Siamese Fighting Fish (Betta splendens Regan) Gut Microbiota Associated with Age and Gender. Fishes, 2022, 7, 347.	0.7	1
2671	<i>Saussurea involucrata</i> oral liquid regulates gut microbiota and serum metabolism during alleviation of collagenâ€induced arthritis in rats. Phytotherapy Research, 2023, 37, 1242-1259.	2.8	5
2672	Analysis of the gut microbiome in obese native Tibetan children living at different altitudes: A case–control study. Frontiers in Public Health, 0, 10, .	1.3	4
2673	Potential for Polyethylene Terephthalate (PET) Degradation Revealed by Metabarcoding and Bacterial Isolates from Soil Around a Bitumen Source in Southwestern Iran. Journal of Polymers and the Environment, 2023, 31, 1279-1291.	2.4	5
2674	Microbial Communities in the Lungs of Bats in China. Zoonoses, 2022, 2, .	0.5	0
2675	Analysis of gut microbiome composition, function, and phenotype in patients with osteoarthritis. Frontiers in Microbiology, 0, 13, .	1.5	1
2676	Polysaccharides from Pseudostellaria heterophylla modulate gut microbiota and alleviate syndrome of spleen deficiency in rats. Scientific Reports, 2022, 12, .	1.6	3
2677	Characterization and Dynamics of the Gut Microbiota in Rice Fishes at Different Developmental Stages in Rice-Fish Coculture Systems. Microorganisms, 2022, 10, 2373.	1.6	3
2678	Effects of Dietary Quinoa Seeds on Cecal Microorganisms and Muscle Fatty Acids of Female Luhua Chickens. Animals, 2022, 12, 3334.	1.0	1
2679	Effects of Dietary Oregano Essential Oil on Cecal Microorganisms and Muscle Fatty Acids of Luhua Chickens. Animals, 2022, 12, 3215.	1.0	4
2680	Response of rhizosphere microbial community of Chinese chives under different fertilization treatments. Frontiers in Microbiology, 0, 13, .	1.5	5
2681	Effects of challenge with Clostridium perfringens, Eimeria and both on ileal microbiota of yellow feather broilers. Frontiers in Microbiology, 0, 13, .	1.5	3
2682	Genetic diversity in the metronidazole metabolism genes nitroreductases and pyruvate ferredoxin oxidoreductases in susceptible and refractory clinical samples of Giardia lamblia. International Journal for Parasitology: Drugs and Drug Resistance, 2023, 21, 51-60.	1.4	4
2683	The effects of a set amount of regular maternal exercise during pregnancy on gut microbiota are diet-dependent in mice and do not cause significant diversity changes. PeerJ, 0, 10, e14459.	0.9	2
2684	Nodule-associated diazotrophic community succession is driven by developmental phases combined with microhabitat of Sophora davidii. Frontiers in Microbiology, 0, 13, .	1.5	1

#	Article	IF	CITATIONS
2685	Protein fractionation and shotgun proteomics analysis of enriched bacterial cultures shed new light on the enzymatically catalyzed degradation of acesulfame. Water Research, 2023, 230, 119535.	5.3	4
2686	Diversity and antibacterial potential of the Actinobacteria associated with Apis mellifera ligustica. Frontiers in Microbiology, 0, 13, .	1.5	2
2687	DNA High-Throughput Sequencing for Arthropod Gut Content Analysis to Evaluate Effectiveness and Safety of Biological Control Agents. Neotropical Entomology, 2023, 52, 302-332.	0.5	3
2688	Insights into Bacterial Communities and Diversity of Mangrove Forest Soils along the Upper Gulf of Thailand in Response to Environmental Factors. Biology, 2022, 11, 1787.	1.3	5
2689	Soil Microbiome Study Based on DNA Extraction: A Review. Water (Switzerland), 2022, 14, 3999.	1.2	9
2690	The Quality and Bacterial Community Changes in Freshwater Crawfish Stored at 4 °C in Vacuum Packaging. Molecules, 2022, 27, 8618.	1.7	6
2691	The effect of a multi-carbohydrase enzyme and yeast-derived product on intestinal microbiome structure, activity, and gut function of turkeys. Canadian Journal of Animal Science, 0, , .	0.7	0
2692	Gut microbiota as an antioxidant system in centenarians associated with high antioxidant activities of gut-resident Lactobacillus. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	13
2693	Characterization of Intestinal Microbiota in Lambs with Different Susceptibility to Escherichia coli F17. Veterinary Sciences, 2022, 9, 670.	0.6	2
2694	Changes in Soil Microbial Communities under Mixed Organic and Inorganic Nitrogen Addition in Temperate Forests. Forests, 2023, 14, 21.	0.9	3
2695	Effect and mechanism of the improvement of coastal silt soil by application of organic fertilizer and gravel combined with Sesbania cannabina cultivation. Frontiers in Plant Science, 0, 13, .	1.7	3
2696	Continuous Wheat/Soybean Cropping Influences Soybean Yield and Rhizosphere Microbial Community Structure and Function. Agronomy, 2023, 13, 28.	1.3	6
2697	Bacterial dynamics during the burial of starch-based bioplastic and oxo-low-density-polyethylene in compost soil. BMC Microbiology, 2022, 22, .	1.3	5
2699	Hidden Decomposers: the Role of Bacteria and Fungi in Recently Intermittent Alpine Streams Heterotrophic Pathways. Microbial Ecology, 2023, 86, 1499-1512.	1.4	3
2700	Roles of vaginal flora in human papillomavirus infection, virus persistence and clearance. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	4
2701	Response of Intestinal Microbiota of Tiger Puffer (Takifugu rubripes) to the Fish Oil Finishing Strategy. Microorganisms, 2023, 11, 208.	1.6	2
2704	Diversity analysis of vineyards soil bacterial community in different planting years at eastern foot of Helan Mountain, Ningxia. Rhizosphere, 2023, 25, 100650.	1.4	5
2705	Seasonal Changes Modulate the Rhizosphere of Desert Plant Species. Agronomy, 2023, 13, 57.	1.3	О

		15	6
#		IF	CITATIONS
2706	Exogenous antibiotic resistance gene contributes to intestinal inflammation by modulating the gut microbiome and inflammatory cytokine responses in mouse. Gut Microbes, 2023, 15, .	4.3	1
2707	Gut microbiota diversity in human strongyloidiasis differs little in two different regions in endemic areas of Thailand. PLoS ONE, 2022, 17, e0279766.	1.1	1
2708	The ground beetle Pseudoophonus rufipes gut microbiome is influenced by the farm management system. Scientific Reports, 2022, 12, .	1.6	3
2709	Corn Straw Total Mix Dietary Supplementation of Bacillus Subtilis-Enhanced Growth Performance of Lambs by Favorably Modulating Rumen Bacterial Microbiome. Fermentation, 2023, 9, 32.	1.4	6
2710	Contrasting effects of elevated CO2 on autotrophic prokaryotes with different CO2 fixation strategies in tea plantation soil. Biology and Fertility of Soils, 2023, 59, 205-215.	2.3	3
2711	Development of the gut microbiota during early life in premature and term infants. Gut Pathogens, 2023, 15, .	1.6	3
2712	Response of fermentation quality and microbial community of oat silage to homofermentative lactic acid bacteria inoculation. Frontiers in Microbiology, 0, 13, .	1.5	5
2714	Change of Gut Microbiome Structure in Preterm Infants with Hypoxic Ischemic Encephalopathy Induced by Apnea. Pediatrics and Neonatology, 2023, , .	0.3	0
2715	Insights into the bacterial and archaeal population dynamics in the deep-sea hydrothermal sediments exposed to lights with different wavelengths. Deep-Sea Research Part I: Oceanographic Research Papers, 2023, 195, 103996.	0.6	0
2716	Uncovering Bacterial Diversity during Mesophilic and Thermophilic Phases of Biowaste Composting through Next-Generation Sequencing. Applied Sciences (Switzerland), 2023, 13, 3111.	1.3	3
2718	Inhibitory effects of Clostridium butyricum culture and supernatant on inflammatory colorectal cancer in mice. Frontiers in Immunology, 0, 14, .	2.2	4
2719	Fishmeal Protein Replacement by Defatted and Full-Fat Black Soldier Fly Larvae Meal in Juvenile Turbot Diet: Effects on the Growth Performance and Intestinal Microbiota. Aquaculture Nutrition, 2023, 2023, 1-14.	1.1	1
2720	Gut microbial and metabolic characterization of Atlantic salmon (Salmon salar) challenged with Aeromonas salmonicida. Aquaculture, 2023, 570, 739420.	1.7	0
2721	Effects of salinity on growth, physiology, biochemistry and gut microbiota of juvenile grass carp (Ctenopharyngodon idella). Aquatic Toxicology, 2023, 258, 106482.	1.9	5
2722	The mitigating effects of diatom-bacteria biofilm on coastal harmful algal blooms: A lab-based study concerning species-specific competition and biofilm formation. Journal of Environmental Management, 2023, 335, 117544.	3.8	1
2723	Bacterial diversity and its correlation with sensory quality of two types of zha-chili from Shennongjia region, China. Food Research International, 2023, 168, 112789.	2.9	6
2724	Evaluation of the effects of dietary mycotoxin-degrading adsorbent on juvenile turbot (Scophthalmus maximus L.) fed aflatoxin B1-contaminated diets. Aquaculture Reports, 2023, 30, 101539.	0.7	0
2725	Effects of microbial succession on the dynamics of flavor metabolites and physicochemical properties during soy sauce koji making. Food Bioscience, 2023, 53, 102636.	2.0	4

#	Article	IF	CITATIONS
2726	Impact of aged and virgin microplastics on sedimentary nitrogen cycling and microbial ecosystems in estuaries. Science of the Total Environment, 2023, 878, 162977.	3.9	7
2727	Immobilization of Klebsiella jilinsis strain 2N3 by corn straw biochar enhanced the degradation of nicosulfuron and restores the soil microbiome function and composition. Applied Soil Ecology, 2023, 189, 104917.	2.1	6
2728	Effect of antibiotic and/or heavy metal on nitrogen cycle of sediment-water interface in aquaculture system: Implications from sea cucumber culture. Environmental Pollution, 2023, 325, 121453.	3.7	4
2729	The vertical distribution and control factor of microbial biomass and bacterial community at macroecological scales. Science of the Total Environment, 2023, 869, 161754.	3.9	12
2730	Effects of Continuous Straw Returning on Soil Functional Microorganisms and Microbial Communities. Journal of Microbiology, 2023, 61, 49-62.	1.3	3
2731	Comparison of network connectivity and environmental driving factors of root-associated fungal communities of desert ephemeral plants in two habitat soils. Journal of Environmental Management, 2023, 332, 117375.	3.8	8
2732	Non-Surgical Periodontal Treatment Impact on Subgingival Microbiome and Intra-Oral Halitosis. International Journal of Molecular Sciences, 2023, 24, 2518.	1.8	3
2733	Establishment of a Standard Tongue Coating Collection Method for Microbiome Studies. Biopreservation and Biobanking, 2023, 21, 599-609.	0.5	0
2734	Microbial community stratification in scale-up Anaerobic Fluidized Bed Reactor applied for 4-Nonylphenol degradation. Bioresource Technology Reports, 2023, 21, 101359.	1.5	0
2735	Chondroitin sulfate alleviates osteoporosis caused by calcium deficiency by regulating lipid metabolism. Nutrition and Metabolism, 2023, 20, .	1.3	4
2736	Gut Microbiota and Metabolites may Play a Crucial Role in Sea Cucumber Apostichopus Japonicus Aestivation. Microorganisms, 2023, 11, 416.	1.6	6
2738	The effects of a <i>Bacillus licheniformis</i> and phytase mixture added to broiler diets on growth performance, nutrient digestibility, and cecal microecosystem. Annals of Animal Science, 2023, .	0.6	0
2739	The Intestinal Microbiota Involves in the Deterioration of Live Sea Cucumber During Storage. Journal of Aquatic Food Product Technology, 2023, 32, 129-141.	0.6	0
2740	Compositional and functional diversities of core microbial communities in wild and artificial Ophiocordyceps sinensis. International Microbiology, 2023, 26, 791-806.	1.1	1
2741	The influences of acidic electrolyzed water on quality and bacteria community of fresh-cut jackfruit in storage. International Journal of Food Engineering, 2023, 19, 27-36.	0.7	0
2742	Relationship between the effects of heat pre-treatment on anaerobic performance of pig manure and the microbial variation within reactors. Chemical Engineering Journal, 2023, 461, 141991.	6.6	2
2743	Characteristics of Microbiota in Different Segments of the Digestive Tract of Lycodon rufozonatus. Animals, 2023, 13, 731.	1.0	1
2744	Impacts of dietary supplementation of bamboo vinegar and charcoal powder on growth performance, intestinal morphology, and gut microflora of large-scale loach Paramisgurnus dabryanus. Journal of Oceanology and Limnology, 2023, 41, 1187-1196.	0.6	1

#	Article	IF	CITATIONS
2745	Shift of Feeding Strategies from Grazing to Different Forage Feeds Reshapes the Rumen Microbiota To Improve the Ability of Tibetan Sheep (Ovis aries) To Adapt to the Cold Season. Microbiology Spectrum, 2023, 11, .	1.2	7
2746	Influence of Parturition on Rumen Bacteria and SCFAs in Holstein Cows Based on 16S rRNA Sequencing and Targeted Metabolomics. Animals, 2023, 13, 782.	1.0	3
2747	Variations in gut microbiome and metabolites of dogs with acute diarrhea in poodles and Labrador retrievers. Archives of Microbiology, 2023, 205, .	1.0	2
2748	The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. MSphere, 2023, 8, .	1.3	4
2749	Soil Fungal Community Structure and Its Effect on CO2 Emissions in the Yellow River Delta. International Journal of Environmental Research and Public Health, 2023, 20, 4190.	1.2	3
2750	Effects of Coumarin on Rhizosphere Microbiome and Metabolome of Lolium multiflorum. Plants, 2023, 12, 1096.	1.6	3
2751	Astragalus-cultivated soil was a suitable bed soil for nurturing Angelica sinensis seedlings from the rhizosphere microbiome perspective. Scientific Reports, 2023, 13, .	1.6	1
2752	Microbiome Structure and Mucosal Morphology of Jejunum Appendix and Colon of Rats in Health and Dysbiosis. Current Microbiology, 2023, 80, .	1.0	0
2753	Alterations in the gut microbiome and metabolome profiles of septic mice treated with Shen FuHuang formula. Frontiers in Microbiology, 0, 14, .	1.5	2
2754	Alteration of the Respiratory Microbiome in Hospitalized Patients with Asthma–COPD Overlap during and after an Exacerbation. Journal of Clinical Medicine, 2023, 12, 2118.	1.0	7
2755	Algal amendment enhances biogenic methane production from coals of different thermal maturity. Frontiers in Microbiology, 0, 14, .	1.5	0
2756	Eukaryotic food sources analysis in situ of tropical common sea cucumber Holothuria leucospilota based on 18S rRNA gene high-throughput sequencing. Journal of Oceanology and Limnology, 0, , .	0.6	0
2757	Characterization of dysbiosis of the conjunctival microbiome and nasal microbiome associated with allergic rhinoconjunctivitis and allergic rhinitis. Frontiers in Immunology, 0, 14, .	2.2	3
2759	Establishment of Residual Methods for Matrine in Quinoa Plants and Soil and the Effect on Soil Bacterial Community and Composition. Foods, 2023, 12, 1337.	1.9	2
2762	Construction of hybrid constructed wetlands for phosphorus chemical industry tailwater treatment in the middle Yangtze river basin: Responses of plant growth and root-associated microbial communities. , 2023, 2, 100144.		0
2763	Klebsiella quasipneumoniae in intestine damages bile acid metabolism in hematopoietic stem cell transplantation patients with bloodstream infection. Journal of Translational Medicine, 2023, 21, .	1.8	0
2764	The Gut Microbiota of Broilers Reared with and without Antibiotic Treatment. Microorganisms, 2023, 11, 876.	1.6	1
2765	Effect of Limosilactobacillus reuteri ZJF036 on Growth Performance and Gut Microbiota in Juvenile Beagle Dogs. Current Microbiology, 2023, 80, .	1.0	1

#	Article	IF	CITATIONS
2766	Accurate profiling of full-length Fv in highly homologous antibody libraries using UMI tagged short reads. Nucleic Acids Research, 2023, 51, e61-e61.	6.5	2
2767	Vitamin C and vitamin D3 alleviate metabolic-associated fatty liver disease by regulating the gut microbiota and bile acid metabolism via the gut-liver axis. Frontiers in Pharmacology, 0, 14, .	1.6	3
2768	Lung microbiome and cytokine profiles in different disease states of COPD: a cohort study. Scientific Reports, 2023, 13, .	1.6	2
2769	Aquafeed fermentation improves dietary nutritional quality and benefits feeding behavior, meat flavor, and intestinal microbiota of Chinese mitten crab (Eriocheir sinensis). Animal Nutrition, 2023, 14, 1-19.	2.1	3
2770	MiSurv: an Integrative Web Cloud Platform for User-Friendly Microbiome Data Analysis with Survival Responses. Microbiology Spectrum, 2023, 11, .	1.2	2
2772	First Study on profiling of gut microbiome in wild and captive Sumatran orangutans (Pongo abelii). Veterinary World, 2023, , 717-727.	0.7	1
2773	Age Rather Than Supplementation with Oat β-Glucan Influences Development of the Intestinal Microbiota and SCFA Concentrations in Suckling Piglets. Animals, 2023, 13, 1349.	1.0	1
2774	Pave the way for successful treatment of Nylon wastewater by performance enhancement via unit stacking scale up of dual cathodes up-flow microbial fuel cell and C/N adjustment with urea. Journal of Environmental Chemical Engineering, 2023, 11, 109930.	3.3	3
2775	Widespread coexistence of genetically distinct morphotypes in the <i>Satyrium longicauda</i> complex (Orchidaceae). Botanical Journal of the Linnean Society, 0, , .	0.8	0
2776	Prevention effect of total ginsenosides and ginseng extract from <i>Panax ginseng</i> on <scp>cyclophosphamideâ€induced</scp> immunosuppression in mice. Phytotherapy Research, 2023, 37, 3583-3601.	2.8	4
2777	Changes of Fatty Acid Compositions, Volatile Compounds, and Microbial Flora of Bighead Carp (Aristichthys nobilis) Heads during the Simulated Fresh Logistics Transportation. Journal of Food Processing and Preservation, 2023, 2023, 1-16.	0.9	0
2778	Hydrogen peroxide treatment mitigates antibiotic resistance gene and mobile genetic element propagation in mariculture sediment. Environmental Pollution, 2023, 328, 121652.	3.7	18
2819	Moving Beyond OTU Methods. , 2023, , 227-288.		0
2911	Metabarcoding for Biodiversity Estimation. , 2024, , 388-407.		0

Bioinformatics in the study of microbial infections. , 2024, , 1975-1992.