

FLASH: fast length adjustment of short reads to improv

Bioinformatics

27, 2957-2963

DOI: [10.1093/bioinformatics/btr507](https://doi.org/10.1093/bioinformatics/btr507)

Citation Report

#	ARTICLE	IF	CITATIONS
7	The role of memory for past test in the underconfidence with practice effect.. Journal of Experimental Psychology: Learning Memory and Cognition, 2007, 33, 238-244.	0.7	128
8	COPE: an accurate k-mer-based pair-end reads connection tool to facilitate genome assembly. Bioinformatics, 2012, 28, 2870-2874.	1.8	145
9	Current challenges in de novo plant genome sequencing and assembly. Genome Biology, 2012, 13, 243.	13.9	157
10	Intestinal Inflammation Targets Cancer-Inducing Activity of the Microbiota. Science, 2012, 338, 120-123.	6.0	1,785
11	GapFiller: a de novo assembly approach to fill the gap within paired reads. BMC Bioinformatics, 2012, 13, S8.	1.2	324
12	AdapterRemoval: easy cleaning of next-generation sequencing reads. BMC Research Notes, 2012, 5, 337.	0.6	548
13	Exploiting sparseness in de novo genome assembly. BMC Bioinformatics, 2012, 13, S1.	1.2	279
14	Reference genomes and transcriptomes of <i>Nicotiana glauca</i> and <i>Nicotiana glauca</i> . Genome Biology, 2013, 14, R60.	3.8	192
15	Ultra-deep mutant spectrum profiling: improving sequencing accuracy using overlapping read pairs. BMC Genomics, 2013, 14, 96.	1.2	40
16	Practical innovations for high-throughput amplicon sequencing. Nature Methods, 2013, 10, 999-1002.	9.0	787
17	The Long-Term Stability of the Human Gut Microbiota. Science, 2013, 341, 1237-1243.	6.0	1,696
18	Nuclear Wave1 Is Required for Reprogramming Transcription in Oocytes and for Normal Development. Science, 2013, 341, 1002-1005.	6.0	82
19	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. BMC Genomics, 2013, 14, 711.	1.2	12
20	SSR_pipeline: A Bioinformatic Infrastructure for Identifying Microsatellites From Paired-End Illumina High-Throughput DNA Sequencing Data. Journal of Heredity, 2013, 104, 881-885.	1.0	49
21	Bacterial community diversity in a low-permeability oil reservoir and its potential for enhancing oil recovery. Bioresource Technology, 2013, 147, 110-116.	4.8	41
22	Endogenous Retrotransposition Activates Oncogenic Pathways in Hepatocellular Carcinoma. Cell, 2013, 153, 101-111.	13.5	352
23	De novo transcriptomic analyses for non-model organisms: an evaluation of methods across a multi-species data set. Molecular Ecology Resources, 2013, 13, 403-416.	2.2	71
24	Horizontal Gene Transfer from Diverse Bacteria to an Insect Genome Enables a Tripartite Nested Mealybug Symbiosis. Cell, 2013, 153, 1567-1578.	13.5	373

#	ARTICLE	IF	CITATIONS
25	Development of genomic microsatellites in <i>Gleditsia triacanthos</i> (Fabaceae) using Illumina sequencing. Applications in Plant Sciences, 2013, 1, 1300050.	0.8	10
26	In-depth analysis of interrelation between quality scores and real errors in illumina reads. , 2013, 2013, 635-8.		15
27	The Genome of the Anaerobic Fungus Orpinomyces sp. Strain C1A Reveals the Unique Evolutionary History of a Remarkable Plant Biomass Degrader. Applied and Environmental Microbiology, 2013, 79, 4620-4634.	1.4	224
28	The Draft Genome Sequence of Sphingomonas paucimobilis Strain HER1398 (<i>Proteobacteria</i>), Host to the Giant PAU Phage, Indicates That It Is a Member of the Genus <i>Sphingobacterium</i> () Tj ETQq1 1 0.784314 rgBT /Over	1.1	78
29	Metagenomics of rumen bacteriophage from thirteen lactating dairy cattle. BMC Microbiology, 2013, 13, 242.	1.3	51
30	The Poultry-Associated Microbiome: Network Analysis and Farm-to-Fork Characterizations. PLoS ONE, 2013, 8, e57190.	1.1	104
31	Co-Enriching Microflora Associated with Culture Based Methods to Detect Salmonella from Tomato Phyllosphere. PLoS ONE, 2013, 8, e73079.	1.1	49
32	Defining the Vulnerable Period for Re-Establishment of Clostridium difficile Colonization after Treatment of C. difficile Infection with Oral Vancomycin or Metronidazole. PLoS ONE, 2013, 8, e76269.	1.1	88
33	Quantitative PCR as a predictor of aligned ancient DNA read counts following targeted enrichment. BioTechniques, 2013, 55, 300-9.	0.8	39
34	The epsomitic phototrophic microbial mat of Hot Lake, Washington: community structural responses to seasonal cycling. Frontiers in Microbiology, 2013, 4, 323.	1.5	75
35	MP3: A Software Tool for the Prediction of Pathogenic Proteins in Genomic and Metagenomic Data. PLoS ONE, 2014, 9, e93907.	1.1	112
36	Host Control of Symbiont Natural Product Chemistry in Cryptic Populations of the Tunicate Lissoclinum patella. PLoS ONE, 2014, 9, e95850.	1.1	31
37	Systematic Characterization and Comparative Analysis of the Rabbit Immunoglobulin Repertoire. PLoS ONE, 2014, 9, e101322.	1.1	61
38	Illumina Amplicon Sequencing of 16S rRNA Tag Reveals Bacterial Community Development in the Rhizosphere of Apple Nurseries at a Replant Disease Site and a New Planting Site. PLoS ONE, 2014, 9, e111744.	1.1	109
39	Assessment of insert sizes and adapter content in fastq data from NexteraXT libraries. Frontiers in Genetics, 2014, 5, 5.	1.1	33
40	Phototrophic biofilm assembly in microbial-mat-derived unicyanobacterial consortia: model systems for the study of autotroph-heterotroph interactions. Frontiers in Microbiology, 2014, 5, 109.	1.5	97
41	Strain-specific parallel evolution drives short-term diversification during <i>Pseudomonas aeruginosa</i> biofilm formation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1419-27.	3.3	81
42	The effect of omeprazole on the development of experimental autoimmune encephalomyelitis in C57BL/6J and SJL/J mice. BMC Research Notes, 2014, 7, 605.	0.6	19

#	ARTICLE	IF	CITATIONS
43	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , 2014, 2, 30.	4.9	233
44	The SIRT1 deacetylase protects mice against the symptoms of metabolic syndrome. <i>FASEB Journal</i> , 2014, 28, 1306-1316.	0.2	74
45	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph. , 2014, , .		8
46	Sequencing and de novo assembly of a Dahlia hybrid cultivar transcriptome. <i>Frontiers in Plant Science</i> , 2014, 5, 340.	1.7	8
47	Genome Sequencing and Comparative Genomics of the Broad Host-Range Pathogen <i>Rhizoctonia solani</i> AG8. <i>PLoS Genetics</i> , 2014, 10, e1004281.	1.5	145
48	Oligotyping reveals differences between gut microbiomes of free-ranging sympatric Namibian carnivores (<i>Acinonyx jubatus</i> , <i>Canis mesomelas</i>) on a bacterial species-like level. <i>Frontiers in Microbiology</i> , 2014, 5, 526.	1.5	43
49	Draft Genome Sequence of <i>Salmonella enterica</i> Serovar Typhi Strain STH2370. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
50	Genome Sequences of <i>Lactobacillus</i> sp. Strains wkB8 and wkB10, Members of the Firm-5 Clade, from Honey Bee Guts. <i>Genome Announcements</i> , 2014, 2, .	0.8	30
51	HCoDES Reveals Chromosomal DNA End Structures with Single-Nucleotide Resolution. <i>Molecular Cell</i> , 2014, 56, 808-818.	4.5	31
52	Extensive Differences in Gene Expression Between Symbiotic and Aposymbiotic Cnidarians. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 277-295.	0.8	150
53	Diminishing return for increased Mappability with longer sequencing reads: implications of the k-mer distributions in the human genome. <i>BMC Bioinformatics</i> , 2014, 15, 2.	1.2	39
54	Draft Genome Sequence of <i>Weissella oryzae</i> SG25 T , Isolated from Fermented Rice Grains. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
55	PEAR: a fast and accurate Illumina Paired-End reAd merger. <i>Bioinformatics</i> , 2014, 30, 614-620.	1.8	3,776
56	Characterization of bacterial communities in solarized soil amended with lignocellulosic organic matter. <i>Applied Soil Ecology</i> , 2014, 73, 97-104.	2.1	37
57	Sequence capture using PCR-generated probes: a cost-effective method of targeted high-throughput sequencing for nonmodel organisms. <i>Molecular Ecology Resources</i> , 2014, 14, 1000-1010.	2.2	89
58	Ultra-deep Illumina sequencing accurately identifies MHC class IIb alleles and provides evidence for copy number variation in the guppy (<i>Poecilia reticulata</i>). <i>Molecular Ecology Resources</i> , 2014, 14, 753-767.	2.2	84
59	Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild <i>Arabidopsis</i> relative. <i>Ecology Letters</i> , 2014, 17, 717-726.	3.0	266
60	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <i>ISME Journal</i> , 2014, 8, 1101-1114.	4.4	174

#	ARTICLE	IF	CITATIONS
61	A <i>de novo</i> transcriptome of European pollen beetle populations and its analysis, with special reference to insecticide action and resistance. <i>Insect Molecular Biology</i> , 2014, 23, 511-526.	1.0	29
62	The tobacco genome sequence and its comparison with those of tomato and potato. <i>Nature Communications</i> , 2014, 5, 3833.	5.8	503
63	Gene expression of lactobacilli in murine forestomach biofilms. <i>Microbial Biotechnology</i> , 2014, 7, 347-359.	2.0	31
64	<i>Yersinia pestis</i> and the Plague of Justinian 541–543 AD: a genomic analysis. <i>Lancet Infectious Diseases</i> , 2014, 14, 319-326.	4.6	358
65	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , 2014, 46, 1303-1310.	9.4	174
66	Prevention, diagnosis and treatment of high-throughput sequencing data pathologies. <i>Molecular Ecology</i> , 2014, 23, 1679-1700.	2.0	24
67	Functional characterization of the TERRA transcriptome at damaged telomeres. <i>Nature Communications</i> , 2014, 5, 5379.	5.8	212
68	Profiling the T-cell receptor repertoire of patient with pleural tuberculosis by high-throughput sequencing. <i>Immunology Letters</i> , 2014, 162, 170-180.	1.1	11
69	Performance of amplicon-based next generation DNA sequencing for diagnostic gene mutation profiling in oncopathology. <i>Cellular Oncology (Dordrecht)</i> , 2014, 37, 353-361.	2.1	43
70	The composition and transmission of microbiome in hard tick, <i>Ixodes persulcatus</i> , during blood meal. <i>Ticks and Tick-borne Diseases</i> , 2014, 5, 864-870.	1.1	93
71	Growth of nitrite-oxidizing bacteria by aerobic hydrogen oxidation. <i>Science</i> , 2014, 345, 1052-1054.	6.0	166
72	Molecular Analysis for Screening Human Bacterial Pathogens in Municipal Wastewater Treatment and Reuse. <i>Environmental Science & Technology</i> , 2014, 48, 11610-11619.	4.6	71
73	Unveiling viral-host interactions within the "microbial dark matter". <i>Nature Communications</i> , 2014, 5, 4542.	5.8	69
74	Getting Started with Microbiome Analysis: Sample Acquisition to Bioinformatics. <i>Current Protocols in Human Genetics</i> , 2014, 82, 18.8.1-29.	3.5	111
75	Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. <i>Nature Communications</i> , 2014, 5, 4724.	5.8	302
76	Whole-Genome Analysis of <i>Exserohilum rostratum</i> from an Outbreak of Fungal Meningitis and Other Infections. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3216-3222.	1.8	52
77	MT-Toolbox: improved amplicon sequencing using molecule tags. <i>BMC Bioinformatics</i> , 2014, 15, 284.	1.2	22
78	Limits of Neutral Drift: Lessons From the In Vitro Evolution of Two Ribozymes. <i>Journal of Molecular Evolution</i> , 2014, 79, 75-90.	0.8	24

#	ARTICLE	IF	CITATIONS
79	An improved dual-indexing approach for multiplexed 16S rRNA gene sequencing on the Illumina MiSeq platform. <i>Microbiome</i> , 2014, 2, 6.	4.9	1,454
80	Nitrifying moving bed biofilm reactor (MBBR) biofilm and biomass response to long term exposure to 1Å°C. <i>Water Research</i> , 2014, 49, 215-224.	5.3	119
81	RNA motif discovery by SHAPE and mutational profiling (SHAPE-MaP). <i>Nature Methods</i> , 2014, 11, 959-965.	9.0	487
82	Neuroblastoma Killing Properties of VÎ2 and VÎ2-Negative Î³T Cells Following Expansion by Artificial Antigen-Presenting Cells. <i>Clinical Cancer Research</i> , 2014, 20, 5720-5732.	3.2	99
83	eQTL Mapping of Transposon Silencing Reveals a Position-Dependent Stable Escape from Epigenetic Silencing and Transposition of <i>AtMu1</i> in the <i>Arabidopsis</i> Lineage. <i>Plant Cell</i> , 2014, 26, 3261-3271.	3.1	12
84	UVB-induced gene expression in the skin of <i>Xiphophorus maculatus</i> Jp 163 B. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2014, 163, 86-94.	1.3	15
85	A mutation burst during the acute phase of <i>Helicobacter pylori</i> infection in humans and rhesus macaques. <i>Nature Communications</i> , 2014, 5, 4165.	5.8	81
86	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	2.4	332
87	Additional Bioinformatic Analyses Involving Nucleic-Acid Sequences. , 2014, , 157-181.		3
88	Enrichment of anodic biofilm inoculated with anaerobic or aerobic sludge in single chambered air-cathode microbial fuel cells. <i>Bioresource Technology</i> , 2014, 167, 124-132.	4.8	120
89	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. <i>Standards in Genomic Sciences</i> , 2014, 9, 1259-1274.	1.5	31
90	CASPER: context-aware scheme for paired-end reads from high-throughput amplicon sequencing. <i>BMC Bioinformatics</i> , 2014, 15, S10.	1.2	56
91	An improved genome reference for the African cichlid, <i>Metriaclima zebra</i> . <i>BMC Genomics</i> , 2015, 16, 724.	1.2	61
92	Draft Genome Sequence of the Moderately Heat-Tolerant <i>Lactococcus lactis</i> subsp. <i>lactis</i> bv. <i>diacetylactis</i> Strain GL2 from Algerian Dromedary Milk. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
93	Ligninâ€modifying processes in the rhizosphere of arid land grasses. <i>Environmental Microbiology</i> , 2015, 17, 4965-4978.	1.8	10
94	Microbial diversity and abundance in the Xinjiang Luliang longâ€term waterâ€flooding petroleum reservoir. <i>MicrobiologyOpen</i> , 2015, 4, 332-342.	1.2	87
95	Shifts in the gut microbiome observed in wildlife faecal samples exposed to natural weather conditions: lessons from timeâ€series analyses using nextâ€generation sequencing for application in field studies. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1080-1087.	2.2	27
96	The hidden â€mycobacteriomeâ€™ of the human healthy oral cavity and upper respiratory tract. <i>Journal of Oral Microbiology</i> , 2015, 7, 26094.	1.2	31

#	ARTICLE	IF	CITATIONS
97	The functional gene composition and metabolic potential of coral-associated microbial communities. <i>Scientific Reports</i> , 2015, 5, 16191.	1.6	71
98	Generation and Analysis of Microbial Metatranscriptomes. , 2015, , 2.4.5-1-2.4.5-19.		1
99	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178
100	Back to Basics â€” The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. <i>PLoS ONE</i> , 2015, 10, e0132783.	1.1	437
101	Konnector v2.0: pseudo-long reads from paired-end sequencing data. <i>BMC Medical Genomics</i> , 2015, 8, S1.	0.7	19
102	Molecular genetic response to varied wavelengths of light in <i>Xiphophorus maculatus</i> skin. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2015, 178, 104-115.	1.3	9
103	Biogeochemical and metagenomic analysis of nitrite accumulation in the <i>Gulf of Mexico</i> hypoxic zone. <i>Limnology and Oceanography</i> , 2015, 60, 1733-1750.	1.6	72
104	The core microbiome bonds the Alpine bog vegetation to a transkingdom metacommunity. <i>Molecular Ecology</i> , 2015, 24, 4795-4807.	2.0	74
105	Xander: employing a novel method for efficient gene-targeted metagenomic assembly. <i>Microbiome</i> , 2015, 3, 32.	4.9	83
106	Terrestrial origin of bacterial communities in complex boreal freshwater networks. <i>Ecology Letters</i> , 2015, 18, 1198-1206.	3.0	227
107	The quality of organic matter shapes the functional biogeography of bacterioplankton across boreal freshwater ecosystems. <i>Global Ecology and Biogeography</i> , 2015, 24, 1487-1498.	2.7	86
108	Screening wild and semi-free ranging great apes for putative sexually transmitted diseases: Evidence of <i>Trichomonadidae</i> infections. <i>American Journal of Primatology</i> , 2015, 77, 1075-1085.	0.8	9
109	High-throughput monitoring of wild bee diversity and abundance via mitogenomics. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1034-1043.	2.2	119
110	Bacterial biogeography in the coastal waters of northern Zhejiang, East China Sea is highly controlled by spatially structured environmental gradients. <i>Environmental Microbiology</i> , 2015, 17, 3898-3913.	1.8	93
111	Differences in microbial community composition between injection and production water samples of water flooding petroleum reservoirs. <i>Biogeosciences</i> , 2015, 12, 3403-3414.	1.3	33
112	Surveying the repair of ancient DNA from bones via high-throughput sequencing. <i>BioTechniques</i> , 2015, 59, 19-25.	0.8	18
113	Comparative Evaluation of DNA Extraction Methods from Feces of Multiple Host Species for Downstream Next-Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0143334.	1.1	112
114	Contesting the presence of wheat in the British Isles 8,000 years ago by assessing ancient DNA authenticity from low-coverage data. <i>ELife</i> , 2015, 4, .	2.8	31

#	ARTICLE	IF	CITATIONS
115	Phyllostomid bat microbiome composition is associated to host phylogeny and feeding strategies. <i>Frontiers in Microbiology</i> , 2015, 6, 447.	1.5	92
116	Combining genomic sequencing methods to explore viral diversity and reveal potential virus-host interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 265.	1.5	72
117	Microbial responses to changes in flow status in temporary headwater streams: a cross-system comparison. <i>Frontiers in Microbiology</i> , 2015, 6, 522.	1.5	41
118	Standard filtration practices may significantly distort planktonic microbial diversity estimates. <i>Frontiers in Microbiology</i> , 2015, 6, 547.	1.5	65
119	Novel molecular markers for the detection of methanogens and phylogenetic analyses of methanogenic communities. <i>Frontiers in Microbiology</i> , 2015, 6, 694.	1.5	31
120	Primer and platform effects on 16S rRNA tag sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 771.	1.5	435
121	Rhizosphere bacterial communities of dominant steppe plants shift in response to a gradient of simulated nitrogen deposition. <i>Frontiers in Microbiology</i> , 2015, 6, 789.	1.5	20
122	Metagenome-based diversity analyses suggest a significant contribution of non-cyanobacterial lineages to carbonate precipitation in modern microbialites. <i>Frontiers in Microbiology</i> , 2015, 6, 797.	1.5	50
123	The effect of D123 wheat as a companion crop on soil enzyme activities, microbial biomass and microbial communities in the rhizosphere of watermelon. <i>Frontiers in Microbiology</i> , 2015, 6, 899.	1.5	30
124	Relations of microbiome characteristics to edaphic properties of tropical soils from Trinidad. <i>Frontiers in Microbiology</i> , 2015, 6, 1045.	1.5	28
125	Variation in fungal microbiome (mycobiome) and aflatoxin in stored in-shell peanuts at four different areas of China. <i>Frontiers in Microbiology</i> , 2015, 6, 1055.	1.5	37
126	Genome sequencing reveals a new lineage associated with lablab bean and genetic exchange between <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> and <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1080.	1.5	29
127	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
128	Transplanting Soil Microbiomes Leads to Lasting Effects on Willow Growth, but not on the Rhizosphere Microbiome. <i>Frontiers in Microbiology</i> , 2015, 6, 1436.	1.5	98
129	Endosymbiont Dominated Bacterial Communities in a Dwarf Spider. <i>PLoS ONE</i> , 2015, 10, e0117297.	1.1	52
130	HCV Genotyping from NGS Short Reads and Its Application in Genotype Detection from HCV Mixed Infected Plasma. <i>PLoS ONE</i> , 2015, 10, e0122082.	1.1	14
131	Determining Microeukaryotic Plankton Community around Xiamen Island, Southeast China, Using Illumina MiSeq and PCR-DGGE Techniques. <i>PLoS ONE</i> , 2015, 10, e0127721.	1.1	29
132	Multi-Analytical Approach Reveals Potential Microbial Indicators in Soil for Sugarcane Model Systems. <i>PLoS ONE</i> , 2015, 10, e0129765.	1.1	52

#	ARTICLE	IF	CITATIONS
133	Inter-Individual Differences in the Oral Bacteriome Are Greater than Intra-Day Fluctuations in Individuals. PLoS ONE, 2015, 10, e0131607.	1.1	47
134	Perilipin-2 Modulates Lipid Absorption and Microbiome Responses in the Mouse Intestine. PLoS ONE, 2015, 10, e0131944.	1.1	43
135	Genomic Analysis and Isolation of RNA Polymerase II Dependent Promoters from Spodoptera frugiperda. PLoS ONE, 2015, 10, e0132898.	1.1	31
136	Identification of Candidate Coral Pathogens on White Band Disease-Infected Staghorn Coral. PLoS ONE, 2015, 10, e0134416.	1.1	61
137	Rescue of Fructose-Induced Metabolic Syndrome by Antibiotics or Faecal Transplantation in a Rat Model of Obesity. PLoS ONE, 2015, 10, e0134893.	1.1	135
138	Bacterial Landscape of Bloodstream Infections in Neutropenic Patients via High Throughput Sequencing. PLoS ONE, 2015, 10, e0135756.	1.1	43
139	Bacterial Diversity and Community Structure in the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> and <i>B. mucronatus</i> with Different Virulence by High-Throughput Sequencing of the 16S rDNA. PLoS ONE, 2015, 10, e0137386.	1.1	27
140	The Effects of Synthetic Estrogen Exposure on the Sexually Dimorphic Liver Transcriptome of the Sex-Role-Reversed Gulf Pipefish. PLoS ONE, 2015, 10, e0139401.	1.1	15
141	Naturally Occurring Stilbenoid TSG Reverses Non-Alcoholic Fatty Liver Diseases via Gut-Liver Axis. PLoS ONE, 2015, 10, e0140346.	1.1	37
142	Antepartum Antibiotic Treatment Increases Offspring Susceptibility to Experimental Colitis: A Role of the Gut Microbiota. PLoS ONE, 2015, 10, e0142536.	1.1	137
143	The Consumption of Bicarbonate-Rich Mineral Water Improves Glycemic Control. Evidence-based Complementary and Alternative Medicine, 2015, 2015, 1-10.	0.5	42
144	Microbial diversity in the deep-sea sediments of Iheya North and Iheya Ridge, Okinawa Trough. Microbiological Research, 2015, 177, 43-52.	2.5	62
145	Effects of aeration strategy on the evolution of dissolved organic matter (DOM) and microbial community structure during sludge bio-drying. Applied Microbiology and Biotechnology, 2015, 99, 7321-7331.	1.7	64
146	Comprehensive analysis of the T-cell receptor beta chain gene in rhesus monkey by high throughput sequencing. Scientific Reports, 2015, 5, 10092.	1.6	35
147	Analyses of soil microbial community compositions and functional genes reveal potential consequences of natural forest succession. Scientific Reports, 2015, 5, 10007.	1.6	162
148	Long-term forest soil warming alters microbial communities in temperate forest soils. Frontiers in Microbiology, 2015, 6, 104.	1.5	270
149	Size-fractionated diversity of eukaryotic microbial communities in the Eastern Tropical North Pacific oxygen minimum zone. FEMS Microbiology Ecology, 2015, 91, .	1.3	34
150	Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. ISME Journal, 2015, 9, 2561-2572.	4.4	134

#	ARTICLE	IF	CITATIONS
151	Genomic features separating ten strains of <i>Neorhizobium galegae</i> with different symbiotic phenotypes. <i>BMC Genomics</i> , 2015, 16, 348.	1.2	12
152	Accelerated methanogenesis from effluents of hydrogen-producing stage in anaerobic digestion by mixed cultures enriched with acetate and nano-sized magnetite particles. <i>Bioresource Technology</i> , 2015, 190, 132-139.	4.8	49
153	Increasing aridity reduces soil microbial diversity and abundance in global drylands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15684-15689.	3.3	728
154	Fecal Bacterial Composition of the Endangered Yangtze Finless Porpoises Living Under Captive and Semi-natural Conditions. <i>Current Microbiology</i> , 2016, 72, 306-14.	1.0	21
155	Interindividual differences in response to treatment with butyrate-producing <i>Butyricoccus pullicaecorum</i> 25â€³T studied in an in vitro gut model. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	50
156	Large-scale transcriptome sequencing reveals novel expression patterns for key sex-related genes in a sex-changing fish. <i>Biology of Sex Differences</i> , 2015, 6, 26.	1.8	100
157	Complete Genome Sequences of Field Isolates of <i>Mycobacterium bovis</i> and <i>Mycobacterium caprae</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
158	Genome Sequences of 11 Shiga Toxin-Producing <i>Escherichia coli</i> Strains. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
159	Complete Genome Sequence of <i>Ehrlichia mineirensis</i> , a Novel Organism Closely Related to <i>Ehrlichia canis</i> with a New Host Association. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
160	Draft Genome Sequences of <i>Mycobacterium setense</i> Type Strain DSM-45070 and the Nonpathogenic Strain <i>Manresensis</i> , Isolated from the Bank of the Cardener River in Manresa, Catalonia, Spain. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
161	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. , 2015, , 563-612.		8
162	A Greenhouse Assay on the Effect of Applied Urea Amount on the Rhizospheric Soil Bacterial Communities. <i>Indian Journal of Microbiology</i> , 2015, 55, 406-414.	1.5	12
163	Broad CTL response is required to clear latent HIV-1 due to dominance of escape mutations. <i>Nature</i> , 2015, 517, 381-385.	13.7	469
164	Nextâ€³generation sequencing workflow for assembly of nonmodel mitogenomes exemplified with North Pacific albatrosses (<i>Phoebastria</i> spp.). <i>Molecular Ecology Resources</i> , 2015, 15, 893-902.	2.2	18
165	Comparative analysis of microbial community of novel lactic acid fermentation inoculated with different undefined mixed cultures. <i>Bioresource Technology</i> , 2015, 179, 268-274.	4.8	48
166	Illumina sequencing-based analysis of free-living bacterial community dynamics during an Akashiwo sanguine bloom in Xiamen sea, China. <i>Scientific Reports</i> , 2015, 5, 8476.	1.6	101
167	Analyses of the mitochondrial genome of <i>Leiopelma hochstetteri</i> argues against the full drowning of New Zealand. <i>Journal of Biogeography</i> , 2015, 42, 1066-1076.	1.4	18
168	Integrated metagenomics and network analysis of soil microbial community of the forest timberline. <i>Scientific Reports</i> , 2015, 5, 7994.	1.6	97

#	ARTICLE	IF	CITATIONS
169	The influence of invasive jellyfish blooms on the aquatic microbiome in a coastal lagoon (Varano, SE) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.2	58
170	Nhumirim virus, a novel flavivirus isolated from mosquitoes from the Pantanal, Brazil. Archives of Virology, 2015, 160, 21-27.	0.9	38
171	Ammonia-oxidizing archaea versus bacteria in two soil aquifer treatment systems. Applied Microbiology and Biotechnology, 2015, 99, 1337-1347.	1.7	29
172	Single Nucleotide Polymorphism Identification in Polyploids: A Review, Example, and Recommendations. Molecular Plant, 2015, 8, 831-846.	3.9	159
173	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. Microbial Ecology, 2015, 70, 411-424.	1.4	118
174	Responses of Microbial Communities to Single-Walled Carbon Nanotubes in Phenol Wastewater Treatment Systems. Environmental Science & Technology, 2015, 49, 4627-4635.	4.6	81
175	Long-term nickel exposure altered the bacterial community composition but not diversity in two contrasting agricultural soils. Environmental Science and Pollution Research, 2015, 22, 10496-10505.	2.7	24
176	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	3.6	6
177	A two-phase binning algorithm using l-mer frequency on groups of non-overlapping reads. Algorithms for Molecular Biology, 2015, 10, 2.	0.3	33
178	Different Inc11 plasmids from Escherichia coli carry ISEcp1-blaCTX-M-15 associated with different Tn2-derived elements. Plasmid, 2015, 80, 118-126.	0.4	39
180	Profiling microbial community structures across six large oilfields in China and the potential role of dominant microorganisms in bioremediation. Applied Microbiology and Biotechnology, 2015, 99, 8751-8764.	1.7	35
181	Plant genotype-specific archaeal and bacterial endophytes but similar Bacillus antagonists colonize Mediterranean olive trees. Frontiers in Microbiology, 2015, 6, 138.	1.5	154
182	MiFish, a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species. Royal Society Open Science, 2015, 2, 150088.	1.1	790
183	PGPR enhanced phytoremediation of petroleum contaminated soil and rhizosphere microbial community response. Chemosphere, 2015, 138, 592-598.	4.2	183
184	The human salivary microbiome exhibits temporal stability in bacterial diversity. FEMS Microbiology Ecology, 2015, 91, fiv091.	1.3	75
185	Analysis of trichloroethylene removal and bacterial community function based on pH-adjusted in an upflow anaerobic sludge blanket reactor. Applied Microbiology and Biotechnology, 2015, 99, 9289-9297.	1.7	12
186	Missense mutations in <i>TENM4</i> , a regulator of axon guidance and central myelination, cause essential tremor. Human Molecular Genetics, 2015, 24, 5677-5686.	1.4	134
187	Optimized deep-targeted proteotranscriptomic profiling reveals unexplored <i>Conus</i> toxin diversity and novel cysteine frameworks. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3782-91.	3.3	85

#	ARTICLE	IF	CITATIONS
188	No assembly required: Full-length MHC class I allele discovery by PacBio circular consensus sequencing. <i>Human Immunology</i> , 2015, 76, 891-896.	1.2	68
189	Illumina-based analysis the microbial diversity associated with <i>Thalassia hemprichii</i> in Xincun Bay, South China Sea. <i>Ecotoxicology</i> , 2015, 24, 1548-1556.	1.1	39
190	Unraveling CRISPR-Cas9 genome engineering parameters via a library-on-library approach. <i>Nature Methods</i> , 2015, 12, 823-826.	9.0	361
191	Ecophysiology of uncultivated marine euryarchaea is linked to particulate organic matter. <i>ISME Journal</i> , 2015, 9, 1747-1763.	4.4	94
192	Comparative Phylodynamics of Rabbit Hemorrhagic Disease Virus in Australia and New Zealand. <i>Journal of Virology</i> , 2015, 89, 9548-9558.	1.5	32
193	Complete Genome Sequences of vB_LmoS_188 and vB_LmoS_293, Two Bacteriophages with Specificity for <i>Listeria monocytogenes</i> Strains of Serotypes 4b and 4e. <i>Genome Announcements</i> , 2015, 3, .	0.8	28
194	Draft Genome Sequence of <i>Bacillus coagulans</i> NL01, a Wonderful <scp> </scp> -Lactic Acid Producer. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
195	Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. <i>Science</i> , 2015, 349, 860-864.	6.0	957
196	Reactor performance and microbial community dynamics during aerobic degradation and detoxification of Acid Red B with activated sludge bioaugmented by a yeast <i>Candida tropicalis</i> TL-F1 in MBR. <i>International Biodeterioration and Biodegradation</i> , 2015, 104, 149-156.	1.9	29
197	Error filtering, pair assembly and error correction for next-generation sequencing reads. <i>Bioinformatics</i> , 2015, 31, 3476-3482.	1.8	1,102
198	Forest harvesting reduces the soil metagenomic potential for biomass decomposition. <i>ISME Journal</i> , 2015, 9, 2465-2476.	4.4	96
199	The Infant Nasopharyngeal Microbiome Impacts Severity of Lower Respiratory Infection and Risk of Asthma Development. <i>Cell Host and Microbe</i> , 2015, 17, 704-715.	5.1	721
200	Assessing the performance of the Oxford Nanopore Technologies MinION. <i>Biomolecular Detection and Quantification</i> , 2015, 3, 1-8.	7.0	436
201	Metagenomic sequencing reveals altered metabolic pathways in the oral microbiota of sailors during a long sea voyage. <i>Scientific Reports</i> , 2015, 5, 9131.	1.6	29
202	Effect of biofertilizer for suppressing <i>Fusarium</i> wilt disease of banana as well as enhancing microbial and chemical properties of soil under greenhouse trial. <i>Applied Soil Ecology</i> , 2015, 93, 111-119.	2.1	97
203	Ubiquitous L1 Mosaicism in Hippocampal Neurons. <i>Cell</i> , 2015, 161, 228-239.	13.5	292
204	Trichloroethylene removal and bacterial variations in the up-flow anaerobic sludge blanket reactor in response to temperature shifts. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6091-6102.	1.7	13
205	Small RNAs derived from tRNAs and rRNAs are highly enriched in exosomes from both old and new world <i>Leishmania</i> providing evidence for conserved exosomal RNA Packaging. <i>BMC Genomics</i> , 2015, 16, 151.	1.2	136

#	ARTICLE	IF	CITATIONS
206	Highly diversified fungi are associated with the achlorophyllous orchid <i>Gastrodia flavilabella</i> . <i>BMC Genomics</i> , 2015, 16, 185.	1.2	19
207	Functional analysis of <i>Girardia tigrina</i> transcriptome seeds pipeline for anthelmintic target discovery. <i>Parasites and Vectors</i> , 2015, 8, 34.	1.0	12
208	Insights from the Metagenome of an Acid Salt Lake: The Role of Biology in an Extreme Depositional Environment. <i>PLoS ONE</i> , 2015, 10, e0122869.	1.1	44
209	Adaptation of soil microbial community structure and function to chronic metal contamination at an abandoned Pb-Zn mine. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	1.3	119
210	Evaluating the performance of anchored hybrid enrichment at the tips of the tree of life: a phylogenetic analysis of Australian <i>Eugongylus</i> group scincid lizards. <i>BMC Evolutionary Biology</i> , 2015, 15, 62.	3.2	57
211	Differential Single Nucleotide Polymorphism-Based Analysis of an Outbreak Caused by <i>Salmonella enterica</i> Serovar Manhattan Reveals Epidemiological Details Missed by Standard Pulsed-Field Gel Electrophoresis. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1227-1238.	1.8	19
212	The location and translocation of <i>ndh</i> genes of chloroplast origin in the Orchidaceae family. <i>Scientific Reports</i> , 2015, 5, 9040.	1.6	143
213	Illumina MiSeq Sequencing Reveals Diverse Microbial Communities of Activated Sludge Systems Stimulated by Different Aromatics for Indigo Biosynthesis from Indole. <i>PLoS ONE</i> , 2015, 10, e0125732.	1.1	41
214	A cysteine-clamp gene drives embryo polarity in the midge <i>Chironomus</i> . <i>Science</i> , 2015, 348, 1040-1042.	6.0	57
215	Enhanced Protein Production in <i>Escherichia coli</i> by Optimization of Cloning Scars at the Vector-Coding Sequence Junction. <i>ACS Synthetic Biology</i> , 2015, 4, 959-965.	1.9	46
216	Two decades of warming increases diversity of a potentially lignolytic bacterial community. <i>Frontiers in Microbiology</i> , 2015, 6, 480.	1.5	73
217	Conductive iron oxide minerals accelerate syntrophic cooperation in methanogenic benzoate degradation. <i>Journal of Hazardous Materials</i> , 2015, 293, 37-45.	6.5	148
218	Exoelectrogenic capacity of host microbiota predicts lymphocyte recruitment to the gut. <i>Physiological Genomics</i> , 2015, 47, 243-252.	1.0	21
219	Bacterial communities in haloalkaliphilic sulfate-reducing bioreactors under different electron donors revealed by 16S rRNA MiSeq sequencing. <i>Journal of Hazardous Materials</i> , 2015, 295, 176-184.	6.5	37
220	The impact of systemic and copper pesticide applications on the phyllosphere microflora of tomatoes. <i>Journal of the Science of Food and Agriculture</i> , 2015, 95, 1116-1125.	1.7	40
221	Isolation of Camelid Single-Domain Antibodies Against Native Proteins Using Recombinant Multivalent Peptide Ligands. <i>Methods in Molecular Biology</i> , 2015, 1348, 167-189.	0.4	2
222	Mechanism, kinetics and microbiology of inhibition caused by long-chain fatty acids in anaerobic digestion of algal biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 141.	6.2	116
223	Scale-dependent effects of climate and geographic distance on bacterial diversity patterns across northern China's grasslands. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv133.	1.3	87

#	ARTICLE	IF	CITATIONS
224	Microsatellite Markers for the New Zealand Endemic <i>Myosotis pygmaea</i> Species Group (Boraginaceae) Amplify Across Species. <i>Applications in Plant Sciences</i> , 2015, 3, 1500027.	0.8	8
225	Noninvasive monitoring of infection and rejection after lung transplantation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13336-13341.	3.3	269
226	TNFR2 Deficiency Acts in Concert with Gut Microbiota To Precipitate Spontaneous Sex-Biased Central Nervous System Demyelinating Autoimmune Disease. <i>Journal of Immunology</i> , 2015, 195, 4668-4684.	0.4	53
227	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. <i>BMC Bioinformatics</i> , 2015, 16, 203.	1.2	49
228	Assembly independent functional annotation of short-read data using SOFA: Short-ORF functional annotation. , 2015, , .		2
229	The Genome and Methyloome of a Beetle with Complex Social Behavior, <i>Nicrophorus vespilloides</i> (Coleoptera: Silphidae). <i>Genome Biology and Evolution</i> , 2015, 7, 3383-3396.	1.1	87
230	Dietary analysis on the shallow-water hydrothermal vent crab <i>Xenograpsus testudinatus</i> using Illumina sequencing. <i>Marine Biology</i> , 2015, 162, 1787-1798.	0.7	21
231	Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. <i>BMC Microbiology</i> , 2015, 15, 125.	1.3	222
232	Cultureâ€dependent and cultureâ€independent characterization of potentially functional biphenylâ€degrading bacterial community in response to extracellular organic matter from <i>Micrococcus luteus</i> . <i>Microbial Biotechnology</i> , 2015, 8, 569-578.	2.0	26
233	Successional Trajectories of Rhizosphere Bacterial Communities over Consecutive Seasons. <i>MBio</i> , 2015, 6, e00746.	1.8	232
234	Poly(A)-specific ribonuclease (PARN) mediates 3â€end maturation of the telomerase RNA component. <i>Nature Genetics</i> , 2015, 47, 1482-1488.	9.4	149
235	Ubiquitous healthy diatoms in the deep sea confirm deep carbon injection by the biological pump. <i>Nature Communications</i> , 2015, 6, 7608.	5.8	177
236	Limited dissemination of the wastewater treatment plant core resistome. <i>Nature Communications</i> , 2015, 6, 8452.	5.8	173
237	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science & Technology</i> , 2015, 49, 12628-12640.	4.6	72
238	Biostimulation of biogas producing microcosm for enhancing oil recovery in low-permeability oil reservoir. <i>RSC Advances</i> , 2015, 5, 91869-91877.	1.7	8
239	Description of a novel pectin-degrading bacterial species <i>Prevotella pectinovora</i> sp. nov., based on its phenotypic and genomic traits. <i>Journal of Microbiology</i> , 2015, 53, 503-510.	1.3	21
240	Draft Genome Sequences of 10 <i>Microbacterium</i> spp., with Emphasis on Heavy Metal-Contaminated Environments. <i>Genome Announcements</i> , 2015, 3, .	0.8	19
241	The complicated substrates enhance the microbial diversity and zinc leaching efficiency in sphalerite bioleaching system. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10311-10322.	1.7	26

#	ARTICLE	IF	CITATIONS
242	Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10967-10972.	3.3	1,023
243	Fecal Microbial Community Structure Is Stable over Time and Related to Variation in Macronutrient and Micronutrient Intakes in Lactating Women. <i>Journal of Nutrition</i> , 2015, 145, 2379-2388.	1.3	65
244	Quantitative Microbial Ecology through Stable Isotope Probing. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7570-7581.	1.4	242
245	Identification of cross-reactive single-domain antibodies against serum albumin using next-generation DNA sequencing. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 379-383.	1.0	29
246	Advancements in the application of NanoSIMS and Raman microspectroscopy to investigate the activity of microbial cells in soils. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv106.	1.3	105
247	Characterization of bacterial diversity associated with deep sea ferromanganese nodules from the South China Sea. <i>Journal of Microbiology</i> , 2015, 53, 598-605.	1.3	18
248	Cas9 gRNA engineering for genome editing, activation and repression. <i>Nature Methods</i> , 2015, 12, 1051-1054.	9.0	272
249	Responses in ileal and cecal bacteria to low and high amylose/amylopectin ratio diets in growing pigs. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10627-10638.	1.7	25
250	Biogas production from <i>Macrocystis pyrifera</i> biomass in seawater system. <i>Bioresource Technology</i> , 2015, 197, 339-347.	4.8	19
251	Cathelicidin Antimicrobial Peptide: A Novel Regulator of Islet Function, Islet Regeneration, and Selected Gut Bacteria. <i>Diabetes</i> , 2015, 64, 4135-4147.	0.3	50
252	ATP selection in a random peptide library consisting of prebiotic amino acids. <i>Biochemical and Biophysical Research Communications</i> , 2015, 466, 400-405.	1.0	13
253	Modified Genomic Sequencing PCR Using the MiSeq Platform to Identify Retroviral Integration Sites. <i>Human Gene Therapy Methods</i> , 2015, 26, 221-227.	2.1	15
254	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
255	Sex-specific molecular genetic response to UVB exposure in <i>Xiphophorus maculatus</i> skin. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2015, 178, 76-85.	1.3	14
256	Is the whole greater than the sum of its parts? De novo assembly strategies for bacterial genomes based on paired-end sequencing. <i>BMC Genomics</i> , 2015, 16, 648.	1.2	8
257	Shifts of tundra bacterial and archaeal communities along a permafrost thaw gradient in Alaska. <i>Molecular Ecology</i> , 2015, 24, 222-234.	2.0	127
258	Microbial community analysis in rice paddy soils irrigated by acid mine drainage contaminated water. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 2911-2922.	1.7	131
259	Whole-Genome Phylogenomic Heterogeneity of <i>Neisseria gonorrhoeae</i> Isolates with Decreased Cephalosporin Susceptibility Collected in Canada between 1989 and 2013. <i>Journal of Clinical Microbiology</i> , 2015, 53, 191-200.	1.8	103

#	ARTICLE	IF	CITATIONS
260	Protistan diversity in a permanently stratified meromictic lake (Lake <i>A</i> latsee, <i>SW</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.8	39
261	Enhanced degradation of biphenyl from PCB-contaminated sediments: the impact of extracellular organic matter from <i>Micrococcus luteus</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1989-2000.	1.7	48
262	Influence of organic loading rate and solid retention time on polyhydroxybutyrate production from hybrid poplar hydrolysates using mixed microbial cultures. <i>Bioresource Technology</i> , 2015, 175, 23-33.	4.8	36
263	Draft Genome Sequence for the Type Strain of <i>Corynebacterium afermentans</i> LCDC 88-0199 T, Isolated from a Human Blood Culture. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
264	Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers. <i>F1000Research</i> , 2015, 4, 1422.	0.8	36
265	Mitochondrion-to-Chloroplast DNA Transfers and Intragenomic Proliferation of Chloroplast Group II Introns in <i>Gloeotilopsis</i> Green Algae (Ulotrichales, Ulvophyceae). <i>Genome Biology and Evolution</i> , 2016, 8, 2789-2805.	1.1	34
266	Biodiversity management of organic orchard enhances both ecological and economic profitability. <i>PeerJ</i> , 2016, 4, e2137.	0.9	29
267	The Gut Microbial Community of Antarctic Fish Detected by 16S rRNA Gene Sequence Analysis. <i>BioMed Research International</i> , 2016, 2016, 1-7.	0.9	37
268	Laboratory Evaluation of Co-digesting Beef Manure and Waste Kitchen Oil. , 2016, , .		0
269	<i>Lactobacillus fermentum</i> CRL1446 Ameliorates Oxidative and Metabolic Parameters by Increasing Intestinal Feruloyl Esterase Activity and Modulating Microbiota in Caloric-Restricted Mice. <i>Nutrients</i> , 2016, 8, 415.	1.7	37
270	Benchmarking DNA Metabarcoding for Biodiversity-Based Monitoring and Assessment. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	157
271	Bacterial Communities Vary between Sinuses in Chronic Rhinosinusitis Patients. <i>Frontiers in Microbiology</i> , 2015, 6, 1532.	1.5	30
272	Comparison of Fungal Community in Black Pepper-Vanilla and Vanilla Monoculture Systems Associated with Vanilla Fusarium Wilt Disease. <i>Frontiers in Microbiology</i> , 2016, 7, 117.	1.5	78
273	An Exogenous Surfactant-Producing <i>Bacillus subtilis</i> Facilitates Indigenous Microbial Enhanced Oil Recovery. <i>Frontiers in Microbiology</i> , 2016, 7, 186.	1.5	34
274	Diversity and Metabolic Potentials of Subsurface Crustal Microorganisms from the Western Flank of the Mid-Atlantic Ridge. <i>Frontiers in Microbiology</i> , 2016, 7, 363.	1.5	37
275	<i>Mycobacterium avium</i> Subspecies <i>paratuberculosis</i> Infection Modifies Gut Microbiota under Different Dietary Conditions in a Rabbit Model. <i>Frontiers in Microbiology</i> , 2016, 7, 446.	1.5	56
276	Reconstruction of Bacterial and Viral Genomes from Multiple Metagenomes. <i>Frontiers in Microbiology</i> , 2016, 7, 469.	1.5	13
277	Investigation of the Activity of the Microorganisms in a Reblochon-Style Cheese by Metatranscriptomic Analysis. <i>Frontiers in Microbiology</i> , 2016, 7, 536.	1.5	56

#	ARTICLE	IF	CITATIONS
278	Comparison of Microbial Communities Isolated from Feces of Asymptomatic Salmonella-Shedding and Non-Salmonella Shedding Dairy Cows. <i>Frontiers in Microbiology</i> , 2016, 7, 691.	1.5	7
279	Pika Population Density Is Associated with the Composition and Diversity of Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 758.	1.5	68
280	Fungal and Prokaryotic Activities in the Marine Subsurface Biosphere at Peru Margin and Canterbury Basin Inferred from RNA-Based Analyses and Microscopy. <i>Frontiers in Microbiology</i> , 2016, 7, 846.	1.5	52
281	A Modified SDS-Based DNA Extraction Method for High Quality Environmental DNA from Seafloor Environments. <i>Frontiers in Microbiology</i> , 2016, 07, 986.	1.5	80
282	Insights into Abundant Rumen Ureolytic Bacterial Community Using Rumen Simulation System. <i>Frontiers in Microbiology</i> , 2016, 7, 1006.	1.5	52
283	Metatranscriptional Response of Chemoautotrophic <i>Ifremeria nautili</i> Endosymbionts to Differing Sulfur Regimes. <i>Frontiers in Microbiology</i> , 2016, 7, 1074.	1.5	11
284	Biogeographic Distribution Patterns of Bacteria in Typical Chinese Forest Soils. <i>Frontiers in Microbiology</i> , 2016, 7, 1106.	1.5	90
285	Diet Diversity Is Associated with Beta but not Alpha Diversity of Pika Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 1169.	1.5	117
286	Diversity and Composition of Bacterial Community in Soils and Lake Sediments from an Arctic Lake Area. <i>Frontiers in Microbiology</i> , 2016, 7, 1170.	1.5	59
287	Microbial Communities in Sediments of Lagos Lagoon, Nigeria: Elucidation of Community Structure and Potential Impacts of Contamination by Municipal and Industrial Wastes. <i>Frontiers in Microbiology</i> , 2016, 7, 1213.	1.5	52
288	Lichen-Associated Fungal Community in <i>Hypogymnia hypotrypa</i> (Parmeliaceae, Ascomycota) Affected by Geographic Distribution and Altitude. <i>Frontiers in Microbiology</i> , 2016, 7, 1231.	1.5	26
289	Physiological and Metagenomic Analyses of Microbial Mats Involved in Self-Purification of Mine Waters Contaminated with Heavy Metals. <i>Frontiers in Microbiology</i> , 2016, 7, 1252.	1.5	57
290	A Multi-Omics Approach to Evaluate the Quality of Milk Whey Used in Ricotta Cheese Production. <i>Frontiers in Microbiology</i> , 2016, 7, 1272.	1.5	24
291	The Probiotic <i>Butyricoccus pullicaecorum</i> Reduces Feed Conversion and Protects from Potentially Harmful Intestinal Microorganisms and Necrotic Enteritis in Broilers. <i>Frontiers in Microbiology</i> , 2016, 7, 1416.	1.5	99
292	Microbiome Dynamics of a Polychlorobiphenyl (PCB) Historically Contaminated Marine Sediment under Conditions Promoting Reductive Dechlorination. <i>Frontiers in Microbiology</i> , 2016, 7, 1502.	1.5	40
293	High Ozone (O ₃) Affects the Fitness Associated with the Microbial Composition and Abundance of <i>Q</i> Biotype <i>Bemisia tabaci</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1593.	1.5	6
294	Distinct Factors Shape Aquatic and Sedimentary Microbial Community Structures in the Lakes of Western China. <i>Frontiers in Microbiology</i> , 2016, 7, 1782.	1.5	74
295	Rapid Fermentable Substance Modulates Interactions between Ruminant Commensals and Toll-Like Receptors in Promotion of Immune Tolerance of Goat Rumen. <i>Frontiers in Microbiology</i> , 2016, 7, 1812.	1.5	57

#	ARTICLE	IF	CITATIONS
296	The Shifts of Diazotrophic Communities in Spring and Summer Associated with Coral <i>Galaxea astreata</i> , <i>Pavona decussata</i> , and <i>Porites lutea</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1870.	1.5	12
297	Microbial Community of High Arsenic Groundwater in Agricultural Irrigation Area of Hetao Plain, Inner Mongolia. <i>Frontiers in Microbiology</i> , 2016, 7, 1917.	1.5	44
298	Microbial Community Structure and Function of Soil Following Ecosystem Conversion from Native Forests to Teak Plantation Forests. <i>Frontiers in Microbiology</i> , 2016, 7, 1976.	1.5	28
299	A High-Level Fungal Diversity in the Intertidal Sediment of Chinese Seas Presents the Spatial Variation of Community Composition. <i>Frontiers in Microbiology</i> , 2016, 7, 2098.	1.5	45
300	Early Recovery of <i>Salmonella</i> from Food Using a 6-Hour Non-selective Pre-enrichment and Reformulation of Tetrathionate Broth. <i>Frontiers in Microbiology</i> , 2016, 7, 2103.	1.5	38
301	Evaluating the Contribution of Gut Microbiota to the Variation of Porcine Fatness with the Cecum and Fecal Samples. <i>Frontiers in Microbiology</i> , 2016, 07, 2108.	1.5	66
302	Analysis of DNA Methylation and Hydroxymethylation in the Genome of Crustacean <i>Daphnia pulex</i> . <i>Genes</i> , 2016, 7, 1.	1.0	47
303	Construction and Characterization of a Cellulolytic Consortium Enriched from the Hindgut of <i>Holotrichia parallela</i> Larvae. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1646.	1.8	18
304	First Comparative Analysis of the Community Structures and Carbon Metabolic Pathways of the Bacteria Associated with <i>Alvinocaris longirostris</i> in a Hydrothermal Vent of Okinawa Trough. <i>PLoS ONE</i> , 2016, 11, e0154359.	1.1	15
305	Selection on Coding and Regulatory Variation Maintains Individuality in Major Urinary Protein Scent Marks in Wild Mice. <i>PLoS Genetics</i> , 2016, 12, e1005891.	1.5	46
306	The Challenges of Implementing Next Generation Sequencing Across a Large Healthcare System, and the Molecular Epidemiology and Antibiotic Susceptibilities of Carbapenemase-Producing Bacteria in the Healthcare System of the U.S. Department of Defense. <i>PLoS ONE</i> , 2016, 11, e0155770.	1.1	22
307	Effects of Diets Supplemented with Ensiled Mulberry Leaves and Sun-Dried Mulberry Fruit Pomace on the Ruminal Bacterial and Archaeal Community Composition of Finishing Steers. <i>PLoS ONE</i> , 2016, 11, e0156836.	1.1	18
308	Five Complete Chloroplast Genome Sequences from <i>Diospyros</i> : Genome Organization and Comparative Analysis. <i>PLoS ONE</i> , 2016, 11, e0159566.	1.1	48
309	Preservation Obscures Pelagic Deep-Sea Fish Diversity: Doubling the Number of Sole-Bearing Opisthoproctids and Resurrection of the Genus <i>Monacoa</i> (Opisthoproctidae, Argentiniformes). <i>PLoS ONE</i> , 2016, 11, e0159762.	1.1	11
310	A Rational Engineering Strategy for Designing Protein A-Binding Camelid Single-Domain Antibodies. <i>PLoS ONE</i> , 2016, 11, e0163113.	1.1	24
311	Cross-Neutralising Nanobodies Bind to a Conserved Pocket in the Hemagglutinin Stem Region Identified Using Yeast Display and Deep Mutational Scanning. <i>PLoS ONE</i> , 2016, 11, e0164296.	1.1	25
312	HIV-1 Integrates Widely throughout the Genome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005931.	2.1	20
313	Transcriptome Analysis of <i>Gerbera hybrida</i> Including in silico Confirmation of Defense Genes Found. <i>Frontiers in Plant Science</i> , 2016, 7, 247.	1.7	23

#	ARTICLE	IF	CITATIONS
314	An evaluation of transcriptome-based exon capture for frog phylogenomics across multiple scales of divergence (Class: Amphibia, Order: Anura). <i>Molecular Ecology Resources</i> , 2016, 16, 1069-1083.	2.2	92
315	Roles of the <i>L</i> aodelphax striatellus Down syndrome cell adhesion molecule in Rice stripe virus infection of its insect vector. <i>Insect Molecular Biology</i> , 2016, 25, 413-421.	1.0	7
316	Application of a dense genetic map for assessment of genomic responses to selection and inbreeding in <i>Heliothis virescens</i> . <i>Insect Molecular Biology</i> , 2016, 25, 385-400.	1.0	16
317	Influences of plant type on bacterial and archaeal communities in constructed wetland treating polluted river water. <i>Environmental Science and Pollution Research</i> , 2016, 23, 19570-19579.	2.7	32
318	MHC, parasites and antler development in red deer: no support for the Hamilton & Zuk hypothesis. <i>Journal of Evolutionary Biology</i> , 2016, 29, 617-632.	0.8	21
319	Characterization of the cyanobacteria and associated bacterial community from an ephemeral wetland in New Zealand. <i>Journal of Phycology</i> , 2016, 52, 761-773.	1.0	12
320	The evolution of silicon transporters in diatoms. <i>Journal of Phycology</i> , 2016, 52, 716-731.	1.0	44
321	Cover crops prevent the deleterious effect of nitrogen fertilisation on bacterial diversity by maintaining the carbon content of ploughed soil. <i>Geoderma</i> , 2016, 281, 49-57.	2.3	75
322	Environmental DNA metabarcoding of lake fish communities reflects long-term data from established survey methods. <i>Molecular Ecology</i> , 2016, 25, 3101-3119.	2.0	452
323	Development and Validation of a Template-Independent Next-Generation Sequencing Assay for Detecting Low-Level Resistance-Associated Variants of Hepatitis C Virus. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 643-656.	1.2	11
324	Characterization of the indigenous microflora in raw and pasteurized buffalo milk during storage at refrigeration temperature by high-throughput sequencing. <i>Journal of Dairy Science</i> , 2016, 99, 7016-7024.	1.4	25
325	Draft Genome Sequence of <i>Trueperella bernardiae</i> LCDC 89-0504 T, Isolated from a Human Blood Culture. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
326	Relationships of decomposability and C/N ratio in different types of organic matter with suppression of <i>Fusarium oxysporum</i> and microbial communities during reductive soil disinfestation. <i>Biological Control</i> , 2016, 101, 103-113.	1.4	78
327	Phylogenetic marker development for target enrichment from transcriptome and genome skim data: the pipeline and its application in southern African <i>Oxalis</i> (Oxalidaceae). <i>Molecular Ecology Resources</i> , 2016, 16, 1124-1135.	2.2	101
328	Carbon content and climate variability drive global soil bacterial diversity patterns. <i>Ecological Monographs</i> , 2016, 86, 373-390.	2.4	173
329	Comparison of three human papillomavirus DNA detection methods: Next generation sequencing, multiplex-PCR and nested-PCR followed by Sanger based sequencing. <i>Journal of Medical Virology</i> , 2016, 88, 888-894.	2.5	22
330	Effects of Specimen Collection Methodologies and Storage Conditions on the Short-Term Stability of Oral Microbiome Taxonomy. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5519-5529.	1.4	30
331	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. <i>Digestive Diseases and Sciences</i> , 2016, 61, 2908-2920.	1.1	121

#	ARTICLE	IF	CITATIONS
332	Elevated IgA Plasmablast Levels in Subjects at Risk of Developing Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2016, 68, 2372-2383.	2.9	74
333	Exon capture phylogenomics: efficacy across scales of divergence. <i>Molecular Ecology Resources</i> , 2016, 16, 1059-1068.	2.2	132
334	Current Research Topics in Plant Virology. , 2016, , .		28
335	Construction and Characterization of Two Novel Transcriptome Assemblies in the Congeneric Porcelain Crabs <i>Petrolisthes cinctipes</i> and <i>P. manimaculis</i> . <i>Integrative and Comparative Biology</i> , 2016, 56, 1092-1102.	0.9	6
336	Coprophilic amoebae and flagellates, including <i>Guttulinopsis</i> , <i>Rosculus</i> and <i>Helkesimastix</i> , characterise a divergent and diverse rhizarian radiation and contribute to a large diversity of faecal-associated protists. <i>Environmental Microbiology</i> , 2016, 18, 1604-1619.	1.8	42
337	Simultaneous identification of host, ectoparasite and pathogen <i>scp</i> DNA via in-solution capture. <i>Molecular Ecology Resources</i> , 2016, 16, 1224-1239.	2.2	31
338	Diversity of ribosomal 16S DNA- and RNA-based bacterial community in an office building drinking water system. <i>Journal of Applied Microbiology</i> , 2016, 120, 1723-1738.	1.4	47
339	Coupling of soil prokaryotic diversity and plant diversity across latitudinal forest ecosystems. <i>Scientific Reports</i> , 2016, 6, 19561.	1.6	50
340	Mucosa-Associated Ileal Microbiota in New-Onset Pediatric Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 1533-1539.	0.9	43
341	Changes in intestinal microflora of <i>Caenorhabditis elegans</i> following <i>Bacillus nematocida</i> B16 infection. <i>Scientific Reports</i> , 2016, 6, 20178.	1.6	21
342	Draft <i>Anaplasma phagocytophilum</i> Genome Sequences from Five Cows, Two Horses, and One Roe Deer Collected in Europe. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
343	Mucosal adherent bacterial dysbiosis in patients with colorectal adenomas. <i>Scientific Reports</i> , 2016, 6, 26337.	1.6	157
344	Beneficial Effects of a Dietary Weight Loss Intervention on Human Gut Microbiome Diversity and Metabolism Are Not Sustained during Weight Maintenance. <i>Obesity Facts</i> , 2016, 9, 379-391.	1.6	48
345	Draft Genome Sequences of <i>Microbacterium hominis</i> LCDC-84-0209 ^T Isolated from a Human Lung Aspirate and <i>Microbacterium laevaniformans</i> LCDC 91-0039 Isolated from a Human Blood Culture. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
346	Draft Genome Sequence of a Novel Mucilaginibacter Member Isolated from Brazilian Amazon Soil. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
347	Evolutionary redesign of the Atlantic cod (<i>Gadus morhua</i> L.) Toll-like receptor repertoire by gene losses and expansions. <i>Scientific Reports</i> , 2016, 6, 25211.	1.6	89
348	Draft Genome Sequences of One Marine and One Clinical <i>Vibrio parahaemolyticus</i> Strain, Both Isolated in Sweden. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
349	Olfactory epithelium changes in germfree mice. <i>Scientific Reports</i> , 2016, 6, 24687.	1.6	49

#	ARTICLE	IF	CITATIONS
350	Prediction of peptidoglycan hydrolases- a new class of antibacterial proteins. BMC Genomics, 2016, 17, 411.	1.2	22
351	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. Biotechnology for Biofuels, 2016, 9, 171.	6.2	134
352	MeFiT: merging and filtering tool for illumina paired-end reads for 16S rRNA amplicon sequencing. BMC Bioinformatics, 2016, 17, 491.	1.2	79
353	Microbial communities and arsenic biogeochemistry at the outflow of an alkaline sulfide-rich hot spring. Scientific Reports, 2016, 6, 25262.	1.6	13
354	Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. BMC Microbiology, 2016, 16, 275.	1.3	143
355	Regional variations in the diversity and predicted metabolic potential of benthic prokaryotes in coastal northern Zhejiang, East China Sea. Scientific Reports, 2016, 6, 38709.	1.6	35
356	pBACode: a random-barcode-based high-throughput approach for BAC paired-end sequencing and physical clone mapping. Nucleic Acids Research, 2017, 45, gkw1261.	6.5	9
357	Genome sequence, population history, and pelage genetics of the endangered African wild dog (<i>Lycaon</i>) Tj ETQq1 1, 0.784314 rgBT /Ove	1.2	23
358	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. DNA Research, 2017, 24, dsw049.	1.5	38
359	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. GigaScience, 2016, 5, 21.	3.3	204
360	The human milk oligosaccharide 2- <i>fucosyllactose</i> attenuates the severity of experimental necrotising enterocolitis by enhancing mesenteric perfusion in the neonatal intestine. British Journal of Nutrition, 2016, 116, 1175-1187.	1.2	145
361	The genome of the Gulf pipefish enables understanding of evolutionary innovations. Genome Biology, 2016, 17, 258.	3.8	76
362	Spotted phenotypes in horses lost attractiveness in the Middle Ages. Scientific Reports, 2016, 6, 38548.	1.6	31
363	Nutrient availability shapes the microbial community structure in sugarcane bagasse compost-derived consortia. Scientific Reports, 2016, 6, 38781.	1.6	56
364	Bacterial communities of the cotton aphid <i>Aphis gossypii</i> associated with Bt cotton in northern China. Scientific Reports, 2016, 6, 22958.	1.6	46
365	Metagenomic analysis of bloodstream infections in patients with acute leukemia and therapy-induced neutropenia. Scientific Reports, 2016, 6, 23532.	1.6	78
366	Scalable metagenomics alignment research tool (SMART): a scalable, rapid, and complete search heuristic for the classification of metagenomic sequences from complex sequence populations. BMC Bioinformatics, 2016, 17, 292.	1.2	25
367	Gut Microbiota and Metabolic Phenotype of <i>Portunus Trituberculatus</i> . Chinese Journal of Analytical Chemistry, 2016, 44, 1867-1873.	0.9	10

#	ARTICLE	IF	CITATIONS
368	The effects of Bt Cry1Ie toxin on bacterial diversity in the midgut of <i>Apis mellifera ligustica</i> (Hymenoptera: Apidae). <i>Scientific Reports</i> , 2016, 6, 24664.	1.6	51
369	Insight into structure dynamics of soil microbiota mediated by the richness of replanted <i>Pseudostellaria heterophylla</i> . <i>Scientific Reports</i> , 2016, 6, 26175.	1.6	47
370	Metagenomic profiling of historic Colorado Front Range flood impact on distribution of riverine antibiotic resistance genes. <i>Scientific Reports</i> , 2016, 6, 38432.	1.6	55
371	Host genome integration and giant virus-induced reactivation of the virophage mavirus. <i>Nature</i> , 2016, 540, 288-291.	13.7	126
372	Colonic luminal microbiota and bacterial metabolite composition in pregnant Huanjiang mini-pigs: effects of food composition at different times of pregnancy. <i>Scientific Reports</i> , 2016, 6, 37224.	1.6	74
373	T Cell Repertoire Diversity Is Decreased in Type 1 Diabetes Patients. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 338-348.	3.0	27
374	Dataset for a <i>Dugesia japonica</i> de novo transcriptome assembly, utilized for defining the voltage-gated like ion channel superfamily. <i>Data in Brief</i> , 2016, 9, 1044-1047.	0.5	12
375	Comparative Phylogenomic Assessment of Mitochondrial Introgression among Several Species of Chipmunks (<i>TAMIAS</i>). <i>Genome Biology and Evolution</i> , 2016, 9, evw254.	1.1	12
376	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. <i>Gut</i> , 2016, 65, 1681-1689.	6.1	312
377	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. <i>Biotechnology for Biofuels</i> , 2016, 9, 156.	6.2	120
378	Variation in fungal microbiome (mycobiome) and aflatoxins during simulated storage of in-shell peanuts and peanut kernels. <i>Scientific Reports</i> , 2016, 6, 25930.	1.6	33
379	MetaDP: a comprehensive web server for disease prediction of 16S rRNA metagenomic datasets. <i>Biophysics Reports</i> , 2016, 2, 106-115.	0.2	9
380	Community and functional diversity of bacteria associated with propagative and dispersal forms of <i>Bursaphelenchus xylophilus</i> . <i>Nematology</i> , 2016, 18, 1185-1198.	0.2	7
381	Complete mitochondrial genome of the endangered Mary River turtle (<i>Elusor macrurus</i>) and low mtDNA variation across the species' range. <i>Australian Journal of Zoology</i> , 2016, 64, 117.	0.6	4
382	A minimalistic microbial food web in an excavated deep subsurface clay rock. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv138.	1.3	29
383	The population genomics of rapid adaptation: disentangling signatures of selection and demography in white sands lizards. <i>Molecular Ecology</i> , 2016, 25, 306-323.	2.0	56
384	Fungal communities from the calcareous deep-sea sediments in the Southwest India Ridge revealed by Illumina sequencing technology. <i>World Journal of Microbiology and Biotechnology</i> , 2016, 32, 78.	1.7	21
385	One step closer to understanding the role of bacteria in diabetic foot ulcers: characterising the microbiome of ulcers. <i>BMC Microbiology</i> , 2016, 16, 54.	1.3	113

#	ARTICLE	IF	CITATIONS
386	Transcriptomic and epigenomic characterization of the developing bat wing. <i>Nature Genetics</i> , 2016, 48, 528-536.	9.4	64
387	Towards the development of multifunctional molecular indicators combining soil biogeochemical and microbiological variables to predict the ecological integrity of silvicultural practices. <i>Microbial Biotechnology</i> , 2016, 9, 316-329.	2.0	3
388	Bacterial characterization of Beijing drinking water by flow cytometry and metagenomic sequencing of the 16S rRNA gene. <i>Ecology and Evolution</i> , 2016, 6, 923-934.	0.8	28
389	Developmental cell death programs license cytotoxic cells to eliminate histocompatible partners. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6520-6525.	3.3	21
390	Deeper insight into the structure of the anaerobic digestion microbial community; the biogas microbiome database is expanded with 157 new genomes. <i>Bioresource Technology</i> , 2016, 216, 260-266.	4.8	132
391	Whole-organism lineage tracing by combinatorial and cumulative genome editing. <i>Science</i> , 2016, 353, aaf7907.	6.0	570
392	Illumina-based analysis of core actinobacteriome in roots, stems, and grains of rice. <i>Microbiological Research</i> , 2016, 190, 12-18.	2.5	34
393	Metagenomic analysis between free-living and cultured <i>Epinephelus fuscoguttatus</i> under different environmental conditions in Indonesian waters. <i>Marine Pollution Bulletin</i> , 2016, 110, 726-734.	2.3	19
394	Detection of Antibiotic Resistance Genes in Source and Drinking Water Samples from a First Nations Community in Canada. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4767-4775.	1.4	103
395	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. <i>ISME Journal</i> , 2016, 10, 2352-2364.	4.4	62
396	Analysis of Gut Microbiome Reveals Significant Differences between Men with Chronic Prostatitis/Chronic Pelvic Pain Syndrome and Controls. <i>Journal of Urology</i> , 2016, 196, 435-441.	0.2	79
397	Genomic Epidemiology and Molecular Resistance Mechanisms of Azithromycin-Resistant <i>Neisseria gonorrhoeae</i> in Canada from 1997 to 2014. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1304-1313.	1.8	124
398	Epithelial calcineurin controls microbiota-dependent intestinal tumor development. <i>Nature Medicine</i> , 2016, 22, 506-515.	15.2	93
399	Seasonality of antibiotic prescriptions for outpatients and resistance genes in sewers and wastewater treatment plant outflow. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw060.	1.3	124
400	The effects of family, dentition, and dental caries on the salivary microbiome. <i>Annals of Epidemiology</i> , 2016, 26, 348-354.	0.9	19
401	The salivary microbiome for differentiating individuals: proof of principle. <i>Microbes and Infection</i> , 2016, 18, 399-405.	1.0	75
402	The Genome and Methylome of a Subsocial Small Carpenter Bee, <i>Ceratina calcarata</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1401-1410.	1.1	71
403	CARD9 impacts colitis by altering gut microbiota metabolism of tryptophan into aryl hydrocarbon receptor ligands. <i>Nature Medicine</i> , 2016, 22, 598-605.	15.2	1,001

#	ARTICLE	IF	CITATIONS
404	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	6.0	1,716
405	Defining the normal core microbiome of conjunctival microbial communities. <i>Clinical Microbiology and Infection</i> , 2016, 22, 643.e7-643.e12.	2.8	159
406	Community proteomics provides functional insight into polyhydroxyalkanoate production by a mixed microbial culture cultivated on fermented dairy manure. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7957-7976.	1.7	17
407	Performance and characteristics of a nitrification air-lift reactor under long-term HRT shortening. <i>International Biodeterioration and Biodegradation</i> , 2016, 111, 45-53.	1.9	38
408	Next-generation sequencing revolution through big data analytics. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2016, 9, 119-149.	1.1	40
409	Genomic variation in the porcine immunoglobulin lambda variable region. <i>Immunogenetics</i> , 2016, 68, 285-293.	1.2	12
410	Bacteriocin from epidemic <i>Listeria</i> strains alters the host intestinal microbiota to favor infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5706-5711.	3.3	166
411	Illumina-based analysis of the rhizosphere microbial communities associated with healthy and wilted Lanzhou lily (<i>Lilium davidii</i> var. <i>unicolor</i>) plants grown in the field. <i>World Journal of Microbiology and Biotechnology</i> , 2016, 32, 95.	1.7	48
412	Exploring fungal diversity in deep-sea sediments from Okinawa Trough using high-throughput Illumina sequencing. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2016, 116, 99-105.	0.6	46
413	Oligotrophic lagoons of the South Pacific Ocean are home to a surprising number of novel eukaryotic microorganisms. <i>Environmental Microbiology</i> , 2016, 18, 4549-4563.	1.8	23
414	Distinctive gut microbial community structure in both the wild and farmed Swan goose (<i>Anser</i>)	1.8	36
415	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. <i>International Forum of Allergy and Rhinology</i> , 2016, 6, 1229-1237.	1.5	15
416	Excess phosphate loading shifts bacterioplankton community composition in oligotrophic coastal water microcosms over time. <i>Journal of Experimental Marine Biology and Ecology</i> , 2016, 483, 139-146.	0.7	16
417	Isolation of TGF- β -neutralizing single-domain antibodies of predetermined epitope specificity using next-generation DNA sequencing. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 439-443.	1.0	25
418	Behavioural and neurochemical consequences of chronic gut microbiota depletion during adulthood in the rat. <i>Neuroscience</i> , 2016, 339, 463-477.	1.1	196
419	Medicinal herbs as a potential strategy to decrease methane production by rumen microbiota: a systematic evaluation with a focus on <i>Perilla frutescens</i> seed extract. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9757-9771.	1.7	12
420	Repertoire comparison of the β -cell receptor encoding loci in humans and rhesus macaques by next-generation sequencing. <i>Clinical and Translational Immunology</i> , 2016, 5, e93.	1.7	43
421	SAMSA: a comprehensive metatranscriptome analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 399.	1.2	49

#	ARTICLE	IF	CITATIONS
422	Effects of Mariculture and Solar-Salt Production on Sediment Microbial Community Structure in a Coastal Wetland. <i>Journal of Coastal Research</i> , 2016, 33, 573.	0.1	5
423	Highlighting the microbial diversity of 12 French cheese varieties. <i>International Journal of Food Microbiology</i> , 2016, 238, 265-273.	2.1	108
424	Polyhydroxyalkanoate synthesis by mixed microbial consortia cultured on fermented dairy manure: Effect of aeration on process rates/yields and the associated microbial ecology. <i>Water Research</i> , 2016, 106, 26-40.	5.3	71
425	Accumulation of transposable elements in <i>Hox</i> gene clusters during adaptive radiation of <i>Anolis</i> lizards. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161555.	1.2	40
426	Accounting for Uncertainty in Gene Tree Estimation: Summary-Coalescent Species Tree Inference in a Challenging Radiation of Australian Lizards. <i>Systematic Biology</i> , 2017, 66, syw089.	2.7	56
427	Rapid identification of bovine MHCII haplotypes in genetically divergent cattle populations using next-generation sequencing. <i>Immunogenetics</i> , 2016, 68, 765-781.	1.2	14
428	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. <i>Nature Genetics</i> , 2016, 48, 1396-1406.	9.4	533
429	The effect of potential heap construction methods on column bioleaching of copper flotation tailings containing high levels of fines by mixed cultures. <i>Minerals Engineering</i> , 2016, 98, 279-285.	1.8	29
430	Qualitatively and quantitatively investigating the regulation of intestinal microbiota on the metabolism of panax notoginseng saponins. <i>Journal of Ethnopharmacology</i> , 2016, 194, 324-336.	2.0	46
431	Sea cucumber (<i>Apostichopus japonicus</i>) eukaryotic food source composition determined by 18s rDNA barcoding. <i>Marine Biology</i> , 2016, 163, 1.	0.7	13
432	Does adaptive radiation of a host lineage promote ecological diversity of its bacterial communities? A test using gut microbiota of <i>Anolis</i> lizards. <i>Molecular Ecology</i> , 2016, 25, 4793-4804.	2.0	63
433	Changes in the microbiota of lamb packaged in a vacuum and in modified atmospheres during chilled storage analysed by high-throughput sequencing. <i>Meat Science</i> , 2016, 121, 253-260.	2.7	33
434	A putative amino acid transporter determines sensitivity to the two-peptide bacteriocin plantaricin JK. <i>MicrobiologyOpen</i> , 2016, 5, 700-708.	1.2	30
435	Biochar decreased microbial metabolic quotient and shifted community composition four years after a single incorporation in a slightly acid rice paddy from southwest China. <i>Science of the Total Environment</i> , 2016, 571, 206-217.	3.9	236
436	Impact of enrichment conditions on cross-species capture of fresh and degraded <i>scp</i> DNA. <i>Molecular Ecology Resources</i> , 2016, 16, 42-55.	2.2	70
437	Analysis of Illumina MiSeq Metabarcoding Data: Application to Benthic Indices for Environmental Monitoring. <i>Methods in Molecular Biology</i> , 2016, 1452, 237-249.	0.4	12
438	Disease Severity and Immune Activity Relate to Distinct Interkingdom Gut Microbiome States in Ethnically Distinct Ulcerative Colitis Patients. <i>MBio</i> , 2016, 7, .	1.8	90
439	A preliminary investigation on the relationship between gut microbiota and gene expressions in peripheral mononuclear cells of infants with autism spectrum disorders. <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 2450-2458.	0.6	104

#	ARTICLE	IF	CITATIONS
440	Evolutionary processes and cellular functions underlying divergence in <i>Alexandrium minutum</i> . <i>Molecular Ecology</i> , 2016, 25, 5129-5143.	2.0	25
441	Composition of the soil fungal community is more sensitive to phosphorus than nitrogen addition in the alpine meadow on the Qinghai-Tibetan Plateau. <i>Biology and Fertility of Soils</i> , 2016, 52, 1059-1072.	2.3	121
442	Successions and diversity of humic-reducing microorganisms and their association with physical-chemical parameters during composting. <i>Bioresource Technology</i> , 2016, 219, 204-211.	4.8	98
443	Selecting Hypomethylated Genomic Regions Using MRE-Seq. <i>Methods in Molecular Biology</i> , 2016, 1482, 83-102.	0.4	5
444	Bisphenol A alters gut microbiome: Comparative metagenomics analysis. <i>Environmental Pollution</i> , 2016, 218, 923-930.	3.7	122
445	Defining antigen-specific plasmablast and memory B cell subsets in human blood after viral infection or vaccination. <i>Nature Immunology</i> , 2016, 17, 1226-1234.	7.0	348
446	Amplification of RNA by an RNA polymerase ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9786-9791.	3.3	190
447	Performance evaluation and microbial community of a sequencing batch biofilm reactor (SBBR) treating mariculture wastewater at different chlortetracycline concentrations. <i>Journal of Environmental Management</i> , 2016, 182, 496-504.	3.8	38
448	Random Mating Between Two Widely Divergent Mitochondrial Lineages of <i>Cryptolestes ferrugineus</i> (Coleoptera: Laemophloeidae): A Test of Species Limits in a Phosphine-Resistant Stored Product Pest. <i>Journal of Economic Entomology</i> , 2016, 109, 2221-2228.	0.8	23
449	Linking biochemical properties of particles to particle-attached and free-living bacterial community structure along the particle density gradient from freshwater to open ocean. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2016, 121, 2261-2274.	1.3	73
450	Landscape-scale spatial abundance distributions discriminate core from random components of boreal lake bacterioplankton. <i>Ecology Letters</i> , 2016, 19, 1506-1515.	3.0	37
451	Assembly and Application to the Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , 139-158.	0.3	0
452	Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. <i>Nature Communications</i> , 2016, 7, 12151.	5.8	754
453	Transcript, protein and metabolite temporal dynamics in the CAM plant <i>Agave</i> . <i>Nature Plants</i> , 2016, 2, 16178.	4.7	158
454	Single-stranded DNA library preparation uncovers the origin and diversity of ultrashort cell-free DNA in plasma. <i>Scientific Reports</i> , 2016, 6, 27859.	1.6	158
455	<i>Lactobacillus plantarum</i> attenuates anxiety-related behavior and protects against stress-induced dysbiosis in adult zebrafish. <i>Scientific Reports</i> , 2016, 6, 33726.	1.6	125
456	Temperature mediates continental-scale diversity of microbes in forest soils. <i>Nature Communications</i> , 2016, 7, 12083.	5.8	419
457	Altered intestinal microbiota-host mitochondria crosstalk in new onset Crohn's disease. <i>Nature Communications</i> , 2016, 7, 13419.	5.8	326

#	ARTICLE	IF	CITATIONS
458	Multi-marker metabarcoding of coral skeletons reveals a rich microbiome and diverse evolutionary origins of endolithic algae. <i>Scientific Reports</i> , 2016, 6, 31508.	1.6	103
459	Gut microbiome and dietary patterns in different Saudi populations and monkeys. <i>Scientific Reports</i> , 2016, 6, 32191.	1.6	55
460	The Effects of LW-AFC on Intestinal Microbiome in Senescence-Accelerated Mouse Prone 8 Strain, a Mouse Model of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2016, 53, 907-919.	1.2	46
461	Deciphering the evolution of the functional genes and microbial community of the combined partial nitrification-anammox process with nitrate build-up and its in situ restoration. <i>RSC Advances</i> , 2016, 6, 111702-111712.	1.7	11
462	The Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , .	0.3	9
463	Thermal discharge-created increasing temperatures alter the bacterioplankton composition and functional redundancy. <i>AMB Express</i> , 2016, 6, 68.	1.4	22
464	Molecular Characterization of the Total Bacteria and Dissimilatory Arsenate-Reducing Bacteria in Core Sediments of the Jiangnan Plain, Central China. <i>Geomicrobiology Journal</i> , 0, , 1-13.	1.0	5
465	Contrasting elevational diversity patterns for soil bacteria between two ecosystems divided by the treeline. <i>Science China Life Sciences</i> , 2016, 59, 1177-1186.	2.3	25
466	Effects of exposure to bisphenol A and ethinyl estradiol on the gut microbiota of parents and their offspring in a rodent model. <i>Gut Microbes</i> , 2016, 7, 471-485.	4.3	121
467	Mungo bean sprout microbiome and changes associated with culture based enrichment protocols used in detection of Gram-negative foodborne pathogens. <i>Microbiome</i> , 2016, 4, 48.	4.9	10
468	<i>Helicobacter pylori</i> Infection Aggravates Diet-induced Insulin Resistance in Association With Gut Microbiota of Mice. <i>EBioMedicine</i> , 2016, 12, 247-254.	2.7	29
469	Characterization of a phenanthrene-degrading microbial consortium enriched from petrochemical contaminated environment. <i>International Biodeterioration and Biodegradation</i> , 2016, 115, 286-292.	1.9	62
470	High-fat diet modifies the PPAR- β pathway leading to disruption of microbial and physiological ecosystem in murine small intestine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5934-E5943.	3.3	180
471	Neonatal gut microbiota associates with childhood multisensitized atopy and T cell differentiation. <i>Nature Medicine</i> , 2016, 22, 1187-1191.	15.2	844
472	De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic <i>Daphnia galeata</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 3120-3139.	1.1	38
473	Diagnosis of Plant Viruses Using Next-Generation Sequencing and Metagenomic Analysis. , 2016, , 323-335.		30
474	Marine Genomics. <i>Methods in Molecular Biology</i> , 2016, , .	0.4	3
475	Dietary breadth is positively correlated with venom complexity in cone snails. <i>BMC Genomics</i> , 2016, 17, 401.	1.2	81

#	ARTICLE	IF	CITATIONS
476	Quality assessment of ice-stored tropical yellowfin tuna (<i>Thunnus albacares</i>) and influence of vacuum and modified atmosphere packaging. <i>Food Microbiology</i> , 2016, 60, 62-72.	2.1	47
477	Variations of rhizosphere bacterial communities in tea (<i>Camellia sinensis</i> L.) continuous cropping soil by high-throughput pyrosequencing approach. <i>Journal of Applied Microbiology</i> , 2016, 121, 787-799.	1.4	95
478	16S rRNA amplicon sequencing dataset for conventionalized and conventionally raised zebrafish larvae. <i>Data in Brief</i> , 2016, 8, 938-943.	0.5	11
479	Genetic code expansion for multiprotein complex engineering. <i>Nature Methods</i> , 2016, 13, 997-1000.	9.0	63
480	Using metabarcoding to reveal and quantify plant-pollinator interactions. <i>Scientific Reports</i> , 2016, 6, 27282.	1.6	118
481	A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232.	3.8	12
482	Microbial consortia controlling biogenic gas formation in the Qaidam Basin of western China. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2016, 121, 2296-2309.	1.3	5
483	Bacterial and archaeal communities in the deep-sea sediments of inactive hydrothermal vents in the Southwest India Ridge. <i>Scientific Reports</i> , 2016, 6, 25982.	1.6	52
484	Sensitive responders among bacterial and fungal microbiome to pyrogenic organic matter (biochar) addition differed greatly between rhizosphere and bulk soils. <i>Scientific Reports</i> , 2016, 6, 36101.	1.6	51
485	Two species of Southeast Asian cats in the genus <i>Catopuma</i> with diverging histories: an island endemic forest specialist and a widespread habitat generalist. <i>Royal Society Open Science</i> , 2016, 3, 160350.	1.1	17
486	<i>Akkermansia muciniphila</i> mediates negative effects of IFN β on glucose metabolism. <i>Nature Communications</i> , 2016, 7, 13329.	5.8	232
487	Changes in duodenal tissue-associated microbiota following hookworm infection and consecutive gluten challenges in humans with coeliac disease. <i>Scientific Reports</i> , 2016, 6, 36797.	1.6	59
488	Joint effects of pregnancy, sociocultural, and environmental factors on early life gut microbiome structure and diversity. <i>Scientific Reports</i> , 2016, 6, 31775.	1.6	122
489	Bamboo shoot fiber prevents obesity in mice by modulating the gut microbiota. <i>Scientific Reports</i> , 2016, 6, 32953.	1.6	104
490	Quantitative analysis of dinoflagellates and diatoms community via Miseq sequencing of actin gene and v9 region of 18S rDNA. <i>Scientific Reports</i> , 2016, 6, 34709.	1.6	27
491	Metagenomic analysis and functional characterization of the biogas microbiome using high throughput shotgun sequencing and a novel binning strategy. <i>Biotechnology for Biofuels</i> , 2016, 9, 26.	6.2	248
492	Evaluation of a membrane bioreactor system as post-treatment in waste water treatment for better removal of micropollutants. <i>Water Research</i> , 2016, 107, 37-46.	5.3	44
493	Local adaptation of a bacterium is as important as its presence in structuring a natural microbial community. <i>Nature Communications</i> , 2016, 7, 12453.	5.8	79

#	ARTICLE	IF	CITATIONS
494	Endemic hydrothermal vent species identified in the open ocean seed bank. <i>Nature Microbiology</i> , 2016, 1, 16086.	5.9	55
495	Discovery of a Novel Seminal Fluid Microbiome and Influence of Estrogen Receptor Alpha Genetic Status. <i>Scientific Reports</i> , 2016, 6, 23027.	1.6	59
496	Consistent responses of the microbial community structure to organic farming along the middle and lower reaches of the Yangtze River. <i>Scientific Reports</i> , 2016, 6, 35046.	1.6	86
497	Analysis of bacterial diversity in two oil blocks from two low-permeability reservoirs with high salinities. <i>Scientific Reports</i> , 2016, 6, 19600.	1.6	29
498	Microbial community dynamics in an anaerobic biofilm reactor treating heavy oil refinery wastewater. <i>RSC Advances</i> , 2016, 6, 107442-107451.	1.7	9
499	HIV-1 Sequencing. , 2016, , 59-76.		0
500	Uncovering the composition of microbial community structure and metagenomics among three gut locations in pigs with distinct fatness. <i>Scientific Reports</i> , 2016, 6, 27427.	1.6	168
501	Dynamic functional characterization and phylogenetic changes due to Long Chain Fatty Acids pulses in biogas reactors. <i>Scientific Reports</i> , 2016, 6, 28810.	1.6	58
502	Gut microbiota Modulated by Probiotics and Garcinia cambogia Extract Correlate with Weight Gain and Adipocyte Sizes in High Fat-Fed Mice. <i>Scientific Reports</i> , 2016, 6, 33566.	1.6	45
503	Skin fungal community and its correlation with bacterial community of urban Chinese individuals. <i>Microbiome</i> , 2016, 4, 46.	4.9	79
505	Different responses of rhizosphere and non-rhizosphere soil microbial communities to consecutive <i>Piper nigrum</i> L. monoculture. <i>Scientific Reports</i> , 2016, 6, 35825.	1.6	65
506	Vaccinating with conserved <i>Escherichia coli</i> antigens does not alter the mouse intestinal microbiome. <i>BMC Research Notes</i> , 2016, 9, 401.	0.6	16
507	Comprehensive identification of internal structure and alternative splicing events in circular RNAs. <i>Nature Communications</i> , 2016, 7, 12060.	5.8	249
508	Potential use of bacterial community succession for estimating post-mortem interval as revealed by high-throughput sequencing. <i>Scientific Reports</i> , 2016, 6, 24197.	1.6	77
509	Effects of consecutive monoculture of <i>Pseudostellaria heterophylla</i> on soil fungal community as determined by pyrosequencing. <i>Scientific Reports</i> , 2016, 6, 26601.	1.6	62
510	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , 2016, 28, 2700-2714.	3.1	183
511	Obese Mice Fed a Diet Supplemented with Enzyme-Treated Wheat Bran Display Marked Shifts in the Liver Metabolome Concurrent with Altered Gut Bacteria. <i>Journal of Nutrition</i> , 2016, 146, 2445-2460.	1.3	16
512	Chlorine Dose Determines Bacterial Community Structure of Subsequent Regrowth in Reclaimed Water. <i>Journal of Water and Environment Technology</i> , 2016, 14, 15-24.	0.3	11

#	ARTICLE	IF	CITATIONS
513	Cut microbiota associated with HIV infection is significantly enriched in bacteria tolerant to oxygen. <i>BMJ Open Gastroenterology</i> , 2016, 3, e000080.	1.1	66
514	High frequency of +1 programmed ribosomal frameshifting in <i>Euplotes octocarinatus</i> . <i>Scientific Reports</i> , 2016, 6, 21139.	1.6	48
515	Soil bacterial endemism and potential functional redundancy in natural broadleaf forest along a latitudinal gradient. <i>Scientific Reports</i> , 2016, 6, 28819.	1.6	15
516	Assembling the <i>Setaria italica</i> L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. <i>Scientific Reports</i> , 2016, 6, 35076.	1.6	10
517	Temporal patterns of damage and decay kinetics of DNA retrieved from plant herbarium specimens. <i>Royal Society Open Science</i> , 2016, 3, 160239.	1.1	108
518	A Protocol for Functional Assessment of Whole-Protein Saturation Mutagenesis Libraries Utilizing High-Throughput Sequencing. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	5
519	Draft Genome Sequences of <i>Burkholderia contaminans</i> FFI-28, a Strain Isolated from a Contaminated Pharmaceutical Solution. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
520	Draft Genome Sequence of <i>Corynebacterium variabile</i> Mu292, Isolated from Munster, a French Smear-Ripened Cheese. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
521	Tracing HIV-1 transmission: envelope traits of HIV-1 transmitter and recipient pairs. <i>Retrovirology</i> , 2016, 13, 62.	0.9	45
522	Illumina sequencing-based community analysis of bacteria associated with different bryophytes collected from Tibet, China. <i>BMC Microbiology</i> , 2016, 16, 276.	1.3	20
523	Evidence for L1-associated DNA rearrangements and negligible L1 retrotransposition in glioblastoma multiforme. <i>Mobile DNA</i> , 2016, 7, 21.	1.3	32
524	Influence of GABA and GABA-producing <i>Lactobacillus brevis</i> DPC 6108 on the development of diabetes in a streptozotocin rat model. <i>Beneficial Microbes</i> , 2016, 7, 409-420.	1.0	46
525	Draft Genome Sequence of the Syntrophic Lactate-Degrading Bacterium <i>Tepidanaerobacter syntrophicus</i> JL ^T . <i>Genome Announcements</i> , 2016, 4, .	0.8	4
526	Mitochondrial Genome Sequence of the Galápagos Endemic Land Snail <i>Naesiotus nux</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5
527	Surface-attached and suspended bacterial community structure as affected by C/N ratios: relationship between bacteria and fish production. <i>World Journal of Microbiology and Biotechnology</i> , 2016, 32, 116.	1.7	22
528	Pond Crash Forensics: Presumptive identification of pond crash agents by next generation sequencing in replicate raceway mass cultures of <i>Nannochloropsis salina</i> . <i>Algal Research</i> , 2016, 17, 341-347.	2.4	51
529	Environmental Filtering Process Has More Important Roles than Dispersal Limitation in Shaping Large-Scale Prokaryotic Beta Diversity Patterns of Grassland Soils. <i>Microbial Ecology</i> , 2016, 72, 221-230.	1.4	28
530	A Recent Whole-Genome Duplication Divides Populations of a Globally Distributed Microsporidian. <i>Molecular Biology and Evolution</i> , 2016, 33, 2002-2015.	3.5	16

#	ARTICLE	IF	CITATIONS
531	Long-term effects of ZnO nanoparticles on nitrogen and phosphorus removal, microbial activity and microbial community of a sequencing batch reactor. <i>Bioresource Technology</i> , 2016, 216, 428-436.	4.8	109
532	Mode of Delivery Determines Neonatal Pharyngeal Bacterial Composition and Early Intestinal Colonization. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 63, 320-328.	0.9	43
533	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	4.4	226
534	Microbial modulation of behavior and stress responses in zebrafish larvae. <i>Behavioural Brain Research</i> , 2016, 311, 219-227.	1.2	113
535	Rhizoma Coptidis alkaloids alleviate hyperlipidemia in B6 mice by modulating gut microbiota and bile acid pathways. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1696-1709.	1.8	111
536	Massively parallel sequencing of short tandem repeats—Population data and mixture analysis results for the PowerSeq [®] system. <i>Forensic Science International: Genetics</i> , 2016, 24, 86-96.	1.6	118
537	Effects of Walnut Consumption on Colon Carcinogenesis and Microbial Community Structure. <i>Cancer Prevention Research</i> , 2016, 9, 692-703.	0.7	50
538	Effects of different media on the enrichment of low numbers of Shiga toxin-producing <i>Escherichia coli</i> in mung bean sprouts and on the development of the sprout microbiome. <i>International Journal of Food Microbiology</i> , 2016, 232, 26-34.	2.1	9
539	Multiple effects of trace elements on methanogenesis in a two-phase anaerobic membrane bioreactor treating starch wastewater. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6631-6642.	1.7	11
540	Predictive functional profiling using marker gene sequences and community diversity analyses of microbes in full-scale anaerobic sludge digesters. <i>Bioprocess and Biosystems Engineering</i> , 2016, 39, 1115-1127.	1.7	41
541	Endophytic bacterial and fungal microbiota in sprouts, roots and stems of rice (<i>Oryza sativa</i> L.). <i>Microbiological Research</i> , 2016, 188-189, 1-8.	2.5	102
542	The gene cortex controls mimicry and crypsis in butterflies and moths. <i>Nature</i> , 2016, 534, 106-110.	13.7	212
543	Delineating ecologically significant taxonomic units from global patterns of marine picocyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3365-74.	3.3	159
544	Comparative genomics and prediction of conditionally dispensable sequences in legume—“infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	1.2	109
545	Deep-fried oil consumption in rats impairs glycerolipid metabolism, gut histology and microbiota structure. <i>Lipids in Health and Disease</i> , 2016, 15, 86.	1.2	38
546	EAGER: efficient ancient genome reconstruction. <i>Genome Biology</i> , 2016, 17, 60.	3.8	305
547	Genotyping-by-sequencing in an orphan plant species <i>Physocarpus opulifolius</i> helps identify the evolutionary origins of the genus <i>Prunus</i> . <i>BMC Research Notes</i> , 2016, 9, 268.	0.6	4
548	Effect of room temperature transport vials on DNA quality and phylogenetic composition of faecal microbiota of elderly adults and infants. <i>Microbiome</i> , 2016, 4, 19.	4.9	51

#	ARTICLE	IF	CITATIONS
549	Diversity and divergence of the glioma-infiltrating T-cell receptor repertoire. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3529-37.	3.3	103
550	Discerning biodegradation and adsorption of microcystin-LR in a shallow semi-enclosed bay and bacterial community shifts in response to associated process. Ecotoxicology and Environmental Safety, 2016, 132, 123-131.	2.9	33
551	The Draft Genome Sequence of Paenibacillus polymyxa Strain CCI-25 Encompasses High Potential for Secondary Metabolite Production. Genome Announcements, 2016, 4, .	0.8	3
552	Analysis of bacterial diversity of Chinese Luzhou-flavor liquor brewed in different seasons by Illumina Miseq sequencing. Annals of Microbiology, 2016, 66, 1293-1301.	1.1	56
553	Molecular Evolution of a <i>Klebsiella pneumoniae</i> ST278 Isolate Harboring <i>bla</i> _{NDM-7} and Involved in Nosocomial Transmission. Journal of Infectious Diseases, 2016, 214, 798-806.	1.9	27
554	IPED: a highly efficient denoising tool for Illumina MiSeq Paired-end 16S rRNA gene amplicon sequencing data. BMC Bioinformatics, 2016, 17, 192.	1.2	30
555	AdapterRemoval v2: rapid adapter trimming, identification, and read merging. BMC Research Notes, 2016, 9, 88.	0.6	1,255
556	Evaluation of microbial population dynamics in the co-composting of cow manure and rice straw using high throughput sequencing analysis. World Journal of Microbiology and Biotechnology, 2016, 32, 101.	1.7	119
557	A hollow bacterial diversity pattern with elevation in Wolong Nature Reserve, Western Sichuan Plateau. Journal of Soils and Sediments, 2016, 16, 2365-2374.	1.5	20
558	An extended single-index multiplexed 16S rRNA sequencing for microbial community analysis on MiSeq illumina platforms. Journal of Basic Microbiology, 2016, 56, 321-326.	1.8	93
559	Biogeographic patterns of soil diazotrophic communities across six forests in the North America. Molecular Ecology, 2016, 25, 2937-2948.	2.0	76
560	Microbiome Survey of the Inflamed and Noninflamed Gut at Different Compartments Within the Gastrointestinal Tract of Inflammatory Bowel Disease Patients. Inflammatory Bowel Diseases, 2016, 22, 817-825.	0.9	114
561	Ice cover extent drives phytoplankton and bacterial community structure in a large north-temperate lake: implications for a warming climate. Environmental Microbiology, 2016, 18, 1704-1719.	1.8	68
562	Meso and micro-scale response of post carbon removal nitrifying MBBR biofilm across carrier type and loading. Water Research, 2016, 91, 235-243.	5.3	45
563	Enhanced biodegradation of pyrene and indeno(1,2,3-cd)pyrene using bacteria immobilized in cinder beads in estuarine wetlands. Marine Pollution Bulletin, 2016, 102, 128-133.	2.3	30
564	Microbial dynamics during shelf-life of industrial Ricotta cheese and identification of a Bacillus strain as a cause of a pink discoloration. Food Microbiology, 2016, 57, 8-15.	2.1	31
565	Impacts of addition of natural zeolite or a nitrification inhibitor on antibiotic resistance genes during sludge composting. Water Research, 2016, 91, 339-349.	5.3	255
566	Diversity and distribution patterns of acidobacterial communities in the black soil zone of northeast China. Soil Biology and Biochemistry, 2016, 95, 212-222.	4.2	113

#	ARTICLE	IF	CITATIONS
567	Bacterial dynamics and metabolite changes in solid-state acetic acid fermentation of Shanxi aged vinegar. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 4395-4411.	1.7	84
568	Conversion of methane-derived carbon and microbial community in enrichment cultures in response to O ₂ availability. <i>Environmental Science and Pollution Research</i> , 2016, 23, 7517-7528.	2.7	20
569	Episodic Diversifying Selection Shaped the Genomes of Gibbon Ape Leukemia Virus and Related Gammaretroviruses. <i>Journal of Virology</i> , 2016, 90, 1757-1772.	1.5	8
570	The dual oxidase gene <i>BdDuoX</i> regulates the intestinal bacterial community homeostasis of <i>Bactrocera dorsalis</i> . <i>ISME Journal</i> , 2016, 10, 1037-1050.	4.4	118
571	Differential responses of soil bacterial taxa to long-term P, N, and organic manure application. <i>Journal of Soils and Sediments</i> , 2016, 16, 1046-1058.	1.5	40
572	Influence of rice straw amendment on mercury methylation and nitrification in paddy soils. <i>Environmental Pollution</i> , 2016, 209, 53-59.	3.7	56
573	Composition and Metabolic Activities of the Bacterial Community in Shrimp Sauce at the Flavor-Forming Stage of Fermentation As Revealed by Metatranscriptome and 16S rRNA Gene Sequencings. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 2591-2603.	2.4	31
574	Population genomics reveals that within-fungus polymorphism is common and maintained in populations of the mycorrhizal fungus <i>Rhizophagus irregularis</i> . <i>ISME Journal</i> , 2016, 10, 2514-2526.	4.4	54
575	Draft Genome Sequence of <i>Thermodesulfovibrio aggregans</i> TGE-P1 T, an Obligately Anaerobic, Thermophilic, Sulfate-Reducing Bacterium in the Phylum Nitrospirae. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
576	Exploring potential bacterial and fungal biocontrol agents transmitted from seeds to sprouts of wheat. <i>Biological Control</i> , 2016, 98, 27-33.	1.4	119
577	Bacterial diversity and distribution in seven different estuarine sediments of Poyang Lake, China. <i>Environmental Earth Sciences</i> , 2016, 75, 1.	1.3	36
578	Potential and pitfalls of eukaryotic metagenome skimming: a test case for lichens. <i>Molecular Ecology Resources</i> , 2016, 16, 511-523.	2.2	24
579	High-throughput sequencing reveals the core gut microbiome of Bar-headed goose (<i>Anser t. t.</i>). <i>Microbiome</i> , 2016, 4, 38.	1.2	38
580	A Comparative Analysis of Mitochondrial Genomes in Eustigmatophyte Algae. <i>Genome Biology and Evolution</i> , 2016, 8, 705-722.	1.1	33
581	Defining the microbial transcriptional response to colitis through integrated host and microbiome profiling. <i>ISME Journal</i> , 2016, 10, 2389-2404.	4.4	40
582	Microbial diversity drives multifunctionality in terrestrial ecosystems. <i>Nature Communications</i> , 2016, 7, 10541.	5.8	1,365
583	Gut bacteria that prevent growth impairments transmitted by microbiota from malnourished children. <i>Science</i> , 2016, 351, .	6.0	580
584	Full Mitochondrial Genome Sequence of the Sugar Beet Wireworm <i>Limonius californicus</i> (Coleoptera: Elateridae), a Common Agricultural Pest. <i>Genome Announcements</i> , 2016, 4, .	0.8	7

#	ARTICLE	IF	CITATIONS
585	Silica fertilization and nano-MnO ₂ amendment on bacterial community composition in high arsenic paddy soils. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 2429-2437.	1.7	45
586	Rapid identification of major histocompatibility complex class I haplotypes using deep sequencing in an endangered Old World monkey. <i>Conservation Genetics Resources</i> , 2016, 8, 23-26.	0.4	4
587	Interactions between hydrology and water chemistry shape bacterioplankton biogeography across boreal freshwater networks. <i>ISME Journal</i> , 2016, 10, 1755-1766.	4.4	183
588	Bacterial community compositions in sediment polluted by perfluoroalkyl acids (PFAAs) using Illumina high-throughput sequencing. <i>Environmental Science and Pollution Research</i> , 2016, 23, 10556-10565.	2.7	72
589	Profiling microbial community in a watershed heavily contaminated by an active antimony (Sb) mine in Southwest China. <i>Science of the Total Environment</i> , 2016, 550, 297-308.	3.9	104
590	Integration of complete chloroplast genome sequences with small amplicon datasets improves phylogenetic resolution in <i>Acacia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 1-8.	1.2	78
591	Development of microsatellite markers and a preliminary assessment of population structuring in the rice weevil, <i>Sitophilus oryzae</i> (L.). <i>Journal of Stored Products Research</i> , 2016, 66, 12-17.	1.2	10
592	Responses of Soil Bacterial Communities to Nitrogen Deposition and Precipitation Increment Are Closely Linked with Aboveground Community Variation. <i>Microbial Ecology</i> , 2016, 71, 974-989.	1.4	86
593	Ultra-high-throughput sequencing of the immune receptor repertoire from millions of lymphocytes. <i>Nature Protocols</i> , 2016, 11, 429-442.	5.5	140
594	Novel soil fumigation method for suppressing cucumber <i>Fusarium</i> wilt disease associated with soil microflora alterations. <i>Applied Soil Ecology</i> , 2016, 101, 28-36.	2.1	53
595	A single three-dimensional chromatin compartment in amphioxus indicates a stepwise evolution of vertebrate Hox bimodal regulation. <i>Nature Genetics</i> , 2016, 48, 336-341.	9.4	113
596	Retrotransposon Capture Sequencing (RC-Seq): A Targeted, High-Throughput Approach to Resolve Somatic L1 Retrotransposition in Humans. <i>Methods in Molecular Biology</i> , 2016, 1400, 47-77.	0.4	18
597	Aflatoxin B ₁ Induced Compositional Changes in Gut Microbial Communities of Male F344 Rats. <i>Toxicological Sciences</i> , 2016, 150, 54-63.	1.4	78
598	Genetic map construction and QTL analysis of nitrogen use efficiency in spinach (<i>Spinacia oleracea</i> L.). <i>Euphytica</i> , 2016, 208, 621-636.	0.6	26
599	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic <i>RAG</i> defects. <i>Journal of Experimental Medicine</i> , 2016, 213, 355-375.	4.2	61
600	T cell fate and clonality inference from single-cell transcriptomes. <i>Nature Methods</i> , 2016, 13, 329-332.	9.0	411
601	Draft Genome Sequence of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> CFL1, a Lactic Acid Bacterium Isolated from French Handcrafted Fermented Milk. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
602	Protistan diversity and activity inferred from RNA and DNA at a coastal ocean site in the eastern North Pacific. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw050.	1.3	74

#	ARTICLE	IF	CITATIONS
603	Isolation of Microsatellite Loci by Next-Generation Sequencing of the Critically Endangered Northern Bald Ibis, <i>Geronticus eremita</i> : Table 1.. Journal of Heredity, 2016, 107, 363-366.	1.0	11
604	Gradient Distribution Patterns of Rhizosphere Bacteria Associated with the Coastal Reclamation Wetlands, 2016, 36, 69-80.	0.7	9
605	The Urinary Microbiome Differs Significantly Between Patients With Chronic Prostatitis/Chronic Pelvic Pain Syndrome and Controls as Well as Between Patients With Different Clinical Phenotypes. Urology, 2016, 92, 26-32.	0.5	106
606	Identification of Unknown Carboxydovore Bacteria Dominant in Deciduous Forest Soil via Succession of Bacterial Communities, <i>coxL</i> Genotypes, and Carbon Monoxide Oxidation Activity in Soil Microcosms. Applied and Environmental Microbiology, 2016, 82, 1324-1333.	1.4	18
607	Changes in the composition and diversity of microbial communities during anaerobic nitrate reduction and Fe(II) oxidation at circumneutral pH in paddy soil. Soil Biology and Biochemistry, 2016, 94, 70-79.	4.2	134
608	Engineering an allosteric transcription factor to respond to new ligands. Nature Methods, 2016, 13, 177-183.	9.0	274
609	Characterization of VCC-1, a Novel Ambler Class A Carbapenemase from <i>Vibrio cholerae</i> Isolated from Imported Retail Shrimp Sold in Canada. Antimicrobial Agents and Chemotherapy, 2016, 60, 1819-1825.	1.4	45
610	High throughput sequencing analysis reveals amelioration of intestinal dysbiosis by squid ink polysaccharide. Journal of Functional Foods, 2016, 20, 506-515.	1.6	44
611	Microbial composition of biofilms associated with lithifying rubble of <i>Acropora palmatobranches</i> . FEMS Microbiology Ecology, 2016, 92, fiv162.	1.3	10
612	Taxonomic analysis of the microbial community in stored sugar beets using high-throughput sequencing of different marker genes. FEMS Microbiology Ecology, 2016, 92, fiv004.	1.3	36
613	Electrical stimulation on biodegradation of phenol and responses of microbial communities in conductive carriers supported biofilms of the bioelectrochemical reactor. Bioresource Technology, 2016, 201, 1-7.	4.8	108
614	Fungal Dysbiosis in Mucosa-associated Microbiota of Crohn's Disease Patients. Journal of Crohn's and Colitis, 2016, 10, 296-305.	0.6	252
615	Microbial Mat Communities along an Oxygen Gradient in a Perennially Ice-Covered Antarctic Lake. Applied and Environmental Microbiology, 2016, 82, 620-630.	1.4	69
616	Gene Expression and Chromatin Modifications Associated with Maize Centromeres. G3: Genes, Genomes, Genetics, 2016, 6, 183-192.	0.8	30
617	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. Nature Methods, 2016, 13, 74-80.	9.0	225
618	Comparative Genomics of an Emerging Amphibian Virus. G3: Genes, Genomes, Genetics, 2016, 6, 15-27.	0.8	18
619	The phylogenetic position of the giant devil ray <i>Mobula mobular</i> (Bonnaterre, 1788) (Myliobatiformes, Myliobatidae) inferred from the mitochondrial genome. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3540-3541.	0.7	8
620	Forage crops alter soil bacterial and fungal communities in an apple orchard. Acta Agriculturae Scandinavica - Section B Soil and Plant Science, 2016, 66, 229-236.	0.3	2

#	ARTICLE	IF	CITATIONS
621	Comparative analysis of the gastrointestinal microbial communities of bar-headed goose (<i>Anser</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7 2016, 182, 59-67.	2.5	65
622	Identification of key taxa that favor intestinal colonization of <i>Clostridium difficile</i> in an adult Chinese population. <i>Microbes and Infection</i> , 2016, 18, 30-38.	1.0	73
623	Optimization and microbial community analysis of anaerobic co-digestion of food waste and sewage sludge based on microwave pretreatment. <i>Bioresource Technology</i> , 2016, 200, 253-261.	4.8	191
624	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 157-166.	1.4	73
625	Human B-cell isotype switching origins of IgE. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 579-586.e7.	1.5	132
626	The phylogenetic position of the roughskin skate <i>Dipturus trachyderma</i> (Krefft & Stehmann,) Tj ETQq1 1 0.784314 rgBT /Ov Mapping, Sequencing, and Analysis, 2016, 27, 2965-2966.	0.7	8
627	The gut microbial profile in patients with primary sclerosing cholangitis is distinct from patients with ulcerative colitis without biliary disease and healthy controls. <i>Gut</i> , 2017, 66, 611-619.	6.1	308
628	Taxon-specific responses of soil microbial communities to different soil priming effects induced by addition of plant residues and their biochars. <i>Journal of Soils and Sediments</i> , 2017, 17, 674-684.	1.5	52
629	Regional and global elevational patterns of microbial species richness and evenness. <i>Ecography</i> , 2017, 40, 393-402.	2.1	79
630	Identification of oral bacteria on titanium implant surfaces by 16S rDNA sequencing. <i>Clinical Oral Implants Research</i> , 2017, 28, 697-703.	1.9	22
631	Exploring the microbial diversity of the distal intestinal lumen and mucosa of farmed rainbow trout <i>Oncorhynchus mykiss</i> (Walbaum) using next generation sequencing (NGS). <i>Aquaculture Research</i> , 2017, 48, 77-91.	0.9	70
632	Bacterial diversity in the rhizosphere of two phylogenetically closely related plant species across environmental gradients. <i>Journal of Soils and Sediments</i> , 2017, 17, 122-132.	1.5	13
633	Unraveling the microbial processes of black band disease in corals through integrated genomics. <i>Scientific Reports</i> , 2017, 7, 40455.	1.6	36
634	The Composition of Human Milk and Infant Faecal Microbiota Over the First Three Months of Life: A Pilot Study. <i>Scientific Reports</i> , 2017, 7, 40597.	1.6	279
635	Evolution of gut microbiota composition from birth to 24 weeks in the INFANTMET Cohort. <i>Microbiome</i> , 2017, 5, 4.	4.9	390
636	Conservative tracer bromide inhibits pesticide mineralisation in soil. <i>Environmental Pollution</i> , 2017, 222, 404-411.	3.7	7
637	Impact of root diversity upon coupling between soil C and N accumulation and bacterial community dynamics and activity: Result of a 30 year rotation experiment. <i>Geoderma</i> , 2017, 292, 87-95.	2.3	32
638	The normal vaginal and uterine bacterial microbiome in giant pandas (<i>Ailuropoda melanoleu</i> ca). <i>Microbiological Research</i> , 2017, 199, 1-9.	2.5	56

#	ARTICLE	IF	CITATIONS
639	Identity of biocrust species and microbial communities drive the response of soil multifunctionality to simulated global change. <i>Soil Biology and Biochemistry</i> , 2017, 107, 208-217.	4.2	78
640	Low temperature MBBR nitrification: Microbiome analysis. <i>Water Research</i> , 2017, 111, 224-233.	5.3	115
641	Identify biosorption effects of <i>Thiobacillus</i> towards perfluorooctanoic acid (PFOA): Pilot study from field to laboratory. <i>Chemosphere</i> , 2017, 171, 31-39.	4.2	27
642	Alteration in successional trajectories of bacterioplankton communities in response to co-exposure of cadmium and phenanthrene in coastal water microcosms. <i>Environmental Pollution</i> , 2017, 221, 480-490.	3.7	10
643	<sc>DNA</sc> metabarcoding reveals that 200â€ <i>i>¼</i>â€fractionated filtering is unable to discriminate between planktonic microbial and large eukaryotes. <i>Molecular Ecology Resources</i>, 2017, 17, 991-1002.</i>	2.2	50
644	Microbial flora analysis for the degradation of beta-cypermethrin. <i>Environmental Science and Pollution Research</i> , 2017, 24, 6554-6562.	2.7	17
645	Degradation in forensic trace DNA samples explored by massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2017, 27, 160-166.	1.6	16
646	Environmental DNA metabarcoding reveals local fish communities in a species-rich coastal sea. <i>Scientific Reports</i> , 2017, 7, 40368.	1.6	348
647	Population expansion and individual age affect endoparasite richness and diversity in a recolonising large carnivore population. <i>Scientific Reports</i> , 2017, 7, 41730.	1.6	35
648	Chemical characterization of the glycated myofibrillar proteins from grass carp (<i>Ctenopharyngodon</i>) Tj ETQq1 1 0.784314 rgBT /Over 8, 1184-1194.	2.1	31
649	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. <i>American Journal of Human Genetics</i> , 2017, 100, 238-256.	2.6	60
650	Complete genome sequence of the heavy metal resistant bacterium <i>Agromyces aureus</i> AR33T and comparison with related Actinobacteria. <i>Standards in Genomic Sciences</i> , 2017, 12, 2.	1.5	15
651	Anaerobic Dechlorination of Tetrachlorobisphenol A in River Sediment and Associated Changes in Bacterial Communities. <i>Water, Air, and Soil Pollution</i> , 2017, 228, 1.	1.1	9
652	Association of HPV infection and clearance with cervicovaginal immunology and the vaginal microbiota. <i>Mucosal Immunology</i> , 2017, 10, 1310-1319.	2.7	148
653	Whole genome sequencing data and de novo draft assemblies for 66 teleost species. <i>Scientific Data</i> , 2017, 4, 160132.	2.4	67
654	Distinct roles for soil fungal and bacterial communities associated with the suppression of vanilla <i>Fusarium</i> wilt disease. <i>Soil Biology and Biochemistry</i> , 2017, 107, 198-207.	4.2	243
655	Bioavailability and Kidney Responses to Diclofenac in the Fathead Minnow (<i>Pimephales</i>) Tj ETQq0 0 0 rgBT /OverJock 10 Tf 50 102 Td 4.6 46	4.6	46
656	De novo transcriptome assembly of heavy metal tolerant <i>Silene dioica</i> . <i>Genomics Data</i> , 2017, 11, 118-119.	1.3	3

#	ARTICLE	IF	CITATIONS
657	Microbial population dynamics in continuous anaerobic digester systems during start up, stable conditions and recovery after starvation. <i>Bioresource Technology</i> , 2017, 232, 313-320.	4.8	41
658	Metataxonomics reveal vultures as a reservoir for <i>Clostridium perfringens</i> . <i>Emerging Microbes and Infections</i> , 2017, 6, 1-8.	3.0	40
659	In-situ biogas upgrading with pulse H ₂ additions: The relevance of methanogen adaption and inorganic carbon level. <i>Bioresource Technology</i> , 2017, 233, 256-263.	4.8	146
660	Method for Dual Viral Vector Mediated CRISPR-Cas9 Gene Disruption in Primary Human Endothelial Cells. <i>Scientific Reports</i> , 2017, 7, 42127.	1.6	23
661	Integrating gut microbiota immaturity and disease-discriminatory taxa to diagnose the initiation and severity of shrimp disease. <i>Environmental Microbiology</i> , 2017, 19, 1490-1501.	1.8	213
662	Integrated metagenomic data analysis demonstrates that a loss of diversity in oral microbiota is associated with periodontitis. <i>BMC Genomics</i> , 2017, 18, 1041.	1.2	82
663	A CRISPR-Cpf1 system for efficient genome editing and transcriptional repression in plants. <i>Nature Plants</i> , 2017, 3, 17018.	4.7	425
664	The effect of environmental contamination on the community structure and fructification of ectomycorrhizal fungi. <i>MicrobiologyOpen</i> , 2017, 6, e00396.	1.2	7
665	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017, 66, 1968-1974.	6.1	370
666	The metabolic pathway of metamifop degradation by consortium ME-1 and its bacterial community structure. <i>Biodegradation</i> , 2017, 28, 181-194.	1.5	11
667	Long-term performance of sediment microbial fuel cells with multiple anodes. <i>Bioresource Technology</i> , 2017, 237, 178-185.	4.8	39
668	Quantitative Analysis of Synthetic Cell Lineage Tracing Using Nuclease Barcoding. <i>ACS Synthetic Biology</i> , 2017, 6, 936-942.	1.9	88
669	Revegetation rewilds the soil bacterial microbiome of an old field. <i>Molecular Ecology</i> , 2017, 26, 2895-2904.	2.0	68
670	An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. <i>BMC Genomics</i> , 2017, 18, 95.	1.2	153
671	Habitat-specific patterns and drivers of bacterial α -diversity in China's drylands. <i>ISME Journal</i> , 2017, 11, 1345-1358.	4.4	218
672	Distribution of Ciliates in Intertidal Sediments across Geographic Distances: A Molecular View. <i>Protist</i> , 2017, 168, 171-182.	0.6	21
673	Influence of dairy by-product waste milk on the microbiomes of different gastrointestinal tract components in pre-weaned dairy calves. <i>Scientific Reports</i> , 2017, 7, 42689.	1.6	41
674	Effect of different enrichment strategies on microbial community structure in petroleum-contaminated marine sediment in Dalian, China. <i>Marine Pollution Bulletin</i> , 2017, 117, 274-282.	2.3	13

#	ARTICLE	IF	CITATIONS
675	Diversity in sequences, post-translational modifications and expected pharmacological activities of toxins from four <i>Conus</i> species revealed by the combination of cutting-edge proteomics, transcriptomics and bioinformatics. <i>Toxicon</i> , 2017, 130, 116-125.	0.8	14
676	Efficient degradation of chlorimuron-ethyl by a bacterial consortium and shifts in the aboriginal microorganism community during the bioremediation of contaminated-soil. <i>Ecotoxicology and Environmental Safety</i> , 2017, 139, 423-430.	2.9	18
677	The complete mitochondrial genome of the White-Nose Syndrome pathogen, <i>Pseudogymnoascus destructans</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 48-49.	0.2	1
678	Microbiome Remodeling via the Montmorillonite Adsorption-Excretion Axis Prevents Obesity-related Metabolic Disorders. <i>EBioMedicine</i> , 2017, 16, 251-261.	2.7	57
679	No effect of Bt Cry1Ie toxin on bacterial diversity in the midgut of the Chinese honey bees, <i>Apis cerana cerana</i> (Hymenoptera, Apidae). <i>Scientific Reports</i> , 2017, 7, 41688.	1.6	12
680	Population genomics reveals that an anthropophilic population of <i>Aedes aegypti</i> mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. <i>BMC Biology</i> , 2017, 15, 16.	1.7	96
681	GH11 xylanase increases prebiotic oligosaccharides from wheat bran favouring butyrate-producing bacteria in vitro. <i>Animal Feed Science and Technology</i> , 2017, 226, 113-123.	1.1	25
682	Potent and broad HIV-neutralizing antibodies in memory B cells and plasma. <i>Science Immunology</i> , 2017, 2, .	5.6	119
683	Differential effects of monensin and a blend of essential oils on rumen microbiota composition of transition dairy cows. <i>Journal of Dairy Science</i> , 2017, 100, 2765-2783.	1.4	109
684	Population genetic structure of the endangered Sierra Nevada yellow-legged frog (<i>Rana sierrae</i>) in Yosemite National Park based on multi-locus nuclear data from swab samples. <i>Conservation Genetics</i> , 2017, 18, 731-744.	0.8	10
685	High-throughput sequencing of multiple amplicons for barcoding and integrative taxonomy. <i>Scientific Reports</i> , 2017, 7, 41948.	1.6	101
686	Retrospective analysis of phytoplankton assemblages on the Iwate coast before and after the 2011 tsunami using cryopreserved <sc>DNA</sc> samples. <i>Fisheries Oceanography</i> , 2017, 26, 234-250.	0.9	5
687	Complete mitochondrial genome from South American catfish <i>Pseudoplatystoma reticulatum</i> (Eigenmann & Eigenmann) and its impact in Siluriformes phylogenetic tree. <i>Genetica</i> , 2017, 145, 51-66.	0.5	9
688	Evolutionary affinities of the unfathomable Parabrotulidae: Molecular data indicate placement of <i>Parabrotula</i> within the family Bythitidae, Ophidiiformes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 337-342.	1.2	6
689	Changes in Microbiota in Rumen Digesta and Feces Due to a Grain-Based Subacute Ruminant Acidosis (SARA) Challenge. <i>Microbial Ecology</i> , 2017, 74, 485-495.	1.4	122
690	Tumour-associated and non-tumour-associated microbiota in colorectal cancer. <i>Gut</i> , 2017, 66, 633-643.	6.1	623
691	Wildfire impact: Natural experiment reveals differential short-term changes in soil microbial communities. <i>Soil Biology and Biochemistry</i> , 2017, 109, 1-13.	4.2	68
692	A new perspective on studying burial environment before archaeological excavation: analyzing bacterial community distribution by high-throughput sequencing. <i>Scientific Reports</i> , 2017, 7, 41691.	1.6	16

#	ARTICLE	IF	CITATIONS
693	Maintaining stability of the rumen ecosystem is associated with changes of microbial composition and epithelial TLR signaling. <i>MicrobiologyOpen</i> , 2017, 6, e00436.	1.2	14
694	Metatranscriptomic Evidence for Direct Interspecies Electron Transfer between <i>Geobacter</i> and <i>Methanotrix</i> Species in Methanogenic Rice Paddy Soils. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	247
695	Microbiome dynamic modulation through functional diets based on pre- and probiotics (mannan-oligosaccharides and <i>Saccharomyces cerevisiae</i>) in juvenile rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Journal of Applied Microbiology</i> , 2017, 122, 1333-1347.	1.4	52
696	Microbiota alteration is associated with the development of stress-induced despair behavior. <i>Scientific Reports</i> , 2017, 7, 43859.	1.6	259
697	Single molecule RNA sequencing uncovers <i>trans</i> -splicing and improves annotations in <i>Anopheles stephensi</i> . <i>Insect Molecular Biology</i> , 2017, 26, 298-307.	1.0	14
698	Soil microbial communities in cucumber monoculture and rotation systems and their feedback effects on cucumber seedling growth. <i>Plant and Soil</i> , 2017, 415, 507-520.	1.8	134
699	Ultra-deep next generation mitochondrial genome sequencing reveals widespread heteroplasmy in Chinese hamster ovary cells. <i>Metabolic Engineering</i> , 2017, 41, 11-22.	3.6	22
700	Glycomacropeptide Sustains Microbiota Diversity and Promotes Specific Taxa in an Artificial Colon Model of Elderly Gut Microbiota. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 1836-1846.	2.4	35
701	Deciphering composition and function of the root microbiome of a legume plant. <i>Microbiome</i> , 2017, 5, 2.	4.9	152
702	Structural dynamics of microbial communities in polycyclic aromatic hydrocarbon-contaminated tropical estuarine sediments undergoing simulated aerobic biotreatment. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4299-4314.	1.7	20
703	Rapid start-up of nitrifying MBBRs at low temperatures: nitrification, biofilm response and microbiome analysis. <i>Bioprocess and Biosystems Engineering</i> , 2017, 40, 731-739.	1.7	35
704	No evidence for MHC class II-based non-random mating at the gametic haplotype in Atlantic salmon. <i>Heredity</i> , 2017, 118, 563-567.	1.2	9
705	Microsatellite markers for the dinoflagellate <i>Gambierdiscus caribaeus</i> from high-throughput sequencing data. <i>Journal of Applied Phycology</i> , 2017, 29, 1927-1932.	1.5	5
706	Melatonin prevents obesity through modulation of gut microbiota in mice. <i>Journal of Pineal Research</i> , 2017, 62, e12399.	3.4	219
707	Physicochemical and microbial properties of settled and floating anammox granules in upflow reactor. <i>Biochemical Engineering Journal</i> , 2017, 123, 75-85.	1.8	54
708	Simultaneous processing and degradation of mitochondrial RNAs revealed by circularized RNA sequencing. <i>Nucleic Acids Research</i> , 2017, 45, 5487-5500.	6.5	36
709	The influence of diet on the grass carp intestinal microbiota and bile acids. <i>Aquaculture Research</i> , 2017, 48, 4934-4944.	0.9	26
710	Patterns of Diversity and Spatial Variability of β -Defensin Innate Immune Genes in a Declining Wild Population of Tree Swallows. <i>Journal of Heredity</i> , 2017, 108, 262-269.	1.0	3

#	ARTICLE	IF	CITATIONS
711	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. <i>Genome Research</i> , 2017, 27, 885-896.	2.4	464
712	Fecal microbiota signatures of adult patients with different types of short bowel syndrome. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2017, 32, 1949-1957.	1.4	44
713	Large-scale seaweed cultivation diverges water and sediment microbial communities in the coast of Nan'ao Island, South China Sea. <i>Science of the Total Environment</i> , 2017, 598, 97-108.	3.9	49
714	A submarine volcanic eruption leads to a novel microbial habitat. <i>Nature Ecology and Evolution</i> , 2017, 1, 144.	3.4	42
715	Development and characterization of 21 novel microsatellite markers for the Australian smelt <i>Retropinna semoni</i> (Weber, 1895). <i>Journal of Applied Ichthyology</i> , 2017, 33, 824-828.	0.3	4
716	The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. <i>Molecular Ecology</i> , 2017, 26, 3676-3686.	2.0	22
717	Sensory profile and volatile aroma composition of reduced alcohol Merlot wines fermented with <i>Metschnikowia pulcherrima</i> and <i>Saccharomyces uvarum</i> . <i>International Journal of Food Microbiology</i> , 2017, 252, 1-9.	2.1	97
718	Inulin with different degrees of polymerization modulates composition of intestinal microbiota in mice. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	61
719	Post carbon removal nitrifying MBBR operation at high loading and exposure to starvation conditions. <i>Bioresource Technology</i> , 2017, 239, 318-325.	4.8	12
720	Effect of fumigation with chloropicrin on soil bacterial communities and genes encoding key enzymes involved in nitrogen cycling. <i>Environmental Pollution</i> , 2017, 227, 534-542.	3.7	84
721	Pilot plant demonstration of stable and efficient high rate biological nutrient removal with low dissolved oxygen conditions. <i>Water Research</i> , 2017, 121, 72-85.	5.3	80
722	<i>Bifidobacterium</i> CECT 7765 modulates early stress-induced immune, neuroendocrine and behavioral alterations in mice. <i>Brain, Behavior, and Immunity</i> , 2017, 65, 43-56.	2.0	124
723	DNA-based study of the diet of the marine calanoid copepod <i>Calanus sinicus</i> . <i>Journal of Experimental Marine Biology and Ecology</i> , 2017, 494, 1-9.	0.7	29
724	Comparative profiling of microbial community of three economically important fishes reared in sea cages under tropical offshore environment. <i>Marine Genomics</i> , 2017, 34, 57-65.	0.4	23
725	Characterization of the gut microbiota in the golden takin (<i>Budorcas taxicolor bedfordi</i>). <i>AMB Express</i> , 2017, 7, 81.	1.4	23
726	Responses of soil N-fixing bacteria communities to invasive plant species under different types of simulated acid deposition. <i>Die Naturwissenschaften</i> , 2017, 104, 43.	0.6	17
727	Distribution patterns of soil microbial eukaryotes suggests widespread algivory by phagotrophic protists as an alternative pathway for nutrient cycling. <i>Soil Biology and Biochemistry</i> , 2017, 112, 68-76.	4.2	104
728	Tropical-forest mammals as detected by environmental DNA at natural saltlicks in Borneo. <i>Biological Conservation</i> , 2017, 210, 281-285.	1.9	54

#	ARTICLE	IF	CITATIONS
729	Comparison of rumen archaeal diversity in adult and elderly yaks (<i>Bos grunniens</i>) using 16S rRNA gene high-throughput sequencing. <i>Journal of Integrative Agriculture</i> , 2017, 16, 1130-1137.	1.7	4
730	Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes. <i>Briefings in Bioinformatics</i> , 2018, 19, 1415-1429.	3.2	34
731	Heritable L1 retrotransposition in the mouse primordial germline and early embryo. <i>Genome Research</i> , 2017, 27, 1395-1405.	2.4	90
732	The environmental and host-associated bacterial microbiota of Arctic seawater-farmed Atlantic salmon with ulcerative disorders. <i>Journal of Fish Diseases</i> , 2017, 40, 1645-1663.	0.9	74
733	An Agile Functional Analysis of Metagenomic Data Using SUPER-FOCUS. <i>Methods in Molecular Biology</i> , 2017, 1611, 35-44.	0.4	2
734	Actual measurement, hygrothermal response experiment and growth prediction analysis of microbial contamination of central air conditioning system in Dalian, China. <i>Scientific Reports</i> , 2017, 7, 44190.	1.6	3
735	Quantitative assessment of timing, efficiency, specificity and genetic mosaicism of CRISPR/Cas9-mediated gene editing of hemoglobin beta gene in rhesus monkey embryos. <i>Human Molecular Genetics</i> , 2017, 26, 2678-2689.	1.4	32
736	Circularized Visualisation of Genetic Interactions. , 2017, , .		2
737	The microbial community of the gut differs between piglets fed sow milk, milk replacer or bovine colostrum. <i>British Journal of Nutrition</i> , 2017, 117, 964-978.	1.2	30
738	Effects of fumigation with metam-sodium on soil microbial biomass, respiration, nitrogen transformation, bacterial community diversity and genes encoding key enzymes involved in nitrogen cycling. <i>Science of the Total Environment</i> , 2017, 598, 1027-1036.	3.9	63
739	Geographic distribution of cadmium and its interaction with the microbial community in the Longjiang River: risk evaluation after a shocking pollution accident. <i>Scientific Reports</i> , 2017, 7, 227.	1.6	18
740	Hot topic: 16S rRNA gene sequencing reveals the microbiome of the virgin and pregnant bovine uterus. <i>Journal of Dairy Science</i> , 2017, 100, 4953-4960.	1.4	100
741	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
742	Land scale biogeography of arsenic biotransformation genes in estuarine wetland. <i>Environmental Microbiology</i> , 2017, 19, 2468-2482.	1.8	45
743	Soil aggregation and associated microbial communities modify the impact of agricultural management on carbon content. <i>Environmental Microbiology</i> , 2017, 19, 3070-3086.	1.8	180
744	Competition drives the response of soil microbial diversity to increased grazing by vertebrate herbivores. <i>Ecology</i> , 2017, 98, 1922-1931.	1.5	96
745	Effect of phosphorus addition on the reductive transformation of pentachlorophenol (PCP) and iron reduction with microorganism involvement. <i>Environmental Science and Pollution Research</i> , 2017, 24, 22852-22860.	2.7	1
746	Effect of benzoic acid on soil microbial communities associated with soilborne peanut diseases. <i>Applied Soil Ecology</i> , 2017, 110, 34-42.	2.1	58

#	ARTICLE	IF	CITATIONS
747	Molecular diversity and ecological characteristics of the eukaryotic phytoplankton community in the coastal waters of the Bohai Sea, China. <i>Harmful Algae</i> , 2017, 61, 13-22.	2.2	38
748	FDSTools: A software package for analysis of massively parallel sequencing data with the ability to recognise and correct STR stutter and other PCR or sequencing noise. <i>Forensic Science International: Genetics</i> , 2017, 27, 27-40.	1.6	73
749	A combined meta-barcoding and shotgun metagenomic analysis of spontaneous wine fermentation. <i>GigaScience</i> , 2017, 6, 1-10.	3.3	67
750	Local and geographical factors jointly drive elevational patterns in three microbial groups across subarctic ponds. <i>Global Ecology and Biogeography</i> , 2017, 26, 973-982.	2.7	34
751	Survey of High-Affinity H ₂ -Oxidizing Bacteria in Soil Reveals Their Vast Diversity Yet Underrepresentation in Genomic Databases. <i>Microbial Ecology</i> , 2017, 74, 771-775.	1.4	14
752	Illumina-Based Analysis of Bulk and Rhizosphere Soil Bacterial Communities in Paddy Fields Under Mixed Heavy Metal Contamination. <i>Pedosphere</i> , 2017, 27, 569-578.	2.1	82
753	Exogenous addition of H ₂ for an in situ biogas upgrading through biological reduction of carbon dioxide into methane. <i>Waste Management</i> , 2017, 68, 146-156.	3.7	110
754	Biogeography of cryoconite bacterial communities on glaciers of the Tibetan Plateau. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	34
755	Next-generation sequencing virulome analysis of a <i>Yersinia enterocolitica</i> subsp. <i>paleartica</i> bioserotype 4/O:3 ST18 isolated from human blood in Brazil. <i>Brazilian Journal of Infectious Diseases</i> , 2017, 21, 550-553.	0.3	5
756	Structure of protein emulsion in food impacts intestinal microbiota, caecal luminal content composition and distal intestine characteristics in rats. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1700078.	1.5	12
757	A high-efficiency denitrification bioreactor for the treatment of acrylonitrile wastewater using waterborne polyurethane immobilized activated sludge. <i>Bioresource Technology</i> , 2017, 239, 472-481.	4.8	45
758	Bamboo invasion of broadleaf forests altered soil fungal community closely linked to changes in soil organic C chemical composition and mineral N production. <i>Plant and Soil</i> , 2017, 418, 507-521.	1.8	54
759	Stormwater loadings of antibiotic resistance genes in an urban stream. <i>Water Research</i> , 2017, 123, 144-152.	5.3	101
760	Complex interactions between potentially pathogenic, opportunistic, and resident bacteria emerge during infection on a reef-building coral. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	57
761	Adaptation of gut microbiome to different dietary nonstarch polysaccharide fractions in a porcine model. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1700012.	1.5	32
762	Effect of urea-supplemented diets on the ruminal bacterial and archaeal community composition of finishing bulls. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6205-6216.	1.7	22
763	Profiles and drivers of antibiotic resistance genes distribution in one-stage and two-stage sludge anaerobic digestion based on microwave-H ₂ O ₂ pretreatment. <i>Bioresource Technology</i> , 2017, 241, 573-581.	4.8	42
764	Evolutionary dynamics of an expressed MHC class II β locus in the Ranidae (Anura) uncovered by genome walking and high-throughput amplicon sequencing. <i>Developmental and Comparative Immunology</i> , 2017, 76, 177-188.	1.0	10

#	ARTICLE	IF	CITATIONS
765	Fecal microbiota variation across the lifespan of the healthy laboratory rat. <i>Gut Microbes</i> , 2017, 8, 428-439.	4.3	93
766	History cleans up messes: The impact of time in driving divergence and introgression in a tropical suture zone. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1888-1899.	1.1	17
767	Decreased plant productivity resulting from plant group removal experiment constrains soil microbial functional diversity. <i>Global Change Biology</i> , 2017, 23, 4318-4332.	4.2	45
768	Draft Genome Sequences of <i>Listeria monocytogenes</i> , Isolated from Fresh Leaf Vegetables in Owerri City, Nigeria. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
769	Performance and microbial community dynamics of electricity-assisted sequencing batch reactor (SBR) for treatment of saline petrochemical wastewater. <i>Environmental Science and Pollution Research</i> , 2017, 24, 17556-17565.	2.7	20
770	Polymannuronic acid ameliorated obesity and inflammation associated with a high-fat and high-sucrose diet by modulating the gut microbiome in a murine model. <i>British Journal of Nutrition</i> , 2017, 117, 1332-1342.	1.2	38
771	Soil fungal diversity in natural grasslands of the Tibetan Plateau: associations with plant diversity and productivity. <i>New Phytologist</i> , 2017, 215, 756-765.	3.5	248
772	Development of a Medium Density Combined-Species SNP Array for Pacific and European Oysters (<i>Crassostrea gigas</i> and <i>Ostrea edulis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2209-2218.	0.8	97
773	Biotransformation of nitrogen- and sulfur-containing pollutants during coking wastewater treatment: Correspondence of performance to microbial community functional structure. <i>Water Research</i> , 2017, 121, 338-348.	5.3	52
774	PipeCraft: Flexible open-source toolkit for bioinformatics analysis of custom high-throughput amplicon sequencing data. <i>Molecular Ecology Resources</i> , 2017, 17, e234-e240.	2.2	116
775	Early Emergence of CD19-Negative Human Antibody-Secreting Cells at the Plasmablast to Plasma Cell Transition. <i>Journal of Immunology</i> , 2017, 198, 4618-4628.	0.4	40
776	High-resolution analyses reveal structural diversity patterns of microbial communities in Chromite Ore Processing Residue (COPR) contaminated soils. <i>Chemosphere</i> , 2017, 183, 266-276.	4.2	49
777	Anti-hyperlipidemic effects of <i>Rhizoma Coptidis</i> alkaloids are achieved through modulation of the enterohepatic circulation of bile acids and cross-talk between the gut microbiota and the liver. <i>Journal of Functional Foods</i> , 2017, 35, 205-215.	1.6	14
778	Biological nutrient removal and molecular biological characteristics in an anaerobic-multistage anaerobic/oxic (A-MAO) process to treat municipal wastewater. <i>Bioresource Technology</i> , 2017, 241, 969-978.	4.8	79
779	Metabolic network analysis reveals microbial community interactions in anammox granules. <i>Nature Communications</i> , 2017, 8, 15416.	5.8	489
780	Bacterial diversity in Shahu lake, northwest China is significantly affected by nutrient composition rather than location. <i>Annals of Microbiology</i> , 2017, 67, 469-478.	1.1	7
781	Effect of biocontrol agent <i>Bacillus amyloliquefaciens</i> SN16-1 and plant pathogen <i>Fusarium oxysporum</i> on tomato rhizosphere bacterial community composition. <i>Biological Control</i> , 2017, 112, 1-9.	1.4	32
782	Divergent taxonomic and functional responses of microbial communities to field simulation of aeolian soil erosion and deposition. <i>Molecular Ecology</i> , 2017, 26, 4186-4196.	2.0	14

#	ARTICLE	IF	CITATIONS
783	RNA-Based Amplicon Sequencing Reveals Microbiota Development during Ripening of Artisanal versus Industrial Lard d'Arnad. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	26
784	Complete mitochondrial genome of a bat-eared fox (<i>Otocyon megalotis</i>), along with phylogenetic considerations. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 298-299.	0.2	2
785	Multi-locus and long amplicon sequencing approach to study microbial diversity at species level using the MinION [®] , a portable nanopore sequencer. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	83
786	Genetic Structure and Phylogeography of the Leopard Cat (<i>Prionailurus bengalensis</i>) Inferred from Mitochondrial Genomes. <i>Journal of Heredity</i> , 2017, 108, 349-360.	1.0	31
787	Circular linkages between soil biodiversity, fertility and plant productivity are limited to topsoil at the continental scale. <i>New Phytologist</i> , 2017, 215, 1186-1196.	3.5	103
788	Selective depletion of uropathogenic <i>E. coli</i> from the gut by a FimH antagonist. <i>Nature</i> , 2017, 546, 528-532.	13.7	231
789	Bacterial Signatures of "Red-Operculum" Disease in the Gut of Crucian Carp (<i>Carassius auratus</i>). <i>Microbial Ecology</i> , 2017, 74, 510-521.	1.4	112
790	Spatial Abundance, Diversity, and Activity of Ammonia-Oxidizing Bacteria in Coastal Sediments of the Liaohu Estuary. <i>Current Microbiology</i> , 2017, 74, 632-640.	1.0	6
791	Protective effects of mannan oligosaccharides on turbot <i>Scophthalmus maximus</i> suffering from soy enteropathy. <i>Aquaculture</i> , 2017, 476, 141-151.	1.7	40
792	Molecular investigation of bacterial communities during the manufacturing and ripening of semi-hard Iranian Liqvan cheese. <i>Food Microbiology</i> , 2017, 66, 64-71.	2.1	29
793	Identification of microbial communities, with a focus on foodborne pathogens, during kimchi manufacturing process using culture-independent and -dependent analyses. <i>LWT - Food Science and Technology</i> , 2017, 81, 153-159.	2.5	31
794	Genomic diversity guides conservation strategies among rare terrestrial orchid species when taxonomy remains uncertain. <i>Annals of Botany</i> , 2017, 119, 1267-1277.	1.4	18
795	Use of municipal solid wastes for chemical and microbiological recovery of soils contaminated with metal(loid)s. <i>Soil Biology and Biochemistry</i> , 2017, 111, 25-35.	4.2	47
796	Patterns of temporal and enemy niche use by a community of leaf cone moths (<i>Caloptilia</i>) coexisting on maples (<i>Acer</i>) as revealed by metabarcoding. <i>Molecular Ecology</i> , 2017, 26, 3309-3319.	2.0	9
797	Community-Level Differences in the Microbiome of Healthy Wild Mallards and Those Infected by Influenza A Viruses. <i>MSystems</i> , 2017, 2, .	1.7	41
798	Novel 16S rDNA primers revealed the diversity and habitats-related community structure of sphingomonads in 10 different niches. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 877-889.	0.7	9
799	Next-generation sequencing enables the discovery of more diverse positive clones from a phage-displayed antibody library. <i>Experimental and Molecular Medicine</i> , 2017, 49, e308-e308.	3.2	55
800	Rectal microbiota among HIV-uninfected, untreated HIV, and treated HIV-infected in Nigeria. <i>Aids</i> , 2017, 31, 857-862.	1.0	46

#	ARTICLE	IF	CITATIONS
801	Factors influencing ruminal bacterial community diversity and composition and microbial fibrolytic enzyme abundance in lactating dairy cows with a focus on the role of active dry yeast. <i>Journal of Dairy Science</i> , 2017, 100, 4377-4393.	1.4	53
802	High-quality genome assembly of <i>Capsella bursa-pastoris</i> reveals asymmetry of regulatory elements at early stages of polyploid genome evolution. <i>Plant Journal</i> , 2017, 91, 278-291.	2.8	40
803	Invasive <i>Drosophila suzukii</i> facilitates <i>Drosophila melanogaster</i> infestation and sour rot outbreaks in the vineyards. <i>Royal Society Open Science</i> , 2017, 4, 170117.	1.1	66
804	Microbial community and metabolic pathway succession driven by changed nutrient inputs in tailings: effects of different nutrients on tailing remediation. <i>Scientific Reports</i> , 2017, 7, 474.	1.6	37
805	Gut metagenomic analysis reveals prominent roles of <i>Lactobacillus</i> and cecal microbiota in chicken feed efficiency. <i>Scientific Reports</i> , 2017, 7, 45308.	1.6	193
806	Intestinal Barrier Function and the Gut Microbiome Are Differentially Affected in Mice Fed a Western-Style Diet or Drinking Water Supplemented with Fructose. <i>Journal of Nutrition</i> , 2017, 147, 770-780.	1.3	118
807	Microbial dynamics in anaerobic digestion reactors for treating organic urban residues during the start-up process. <i>Letters in Applied Microbiology</i> , 2017, 64, 438-445.	1.0	27
808	The role of adaptive immunity as an ecological filter on the gut microbiota in zebrafish. <i>ISME Journal</i> , 2017, 11, 1630-1639.	4.4	93
809	Whole-Community Metagenomics in Two Different Anammox Configurations: Process Performance and Community Structure. <i>Environmental Science & Technology</i> , 2017, 51, 4317-4327.	4.6	98
810	High throughput 16SrRNA gene sequencing reveals the correlation between <i>Propionibacterium acnes</i> and sarcoidosis. <i>Respiratory Research</i> , 2017, 18, 28.	1.4	27
811	Contrasting patterns of diversity of abundant and rare bacterioplankton in freshwater lakes along an elevation gradient. <i>Limnology and Oceanography</i> , 2017, 62, 1570-1585.	1.6	49
812	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. <i>Nature Ecology and Evolution</i> , 2017, 1, 91.	3.4	262
813	Evaluation of bacterial pathogen diversity, abundance and health risks in urban recreational water by amplicon next-generation sequencing and quantitative PCR. <i>Journal of Environmental Sciences</i> , 2017, 57, 137-149.	3.2	43
814	Effects of xeric shrubs on soil microbial communities in a desert in northern China. <i>Plant and Soil</i> , 2017, 414, 281-294.	1.8	32
815	High tolerance to glycerol and high production of 1,3-propanediol in batch fermentations by microbial consortium from marine sludge. <i>Engineering in Life Sciences</i> , 2017, 17, 635-644.	2.0	32
816	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	13.7	166
817	Entire nucleotide sequences of <i>Gossypium raimondii</i> and <i>G. arboreum</i> mitochondrial genomes revealed a genome species as cytoplasmic donor of the allotetraploid species. <i>Plant Biology</i> , 2017, 19, 484-493.	1.8	54
818	Impacts of conversion from secondary forests to larch plantations on the structure and function of microbial communities. <i>Applied Soil Ecology</i> , 2017, 111, 73-83.	2.1	70

#	ARTICLE	IF	CITATIONS
819	The expressed TCR ^β CDR3 repertoire is dominated by conserved DNA sequences in channel catfish. <i>Developmental and Comparative Immunology</i> , 2017, 68, 26-33.	1.0	8
820	Bisphenol A (BPA) in the serum of pet dogs following short-term consumption of canned dog food and potential health consequences of exposure to BPA. <i>Science of the Total Environment</i> , 2017, 579, 1804-1814.	3.9	43
821	Temporal dynamics of bacterioplankton communities in response to excessive nitrate loading in oligotrophic coastal water. <i>Marine Pollution Bulletin</i> , 2017, 114, 656-663.	2.3	8
822	Microbial distribution and variation in produced water from separators to storage tanks of shale gas wells in Sichuan Basin, China. <i>Environmental Science: Water Research and Technology</i> , 2017, 3, 340-351.	1.2	24
823	Tobacco bacterial wilt suppression with biochar soil addition associates to improved soil physiochemical properties and increased rhizosphere bacteria abundance. <i>Applied Soil Ecology</i> , 2017, 112, 90-96.	2.1	109
824	Mutational landscape of antibody variable domains reveals a switch modulating the interdomain conformational dynamics and antigen binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E486-E495.	3.3	72
825	Detecting invertebrate species in archived collections using next-generation sequencing. <i>Molecular Ecology Resources</i> , 2017, 17, 915-930.	2.2	11
826	A long-term hybrid poplar plantation on cropland reduces soil organic carbon mineralization and shifts microbial community abundance and composition. <i>Applied Soil Ecology</i> , 2017, 111, 94-104.	2.1	62
827	Soil nitrogen leaching decreases as biogas slurry DOC/N ratio increases. <i>Applied Soil Ecology</i> , 2017, 111, 105-113.	2.1	43
828	The Underlying Ecological Processes of Gut Microbiota Among Cohabiting Retarded, Overgrown and Normal Shrimp. <i>Microbial Ecology</i> , 2017, 73, 988-999.	1.4	102
829	Depth-resolved microbial community analyses in two contrasting soil cores contaminated by antimony and arsenic. <i>Environmental Pollution</i> , 2017, 221, 244-255.	3.7	60
830	Long-Term Nickel Contamination Increases the Occurrence of Antibiotic Resistance Genes in Agricultural Soils. <i>Environmental Science & Technology</i> , 2017, 51, 790-800.	4.6	240
831	Consumption of a high-fat diet alters the seminal fluid and gut microbiomes in male mice. <i>Reproduction, Fertility and Development</i> , 2017, 29, 1602.	0.1	38
832	Unusual Legionnaires' outbreak in cool, dry Western Canada: an investigation using genomic epidemiology. <i>Epidemiology and Infection</i> , 2017, 145, 254-265.	1.0	6
833	Draft Genome Sequence of <i>Rhodococcus</i> sp. Strain 66b. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
834	OCULAR FINDINGS AND SELECT OPHTHALMIC DIAGNOSTIC TESTS IN CAPTIVE AMERICAN WHITE PELICANS (<i>PELECANUS ERYTHRORHYNCHOS</i>). <i>Journal of Zoo and Wildlife Medicine</i> , 2017, 48, 675-682.	0.3	9
835	Managing the excessive proliferation of glycogen accumulating organisms in industrial activated sludge by nitrogen supplementation: A FISH-NanoSIMS approach. <i>Systematic and Applied Microbiology</i> , 2017, 40, 500-507.	1.2	3
836	Genome diversity of tuber-bearing <i>Solanum</i> uncovers complex evolutionary history and targets of domestication in the cultivated potato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9999-E10008.	3.3	271

#	ARTICLE	IF	CITATIONS
837	Open the Sterivex TM casing: An easy and effective way to improve DNA extraction yields. <i>Limnology and Oceanography: Methods</i> , 2017, 15, 1015-1020.	1.0	71
838	Draft Genome Sequences of Four Alkaliphilic Bacteria Belonging to the <i>Anaerobacillus</i> Genus. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
839	Response of soil microbial communities and microbial interactions to long-term heavy metal contamination. <i>Environmental Pollution</i> , 2017, 231, 908-917.	3.7	320
840	Strong impact of anthropogenic contamination on the occurrence patterns of a riverine microbial community. <i>Environmental Microbiology</i> , 2017, 19, 4993-5009.	1.8	213
841	Stepwise impact of urban wastewater treatment on the bacterial community structure, antibiotic contents, and prevalence of antimicrobial resistance. <i>Environmental Pollution</i> , 2017, 231, 1578-1585.	3.7	59
842	Pathogen invasion changes the intestinal microbiota composition and induces innate immune responses in the zebrafish intestine. <i>Fish and Shellfish Immunology</i> , 2017, 71, 35-42.	1.6	119
843	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <i>Nature Biotechnology</i> , 2017, 35, 1077-1086.	9.4	400
844	Interhost dispersal alters microbiome assembly and can overwhelm host innate immunity in an experimental zebrafish model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11181-11186.	3.3	131
845	Diversity and co-occurrence network of soil fungi are more responsive than those of bacteria to shifts in precipitation seasonality in a subtropical forest. <i>Soil Biology and Biochemistry</i> , 2017, 115, 499-510.	4.2	134
846	Exploring the Plant Microbiome Through Multi-omics Approaches. , 2017, , 233-268.		11
847	Differences in root-associated bacterial communities among fine root branching orders of poplar (<i>Populus euramericana</i> (Dode) Guinier.). <i>Plant and Soil</i> , 2017, 421, 123-135.	1.8	17
848	Community structure of gut bacteria of <i>Dendroctonus armandi</i> (Coleoptera: Curculionidae: Tj ETQq1 1 0.784314 r _{BT} /Overlock 10 Tf	1.6	10
849	Bacterial community of a spider, <i>Marpiss magister</i> (Salticidae). <i>3 Biotech</i> , 2017, 7, 371.	1.1	11
850	Oxygen transfer dynamics and nitrification in a novel rotational sponge reactor. <i>Biochemical Engineering Journal</i> , 2017, 128, 162-167.	1.8	25
851	16S rRNA Gene Amplicon Sequencing Reveals Significant Changes in Microbial Compositions during Cyanobacteria-Laden Drinking Water Sludge Storage. <i>Environmental Science & Technology</i> , 2017, 51, 12774-12783.	4.6	25
852	Unravelling the core microbiome of biofilms in cooling tower systems. <i>Biofouling</i> , 2017, 33, 793-806.	0.8	35
853	Shifts in microbial communities with increasing soil fertility across a chronosequence of paddy cultivation in subtropical China. <i>Applied Soil Ecology</i> , 2017, 120, 153-159.	2.1	27
854	Cleavage of the main carbon chain backbone of high molecular weight polyacrylamide by aerobic and anaerobic biological treatment. <i>Chemosphere</i> , 2017, 189, 277-283.	4.2	13

#	ARTICLE	IF	CITATIONS
855	Effects of therapeutic hypothermia on the gut microbiota and metabolome of infants suffering hypoxic-ischemic encephalopathy at birth. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 93, 110-118.	1.2	13
856	Fungal community assemblages in a high elevation desert environment: Absence of dispersal limitation and edaphic effects in surface soil. <i>Soil Biology and Biochemistry</i> , 2017, 115, 393-402.	4.2	42
857	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. <i>Nature Communications</i> , 2017, 8, 858.	5.8	107
858	Interactions of plant growth-promoting rhizobacteria and soil factors in two leguminous plants. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8485-8497.	1.7	76
859	Effect of <i>Propionibacterium acidipropionici</i> P169 on the rumen and faecal microbiota of beef cattle fed a maize-based finishing diet. <i>Beneficial Microbes</i> , 2017, 8, 785-799.	1.0	7
860	High reactivity of deep biota under anthropogenic CO ₂ injection into basalt. <i>Nature Communications</i> , 2017, 8, 1063.	5.8	55
861	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	1.6	24
862	Prokaryotic Community Distribution along an Ecological Gradient of Salinity in Surface and Subsurface Saline Soils. <i>Scientific Reports</i> , 2017, 7, 13332.	1.6	33
863	Blood Meal Source Characterization Using Illumina Sequencing in the Chagas Disease Vector <i>Rhodnius pallescens</i> (Hemiptera: Reduviidae) in Panamá. <i>Journal of Medical Entomology</i> , 2017, 54, 1786-1789.	0.9	36
864	Soil microbial community dynamics and assembly under long-term land use change. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	69
865	Impact of pyrene and cadmium co-contamination on prokaryotic community in coastal sediment microcosms. <i>Chemosphere</i> , 2017, 188, 320-328.	4.2	14
866	Impact of egg disinfection of hatching eggs on the eggshell microbiome and bacterial load. <i>Poultry Science</i> , 2017, 96, 3901-3911.	1.5	39
867	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
868	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	1.9	84
869	Augmentation of acyl homoserine lactones-producing and -quenching bacterium into activated sludge for its granulation. <i>Water Research</i> , 2017, 125, 309-317.	5.3	44
870	Fishmeal Application Induces Antibiotic Resistance Gene Propagation in Mariculture Sediment. <i>Environmental Science & Technology</i> , 2017, 51, 10850-10860.	4.6	100
871	Microbial community structure and diversity within hypersaline Keke Salt Lake environments. <i>Canadian Journal of Microbiology</i> , 2017, 63, 895-908.	0.8	54
872	Diverse bacterial taxa inhabit root nodules of lucerne (<i>Medicago sativa</i> L.) in New Zealand pastoral soils. <i>Plant and Soil</i> , 2017, 420, 253-262.	1.8	15

#	ARTICLE	IF	CITATIONS
873	A novel signature for stratifying the molecular heterogeneity of the tissue-infiltrating T-cell receptor repertoire reflects gastric cancer prognosis. <i>Scientific Reports</i> , 2017, 7, 7762.	1.6	25
874	Microbiome Dynamics in a Shrimp Grow-out Pond with Possible Outbreak of Acute Hepatopancreatic Necrosis Disease. <i>Scientific Reports</i> , 2017, 7, 9395.	1.6	112
875	Distinct gut microbiome patterns associate with consensus molecular subtypes of colorectal cancer. <i>Scientific Reports</i> , 2017, 7, 11590.	1.6	173
876	Organic amendment practices as possible drivers of biogenic Volatile Organic Compounds emitted by soils in agrosystems. <i>Agriculture, Ecosystems and Environment</i> , 2017, 250, 25-36.	2.5	30
877	Effects of iron and calcium carbonate on contaminant removal efficiencies and microbial communities in integrated wastewater treatment systems. <i>Chemosphere</i> , 2017, 189, 10-20.	4.2	10
878	Variations in oral microbiota associated with oral cancer. <i>Scientific Reports</i> , 2017, 7, 11773.	1.6	259
879	Variation of mucin adhesion, cell surface characteristics, and molecular mechanisms among <i>Lactobacillus plantarum</i> isolated from different habitats. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7663-7674.	1.7	34
880	Spatiotemporal heterogeneity of core functional bacteria and their synergetic and competitive interactions in denitrifying sulfur conversion-assisted enhanced biological phosphorus removal. <i>Scientific Reports</i> , 2017, 7, 10927.	1.6	17
881	The impact of immigration on microbial community composition in full-scale anaerobic digesters. <i>Scientific Reports</i> , 2017, 7, 9343.	1.6	127
882	Structural and functional variability in root-associated bacterial microbiomes of Cd/Zn hyperaccumulator <i>Sedum alfredii</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7961-7976.	1.7	52
883	Molecular estimation of alteration in intestinal microbial composition in Hashimoto's thyroiditis patients. <i>Biomedicine and Pharmacotherapy</i> , 2017, 95, 865-874.	2.5	70
884	Guanylate Cyclase C Activation Shapes the Intestinal Microbiota in Patients with Familial Diarrhea and Increased Susceptibility for Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 1752-1761.	0.9	13
885	VHL Deficiency Drives Enhancer Activation of Oncogenes in Clear Cell Renal Cell Carcinoma. <i>Cancer Discovery</i> , 2017, 7, 1284-1305.	7.7	111
886	Biodiversity and species competition regulate the resilience of microbial biofilm community. <i>Molecular Ecology</i> , 2017, 26, 6170-6182.	2.0	299
887	An Efficient Approach to Merging Paired-End Reads and Incorporation of Uncertainties. , 2017, , 299-325.		0
888	Linking Spatial Structure and Community-Level Biotic Interactions through Cooccurrence and Time Series Modeling of the Human Intestinal Microbiota. <i>MSystems</i> , 2017, 2, .	1.7	8
889	Changes in the intestinal microbiota following the administration of azithromycin in a randomised placebo-controlled trial among infants in south India. <i>Scientific Reports</i> , 2017, 7, 9168.	1.6	55
890	Bacterial community diversity on in-shell walnut surfaces from six representative provinces in China. <i>Scientific Reports</i> , 2017, 7, 10054.	1.6	26

#	ARTICLE	IF	CITATIONS
891	Marked seasonality and high spatial variation in estuarine ciliates are driven by exchanges between the "abundant" and "intermediate" biospheres. <i>Scientific Reports</i> , 2017, 7, 9494.	1.6	27
892	A cross-sectional comparative study of gut bacterial community of Indian and Finnish children. <i>Scientific Reports</i> , 2017, 7, 10555.	1.6	37
893	Characterization of sediment bacterial communities in plain lakes with different trophic statuses. <i>MicrobiologyOpen</i> , 2017, 6, e00503.	1.2	71
894	Monitoring of genetically modified <i>Escherichia coli</i> in laboratory wastewater. <i>Environmental Science and Pollution Research</i> , 2017, 24, 23725-23734.	2.7	5
895	<i>Bifidobacterium pseudocatenulatum</i> LI09 and <i>Bifidobacterium catenulatum</i> LI10 attenuate D-galactosamine-induced liver injury by modifying the gut microbiota. <i>Scientific Reports</i> , 2017, 7, 8770.	1.6	70
896	Effect of dairy matrices on the survival of <i>Streptococcus thermophilus</i> , <i>Brevibacterium aurantiacum</i> and <i>Hafnia alvei</i> during digestion. <i>Food Research International</i> , 2017, 100, 477-488.	2.9	11
897	Responses of soil N-fixing bacteria communities to <i>Amaranthus retroflexus</i> invasion under different forms of N deposition. <i>Agriculture, Ecosystems and Environment</i> , 2017, 247, 329-336.	2.5	33
898	DBZ is a putative PPAR β agonist that prevents high fat diet-induced obesity, insulin resistance and gut dysbiosis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2690-2701.	1.1	51
899	The aerial parts of <i>Salvia miltiorrhiza</i> Bge. strengthen intestinal barrier and modulate gut microbiota imbalance in streptozocin-induced diabetic mice. <i>Journal of Functional Foods</i> , 2017, 36, 362-374.	1.6	32
900	Priming in a permissive type I-C CRISPR-Cas system reveals distinct dynamics of spacer acquisition and loss. <i>Rna</i> , 2017, 23, 1525-1538.	1.6	48
901	Increased sequencing depth does not increase captured diversity of arbuscular mycorrhizal fungi. <i>Mycorrhiza</i> , 2017, 27, 761-773.	1.3	58
902	Effect of dietary nucleosides and yeast extracts on composition and metabolic activity of infant gut microbiota in PolyFermS colonic fermentation models. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	34
903	Specific Signatures of the Gut Microbiota and Increased Levels of Butyrate in Children Treated with Fermented Cow's Milk Containing Heat-Killed <i>Lactobacillus paracasei</i> CBA L74. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	92
904	Evaluating hybridization capture with RAD probes as a tool for museum genomics with historical bird specimens. <i>Ecology and Evolution</i> , 2017, 7, 4755-4767.	0.8	34
905	Patterns of seasonality and group membership characterize the gut microbiota in a longitudinal study of wild Verreaux's sifakas (<i>Propithecus verreauxi</i>). <i>Ecology and Evolution</i> , 2017, 7, 5732-5745.	0.8	90
906	Sex determines effect of physical activity on diet preference: Association of striatal opioids and gut microbiota composition. <i>Behavioural Brain Research</i> , 2017, 334, 16-25.	1.2	19
907	Heart failure is associated with depletion of core intestinal microbiota. <i>ESC Heart Failure</i> , 2017, 4, 282-290.	1.4	202
908	Divergent copies of the large inverted repeat in the chloroplast genomes of ulvophycean green algae. <i>Scientific Reports</i> , 2017, 7, 994.	1.6	77

#	ARTICLE	IF	CITATIONS
909	Analysis of large 16S rRNA Illumina data sets: Impact of singleton read filtering on microbial community description. <i>Molecular Ecology Resources</i> , 2017, 17, e122-e132.	2.2	55
910	Bacterial community diversity of traditional fermented vegetables in China. <i>LWT - Food Science and Technology</i> , 2017, 86, 40-48.	2.5	67
911	Range instability leads to cytonuclear discordance in a morphologically cryptic ground squirrel species complex. <i>Molecular Ecology</i> , 2017, 26, 4743-4755.	2.0	23
912	Diversity and stability of coral endolithic microbial communities at a naturally high CO ₂ reef. <i>Molecular Ecology</i> , 2017, 26, 5344-5357.	2.0	43
913	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. <i>MSphere</i> , 2017, 2, .	1.3	114
914	Environment and geographic distance differ in relative importance for determining fungal community of rhizosphere and bulk soil. <i>Environmental Microbiology</i> , 2017, 19, 3649-3659.	1.8	78
915	Interplay between the gut microbiota and immune responses of ayu (<i>Plecoglossus altivelis</i>) during <i>Vibrio anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2017, 68, 479-487.	1.6	100
916	Fate of antibiotic resistance genes in mesophilic and thermophilic anaerobic digestion of chemically enhanced primary treatment (CEPT) sludge. <i>Bioresource Technology</i> , 2017, 244, 433-444.	4.8	57
917	Relative abundance of deformed wing virus, <i>Varroa destructor</i> virus 1, and their recombinants in honey bees (<i>Apis mellifera</i>) assessed by kmer analysis of public RNA-Seq data. <i>Journal of Invertebrate Pathology</i> , 2017, 149, 44-50.	1.5	18
918	Comparison of DNA-, PMA-, and RNA-based 16S rRNA Illumina sequencing for detection of live bacteria in water. <i>Scientific Reports</i> , 2017, 7, 5752.	1.6	116
919	Heterogeneity of tumor-infiltrating lymphocytes ascribed to local immune status rather than neoantigens by multi-omics analysis of glioblastoma multiforme. <i>Scientific Reports</i> , 2017, 7, 6968.	1.6	26
920	Dissimilatory Nitrate Reduction to Ammonium in the Yellow River Estuary: Rates, Abundance, and Community Diversity. <i>Scientific Reports</i> , 2017, 7, 6830.	1.6	71
921	Bottom-up effects on herbivore-induced plant defences: a case study based on compositional patterns of rhizosphere microbial communities. <i>Scientific Reports</i> , 2017, 7, 6251.	1.6	15
922	Soil nutritional status and biogeography influence rhizosphere microbial communities associated with the invasive tree <i>Acacia dealbata</i> . <i>Scientific Reports</i> , 2017, 7, 6472.	1.6	54
923	Rapid de novo assembly of the European eel genome from nanopore sequencing reads. <i>Scientific Reports</i> , 2017, 7, 7213.	1.6	104
924	Characterization of the contaminant bacterial communities in sugarcane first-generation industrial ethanol production. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	20
925	Bio-fertilizer application induces soil suppressiveness against <i>Fusarium</i> wilt disease by reshaping the soil microbiome. <i>Soil Biology and Biochemistry</i> , 2017, 114, 238-247.	4.2	216
926	Elevated auxin biosynthesis and transport underlie high vein density in C ₄ leaves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6884-E6891.	3.3	34

#	ARTICLE	IF	CITATIONS
927	Complete sequence of chloroplast genome from <i>Sargassum vachellianum</i> (Sargassaceae,) Tj ETQq0 0 0 rgBT /Overlogk 10 Tf 50 742 Td	1.2	2
928	Distinct soil bacterial communities in response to the cropping system in a Mollisol of northeast China. <i>Applied Soil Ecology</i> , 2017, 119, 407-416.	2.1	51
929	Assessment of the degradation efficiency of full-scale biogas plants: A comparative study of degradation indicators. <i>Bioresource Technology</i> , 2017, 244, 304-312.	4.8	26
930	Remediation of <i>Thiothrix</i> spp. associated bulking problems by raw wastewater feeding: A full-scale experience. <i>Systematic and Applied Microbiology</i> , 2017, 40, 396-399.	1.2	5
931	Characterization of natural variation in North American Atlantic Salmon populations (Salmonidae:) Tj ETQq0 0 0 rgBT /Overlogk 10 Tf 50 742 Td	0.8	28
932	Metabolic potential and <i>in situ</i> activity of marine Marinimicrobia bacteria in an anoxic water column. <i>Environmental Microbiology</i> , 2017, 19, 4392-4416.	1.8	40
933	A Naturally Transmitted Epitheliotropic Polyomavirus Pathogenic in Immunodeficient Rats: Characterization, Transmission, and Preliminary Epidemiologic Studies. <i>Toxicologic Pathology</i> , 2017, 45, 593-603.	0.9	10
934	Metagenomic Analysis of Silage. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	7
935	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515.	6.0	169
936	Comparison of commercially-available preservatives for maintaining the integrity of bacterial DNA in human milk. <i>Journal of Microbiological Methods</i> , 2017, 141, 73-81.	0.7	18
937	Characterization of <i>Legionella</i> Species from Watersheds in British Columbia, Canada. <i>MSphere</i> , 2017, 2, .	1.3	32
938	Metabolic pathway analysis based on high-throughput sequencing in a batch biogas production process. <i>Energy</i> , 2017, 139, 571-579.	4.5	30
939	Dietary fucoidan of <i>Acaudina molpadioides</i> alters gut microbiota and mitigates intestinal mucosal injury induced by cyclophosphamide. <i>Food and Function</i> , 2017, 8, 3383-3393.	2.1	123
940	Lingual microbiota profiles of patients with geographic tongue. <i>Journal of Oral Microbiology</i> , 2017, 9, 1355206.	1.2	16
941	Gut microbiomes of free-ranging and captive Namibian cheetahs: Diversity, putative functions and occurrence of potential pathogens. <i>Molecular Ecology</i> , 2017, 26, 5515-5527.	2.0	84
942	A <i>Coxiella</i> mutualist symbiont is essential to the development of <i>Rhipicephalus microplus</i> . <i>Scientific Reports</i> , 2017, 7, 17554.	1.6	110
943	High-resolution profiling of the gut microbiome reveals the extent of <i>Clostridium difficile</i> burden. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 35.	2.9	55
944	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051.	6.0	229

#	ARTICLE	IF	CITATIONS
945	Deficiency of essential dietary n-3 PUFA disrupts the caecal microbiome and metabolome in mice. <i>British Journal of Nutrition</i> , 2017, 118, 959-970.	1.2	40
946	High-resolution bacterial 16S rRNA gene profile meta-analysis and biofilm status reveal common colorectal cancer consortia. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 34.	2.9	237
947	Microbial communities in the native habitats of <i>Agaricus sinodeliciosus</i> from Xinjiang Province revealed by amplicon sequencing. <i>Scientific Reports</i> , 2017, 7, 15719.	1.6	23
948	Effects of gravel-sand mulching on soil bacterial community and metabolic capability in the semi-arid Loess Plateau, China. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 209.	1.7	10
949	The unexpected depths of genome-skimming data: A case study examining Goodeniaceae floral symmetry genes. <i>Applications in Plant Sciences</i> , 2017, 5, 1700042.	0.8	24
950	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017, 551, 507-511.	13.7	791
951	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
952	Linking EPCR-Binding PfEMP1 to Brain Swelling in Pediatric Cerebral Malaria. <i>Cell Host and Microbe</i> , 2017, 22, 601-614.e5.	5.1	92
953	Evaluating the contribution of gut microbiome to the variance of porcine serum glucose and lipid concentration. <i>Scientific Reports</i> , 2017, 7, 14928.	1.6	15
954	Distinct microbial communities in the active and permafrost layers on the Tibetan Plateau. <i>Molecular Ecology</i> , 2017, 26, 6608-6620.	2.0	92
955	Bacterial Degradors of Coexisting Dichloromethane, Benzene, and Toluene, Identified by Stable-Isotope Probing. <i>Water, Air, and Soil Pollution</i> , 2017, 228, 418.	1.1	23
956	Metatranscriptomic data reveal the effect of different community properties on multifunctional redundancy. <i>Molecular Ecology</i> , 2017, 26, 6813-6826.	2.0	18
957	Usefulness and limitations of sample pooling for environmental DNA metabarcoding of freshwater fish communities. <i>Scientific Reports</i> , 2017, 7, 14860.	1.6	79
958	Understanding the variation of microbial community in heavy metals contaminated soil using high throughput sequencing. <i>Ecotoxicology and Environmental Safety</i> , 2017, 144, 300-306.	2.9	212
959	Impact of 25 years of inorganic fertilization on diazotrophic abundance and community structure in an acidic soil in southern China. <i>Soil Biology and Biochemistry</i> , 2017, 113, 240-249.	4.2	196
960	Microbial diversity in Chinese temperate steppe: unveiling the most influential environmental drivers. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	21
961	Bacterial diversity as affected by application of manure in red soils of subtropical China. <i>Biology and Fertility of Soils</i> , 2017, 53, 639-649.	2.3	44
962	Threatened but understudied: supporting conservation by understanding the genetic structure of the flat-headed cat. <i>Conservation Genetics</i> , 2017, 18, 1423-1433.	0.8	12

#	ARTICLE	IF	CITATIONS
963	An experimental study on the influence of water stagnation and temperature change on water quality in a full-scale domestic drinking water system. <i>Water Research</i> , 2017, 123, 761-772.	5.3	125
964	Vertical and horizontal assemblage patterns of bacterial communities in a eutrophic river receiving domestic wastewater in southeast China. <i>Environmental Pollution</i> , 2017, 230, 469-478.	3.7	65
965	Response of Soil Microbial Communities to Elevated Antimony and Arsenic Contamination Indicates the Relationship between the Innate Microbiota and Contaminant Fractions. <i>Environmental Science & Technology</i> , 2017, 51, 9165-9175.	4.6	133
966	Diversity and arsenic-tolerance potential of bacterial communities from soil and sediments along a gold tailing contamination gradient. <i>Canadian Journal of Microbiology</i> , 2017, 63, 788-805.	0.8	11
967	Deep-Sea Hydrothermal Vent Viruses Compensate for Microbial Metabolism in Virus-Host Interactions. <i>MBio</i> , 2017, 8, .	1.8	59
968	The gut eukaryotic microbiota influences the growth performance among cohabitating shrimp. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6447-6457.	1.7	77
969	Seasonal and spatial variations of prokaryoplankton communities in a salinity-influenced watershed, China. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	12
970	Natural products and morphogenic activity of β -Proteobacteria associated with the marine hydroid polyp <i>Hydractinia echinata</i> . <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 6088-6097.	1.4	15
971	Culture independent analysis using <i>gnd</i> as a target gene to assess <i>Escherichia coli</i> diversity and community structure. <i>Scientific Reports</i> , 2017, 7, 841.	1.6	22
972	Characterization of a cold-active bacterium isolated from the South Pole "Ice Tunnel". <i>Extremophiles</i> , 2017, 21, 891-901.	0.9	6
973	Gut microbiota of liver transplantation recipients. <i>Scientific Reports</i> , 2017, 7, 3762.	1.6	40
974	Diet-induced reconstruction of mucosal microbiota associated with alterations of epithelium lectin expression and regulation in the maintenance of rumen homeostasis. <i>Scientific Reports</i> , 2017, 7, 3941.	1.6	5
975	Modulation of gut microbiota by berberine and decocted <i>Coptis chinensis</i> Franch. in a high-fat diet-induced metabolic syndrome rat model. <i>Journal of Traditional Chinese Medical Sciences</i> , 2017, 4, 149-157.	0.1	2
976	Effects of vermicompost amendment as a basal fertilizer on soil properties and cucumber yield and quality under continuous cropping conditions in a greenhouse. <i>Journal of Soils and Sediments</i> , 2017, 17, 2718-2730.	1.5	70
977	A mitogenomic timetree for Darwin's enigmatic South American mammal <i>Macrauchenia patachonica</i> . <i>Nature Communications</i> , 2017, 8, 15951.	5.8	71
978	A high quality assembly of the Nile Tilapia (<i>Oreochromis niloticus</i>) genome reveals the structure of two sex determination regions. <i>BMC Genomics</i> , 2017, 18, 341.	1.2	179
979	Bacterial and fungal core microbiomes associated with small grain silages during ensiling and aerobic spoilage. <i>BMC Microbiology</i> , 2017, 17, 50.	1.3	116
980	Characterisation of microbial communities within aggressive prostate cancer tissues. <i>Infectious Agents and Cancer</i> , 2017, 12, 4.	1.2	42

#	ARTICLE	IF	CITATIONS
981	Comparison of rumen bacteria distribution in original rumen digesta, rumen liquid and solid fractions in lactating Holstein cows. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 16.	2.1	48
982	Identifying the core seed bank of a complex boreal bacterial metacommunity. <i>ISME Journal</i> , 2017, 11, 2012-2021.	4.4	18
983	Illumina sequencing of bacterial 16S rDNA and 16S rRNA reveals seasonal and species-specific variation in bacterial communities in four moss species. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6739-6753.	1.7	26
984	Case-Control Comparison of Enteric Viromes in Captive Rhesus Macaques with Acute or Idiopathic Chronic Diarrhea. <i>Journal of Virology</i> , 2017, 91, .	1.5	46
985	Wheat cover crop promoted cucumber seedling growth through regulating soil nutrient resources or soil microbial communities?. <i>Plant and Soil</i> , 2017, 418, 459-475.	1.8	14
986	Gut Dysbiosis and Neurobehavioral Alterations in Rats Exposed to Silver Nanoparticles. <i>Scientific Reports</i> , 2017, 7, 2822.	1.6	91
987	<i>Streptococcus</i> sp. in neonatal endotracheal tube biofilms is associated with ventilator-associated pneumonia and enhanced biofilm formation of <i>Pseudomonas aeruginosa</i> PAO1. <i>Scientific Reports</i> , 2017, 7, 3423.	1.6	5
988	Bacterial community composition and diversity in Kalakuli, an alpine glacial-fed lake in Muztagh Ata of the westernmost Tibetan Plateau. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	23
989	Responses of soil N-fixing bacteria communities to invasive species over a gradient of simulated nitrogen deposition. <i>Ecological Engineering</i> , 2017, 98, 32-39.	1.6	35
990	An Inducible Operon Is Involved in Inulin Utilization in <i>Lactobacillus plantarum</i> Strains, as Revealed by Comparative Proteogenomics and Metabolic Profiling. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	43
991	Features of the bronchial bacterial microbiome associated with atopy, asthma, and responsiveness to inhaled corticosteroid treatment. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 63-75.	1.5	222
992	Effects of the dose and viability of <i>Saccharomyces cerevisiae</i> . 1. Diversity of ruminal microbes as analyzed by Illumina MiSeq sequencing and quantitative PCR. <i>Journal of Dairy Science</i> , 2017, 100, 325-342.	1.4	59
993	Thirty-one years of rice-rice-green manure rotations shape the rhizosphere microbial community and enrich beneficial bacteria. <i>Soil Biology and Biochemistry</i> , 2017, 104, 208-217.	4.2	205
994	Resources for phylogenomic analyses of Australian terrestrial vertebrates. <i>Molecular Ecology Resources</i> , 2017, 17, 869-876.	2.2	13
995	Slope aspect influences arbuscular mycorrhizal fungus communities in arid ecosystems of the Daqingshan Mountains, Inner Mongolia, North China. <i>Mycorrhiza</i> , 2017, 27, 189-200.	1.3	37
996	Characterizing and contrasting the microbial ecology of laboratory and full-scale EBPR systems cultured on synthetic and real wastewaters. <i>Water Research</i> , 2017, 108, 124-136.	5.3	62
997	Utilizing the planarian voltage-gated ion channel transcriptome to resolve a role for a Ca ²⁺ channel in neuromuscular function and regeneration. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 1036-1045.	1.9	17
998	Effects of deep sea water and <i>Lactobacillus paracasei</i> subsp. <i>paracasei</i> NTU 101 on hypercholesterolemia hamsters gut microbiota. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 321-329.	1.7	7

#	ARTICLE	IF	CITATIONS
999	A bacterial community-based index to assess the ecological status of estuarine and coastal environments. <i>Marine Pollution Bulletin</i> , 2017, 114, 679-688.	2.3	120
1000	Testing genotyping strategies for ultra-deep sequencing of a co-amplifying gene family: MHC class I in a passerine bird. <i>Molecular Ecology Resources</i> , 2017, 17, 642-655.	2.2	46
1001	Long-term fertilizer and crop-rotation treatments differentially affect soil bacterial community structure. <i>Plant and Soil</i> , 2017, 413, 145-159.	1.8	119
1002	Comparison of Microbial Community Composition and Diversity in Native Coastal Wetlands and Wetlands that Have Undergone Long-Term Agricultural Reclamation. <i>Wetlands</i> , 2017, 37, 99-108.	0.7	19
1003	Methodologic Considerations in the Application of Next-Generation Sequencing of Human TRB Repertoires for Clinical Use. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 72-83.	1.2	8
1004	Impacts of Seasonal Housing and Teat Preparation on Raw Milk Microbiota: a High-Throughput Sequencing Study. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	104
1005	Nutrients, heavy metals and microbial communities co-driven distribution of antibiotic resistance genes in adjacent environment of Aquaculture. <i>Environmental Pollution</i> , 2017, 220, 909-918.	3.7	137
1006	Cost-effective <i>Chlorella</i> biomass production from dilute wastewater using a novel photosynthetic microbial fuel cell (PMFC). <i>Water Research</i> , 2017, 108, 356-364.	5.3	85
1007	Conversion of grassland to arable decreases microbial diversity and alters community composition. <i>Applied Soil Ecology</i> , 2017, 110, 43-52.	2.1	49
1008	Microbial Factors Associated with Postoperative Crohn's Disease Recurrence. <i>Journal of Crohn's and Colitis</i> , 2017, 11, 191-203.	0.6	86
1009	Practical low-coverage genomewide sequencing of hundreds of individually barcoded samples for population and evolutionary genomics in nonmodel species. <i>Molecular Ecology Resources</i> , 2017, 17, 194-208.	2.2	104
1010	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017, 15, 318-330.	4.1	153
1011	Complex bacterial communities in the deep-sea sediments of the Bay of Bengal and volcanic Barren Island in the Andaman Sea. <i>Marine Genomics</i> , 2017, 31, 33-41.	0.4	23
1012	Temperature sensitivity of soil respiration: Synthetic effects of nitrogen and phosphorus fertilization on Chinese Loess Plateau. <i>Science of the Total Environment</i> , 2017, 574, 1665-1673.	3.9	29
1013	Correlation between microbial community structure and performances of membrane bioreactor for treatment of palm oil mill effluent. <i>Chemical Engineering Journal</i> , 2017, 308, 656-663.	6.6	28
1014	Significant relationship between soil bacterial community structure and incidence of bacterial wilt disease under continuous cropping system. <i>Archives of Microbiology</i> , 2017, 199, 267-275.	1.0	111
1015	Bacteria in drinking water sources of a First Nation reserve in Canada. <i>Science of the Total Environment</i> , 2017, 575, 813-819.	3.9	32
1016	Temporal and Spatial Dynamics of Sediment Anaerobic Ammonium Oxidation (Anammox) Bacteria in Freshwater Lakes. <i>Microbial Ecology</i> , 2017, 73, 285-295.	1.4	34

#	ARTICLE	IF	CITATIONS
1017	Omega-3 polyunsaturated fatty acids critically regulate behaviour and gut microbiota development in adolescence and adulthood. <i>Brain, Behavior, and Immunity</i> , 2017, 59, 21-37.	2.0	195
1018	Molecular biosignatures reveal common benthic microbial sources of organic matter in ooids and grapestones from Pigeon Cay, The Bahamas. <i>Geobiology</i> , 2017, 15, 112-130.	1.1	58
1019	Immune Response and Mortality Risk Relate to Distinct Lung Microbiomes in Patients with HIV and Pneumonia. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 104-114.	2.5	60
1020	Composition and diversity of mucosa-associated microbiota along the entire length of the pig gastrointestinal tract; dietary influences. <i>Environmental Microbiology</i> , 2017, 19, 1425-1438.	1.8	120
1021	Effects of iron and calcium carbonate on the variation and cycling of carbon source in integrated wastewater treatments. <i>Bioresource Technology</i> , 2017, 225, 262-271.	4.8	8
1022	Sex-specific effects of docosahexaenoic acid (DHA) on the microbiome and behavior of socially-isolated mice. <i>Brain, Behavior, and Immunity</i> , 2017, 59, 38-48.	2.0	91
1023	Microbial Community Dynamics and Response to Plant Growth-Promoting Microorganisms in the Rhizosphere of Four Common Food Crops Cultivated in Hydroponics. <i>Microbial Ecology</i> , 2017, 73, 378-393.	1.4	43
1024	Comparison of the gut microbiota composition between wild and captive sika deer (<i>Cervus nippon</i>) Tj ETQq1 1 0.784314 rgBT /Overload	1.4	102
1025	Temporal dynamics of bacterial communities and predicted nitrogen metabolism genes in a full-scale wastewater treatment plant. <i>RSC Advances</i> , 2017, 7, 56317-56327.	1.7	68
1026	Application of <i>Bacillus</i> spp. in Pilot Test of Microbial Huff and Puff to Improve Heavy Oil Recovery. <i>Energy & Fuels</i> , 2017, 31, 13724-13732.	2.5	23
1027	Bacterial community structure and novel species of magnetotactic bacteria in sediments from a seamount in the Mariana volcanic arc. <i>Scientific Reports</i> , 2017, 7, 17964.	1.6	29
1028	Unravelling vaginal microbial genetic diversity and abundance between Holstein and Fleckvieh cattle. <i>RSC Advances</i> , 2017, 7, 56137-56143.	1.7	9
1029	Effective DNA fragmentation technique for simple sequence repeat detection with a microsatellite-enriched library and high-throughput sequencing. <i>BioTechniques</i> , 2017, 62, 180-182.	0.8	5
1030	From reads to operational taxonomic units: an ensemble processing pipeline for MiSeq amplicon sequencing data. <i>GigaScience</i> , 2017, 6, 1-10.	3.3	47
1031	Microbial population analysis of the midgut of <i>Melophagus ovinus</i> via high-throughput sequencing. <i>Parasites and Vectors</i> , 2017, 10, 382.	1.0	19
1032	An approach for detecting groundwater runoff connectivity using cluster analysis. , 2017, , .		0
1033	The microbial community shifts of subgingival plaque in patients with generalized aggressive periodontitis following non-surgical periodontal therapy: a pilot study. <i>Oncotarget</i> , 2017, 8, 10609-10619.	0.8	26
1034	Determination of Nucleopolyhedrovirus™ Taxonomic Position. , 2017, , .		1

#	ARTICLE	IF	CITATIONS
1035	Volatile Oil from Amomi Fructus Attenuates 5-Fluorouracil-Induced Intestinal Mucositis. <i>Frontiers in Pharmacology</i> , 2017, 8, 786.	1.6	52
1036	Chloroplast Genome Analysis of Resurrection Tertiary Relict <i>Haberlea rhodopensis</i> Highlights Genes Important for Desiccation Stress Response. <i>Frontiers in Plant Science</i> , 2017, 8, 204.	1.7	112
1037	<i>Mycoplasma hominis</i> and <i>Mycoplasma genitalium</i> in the Vaginal Microbiota and Persistent High-Risk Human Papillomavirus Infection. <i>Frontiers in Public Health</i> , 2017, 5, 140.	1.3	55
1038	Real-Time Whole-Genome Sequencing for Surveillance of <i>Listeria monocytogenes</i> , France. <i>Emerging Infectious Diseases</i> , 2017, 23, 1462-1470.	2.0	154
1039	Spatial Distribution Patterns of Root-Associated Bacterial Communities Mediated by Root Exudates in Different Aged Ratooning Tea Monoculture Systems. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1727.	1.8	64
1040	RNA-seq: Applications and Best Practices. , 0, , .		17
1041	Changes in bacterial community of soil induced by long-term straw returning. <i>Scientia Agricola</i> , 2017, 74, 349-356.	0.6	55
1042	A Simple Method to Decode the Complete 18-5.8-28S rRNA Repeated Units of Green Algae by Genome Skimming. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2341.	1.8	5
1043	Soil microbial community structure and diversity are largely influenced by soil pH and nutrient quality in 78-year-old tree plantations. <i>Biogeosciences</i> , 2017, 14, 2101-2111.	1.3	94
1044	Enterotype May Drive the Dietary-Associated Cardiometabolic Risk Factors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 47.	1.8	68
1045	Diversity of Cervical Microbiota in Asymptomatic <i>Chlamydia trachomatis</i> Genital Infection: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 321.	1.8	38
1046	Pole-to-Pole Connections: Similarities between Arctic and Antarctic Microbiomes and Their Vulnerability to Environmental Change. <i>Frontiers in Ecology and Evolution</i> , 2017, 5, .	1.1	51
1047	Large Diversity of Functional Nanobodies from a Camelid Immune Library Revealed by an Alternative Analysis of Next-Generation Sequencing Data. <i>Frontiers in Immunology</i> , 2017, 8, 420.	2.2	21
1048	Impact of Age, Caloric Restriction, and Influenza Infection on Mouse Gut Microbiome: An Exploratory Study of the Role of Age-Related Microbiome Changes on Influenza Responses. <i>Frontiers in Immunology</i> , 2017, 8, 1164.	2.2	77
1049	<i>Bifidobacterium infantis</i> Potentially Alleviates Shrimp Tropomyosin-Induced Allergy by Tolerogenic Dendritic Cell-Dependent Induction of Regulatory T Cells and Alterations in Gut Microbiota. <i>Frontiers in Immunology</i> , 2017, 8, 1536.	2.2	76
1050	Metagenomic Binning Recovers a Transcriptionally Active Gammaproteobacterium Linking Methanotrophy to Partial Denitrification in an Anoxic Oxygen Minimum Zone. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	44
1051	Metagenomic Analysis of Hot Springs in Central India Reveals Hydrocarbon Degrading Thermophiles and Pathways Essential for Survival in Extreme Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 2123.	1.5	96
1052	Compositions and Abundances of Sulfate-Reducing and Sulfur-Oxidizing Microorganisms in Water-Flooded Petroleum Reservoirs with Different Temperatures in China. <i>Frontiers in Microbiology</i> , 2017, 08, 143.	1.5	84

#	ARTICLE	IF	CITATIONS
1053	Assessment of Ruminal Bacterial and Archaeal Community Structure in Yak (<i>Bos grunniens</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 179.	1.5	68
1054	Variable Colonization after Reciprocal Fecal Microbiota Transfer between Mice with Low and High Richness Microbiota. <i>Frontiers in Microbiology</i> , 2017, 8, 196.	1.5	64
1055	Anti-obesity Effect of Capsaicin in Mice Fed with High-Fat Diet Is Associated with an Increase in Population of the Gut Bacterium <i>Akkermansia muciniphila</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 272.	1.5	118
1056	Differences in Ureolytic Bacterial Composition between the Rumen Digesta and Rumen Wall Based on ureC Gene Classification. <i>Frontiers in Microbiology</i> , 2017, 8, 385.	1.5	65
1057	Untangling Genomes of Novel Planctomycetal and Verrucomicrobial Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning. <i>Frontiers in Microbiology</i> , 2017, 8, 472.	1.5	70
1058	Inferring Microbial Interactions in the Gut of the Hong Kong Whipping Frog (<i>Polypedates</i>) Tj ETQq1 1 0.784314 rgBT/Overlogk 10 Tf 50	1.5	37
1059	Exploring the Ecological Coherence between the Spatial and Temporal Patterns of Bacterioplankton in Boreal Lakes. <i>Frontiers in Microbiology</i> , 2017, 8, 636.	1.5	13
1060	A Critical Assessment of the Microorganisms Proposed to be Important to Enhanced Biological Phosphorus Removal in Full-Scale Wastewater Treatment Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 718.	1.5	212
1061	Alterations in the Rumen Liquid-, Particle- and Epithelium-Associated Microbiota of Dairy Cows during the Transition from a Silage- and Concentrate-Based Ration to Pasture in Spring. <i>Frontiers in Microbiology</i> , 2017, 8, 744.	1.5	78
1062	Differing Complex Microbiota Alter Disease Severity of the IL-10 ^{−/−} Mouse Model of Inflammatory Bowel Disease. <i>Frontiers in Microbiology</i> , 2017, 8, 792.	1.5	56
1063	A Metagenomic Approach to Cyanobacterial Genomics. <i>Frontiers in Microbiology</i> , 2017, 8, 809.	1.5	98
1064	The Bacteriophage EF-P29 Efficiently Protects against Lethal Vancomycin-Resistant <i>Enterococcus faecalis</i> and Alleviates Gut Microbiota Imbalance in a Murine Bacteremia Model. <i>Frontiers in Microbiology</i> , 2017, 8, 837.	1.5	78
1065	Impact of Ferrous Iron on Microbial Community of the Biofilm in Microbial Fuel Cells. <i>Frontiers in Microbiology</i> , 2017, 8, 920.	1.5	19
1066	Cable Bacteria and the Bioelectrochemical Snorkel: The Natural and Engineered Facets Playing a Role in Hydrocarbons Degradation in Marine Sediments. <i>Frontiers in Microbiology</i> , 2017, 8, 952.	1.5	48
1067	Different Types of Dietary Fibers Trigger Specific Alterations in Composition and Predicted Functions of Colonic Bacterial Communities in BALB/c Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 966.	1.5	47
1068	Zinc Oxide Nanoparticles Influence Microflora in Ileal Digesta and Correlate Well with Blood Metabolites. <i>Frontiers in Microbiology</i> , 2017, 8, 992.	1.5	44
1069	Diversity and Composition of Sulfate-Reducing Microbial Communities Based on Genomic DNA and RNA Transcription in Production Water of High Temperature and Corrosive Oil Reservoir. <i>Frontiers in Microbiology</i> , 2017, 8, 1011.	1.5	63
1070	Non-pylori Helicobacters (NHPHs) Induce Shifts in Gastric Microbiota in <i>Helicobacter pylori</i> -Infected Patients. <i>Frontiers in Microbiology</i> , 2017, 8, 1038.	1.5	16

#	ARTICLE	IF	CITATIONS
1071	The Validation and Implications of Using Whole Genome Sequencing as a Replacement for Traditional Serotyping for a National Salmonella Reference Laboratory. <i>Frontiers in Microbiology</i> , 2017, 8, 1044.	1.5	86
1072	The Arbuscular Mycorrhizal Fungus <i>Funneliformis mosseae</i> Alters Bacterial Communities in Subtropical Forest Soils during Litter Decomposition. <i>Frontiers in Microbiology</i> , 2017, 8, 1120.	1.5	36
1073	Microbial Eukaryote Diversity and Activity in the Water Column of the South China Sea Based on DNA and RNA High Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 1121.	1.5	63
1074	Preparing the Gut with Antibiotics Enhances Gut Microbiota Reprogramming Efficiency by Promoting Xenomicrobiota Colonization. <i>Frontiers in Microbiology</i> , 2017, 8, 1208.	1.5	75
1075	The Gut Microbiota of Healthy Chilean Subjects Reveals a High Abundance of the Phylum Verrucomicrobia. <i>Frontiers in Microbiology</i> , 2017, 8, 1221.	1.5	225
1076	Oral Probiotics Alter Healthy Feline Respiratory Microbiota. <i>Frontiers in Microbiology</i> , 2017, 8, 1287.	1.5	25
1077	The Cyanobacteria-Dominated Sponge <i>Dactylospongia elegans</i> in the South China Sea: Prokaryotic Community and Metagenomic Insights. <i>Frontiers in Microbiology</i> , 2017, 8, 1387.	1.5	15
1078	Watershed Urbanization Linked to Differences in Stream Bacterial Community Composition. <i>Frontiers in Microbiology</i> , 2017, 8, 1452.	1.5	94
1079	Intestinal Bacterial Communities of Trypanosome-Infected and Uninfected <i>Glossina palpalis palpalis</i> from Three Human African Trypanomiasis Foci in Cameroon. <i>Frontiers in Microbiology</i> , 2017, 8, 1464.	1.5	13
1080	Long-term Fertilization Structures Bacterial and Archaeal Communities along Soil Depth Gradient in a Paddy Soil. <i>Frontiers in Microbiology</i> , 2017, 8, 1516.	1.5	72
1081	High Spatial and Temporal Variations of Microbial Community along the Southern Catfish Gastrointestinal Tract: Insights into Dynamic Food Digestion. <i>Frontiers in Microbiology</i> , 2017, 8, 1531.	1.5	29
1082	Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. <i>Frontiers in Microbiology</i> , 2017, 8, 1561.	1.5	265
1083	High-Resolution Microbiome Profiling for Detection and Tracking of <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1587.	1.5	31
1084	Identification of Fungal Communities Associated with the Biodeterioration of Waterlogged Archeological Wood in a Han Dynasty Tomb in China. <i>Frontiers in Microbiology</i> , 2017, 8, 1633.	1.5	27
1085	Modulation of Gut Microbiome Composition and Function in Experimental Colitis Treated with Sulfasalazine. <i>Frontiers in Microbiology</i> , 2017, 8, 1703.	1.5	89
1086	Isolation and Characterization of <i>Pseudomonas</i> spp. Strains That Efficiently Decompose Sodium Dodecyl Sulfate. <i>Frontiers in Microbiology</i> , 2017, 8, 1872.	1.5	28
1087	Patterns and Processes in Marine Microeukaryotic Community Biogeography from Xiamen Coastal Waters and Intertidal Sediments, Southeast China. <i>Frontiers in Microbiology</i> , 2017, 8, 1912.	1.5	108
1088	<i>Myriophyllum aquaticum</i> Constructed Wetland Effectively Removes Nitrogen in Swine Wastewater. <i>Frontiers in Microbiology</i> , 2017, 8, 1932.	1.5	44

#	ARTICLE	IF	CITATIONS
1089	Diversity and Structure of Diazotrophic Communities in Mangrove Rhizosphere, Revealed by High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2032.	1.5	49
1090	Microbial Diversity and Community Structure of Sulfate-Reducing and Sulfur-Oxidizing Bacteria in Sediment Cores from the East China Sea. <i>Frontiers in Microbiology</i> , 2017, 8, 2133.	1.5	53
1091	Stratified Bacterial and Archaeal Community in Mangrove and Intertidal Wetland Mudflats Revealed by High Throughput 16S rRNA Gene Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2148.	1.5	91
1092	An Integrated Insight into the Relationship between Soil Microbial Community and Tobacco Bacterial Wilt Disease. <i>Frontiers in Microbiology</i> , 2017, 8, 2179.	1.5	108
1093	Low-Molecular-Weight Chitosan Supplementation Increases the Population of <i>Prevotella</i> in the Cecal Contents of Weanling Pigs. <i>Frontiers in Microbiology</i> , 2017, 8, 2182.	1.5	31
1094	Illumina-Based Analysis of Endophytic and Rhizosphere Bacterial Diversity of the Coastal Halophyte <i>Messerschmidia sibirica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2288.	1.5	84
1095	The Gut Entomotype of Red Palm Weevil <i>Rhynchophorus ferrugineus</i> Olivier (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td 2291.	1.5	96
1096	Resource Legacies of Organic and Conventional Management Differentiate Soil Microbial Carbon Use. <i>Frontiers in Microbiology</i> , 2017, 8, 2293.	1.5	38
1097	Environmental Factors Shape Water Microbial Community Structure and Function in Shrimp Cultural Enclosure Ecosystems. <i>Frontiers in Microbiology</i> , 2017, 8, 2359.	1.5	137
1098	Balanced Fertilization Decreases Environmental Filtering on Soil Bacterial Community Assemblage in North China. <i>Frontiers in Microbiology</i> , 2017, 8, 2376.	1.5	44
1099	Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. <i>Frontiers in Microbiology</i> , 2017, 8, 2384.	1.5	60
1100	EPSP of <i>L. casei</i> BL23 Protected against the Infection Caused by <i>Aeromonas veronii</i> via Enhancement of Immune Response in Zebrafish. <i>Frontiers in Microbiology</i> , 2017, 8, 2406.	1.5	28
1101	Glyphosate Shapes a Dinoflagellate-Associated Bacterial Community While Supporting Algal Growth as Sole Phosphorus Source. <i>Frontiers in Microbiology</i> , 2017, 8, 2530.	1.5	42
1102	Patterns and Drivers of Vertical Distribution of the Ciliate Community from the Surface to the Abyssopelagic Zone in the Western Pacific Ocean. <i>Frontiers in Microbiology</i> , 2017, 8, 2559.	1.5	37
1103	<i>Bacillus amyloliquefaciens</i> L-S60 Reforms the Rhizosphere Bacterial Community and Improves Growth Conditions in Cucumber Plug Seedling. <i>Frontiers in Microbiology</i> , 2017, 8, 2620.	1.5	39
1104	Uncovering the Potential of Termite Gut Microbiome for Lignocellulose Bioconversion in Anaerobic Batch Bioreactors. <i>Frontiers in Microbiology</i> , 2017, 8, 2623.	1.5	64
1105	L-Glutamine Supplementation Alleviates Constipation during Late Gestation of Mini Sows by Modifying the Microbiota Composition in Feces. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	28
1106	Metagenome of the Siberian Underground Water Reservoir. <i>Genome Announcements</i> , 2017, 5, .	0.8	9

#	ARTICLE	IF	CITATIONS
1107	Draft Genome Sequence of <i>Terrimicrobium sacchariphilum</i> NM-5 ^T , a Facultative Anaerobic Soil Bacterium of the Class <i>Spartobacteria</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1108	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	1.2	51
1109	Rapid evolutionary divergence of diploid and allotetraploid <i>Gossypium</i> mitochondrial genomes. <i>BMC Genomics</i> , 2017, 18, 876.	1.2	23
1110	Effects of dietary nutrient levels on microbial community composition and diversity in the ileal contents of pregnant Huanjiang mini-pigs. <i>PLoS ONE</i> , 2017, 12, e0172086.	1.1	28
1111	An in vivo system for directed experimental evolution of rabbit haemorrhagic disease virus. <i>PLoS ONE</i> , 2017, 12, e0173727.	1.1	10
1112	<i>Tuber indicum</i> shapes the microbial communities of ectomycorrhizosphere soil and ectomycorrhizae of an indigenous tree (<i>Pinus armandii</i>). <i>PLoS ONE</i> , 2017, 12, e0175720.	1.1	25
1113	New gSSR and EST-SSR markers reveal high genetic diversity in the invasive plant <i>Ambrosia artemisiifolia</i> L. and can be transferred to other invasive <i>Ambrosia</i> species. <i>PLoS ONE</i> , 2017, 12, e0176197.	1.1	23
1114	Bacterial community and arsenic functional genes diversity in arsenic contaminated soils from different geographic locations. <i>PLoS ONE</i> , 2017, 12, e0176696.	1.1	40
1115	Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716.	1.1	107
1116	The Agassizâ€™s desert tortoise genome provides a resource for the conservation of a threatened species. <i>PLoS ONE</i> , 2017, 12, e0177708.	1.1	33
1117	Phylogenetic analysis of emergent <i>Streptococcus pneumoniae</i> serotype 22F causing invasive pneumococcal disease using whole genome sequencing. <i>PLoS ONE</i> , 2017, 12, e0178040.	1.1	21
1118	Decreased emergence of HIV-1 drug resistance mutations in a cohort of Ugandan women initiating option B+ for PMTCT. <i>PLoS ONE</i> , 2017, 12, e0178297.	1.1	11
1119	Bacterial communities found in placental tissues are associated with severe chorioamnionitis and adverse birth outcomes. <i>PLoS ONE</i> , 2017, 12, e0180167.	1.1	97
1120	<i>Methanobrevibacter</i> attenuation via probiotic intervention reduces flatulence in adult human: A non-randomised paired-design clinical trial of efficacy. <i>PLoS ONE</i> , 2017, 12, e0184547.	1.1	20
1121	<i>Lactobacillus paracasei</i> feeding improves immune control of influenza infection in mice. <i>PLoS ONE</i> , 2017, 12, e0184976.	1.1	76
1122	BBMerge â€“ Accurate paired shotgun read merging via overlap. <i>PLoS ONE</i> , 2017, 12, e0185056.	1.1	897
1123	Intestinal microbiota profiles associated with low and high residual feed intake in chickens across two geographical locations. <i>PLoS ONE</i> , 2017, 12, e0187766.	1.1	73
1124	Diversity and characterization of bacteria associated with the deep-sea hydrothermal vent crab <i>Austinograea</i> sp. comparing with those of two shallow-water crabs by 16S ribosomal DNA analysis. <i>PLoS ONE</i> , 2017, 12, e0187842.	1.1	22

#	ARTICLE	IF	CITATIONS
1125	Effects of <i>Lactobacillus acidophilus</i> on gut microbiota composition in broilers challenged with <i>Clostridium perfringens</i> . PLoS ONE, 2017, 12, e0188634.	1.1	75
1126	Endosphere microbiome comparison between symptomatic and asymptomatic roots of <i>Brassica napus</i> infected with <i>Plasmodiophora brassicae</i> . PLoS ONE, 2017, 12, e0185907.	1.1	53
1127	Impact of Glyphosate on the Rhizosphere Microbial Communities of An EPSPS-Transgenic Soybean Line ZUTS31 by Metagenome Sequencing. Current Genomics, 2017, 19, 36-49.	0.7	10
1128	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters!. PLoS ONE, 2017, 12, e0169662.	1.1	186
1129	Characterization of the urinary microbiome in healthy dogs. PLoS ONE, 2017, 12, e0177783.	1.1	43
1130	Diversity of <i>Ktedonobacteria</i> with Actinomycetes-Like Morphology in Terrestrial Environments. Microbes and Environments, 2017, 32, 61-70.	0.7	83
1131	16S rRNA gene-based association study identified microbial taxa associated with pork intramuscular fat content in feces and cecum lumen. BMC Microbiology, 2017, 17, 162.	1.3	77
1132	Highly efficient methane generation from untreated microalgae biomass. Biotechnology for Biofuels, 2017, 10, 186.	6.2	63
1133	Coexistence and competition of sulfate-reducing and methanogenic populations in an anaerobic hexadecane-degrading culture. Biotechnology for Biofuels, 2017, 10, 207.	6.2	36
1134	A quantitative and qualitative comparison of illumina MiSeq and 454 amplicon sequencing for genotyping the highly polymorphic major histocompatibility complex (MHC) in a non-model species. BMC Research Notes, 2017, 10, 346.	0.6	12
1135	Gene and transcript abundances of bacterial type III secretion systems from the rumen microbiome are correlated with methane yield in sheep. BMC Research Notes, 2017, 10, 367.	0.6	8
1136	Doxycycline induces dysbiosis in female C57BL/6NCrl mice. BMC Research Notes, 2017, 10, 644.	0.6	29
1137	Metagenomic analysis reveals potential interactions in an artificial coculture. AMB Express, 2017, 7, 193.	1.4	17
1138	A novel ultra high-throughput 16S rRNA gene amplicon sequencing library preparation method for the Illumina HiSeq platform. Microbiome, 2017, 5, 68.	4.9	93
1139	Environmental drivers of viral community composition in Antarctic soils identified by viromics. Microbiome, 2017, 5, 83.	4.9	94
1140	Season, but not symbiont state, drives microbiome structure in the temperate coral <i>Astrangia poculata</i> . Microbiome, 2017, 5, 120.	4.9	105
1141	Associations among dietary non-fiber carbohydrate, ruminal microbiota and epithelium G-protein-coupled receptor, and histone deacetylase regulations in goats. Microbiome, 2017, 5, 123.	4.9	74
1142	Indoor microbiota in severely moisture damaged homes and the impact of interventions. Microbiome, 2017, 5, 138.	4.9	40

#	ARTICLE	IF	CITATIONS
1143	Seasonal, spatial, and maternal effects on gut microbiome in wild red squirrels. <i>Microbiome</i> , 2017, 5, 163.	4.9	148
1144	A multiplex marker set for microsatellite typing and sexing of sooty terns <i>Onychoprion fuscatus</i> . <i>BMC Research Notes</i> , 2017, 10, 756.	0.6	3
1145	The gut microbiota in larvae of the housefly <i>Musca domestica</i> and their horizontal transfer through feeding. <i>AMB Express</i> , 2017, 7, 147.	1.4	49
1146	Endolysin LysEF-P10 shows potential as an alternative treatment strategy for multidrug-resistant <i>Enterococcus faecalis</i> infections. <i>Scientific Reports</i> , 2017, 7, 10164.	1.6	38
1147	The contribution of Late Pleistocene megafauna finds to submerged archaeology and the interpretation of ancient coastal landscapes. <i>Journal of Archaeological Science: Reports</i> , 2017, 15, 290-298.	0.2	2
1148	Effect of <i>Ageratina adenophora</i> invasion on the composition and diversity of soil microbiome. <i>Journal of General and Applied Microbiology</i> , 2017, 63, 114-121.	0.4	14
1149	Draft Genome Sequence of <i>Paludibacter jiangxiensis</i> NM7 ^T , a Propionate-Producing Fermentative Bacterium. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1150	Gut microbial diversity analysis using Illumina sequencing for functional dyspepsia with liver depression-spleen deficiency syndrome and the interventional Xiaoyaosan in a rat model. <i>World Journal of Gastroenterology</i> , 2017, 23, 810.	1.4	38
1151	Exploring the Impacts of Anthropogenic Disturbance on Seawater and Sediment Microbial Communities in Korean Coastal Waters Using Metagenomics Analysis. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 130.	1.2	38
1152	Clonal Clusters and Virulence Factors of Group C and G <i>Streptococcus</i> Causing Severe Infections, Manitoba, Canada, 2012-2014. <i>Emerging Infectious Diseases</i> , 2017, 23, 1079-1088.	2.0	20
1153	Effect of Sewage and Industrial Effluents on Bacterial and Archaeal Communities of Creek Sediments in the Taihu Basin. <i>Water (Switzerland)</i> , 2017, 9, 373.	1.2	17
1154	Contrasting dynamics and environmental controls of dispersed bacteria along a hydrologic gradient. <i>Advances in Oceanography and Limnology</i> , 2017, 8, .	0.2	13
1155	Understory Dwarf Bamboo Affects Microbial Community Structures and Soil Properties in a <i>Betula ermanii</i> Forest in Northern Japan. <i>Microbes and Environments</i> , 2017, 32, 103-111.	0.7	5
1156	Vertical profiles of sediment methanogenic potential and communities in two plateau freshwater lakes. <i>Biogeosciences</i> , 2017, 14, 341-351.	1.3	28
1157	Patterns of host gene expression associated with harboring a foregut microbial community. <i>BMC Genomics</i> , 2017, 18, 697.	1.2	4
1158	Comparative genomic analysis of <i>Brevibacterium</i> strains: insights into key genetic determinants involved in adaptation to the cheese habitat. <i>BMC Genomics</i> , 2017, 18, 955.	1.2	38
1159	Collaborative environmental DNA sampling from petal surfaces of flowering cherry <i>Cerasus yedoensis</i> 'Somei-yoshino' across the Japanese archipelago. <i>Journal of Plant Research</i> , 2018, 131, 709-717.		1
1160	The Variation of Microbial Communities in a Depth Profile of Peat in the Gahai Lake Wetland Natural Conservation Area. <i>Geomicrobiology Journal</i> , 2018, 35, 484-490.	1.0	8

#	ARTICLE	IF	CITATIONS
1161	Acute Drug Effects on the Human Placental Tissue: The Development of a Placental Murine Xenograft Model. <i>Reproductive Sciences</i> , 2018, 25, 1637-1648.	1.1	0
1162	Planktonic bivalve larvae identification and quantification in Gomso Bay, South Korea, using next-generation sequencing analysis and microscopic observations. <i>Aquaculture</i> , 2018, 490, 297-302.	1.7	4
1163	Phenol removal performance and microbial community shift during pH shock in a moving bed biofilm reactor (MBBR). <i>Journal of Hazardous Materials</i> , 2018, 351, 71-79.	6.5	38
1164	Insights into protein structure, stability and function from saturation mutagenesis. <i>Current Opinion in Structural Biology</i> , 2018, 50, 117-125.	2.6	26
1165	Drought consistently alters the composition of soil fungal and bacterial communities in grasslands from two continents. <i>Global Change Biology</i> , 2018, 24, 2818-2827.	4.2	221
1166	The influence of caging, bedding, and diet on the composition of the microbiota in different regions of the mouse gut. <i>Scientific Reports</i> , 2018, 8, 4065.	1.6	137
1167	Alterations in the gut microbiota of patients with acquired immune deficiency syndrome. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2263-2271.	1.6	63
1168	Market Integration Predicts Human Gut Microbiome Attributes across a Gradient of Economic Development. <i>MSystems</i> , 2018, 3, .	1.7	31
1169	Intestinal bacterial signatures of white feces syndrome in shrimp. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3701-3709.	1.7	118
1170	Integrating molecular and ecological approaches to identify potential polymicrobial pathogens over a shrimp disease progression. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3755-3764.	1.7	44
1171	Conservation genomics of desert dwelling California voles (<i>Microtus californicus</i>) and implications for management of endangered Amargosa voles (<i>Microtus californicus scirpensis</i>). <i>Conservation Genetics</i> , 2018, 19, 383-395.	0.8	12
1172	Biochars change the sorption and degradation of thiacloprid in soil: Insights into chemical and biological mechanisms. <i>Environmental Pollution</i> , 2018, 236, 158-167.	3.7	128
1173	Multilocus phylogenetic analysis of the first molecular data from the rare and monotypic Amarsipidae places the family within the Pelagia and highlights limitations of existing data sets in resolving pelagian interrelationships. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 172-180.	1.2	7
1174	Fuzhuan Brick Tea Polysaccharides Attenuate Metabolic Syndrome in High-Fat Diet Induced Mice in Association with Modulation in the Gut Microbiota. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 2783-2795.	2.4	166
1175	Dietary lipid levels could improve growth and intestinal microbiota of juvenile swimming crab, <i>Portunus trituberculatus</i> . <i>Aquaculture</i> , 2018, 490, 208-216.	1.7	65
1176	Neuroprotective effects of fecal microbiota transplantation on MPTP-induced Parkinson's disease mice: Gut microbiota, glial reaction and TLR4/TNF- α signaling pathway. <i>Brain, Behavior, and Immunity</i> , 2018, 70, 48-60.	2.0	448
1177	Land-use type strongly shapes community composition, but not always diversity of soil microbes in tropical China. <i>Catena</i> , 2018, 165, 369-380.	2.2	56
1178	Landscape topography structures the soil microbiome in arctic polygonal tundra. <i>Nature Communications</i> , 2018, 9, 777.	5.8	105

#	ARTICLE	IF	CITATIONS
1180	Dog introduction alters the home dust microbiota. <i>Indoor Air</i> , 2018, 28, 539-547.	2.0	46
1181	The Gills of Reef Fish Support a Distinct Microbiome Influenced by Host-Specific Factors. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	96
1182	Thermal regime and host clade, rather than geography, drive Symbiodinium and bacterial assemblages in the scleractinian coral <i>Pocillopora damicornis</i> sensu lato. <i>Microbiome</i> , 2018, 6, 39.	4.9	100
1183	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	5.8	36
1184	Shrub encroachment is associated with changes in soil bacterial community composition in a temperate grassland ecosystem. <i>Plant and Soil</i> , 2018, 425, 539-551.	1.8	30
1185	The influence of microbial communities for triadimefon enantiomerization in soils with different pH values. <i>Chirality</i> , 2018, 30, 293-301.	1.3	12
1186	The effect of probiotics and polysaccharides on the gut microbiota composition and function of weaned rats. <i>Food and Function</i> , 2018, 9, 1864-1877.	2.1	25
1187	Draft Genome Assemblies of Xylose-Utilizing <i>Candida tropicalis</i> and <i>Candida boidinii</i> with Potential Application in Biochemical and Biofuel Production. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
1188	Featured article: Structure moderation of gut microbiota in liraglutide-treated diabetic male rats. <i>Experimental Biology and Medicine</i> , 2018, 243, 34-44.	1.1	56
1189	The divergence between fungal and bacterial communities in seasonal and spatial variations of wastewater treatment plants. <i>Science of the Total Environment</i> , 2018, 628-629, 969-978.	3.9	79
1190	Polyadenylation and degradation of structurally abnormal mitochondrial tRNAs in human cells. <i>Nucleic Acids Research</i> , 2018, 46, 5209-5226.	6.5	14
1191	Community composition, diversity, and metabolism of intestinal microbiota in cultivated European eel (<i>Anguilla anguilla</i>). <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4143-4157.	1.7	22
1192	Functional groups of soil fungi decline under grazing. <i>Plant and Soil</i> , 2018, 426, 51-60.	1.8	33
1193	Arbuscular mycorrhizal fungal communities associated with two dominant species differ in their responses to long-term nitrogen addition in temperate grasslands. <i>Functional Ecology</i> , 2018, 32, 1575-1588.	1.7	39
1194	Gammaproteobacterial Diversity and Carbon Utilization in Response to Salinity in the Lakes on the Qinghai-Tibetan Plateau. <i>Geomicrobiology Journal</i> , 2018, 35, 392-403.	1.0	19
1195	Changes in community structure of active protistan assemblages from the lower Pearl River to coastal Waters of the South China Sea. <i>European Journal of Protistology</i> , 2018, 63, 72-82.	0.5	34
1196	One-time phosphate fertilizer application to grassland columns modifies the soil microbiota and limits its role in ecosystem services. <i>Science of the Total Environment</i> , 2018, 630, 849-858.	3.9	87
1197	Light-dependent processes on the cathode enhance the electrical outputs of sediment microbial fuel cells. <i>Bioelectrochemistry</i> , 2018, 122, 1-10.	2.4	14

#	ARTICLE	IF	CITATIONS
1198	Targeted Sequencing of Venom Genes from Cone Snail Genomes Improves Understanding of Conotoxin Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 1210-1224.	3.5	33
1199	Dense infraspecific sampling reveals rapid and independent trajectories of plastome degradation in a heterotrophic orchid complex. <i>New Phytologist</i> , 2018, 218, 1192-1204.	3.5	56
1200	Effects of Baicalein on Cortical Proinflammatory Cytokines and the Intestinal Microbiome in Senescence Accelerated Mouse Prone 8. <i>ACS Chemical Neuroscience</i> , 2018, 9, 1714-1724.	1.7	47
1201	Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex1. <i>Journal of Animal Science</i> , 2018, 96, 1405-1418.	0.2	50
1202	Decline of genetic diversity in ancient domestic stallions in Europe. <i>Science Advances</i> , 2018, 4, eaap9691.	4.7	29
1203	A combination of <i>Lactobacillus mali</i> APS1 and dieting improved the efficacy of obesity treatment via manipulating gut microbiome in mice. <i>Scientific Reports</i> , 2018, 8, 6153.	1.6	31
1204	Application of high-throughput sequencing for microbial diversity detection in feces of specific-pathogen-free ducks. <i>Poultry Science</i> , 2018, 97, 2278-2286.	1.5	10
1205	Symbiotic N ₂ -Fixer Community Composition, but Not Diversity, Shifts in Nodules of a Single Host Legume Across a 2-Million-Year Dune Chronosequence. <i>Microbial Ecology</i> , 2018, 76, 1009-1020.	1.4	9
1206	Diversity of herbaceous plants and bacterial communities regulates soil resistome across forest biomes. <i>Environmental Microbiology</i> , 2018, 20, 3186-3200.	1.8	55
1207	The Genome of <i>Artemisia annua</i> Provides Insight into the Evolution of Asteraceae Family and Artemisinin Biosynthesis. <i>Molecular Plant</i> , 2018, 11, 776-788.	3.9	205
1208	Revealing the microbiota of marketed edible insects through PCR-DGGE, metagenomic sequencing and real-time PCR. <i>International Journal of Food Microbiology</i> , 2018, 276, 54-62.	2.1	34
1209	Tuna Oil Alleviates α -Galactose Induced Aging in Mice Accompanied by Modulating Gut Microbiota and Brain Protein Expression. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 5510-5520.	2.4	23
1210	MitoFish and MiFish Pipeline: A Mitochondrial Genome Database of Fish with an Analysis Pipeline for Environmental DNA Metabarcoding. <i>Molecular Biology and Evolution</i> , 2018, 35, 1553-1555.	3.5	169
1211	Changes in intestinal microbiota across an altitudinal gradient in the lizard <i>Phrynocephalus vlangalii</i> . <i>Ecology and Evolution</i> , 2018, 8, 4695-4703.	0.8	51
1212	High-throughput sequencing for algal systematics. <i>European Journal of Phycology</i> , 2018, 53, 256-272.	0.9	33
1213	Highly efficient removal of nitrogen and phosphorus in an electrolysis-integrated horizontal subsurface-flow constructed wetland amended with biochar. <i>Water Research</i> , 2018, 139, 301-310.	5.3	80
1214	Connection Between BMI-Related Plasma Metabolite Profile and Gut Microbiota. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 1491-1501.	1.8	163
1215	Effect of daidzein on fermentation parameters and bacterial community of finishing Xianan cattle. <i>Italian Journal of Animal Science</i> , 2018, 17, 950-958.	0.8	7

#	ARTICLE	IF	CITATIONS
1216	Yeast culture dietary supplementation modulates gut microbiota, growth and biochemical parameters of grass carp. <i>Microbial Biotechnology</i> , 2018, 11, 551-565.	2.0	36
1217	Increasing the utility of barcode databases through high-throughput sequencing of amplicons from dried museum specimens, an example on parasitic hymenoptera (Braconidae). <i>Biological Control</i> , 2018, 122, 93-100.	1.4	10
1218	Bacterial diversity and community structure in the rhizosphere of four <i>Ferula</i> species. <i>Scientific Reports</i> , 2018, 8, 5345.	1.6	33
1219	Development of a New Application for Comprehensive Viability Analysis Based on Microbiome Analysis by Next-Generation Sequencing: Insights into Staphylococcal Carriage in Human Nasal Cavities. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
1220	Gut-dependent microbial translocation induces inflammation and cardiovascular events after ST-elevation myocardial infarction. <i>Microbiome</i> , 2018, 6, 66.	4.9	185
1221	Conversion of sulfur compounds and microbial community in anaerobic treatment of fish and pork waste. <i>Waste Management</i> , 2018, 76, 383-393.	3.7	35
1222	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	3.5	30
1223	High-throughput sequencing reveals microbial communities in drinking water treatment sludge from six geographically distributed plants, including potentially toxic cyanobacteria and pathogens. <i>Science of the Total Environment</i> , 2018, 634, 769-779.	3.9	40
1224	Effect of <i>Lactobacillus rhamnosus</i> GG Supplementation on Intestinal Inflammation Assessed by PET/MRI Scans and Gut Microbiota Composition in HIV-Infected Individuals. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2018, 78, 450-457.	0.9	26
1225	L1 retrotransposition is a common feature of mammalian hepatocarcinogenesis. <i>Genome Research</i> , 2018, 28, 639-653.	2.4	79
1226	The unspecificity of the relationships between the invasive <i>Pennisetum setaceum</i> and mycorrhizal fungi may provide advantages during its establishment at semiarid Mediterranean sites. <i>Science of the Total Environment</i> , 2018, 630, 1464-1471.	3.9	12
1227	HiMAP: Robust phylogenomics from highly multiplexed amplicon sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 1000-1019.	2.2	30
1228	Bacterial communities of four adjacent fresh lakes at different trophic status. <i>Ecotoxicology and Environmental Safety</i> , 2018, 157, 388-394.	2.9	52
1229	Temperature sensitivity of soil respiration to nitrogen and phosphorous fertilization: Does soil initial fertility matter?. <i>Geoderma</i> , 2018, 325, 172-182.	2.3	26
1230	Responses of bacterial community to dibutyl phthalate pollution in a soil-vegetable ecosystem. <i>Journal of Hazardous Materials</i> , 2018, 353, 142-150.	6.5	104
1231	Characterization of the duodenal bacterial microbiota in patients with pancreatic head cancer vs. healthy controls. <i>Pancreatology</i> , 2018, 18, 438-445.	0.5	64
1232	Host-mediated selection impacts the diversity of <i>Plasmodium falciparum</i> antigens within infections. <i>Nature Communications</i> , 2018, 9, 1381.	5.8	27
1233	Impact of a vegan diet on the human salivary microbiota. <i>Scientific Reports</i> , 2018, 8, 5847.	1.6	93

#	ARTICLE	IF	CITATIONS
1234	Cadmium Exposure-Sedum alfredii Planting Interactions Shape the Bacterial Community in the Hyperaccumulator Plant Rhizosphere. Applied and Environmental Microbiology, 2018, 84, .	1.4	60
1235	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
1236	Long-term fertilisation form, level and duration affect the diversity, structure and functioning of soil microbial communities in the field. Soil Biology and Biochemistry, 2018, 122, 91-103.	4.2	134
1237	Quantitative characterization of all single amino acid variants of a viral capsid-based drug delivery vehicle. Nature Communications, 2018, 9, 1385.	5.8	43
1238	Diversity and metabolic potential of the microbiota associated with a soil arthropod. Scientific Reports, 2018, 8, 2491.	1.6	39
1239	Chronic impacts of oxytetracycline on mesophilic anaerobic digestion of excess sludge: Inhibition of hydrolytic acidification and enrichment of antibiotic resistome. Environmental Pollution, 2018, 238, 1017-1026.	3.7	41
1240	Spatial dynamics and mixing of bluefin tuna in the Atlantic Ocean and Mediterranean Sea revealed using next-generation sequencing. Molecular Ecology Resources, 2018, 18, 620-638.	2.2	34
1241	Delayed gut microbiota development in high-risk for asthma infants is temporarily modifiable by Lactobacillus supplementation. Nature Communications, 2018, 9, 707.	5.8	158
1242	Interrelations between the rumen microbiota and production, behavioral, rumen fermentation, metabolic, and immunological attributes of dairy cows. Journal of Dairy Science, 2018, 101, 4615-4637.	1.4	90
1243	Taxonomic structure and function of seed-inhabiting bacterial microbiota from common reed (Phragmites australis) and narrowleaf cattail (Typha angustifolia L.). Archives of Microbiology, 2018, 200, 869-876.	1.0	11
1244	Hemolymph Microbiomes of Three Aquatic Invertebrates as Revealed by a New Cell Extraction Method. Applied and Environmental Microbiology, 2018, 84, .	1.4	49
1245	Comparative study on intestinal bacterial communities of Boleophthalmus pectinirostris and Periophthalmus magnuspinnatus with different sexes and feeding strategies. Annals of Microbiology, 2018, 68, 123-133.	1.1	9
1246	Impact of temperature and substrate concentration on degradation rates of acetate, propionate and hydrogen and their links to microbial community structure. Bioresource Technology, 2018, 256, 44-52.	4.8	41
1247	Barcoded sequencing workflow for high throughput digitization of hybridoma antibody variable domain sequences. Journal of Immunological Methods, 2018, 455, 88-94.	0.6	18
1248	Biogeography and ecological processes affecting root-associated bacterial communities in soybean fields across China. Science of the Total Environment, 2018, 627, 20-27.	3.9	53
1249	Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan. ISME Journal, 2018, 12, 1287-1295.	4.4	44
1250	Impact of beneficial bacteria supplementation on the gut microbiota, colony development and productivity of Apis mellifera L.. Beneficial Microbes, 2018, 9, 269-278.	1.0	56
1251	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

#	ARTICLE	IF	CITATIONS
1252	Microbial diversity and community structure in agricultural soils suffering from 4 years of Pb contamination. <i>Canadian Journal of Microbiology</i> , 2018, 64, 305-316.	0.8	15
1253	Mobility of multiple heavy metalloids in contaminated soil under various redox conditions: Effects of iron sulfide presence and phosphate competition. <i>Chemosphere</i> , 2018, 197, 344-352.	4.2	18
1254	Airborne microbial communities in the atmospheric environment of urban hospitals in China. <i>Journal of Hazardous Materials</i> , 2018, 349, 10-17.	6.5	73
1255	Vaccination Against <i>Lawsonia intracellularis</i> Decreases Shedding of <i>Salmonella enterica</i> serovar Typhimurium in Co-Infected Pigs and Alters the Gut Microbiome. <i>Scientific Reports</i> , 2018, 8, 2857.	1.6	24
1256	Microbial community and short-chain fatty acid profile in gastrointestinal tract of goose. <i>Poultry Science</i> , 2018, 97, 1420-1428.	1.5	46
1257	p-Coumaric can alter the composition of cucumber rhizosphere microbial communities and induce negative plant-microbial interactions. <i>Biology and Fertility of Soils</i> , 2018, 54, 363-372.	2.3	83
1258	Massively Parallel Sequencing of Peritoneal and Splenic B Cell Repertoires Highlights Unique Properties of B-1 Cell Antibodies. <i>Journal of Immunology</i> , 2018, 200, 1702-1717.	0.4	36
1259	Temperature and nutrients as drivers of microbially mediated arsenic oxidation and removal from acid mine drainage. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2413-2424.	1.7	17
1260	Taxonomy of anaerobic digestion microbiome reveals biases associated with the applied high throughput sequencing strategies. <i>Scientific Reports</i> , 2018, 8, 1926.	1.6	70
1261	Comparative Genomics Reveals Accelerated Evolution in Conserved Pathways during the Diversification of Anole Lizards. <i>Genome Biology and Evolution</i> , 2018, 10, 489-506.	1.1	43
1262	Analysis of the succession of structure of the bacteria community in soil from long-term continuous cotton cropping in Xinjiang using high-throughput sequencing. <i>Archives of Microbiology</i> , 2018, 200, 653-662.	1.0	53
1263	Genotyping strategy matters when analyzing hypervariable major histocompatibility complex—Experience from a passerine bird. <i>Ecology and Evolution</i> , 2018, 8, 1680-1692.	0.8	16
1264	Experimental insights into the importance of ecologically dissimilar bacteria to community assembly along a salinity gradient. <i>Environmental Microbiology</i> , 2018, 20, 1170-1184.	1.8	32
1265	Ontogeny of human mucosal-associated invariant T cells and related T cell subsets. <i>Journal of Experimental Medicine</i> , 2018, 215, 459-479.	4.2	115
1266	Tick saliva microbiomes isolated from engorged and partially fed adults of <i>Haemaphysalis flava</i> tick females. <i>Journal of Applied Entomology</i> , 2018, 142, 173-180.	0.8	8
1267	Kudingcha and Fuzhuan Brick Tea Prevent Obesity and Modulate Gut Microbiota in High-Fat Diet Fed Mice. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1700485.	1.5	161
1268	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. <i>ISME Journal</i> , 2018, 12, 1344-1359.	4.4	84
1269	Nitrogen Cycle Evaluation (NICE) Chip for Simultaneous Analysis of Multiple N Cycle-Associated Genes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	23

#	ARTICLE	IF	CITATIONS
1270	Arabidopsis Zinc-Finger-Like Protein ASYMMETRIC LEAVES2 (AS2) and Two Nucleolar Proteins Maintain Gene Body DNA Methylation in the Leaf Polarity Gene ETTIN (ARF3). <i>Plant and Cell Physiology</i> , 2018, 59, 1385-1397.	1.5	19
1271	Differentiated surface fungal communities at point of harvest on apple fruits from rural and peri-urban orchards. <i>Scientific Reports</i> , 2018, 8, 2165.	1.6	31
1272	Identification of an (AC) _n microsatellite in the Six1 gene promoter and its effect on production traits in Pietrain × Duroc × Landrace × Yorkshire pigs1. <i>Journal of Animal Science</i> , 2018, 96, 17-26.	0.2	3
1273	Response of soil microbial communities to red mud-based stabilizer remediation of cadmium-contaminated farmland. <i>Environmental Science and Pollution Research</i> , 2018, 25, 11661-11669.	2.7	16
1274	Starvation influences the microbiota assembly and expression of immunity-related genes in the intestine of grass carp (<i>Ctenopharyngodon idellus</i>). <i>Aquaculture</i> , 2018, 489, 121-129.	1.7	54
1275	A comprehensive insight into the effects of microwave-H ₂ O ₂ pretreatment on concentrated sewage sludge anaerobic digestion based on semi-continuous operation. <i>Bioresource Technology</i> , 2018, 256, 118-127.	4.8	39
1276	Advantages of meta-total RNA sequencing (MeTRS) over shotgun metagenomics and amplicon-based sequencing in the profiling of complex microbial communities. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 2.	2.9	65
1277	Cropping practices manipulate abundance patterns of root and soil microbiome members paving the way to smart farming. <i>Microbiome</i> , 2018, 6, 14.	4.9	399
1278	Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery. <i>Nucleic Acids Research</i> , 2018, 46, e42-e42.	6.5	7
1279	Draft genome and reference transcriptomic resources for the urticating pine defoliator <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). <i>Molecular Ecology Resources</i> , 2018, 18, 602-619.	2.2	23
1280	Succession of microbial communities and changes of incremental oil in a post-polymer flooded reservoir with nutrient stimulation. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2007-2017.	1.7	22
1281	Dominant plant species shape soil bacterial community in semiarid sandy land of northern China. <i>Ecology and Evolution</i> , 2018, 8, 1693-1704.	0.8	31
1282	Comparative analyses of fecal microbiota in Chinese isolated Yao population, minority Zhuang and rural Han by 16sRNA sequencing. <i>Scientific Reports</i> , 2018, 8, 1142.	1.6	32
1283	Deciphering the associations between soil microbial diversity and ecosystem multifunctionality driven by long-term fertilization management. <i>Functional Ecology</i> , 2018, 32, 1103-1116.	1.7	141
1284	Bacterial diversity and composition of alfalfa silage as analyzed by Illumina MiSeq sequencing: Effects of <i>Escherichia coli</i> O157:H7 and silage additives. <i>Journal of Dairy Science</i> , 2018, 101, 2048-2059.	1.4	184
1285	Fungal community structure at pelagic and littoral sites in Lake Biwa determined with high-throughput sequencing. <i>Limnology</i> , 2018, 19, 241-251.	0.8	14
1286	Oral administration of liquid iron preparation containing excess iron induces intestine and liver injury, impairs intestinal barrier function and alters the gut microbiota in rats. <i>Journal of Trace Elements in Medicine and Biology</i> , 2018, 47, 12-20.	1.5	52
1287	Comparison of <i>Iris pseudacorus</i> wetland systems with unplanted systems on pollutant removal and microbial community under nanosilver exposure. <i>Science of the Total Environment</i> , 2018, 624, 1336-1347.	3.9	36

#	ARTICLE	IF	CITATIONS
1288	Imprecision and DNA Break Repair Biased towards Incompatible End Joining in Leukemia. <i>Molecular Cancer Research</i> , 2018, 16, 428-438.	1.5	11
1289	Individual- and Species-Specific Skin Microbiomes in Three Different Estrildid Finch Species Revealed by 16S Amplicon Sequencing. <i>Microbial Ecology</i> , 2018, 76, 518-529.	1.4	29
1290	Long-term fertilization changes bacterial diversity and bacterial communities in the maize rhizosphere of Chinese Mollisols. <i>Applied Soil Ecology</i> , 2018, 125, 88-96.	2.1	94
1291	High-throughput analysis of anammox bacteria in wetland and dryland soils along the altitudinal gradient in Qinghai-Tibet Plateau. <i>MicrobiologyOpen</i> , 2018, 7, e00556.	1.2	21
1292	Analysis of the influence of living environment and age on vaginal fungal microbiome in giant pandas (<i>Ailuropoda melanoleuca</i>) by high throughput sequencing. <i>Microbial Pathogenesis</i> , 2018, 115, 280-286.	1.3	5
1293	The greater roles of indigenous microorganisms in removing nitrobenzene from sediment compared with the exogenous <i>Phragmites australis</i> and strain JS45. <i>Frontiers of Environmental Science and Engineering</i> , 2018, 12, 1.	3.3	9
1294	Pilot investigation on formation of 2,4,6-trichloroanisole via microbial O-methylation of 2,4,6-trichlorophenol in drinking water distribution system: An insight into microbial mechanism. <i>Water Research</i> , 2018, 131, 11-21.	5.3	44
1295	Marine bacterial richness increases towards higher latitudes in the eastern Indian Ocean. <i>Limnology and Oceanography Letters</i> , 2018, 3, 10-19.	1.6	32
1296	Zebrafish Axenic Larvae Colonization with Human Intestinal Microbiota. <i>Zebrafish</i> , 2018, 15, 96-106.	0.5	10
1297	Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. <i>Environmental Microbiology</i> , 2018, 20, 402-419.	1.8	120
1298	Organic carbon availability limiting microbial denitrification in the deep vadose zone. <i>Environmental Microbiology</i> , 2018, 20, 980-992.	1.8	81
1299	Field study reveals core plant microbiota and relative importance of their drivers. <i>Environmental Microbiology</i> , 2018, 20, 124-140.	1.8	255
1300	Ammonium nitrogen content is a dominant predictor of bacterial community composition in an acidic forest soil with exogenous nitrogen enrichment. <i>Science of the Total Environment</i> , 2018, 624, 407-415.	3.9	128
1301	Gut microbiome populations are associated with structure-specific changes in white matter architecture. <i>Translational Psychiatry</i> , 2018, 8, 6.	2.4	63
1302	Ecological plasticity in the gastrointestinal microbiomes of Ethiopian <i>Chlorocebus</i> monkeys. <i>Scientific Reports</i> , 2018, 8, 20.	1.6	37
1303	Rhubarb Supplementation Promotes Intestinal Mucosal Innate Immune Homeostasis through Modulating Intestinal Epithelial Microbiota in Goat Kids. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 1047-1057.	2.4	24
1304	Deep sequence analysis reveals the ovine rumen as a reservoir of antibiotic resistance genes. <i>Environmental Pollution</i> , 2018, 235, 571-575.	3.7	26
1305	Diazotroph abundance and community composition in an acidic soil in response to aluminum-tolerant and aluminum-sensitive maize (<i>Zea mays</i> L.) cultivars under two nitrogen fertilizer forms. <i>Plant and Soil</i> , 2018, 424, 463-478.	1.8	25

#	ARTICLE	IF	CITATIONS
1306	Shifts in soil bacterial and archaeal communities during freeze-thaw cycles in a seasonal frozen marsh, Northeast China. <i>Science of the Total Environment</i> , 2018, 625, 782-791.	3.9	56
1307	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. <i>Nature Chemical Biology</i> , 2018, 14, 256-261.	3.9	143
1308	A <i>Lactobacillus</i> -Deficient Vaginal Microbiota Dominates Postpartum Women in Rural Malawi. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	50
1309	FROGS: Find, Rapidly, OTUs with Galaxy Solution. <i>Bioinformatics</i> , 2018, 34, 1287-1294.	1.8	660
1310	Fingerprint of Exhaust Gases and Database of Microbial Diversity During Silkworm Excrement Composting. <i>Compost Science and Utilization</i> , 2018, 26, 40-51.	1.2	2
1311	Integrating restriction site-associated DNA sequencing (RAD-seq) with morphological cladistic analysis clarifies evolutionary relationships among major species groups of bee orchids. <i>Annals of Botany</i> , 2018, 121, 85-105.	1.4	48
1312	Spatiotemporal changes in bacterial community and microbial activity in a full-scale drinking water treatment plant. <i>Science of the Total Environment</i> , 2018, 625, 449-459.	3.9	79
1313	Epithelial Hes1 maintains gut homeostasis by preventing microbial dysbiosis. <i>Mucosal Immunology</i> , 2018, 11, 716-726.	2.7	35
1314	Effects of short-term fallow managements on soil microbial properties: A case study in China. <i>Applied Soil Ecology</i> , 2018, 125, 128-137.	2.1	11
1315	Correcting for 16S rRNA gene copy numbers in microbiome surveys remains an unsolved problem. <i>Microbiome</i> , 2018, 6, 41.	4.9	514
1316	Metagenome-based diversity analyses suggest a strong locality signal for bacterial communities associated with oyster aquaculture farms in Ofunato Bay. <i>Gene</i> , 2018, 665, 149-154.	1.0	14
1317	Transcripts within rod photoreceptors of the Zebrafish retina. <i>BMC Genomics</i> , 2018, 19, 127.	1.2	41
1318	Genomic architecture of haddock (<i>Melanogrammus aeglefinus</i>) shows expansions of innate immune genes and short tandem repeats. <i>BMC Genomics</i> , 2018, 19, 240.	1.2	58
1319	Differential human gut microbiome assemblages during soil-transmitted helminth infections in Indonesia and Liberia. <i>Microbiome</i> , 2018, 6, 33.	4.9	102
1320	Core gut microbiota in Jinhua pigs and its correlation with strain, farm and weaning age. <i>Journal of Microbiology</i> , 2018, 56, 346-355.	1.3	50
1321	Fecal Microbiota Transplantation in Experimental Ulcerative Colitis Reveals Associated Gut Microbial and Host Metabolic Reprogramming. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
1322	Metagenome, metatranscriptome, and metaproteome approaches unraveled compositions and functional relationships of microbial communities residing in biogas plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5045-5063.	1.7	128
1323	Seasonal changes in the abundance of bacterial genes related to dimethylsulfoniopropionate catabolism in seawater from Ofunato Bay revealed by metagenomic analysis. <i>Gene</i> , 2018, 665, 174-184.	1.0	17

#	ARTICLE	IF	CITATIONS
1324	Impact of HIV and Type 2 diabetes on Gut Microbiota Diversity, Tryptophan Catabolism and Endothelial Dysfunction. <i>Scientific Reports</i> , 2018, 8, 6725.	1.6	35
1325	Electron acceptors for anaerobic oxidation of methane drive microbial community structure and diversity in mud volcanoes. <i>Environmental Microbiology</i> , 2018, 20, 2370-2385.	1.8	34
1326	Social networks, cooperative breeding, and the human milk microbiome. <i>American Journal of Human Biology</i> , 2018, 30, e23131.	0.8	55
1327	Molecular Profiling and Clonal Tracking of Secreted Rheumatoid Factors in Primary Sjögren's Syndrome. <i>Arthritis and Rheumatology</i> , 2018, 70, 1617-1625.	2.9	21
1328	<i>Chrysomya megacephala</i> larvae feeding favourably influences manure microbiome, heavy metal stability and greenhouse gas emissions. <i>Microbial Biotechnology</i> , 2018, 11, 498-509.	2.0	16
1329	Microeukaryotic biogeography in the typical subtropical coastal waters with multiple environmental gradients. <i>Science of the Total Environment</i> , 2018, 635, 618-628.	3.9	37
1330	Contrasting responses of bacterial and fungal communities to aggregate-size fractions and long-term fertilizations in soils of northeastern China. <i>Science of the Total Environment</i> , 2018, 635, 784-792.	3.9	80
1331	Microbial Community Composition in a Simultaneous Nitrification and Denitrification Bioreactor for Domestic Wastewater Treatment. <i>IOP Conference Series: Earth and Environmental Science</i> , 2018, 112, 012007.	0.2	4
1332	Taxonomic profiles in metagenomic analyses of free-living microbial communities in the Ofunato Bay. <i>Gene</i> , 2018, 665, 192-200.	1.0	15
1333	Drug-Resistance and Population Structure of <i>Plasmodium falciparum</i> Across the Democratic Republic of Congo Using High-Throughput Molecular Inversion Probes. <i>Journal of Infectious Diseases</i> , 2018, 218, 946-955.	1.9	78
1334	PGRP-LB homolog acts as a negative modulator of immunity in maintaining the gut-microbe symbiosis of red palm weevil, <i>Rhynchophorus ferrugineus</i> Olivier. <i>Developmental and Comparative Immunology</i> , 2018, 86, 65-77.	1.0	43
1335	Basin-scale seasonal changes in marine free-living bacterioplankton community in the Ofunato Bay. <i>Gene</i> , 2018, 665, 185-191.	1.0	10
1336	The beneficial effects of <i>Gracilaria lemaneiformis</i> polysaccharides on obesity and the gut microbiota in high fat diet-fed mice. <i>Journal of Functional Foods</i> , 2018, 46, 48-56.	1.6	65
1337	Molecular diagnostics for verifying an etiological agent of emaciation disease in cultured olive flounder <i>Paralichthys olivaceus</i> in Korea. <i>Aquaculture</i> , 2018, 493, 18-25.	1.7	12
1338	RTS,S/AS01 malaria vaccine mismatch observed among <i>Plasmodium falciparum</i> isolates from southern and central Africa and globally. <i>Scientific Reports</i> , 2018, 8, 6622.	1.6	37
1339	Conservation tillage and organic farming induce minor variations in <i>Pseudomonas</i> abundance, their antimicrobial function and soil disease resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	10
1340	Methodology challenges in studying human gut microbiota – effects of collection, storage, DNA extraction and next generation sequencing technologies. <i>Scientific Reports</i> , 2018, 8, 5143.	1.6	146
1341	Microbial community dynamics analysis by high-throughput sequencing in chilled beef longissimus steaks packaged under modified atmospheres. <i>Meat Science</i> , 2018, 141, 94-102.	2.7	65

#	ARTICLE	IF	CITATIONS
1342	Effect of live yeast <i>Saccharomyces cerevisiae</i> (Actisaf Sc 47) supplementation on the performance and hindgut microbiota composition of weanling pigs. <i>Scientific Reports</i> , 2018, 8, 5315.	1.6	44
1343	Moss habitats distinctly affect their associated bacterial community structures as revealed by the high-throughput sequencing method. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 58.	1.7	13
1344	Response of the microbial community structure of biofilms to ferric iron in microbial fuel cells. <i>Science of the Total Environment</i> , 2018, 631-632, 695-701.	3.9	43
1345	Structure and dynamics of microbiomes associated with the marine sponge <i>Tedania</i> sp. during its life cycle. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
1346	A High-Throughput Mutational Scan of an Intrinsically Disordered Acidic Transcriptional Activation Domain. <i>Cell Systems</i> , 2018, 6, 444-455.e6.	2.9	135
1347	Bioaugmentation of chlorothalonil-contaminated soil with hydrolytically or reductively dehalogenating strain and its effect on soil microbial community. <i>Journal of Hazardous Materials</i> , 2018, 351, 240-249.	6.5	40
1348	Designer epigenome modifiers enable robust and sustained gene silencing in clinically relevant human cells. <i>Nucleic Acids Research</i> , 2018, 46, 4456-4468.	6.5	63
1349	Nutrient enrichment during shrimp cultivation alters bacterioplankton assemblies and destroys community stability. <i>Ecotoxicology and Environmental Safety</i> , 2018, 156, 366-374.	2.9	30
1350	Transformation, CO ₂ formation and uptake of four organic micropollutants by carrier-attached microorganisms. <i>Water Research</i> , 2018, 141, 405-416.	5.3	27
1351	Earthworm-induced shifts in microbial diversity in soils with rare versus established invasive earthworm populations. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	19
1352	Biodiversity of fungi on <i>Vitis vinifera</i> L. revealed by traditional and high-resolution culture-independent approaches. <i>Fungal Diversity</i> , 2018, 90, 1-84.	4.7	101
1353	<i>Solidago canadensis</i> invasion affects soil N-fixing bacterial communities in heterogeneous landscapes in urban ecosystems in East China. <i>Science of the Total Environment</i> , 2018, 631-632, 702-713.	3.9	64
1354	Phylum-Level Archaeal Distributions in the Sediments of Chinese Lakes With a Large Range of Salinity. <i>Geomicrobiology Journal</i> , 2018, 35, 404-410.	1.0	14
1355	SeekDeep: single-base resolution de novo clustering for amplicon deep sequencing. <i>Nucleic Acids Research</i> , 2018, 46, e21-e21.	6.5	134
1356	Shifts of Sediment Microbial Community Structure along a Salinized and Degraded River Continuum. <i>Journal of Coastal Research</i> , 2018, 342, 443-450.	0.1	5
1357	Gut Microbial Dysbiosis in Indian Children with Autism Spectrum Disorders. <i>Microbial Ecology</i> , 2018, 76, 1102-1114.	1.4	130
1358	Community Structure Analysis and Biodegradation Potential of Aniline-Degrading Bacteria in Biofilters. <i>Current Microbiology</i> , 2018, 75, 918-924.	1.0	33
1359	Effect of exogenous inoculants on enhancing oil recovery and indigenous bacterial community dynamics in long-term field pilot of low permeability reservoir. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 53.	1.7	13

#	ARTICLE	IF	CITATIONS
1360	Differential immune responses and microbiota profiles in children with autism spectrum disorders and co-morbid gastrointestinal symptoms. <i>Brain, Behavior, and Immunity</i> , 2018, 70, 354-368.	2.0	163
1361	Functional evaluation of pollutant transformation in sediment from combined sewer system. <i>Environmental Pollution</i> , 2018, 238, 85-93.	3.7	35
1362	Expansions, diversification, and interindividual copy number variations of AID/APOBEC family cytidine deaminase genes in lampreys. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3211-E3220.	3.3	23
1363	Vanillic acid changed cucumber (<i>Cucumis sativus</i> L.) seedling rhizosphere total bacterial, <i>Pseudomonas</i> and <i>Bacillus</i> spp. communities. <i>Scientific Reports</i> , 2018, 8, 4929.	1.6	31
1364	Gut microbiota analysis of juvenile genetically improved farmed tilapia (<i>Oreochromis niloticus</i>) by dietary supplementation of different resveratrol concentrations. <i>Fish and Shellfish Immunology</i> , 2018, 77, 200-207.	1.6	37
1365	Plant sterols and human gut microbiota relationship: An in vitro colonic fermentation study. <i>Journal of Functional Foods</i> , 2018, 44, 322-329.	1.6	27
1366	Salinity shifts in marine sediment: Importance of number of fluctuation rather than their intensities on bacterial denitrifying community. <i>Marine Pollution Bulletin</i> , 2018, 130, 76-83.	2.3	13
1367	Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, .	1.5	31
1368	Lower dietary concentrate level increases bacterial diversity in the rumen of <i>Cervus elaphus yarkandensis</i> . <i>Canadian Journal of Microbiology</i> , 2018, 64, 501-509.	0.8	10
1369	Biogeochemical cycling of gold: Transforming gold particles from arctic Finland. <i>Chemical Geology</i> , 2018, 483, 511-529.	1.4	24
1370	A global comparison of the microbiome compositions of three gut locations in commercial pigs with extreme feed conversion ratios. <i>Scientific Reports</i> , 2018, 8, 4536.	1.6	121
1371	Soil pH is equally important as salinity in shaping bacterial communities in saline soils under halophytic vegetation. <i>Scientific Reports</i> , 2018, 8, 4550.	1.6	68
1372	Dynamics of the human gut phageome during antibiotic treatment. <i>Computational Biology and Chemistry</i> , 2018, 74, 420-427.	1.1	15
1373	Microbial dynamics and metabolite changes in Chinese Rice Wine fermentation from sorghum with different tannin content. <i>Scientific Reports</i> , 2018, 8, 4639.	1.6	45
1374	Independent of Birth Mode or Gestational Age, Very-Low-Birth-Weight Infants Fed Their Mothers' Milk Rapidly Develop Personalized Microbiotas Low in <i>Bifidobacterium</i> . <i>Journal of Nutrition</i> , 2018, 148, 326-335.	1.3	22
1375	Changes in the soil bacterial community structure and enzyme activities after intercrop mulch with cover crop for eight years in an orchard. <i>European Journal of Soil Biology</i> , 2018, 86, 34-41.	1.4	81
1376	Imbalance of gut microbiome and intestinal epithelial barrier dysfunction in patients with high blood pressure. <i>Clinical Science</i> , 2018, 132, 701-718.	1.8	328
1377	Opportunistic pathogens are abundant in the gut of cultured giant spiny frog (<i>Paa spinosa</i>). <i>Aquaculture Research</i> , 2018, 49, 2033-2041.	0.9	51

#	ARTICLE	IF	CITATIONS
1378	World's Largest Mass Bathing Event Influences the Bacterial Communities of Godavari, a Holy River of India. <i>Microbial Ecology</i> , 2018, 76, 706-718.	1.4	39
1379	Oyster microbial communities and implications for chalky deposit formation. <i>Hydrobiologia</i> , 2018, 816, 121-135.	1.0	22
1380	Extended and Continuous Decline in Effective Population Size Results in Low Genomic Diversity in the World's Rarest Hyena Species, the Brown Hyena. <i>Molecular Biology and Evolution</i> , 2018, 35, 1225-1237.	3.5	72
1381	Microbiome Dynamics in a Large Artificial Seawater Aquarium. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	33
1382	A comparative study of gut microbiota profiles of earthworms fed in three different substrates. <i>Symbiosis</i> , 2018, 74, 21-29.	1.2	51
1383	Bacterial communities associated with <i>Shinkaia crosnieri</i> from the Iheya North, Okinawa Trough: Microbial diversity and metabolic potentials. <i>Journal of Marine Systems</i> , 2018, 180, 228-236.	0.9	5
1384	Isolation and Characterization of <i>Rumex acetosa</i> -Associated Mineral-Weathering Bacteria. <i>Geomicrobiology Journal</i> , 2018, 35, 148-155.	1.0	4
1385	A nitrogen removal system to limit water exchange for recirculating freshwater aquarium using DHS's USB reactor. <i>Environmental Technology (United Kingdom)</i> , 2018, 39, 1577-1585.	1.2	15
1386	Bacterial community dynamics in the rhizosphere of a long-lived, leguminous shrub across a 40-year age sequence. <i>Journal of Soils and Sediments</i> , 2018, 18, 76-84.	1.5	35
1387	Responses of the soil fungal communities to the invasion of two invasive species with different cover classes. <i>Plant Biology</i> , 2018, 20, 151-159.	1.8	43
1388	Mechanisms of HERV-K (HML-2) Transcription during Human Mammary Epithelial Cell Transformation. <i>Journal of Virology</i> , 2018, 92, .	1.5	33
1389	Ophiopogonin D alleviates high-fat diet-induced metabolic syndrome and changes the structure of gut microbiota in mice. <i>FASEB Journal</i> , 2018, 32, 1139-1153.	0.2	35
1390	Antibiotic pretreatment minimizes dietary effects on reconstructure of rumen fluid and mucosal microbiota in goats. <i>MicrobiologyOpen</i> , 2018, 7, e00537.	1.2	6
1391	Evaluation of different 16S rRNA gene V regions for exploring bacterial diversity in a eutrophic freshwater lake. <i>Science of the Total Environment</i> , 2018, 618, 1254-1267.	3.9	115
1392	Supplementation of pancreatic digestive enzymes alters the composition of intestinal microbiota in mice. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 273-279.	1.0	43
1393	Anaerobic digestion of spent mushroom substrate under thermophilic conditions: performance and microbial community analysis. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 499-507.	1.7	25
1394	Fate of antibiotic resistance genes and metal resistance genes during thermophilic aerobic digestion of sewage sludge. <i>Bioresource Technology</i> , 2018, 249, 635-643.	4.8	48
1395	Effect of ozone injection on the long-term performance and microbial community structure of a VOCs biofilter. <i>Journal of Environmental Sciences</i> , 2018, 69, 133-140.	3.2	23

#	ARTICLE	IF	CITATIONS
1396	Residual disease detection using targeted parallel sequencing predicts relapse in cytogenetically normal acute myeloid leukemia. <i>American Journal of Hematology</i> , 2018, 93, 23-30.	2.0	16
1397	Sorption, desorption and degradation of neonicotinoids in four agricultural soils and their effects on soil microorganisms. <i>Science of the Total Environment</i> , 2018, 615, 59-69.	3.9	148
1398	Use of a filtering process to remove solid waste and antibiotic resistance genes from effluent of a flow-through fish farm. <i>Science of the Total Environment</i> , 2018, 615, 289-296.	3.9	26
1399	Influence of resistance breeding in common bean on rhizosphere microbiome composition and function. <i>ISME Journal</i> , 2018, 12, 212-224.	4.4	296
1400	Prevalence of antibiotic resistance genes from effluent of coastal aquaculture, South Korea. <i>Environmental Pollution</i> , 2018, 233, 1049-1057.	3.7	127
1401	Selecting fungal disturbance indicators to compare forest soil profile re-construction regimes. <i>Ecological Indicators</i> , 2018, 84, 662-682.	2.6	9
1402	Bacterial community temporal dynamics and disease-related variations in the seawater of <i>Pyropia</i> (laver) seedling pools. <i>Journal of Applied Phycology</i> , 2018, 30, 1217-1224.	1.5	7
1403	Potentially active spoilage bacteria community during the storage of vacuum packaged beefsteaks treated with aqueous ozone and electrolyzed water. <i>International Journal of Food Microbiology</i> , 2018, 266, 337-345.	2.1	29
1404	Lipoâ€Protein Emulsion Structure in the Diet Affects Protein Digestion Kinetics, Intestinal Mucosa Parameters and Microbiota Composition. <i>Molecular Nutrition and Food Research</i> , 2018, 62, 1700570.	1.5	16
1405	Comparative analysis of microbial communities associated with bacteriomes, reproductive organs and eggs of the cicada <i>Subsalstria yangi</i> . <i>Archives of Microbiology</i> , 2018, 200, 227-235.	1.0	15
1406	Transmission of a common intestinal neoplasm in zebrafish by cohabitation. <i>Journal of Fish Diseases</i> , 2018, 41, 569-579.	0.9	24
1407	Taxonomic and Functional Analyses of the Supragingival Microbiome from Caries-Affected and Caries-Free Hosts. <i>Microbial Ecology</i> , 2018, 75, 543-554.	1.4	23
1408	Obesity increases the risk of small intestinal bacterial overgrowth (<sc>SIBO</sc>). <i>Neurogastroenterology and Motility</i> , 2018, 30, e13199.	1.6	35
1409	<i>Lactobacillus iners</i>-dominated vaginal microbiota is associated with increased susceptibility to <i>Chlamydia trachomatis</i> infection in Dutch women: a caseâ€control study. <i>Sexually Transmitted Infections</i> , 2018, 94, 117-123.	0.8	89
1410	A comparative study of composting the solid fraction of dairy manure with or without bulking material: Performance and microbial community dynamics. <i>Bioresource Technology</i> , 2018, 247, 443-452.	4.8	135
1411	Microbial community and bioelectrochemical activities in MFC for degrading phenol and producing electricity: Microbial consortia could make differences. <i>Chemical Engineering Journal</i> , 2018, 332, 647-657.	6.6	137
1412	Subclonal Evolution of Cancer-Related Gene Mutations in p53 Immunopositive Patches in Human Skin. <i>Journal of Investigative Dermatology</i> , 2018, 138, 189-198.	0.3	28
1413	The diversity and biogeography of abundant and rare intertidal marine microeukaryotes explained by environment and dispersal limitation. <i>Environmental Microbiology</i> , 2018, 20, 462-476.	1.8	112

#	ARTICLE	IF	CITATIONS
1414	Reduced obesity, diabetes, and steatosis upon cinnamon and grape pomace are associated with changes in gut microbiota and markers of gut barrier. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 314, E334-E352.	1.8	119
1415	Bacterial community structures in air conditioners installed in Japanese residential buildings. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 45-53.	0.7	6
1416	Contact with turf algae alters the coral microbiome: contact versus systemic impacts. <i>Coral Reefs</i> , 2018, 37, 1-13.	0.9	47
1417	Distribution of apple and blackcurrant microbiota in Lithuania and the Czech Republic. <i>Microbiological Research</i> , 2018, 206, 1-8.	2.5	44
1418	<i>Tremblaya phenacola</i> PPER: an evolutionary beta-gammaproteobacterium collage. <i>ISME Journal</i> , 2018, 12, 124-135.	4.4	14
1419	Different <i>Lactobacillus</i> populations dominate in "Chorizo de Le ³ "-manufacturing performed in different production plants. <i>Food Microbiology</i> , 2018, 70, 94-102.	2.1	41
1420	Antibiotic-induced microbiota perturbation causes gut endocannabinoidome changes, hippocampal neuroglial reorganization and depression in mice. <i>Brain, Behavior, and Immunity</i> , 2018, 67, 230-245.	2.0	246
1421	Aerobic composting reduces antibiotic resistance genes in cattle manure and the resistome dissemination in agricultural soils. <i>Science of the Total Environment</i> , 2018, 612, 1300-1310.	3.9	190
1422	Anthropogenic Activities Induce Depletion in Microbial Communities at Urban Sites of the River Ganges. <i>Current Microbiology</i> , 2018, 75, 79-83.	1.0	49
1423	Effects of chlortetracycline, Cu and their combination on the performance and microbial community dynamics in swine manure anaerobic digestion. <i>Journal of Environmental Sciences</i> , 2018, 67, 206-215.	3.2	43
1424	Rapid startup of thermophilic anaerobic digester to remove tetracycline and sulfonamides resistance genes from sewage sludge. <i>Science of the Total Environment</i> , 2018, 612, 788-798.	3.9	90
1425	Strong responses of <i>Drosophila melanogaster</i> microbiota to developmental temperature. <i>Fly</i> , 2018, 12, 1-12.	0.9	93
1426	Variation in the bacteriome of the tropical liverwort, <i>Marchantia inflexa</i> , between the sexes and across habitats. <i>Symbiosis</i> , 2018, 75, 93-101.	1.2	12
1427	Characterization of diversified Sb(V)-reducing bacterial communities by various organic or inorganic electron donors. <i>Bioresource Technology</i> , 2018, 250, 239-246.	4.8	25
1428	Contrasting responses of soil respiration and temperature sensitivity to land use types: Cropland vs. apple orchard on the Chinese Loess Plateau. <i>Science of the Total Environment</i> , 2018, 621, 425-433.	3.9	34
1429	Organic amendments shift the phosphorus-correlated microbial co-occurrence pattern in the peanut rhizosphere network during long-term fertilization regimes. <i>Applied Soil Ecology</i> , 2018, 124, 229-239.	2.1	48
1430	Fungal communities influence decomposition rates of plant litter from two dominant tree species. <i>Fungal Ecology</i> , 2018, 32, 1-8.	0.7	35
1431	Nitrogen removal performance and microbial community changes in subsurface wastewater infiltration systems (SWISs) at low temperature with different bioaugmentation strategies. <i>Bioresource Technology</i> , 2018, 250, 603-610.	4.8	50

#	ARTICLE	IF	CITATIONS
1432	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. ISME Journal, 2018, 12, 742-755.	4.4	76
1433	Forest conversion induces seasonal variation in microbial α -diversity. Environmental Microbiology, 2018, 20, 111-123.	1.8	33
1434	The microbiome in PTEN hamartoma tumor syndrome. Endocrine-Related Cancer, 2018, 25, 233-243.	1.6	5
1435	Dietary stachyose altered the intestinal microbiota profile and improved the intestinal mucosal barrier function of juvenile turbot, <i>Scophthalmus maximus</i> L.. Aquaculture, 2018, 486, 98-106.	1.7	66
1436	Effect of microbially mediated iron mineral transformation on temporal variation of arsenic in the Pleistocene aquifers of the central Yangtze River basin. Science of the Total Environment, 2018, 619-620, 1247-1258.	3.9	65
1437	Gancao-Gansui combination impacts gut microbiota diversity and related metabolic functions. Journal of Ethnopharmacology, 2018, 214, 71-82.	2.0	48
1438	Soil bacterial community responses to long-term fertilizer treatments in Paulownia plantations in subtropical China. Applied Soil Ecology, 2018, 124, 317-326.	2.1	30
1439	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
1440	Gut microbiota composition is associated with environmental landscape in honey bees. Ecology and Evolution, 2018, 8, 441-451.	0.8	106
1441	Compositional and functional variations of oral microbiota associated with the mutational changes in oral cancer. Oral Oncology, 2018, 77, 1-8.	0.8	95
1442	Influence of the intestinal microbiota on the immunogenicity of oral rotavirus vaccine given to infants in south India. Vaccine, 2018, 36, 264-272.	1.7	88
1443	Metagenomics profiling for assessing microbial diversity in both active and closed landfills. Science of the Total Environment, 2018, 616-617, 269-278.	3.9	45
1444	Can high-throughput sequencing detect macroinvertebrate diversity for routine monitoring of an urban river?. Ecological Indicators, 2018, 85, 440-450.	2.6	34
1445	Difference of nitrogen-cycling microbes between shallow bay and deep-sea sediments in the South China Sea. Applied Microbiology and Biotechnology, 2018, 102, 447-459.	1.7	33
1446	Impact of <i>Lactobacillus curvatus</i> 54M16 on microbiota composition and growth of <i>Listeria monocytogenes</i> in fermented sausages. Food Microbiology, 2018, 72, 1-15.	2.1	43
1447	Next-Generation DNA Sequencing of VH/VL Repertoires: A Primer and Guide to Applications in Single-Domain Antibody Discovery. Methods in Molecular Biology, 2018, 1701, 425-446.	0.4	14
1448	Monitoring Phage Biopanning by Next-Generation Sequencing. Methods in Molecular Biology, 2018, 1701, 463-473.	0.4	9
1449	Contemporary evolution of a Lepidopteran species, <i>Heliiothis virescens</i> , in response to modern agricultural practices. Molecular Ecology, 2018, 27, 167-181.	2.0	28

#	ARTICLE	IF	CITATIONS
1450	Droplet distribution and airborne bacteria in an experimental shower unit. <i>Water Research</i> , 2018, 130, 47-57.	5.3	24
1451	Microhaplotypes provide increased power from short-read <i>scp</i> DNA sequences for relationship inference. <i>Molecular Ecology Resources</i> , 2018, 18, 296-305.	2.2	101
1452	Overexpression of a newly identified <i>α</i> -amino acid transaminase in <i>Mycobacterium smegmatis</i> complements glutamate racemase deletion. <i>Molecular Microbiology</i> , 2018, 107, 198-213.	1.2	33
1453	Dynamics of Heterotrophic Bacterial Assemblages within <i>Synechococcus</i> Cultures. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	52
1454	Targeted DNA enrichment and whole genome sequencing of <i>Neisseria meningitidis</i> directly from clinical specimens. <i>International Journal of Medical Microbiology</i> , 2018, 308, 256-262.	1.5	36
1455	The mechanical scouring of bio-carriers improves phosphorus removal and mediates functional microbiomes in membrane bioreactors. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 241-252.	1.2	12
1456	Roles of different active metal-reducing bacteria in arsenic release from arsenic-contaminated paddy soil amended with biochar. <i>Journal of Hazardous Materials</i> , 2018, 344, 958-967.	6.5	123
1457	Root type and soil phosphate determine the taxonomic landscape of colonizing fungi and the transcriptome of field-grown maize roots. <i>New Phytologist</i> , 2018, 217, 1240-1253.	3.5	80
1458	Free-living chemoautotrophic and particle-attached heterotrophic prokaryotes dominate microbial assemblages along a pelagic redox gradient. <i>Environmental Microbiology</i> , 2018, 20, 693-712.	1.8	46
1459	Antibiotics reduce genetic diversity of core species in the honeybee gut microbiome. <i>Molecular Ecology</i> , 2018, 27, 2057-2066.	2.0	95
1460	Metaproteomics reveals major microbial players and their metabolic activities during the blooming period of a marine dinoflagellate <i>Prorocentrum donghaiense</i> . <i>Environmental Microbiology</i> , 2018, 20, 632-644.	1.8	35
1461	The Distal Gut Bacterial Community of Some Primates and Carnivora. <i>Current Microbiology</i> , 2018, 75, 213-222.	1.0	18
1462	Increase in taxonomic assignment efficiency of viral reads in metagenomic studies. <i>Virus Research</i> , 2018, 244, 230-234.	1.1	10
1463	Comparison study of the volatile profiles and microbial communities of Wuyi Qu and Gutian Qu, two major types of traditional fermentation starters of Hong Qu glutinous rice wine. <i>Food Microbiology</i> , 2018, 69, 105-115.	2.1	69
1464	Next-generation teaching: a template for bringing genomic and bioinformatic tools into the classroom. <i>Journal of Biological Education</i> , 2018, 52, 301-313.	0.8	4
1465	Root exudates of potato onion are involved in the suppression of clubroot in a Chinese cabbage-potato onion-Chinese cabbage crop rotation. <i>European Journal of Plant Pathology</i> , 2018, 150, 765-777.	0.8	15
1466	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. <i>PeerJ</i> , 2018, 6, e6075.	0.9	64
1467	Fecal microbial dysbiosis in Chinese patients with inflammatory bowel disease. <i>World Journal of Gastroenterology</i> , 2018, 24, 1464-1477.	1.4	49

#	ARTICLE	IF	CITATIONS
1468	Probiotics Strains Modulate Gut Microbiota and Lipid Metabolism in Mule Ducks. <i>Open Microbiology Journal</i> , 2018, 12, 71-93.	0.2	7
1469	Nutrients Availability Shapes Fungal Community Composition and Diversity in the Rare Earth Mine Tailings of Southern Jiangxi, China. <i>Russian Journal of Ecology</i> , 2018, 49, 524-533.	0.3	6
1470	Association of gestational diabetes mellitus and abnormal vaginal flora with adverse pregnancy outcomes. <i>Medicine (United States)</i> , 2018, 97, e11891.	0.4	50
1471	Whole-Genome Sequences of <i>Corynebacterium macginleyi</i> CCUG 32361 ^T and Clinical Isolates NML 080212 and NML 120205. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
1472	Analyses of Aerosol Concentrations and Bacterial Community Structures for Closed Cage Broiler Houses at Different Broiler Growth Stages in Winter. <i>Journal of Food Protection</i> , 2018, 81, 1557-1564.	0.8	13
1473	Similarities and differences in gut microbiome composition correlate with dietary patterns of Indian and Chinese adults. <i>AMB Express</i> , 2018, 8, 104.	1.4	55
1474	Traits of Exogenous Species and Indigenous Community Contribute to the Species Colonization and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 3087.	1.5	9
1475	Composition of Rumen Bacterial Community in Dairy Cows With Different Levels of Somatic Cell Counts. <i>Frontiers in Microbiology</i> , 2018, 9, 3217.	1.5	39
1476	NGmerge: merging paired-end reads via novel empirically-derived models of sequencing errors. <i>BMC Bioinformatics</i> , 2018, 19, 536.	1.2	142
1477	Evaluation of Mixotrophy-Associated Gene Expression in Two Species of Polar Marine Algae. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	19
1478	CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes. <i>BMC Genomics</i> , 2018, 19, 858.	1.2	2
1479	Genotypes and Phenotypes of Enterococci Isolated From Broiler Chickens. <i>Frontiers in Sustainable Food Systems</i> , 2018, 2, .	1.8	26
1480	Comprehensive assessment of free nitrous acid-based technology to establish partial nitrification. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 2113-2124.	1.2	12
1481	<i>Lactobacillus helveticus</i> KLD51.8701 alleviates d-galactose-induced aging by regulating Nrf-2 and gut microbiota in mice. <i>Food and Function</i> , 2018, 9, 6586-6598.	2.1	66
1482	Whole-Genome Sequences of <i>Propionibacterium australiense</i> NML (LCDC) 98A072 T and NML (LCDC) 98A078, Associated with Granulomatous Bovine Lesions. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
1483	Advances in genotyping microsatellite markers through sequencing and consequences of scoring methods for <i>Ceratonia siliqua</i> (Leguminosae). <i>Applications in Plant Sciences</i> , 2018, 6, e01201.	0.8	14
1484	Biofilm diversity, structure and matrix seasonality in a full-scale cooling tower. <i>Biofouling</i> , 2018, 34, 1093-1109.	0.8	3
1485	Microsatellite Capture Sequencing. , 0, , .		0

#	ARTICLE	IF	CITATIONS
1486	Pediatric Obstructive Sleep Apnea is Associated With Changes in the Oral Microbiome and Urinary Metabolomics Profile: A Pilot Study. <i>Journal of Clinical Sleep Medicine</i> , 2018, 14, 1559-1567.	1.4	38
1487	Soil Bacterial Communities Under Different Long-Term Fertilization Regimes in Three Locations Across the Black Soil Region of Northeast China. <i>Pedosphere</i> , 2018, 28, 751-763.	2.1	32
1488	Comparison of differences in microbial compositions between negative controls and subject samples with varying analysis configurations. <i>Allergy Asthma & Respiratory Disease</i> , 2018, 6, 255.	0.3	0
1489	A Pipeline for Variant Calling in Tumor Panels Using Amplicon Sequencing Data. , 2018, , .		0
1490	The first complete genomic structure of <i>Butyrivibrio fibrisolvens</i> and its chromid. <i>Microbial Genomics</i> , 2018, 4, .	1.0	9
1491	Assessment of fecal microbiota in farmed silver fox (<i>Vulpes vulpes fulva</i>) and raccoon dog (<i>Nyctereutes procyonoides</i>). <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2018, 68, 142-151.	0.2	2
1493	Disease outbreak accompanies the dispersive structure of shrimp gut bacterial community with a simple core microbiota. <i>AMB Express</i> , 2018, 8, 120.	1.4	50
1494	Response of soil fungal community to long-term chromium contamination. <i>Transactions of Nonferrous Metals Society of China</i> , 2018, 28, 1838-1846.	1.7	27
1495	Intergenerational effects of macroalgae on a reef coral: major declines in larval survival but subtle changes in microbiomes. <i>Marine Ecology - Progress Series</i> , 2018, 589, 97-114.	0.9	27
1496	The effect of drinking water pH on the human gut microbiota and glucose regulation: results of a randomized controlled cross-over intervention. <i>Scientific Reports</i> , 2018, 8, 16626.	1.6	26
1497	Butyrate Producers as Potential Next-Generation Probiotics: Safety Assessment of the Administration of <i>Butyricoccus pullicaecorum</i> to Healthy Volunteers. <i>MSystems</i> , 2018, 3, .	1.7	99
1498	A complete <i>Leishmania donovani</i> reference genome identifies novel genetic variations associated with virulence. <i>Scientific Reports</i> , 2018, 8, 16549.	1.6	41
1499	Variation of Bacterial and Archaeal Community Structures in a Full-Scale Constructed Wetlands for Wastewater Treatment. <i>Archaea</i> , 2018, 2018, 1-12.	2.3	9
1500	Microbiome-Triggered Transformations of Trace Organic Chemicals in the Presence of Effluent Organic Matter in Managed Aquifer Recharge (MAR) Systems. <i>Environmental Science & Technology</i> , 2018, 52, 14342-14351.	4.6	15
1501	Variation and diversification of the microbiome of <i>Schlechtendalia chinensis</i> on two alternate host plants. <i>PLoS ONE</i> , 2018, 13, e0200049.	1.1	7
1502	Microbial community structure and functional potential of lava-formed Gotjawal soils in Jeju, Korea. <i>PLoS ONE</i> , 2018, 13, e0204761.	1.1	14
1503	Pretreatment of spiramycin fermentation residue using hyperthermophilic digestion: quick startup and performance. <i>Water Science and Technology</i> , 2018, 78, 1823-1832.	1.2	5
1504	Long-term combined application of manure and chemical fertilizer sustained higher nutrient status and rhizospheric bacterial diversity in reddish paddy soil of Central South China. <i>Scientific Reports</i> , 2018, 8, 16554.	1.6	70

#	ARTICLE	IF	CITATIONS
1505	Targeted mutagenesis using the <i>Agrobacterium tumefaciens</i> -mediated CRISPR-Cas9 system in common wheat. <i>BMC Plant Biology</i> , 2018, 18, 302.	1.6	69
1506	Impact of <i>Bacillus</i> spp. spores and gentamicin on the gastrointestinal microbiota of suckling and newly weaned piglets. <i>PLoS ONE</i> , 2018, 13, e0207382.	1.1	33
1507	Insights Into the Bovine Milk Microbiota in Dairy Farms With Different Incidence Rates of Subclinical Mastitis. <i>Frontiers in Microbiology</i> , 2018, 9, 2379.	1.5	46
1508	Effects of IRW and IQW on Oxidative Stress and Gut Microbiota in Dextran Sodium Sulfate-Induced Colitis. <i>Cellular Physiology and Biochemistry</i> , 2018, 51, 441-451.	1.1	40
1509	Effects of Graphene on Bacterial Community Diversity and Soil Environments of Haplic Cambisols in Northeast China. <i>Forests</i> , 2018, 9, 677.	0.9	19
1510	Vanillin Alleviates High Fat Diet-Induced Obesity and Improves the Gut Microbiota Composition. <i>Frontiers in Microbiology</i> , 2018, 9, 2733.	1.5	51
1511	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018, 9, 4894.	5.8	304
1512	Variations in oral microbiome profiles in rheumatoid arthritis and osteoarthritis with potential biomarkers for arthritis screening. <i>Scientific Reports</i> , 2018, 8, 17126.	1.6	68
1513	Geographical Distribution and Risk Assessment of Heavy Metals in Nearby River of Heap Bioleaching Plant: A Case Study At the Zijin Copper Mine, China. <i>IOP Conference Series: Earth and Environmental Science</i> , 2018, 182, 012005.	0.2	0
1514	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	121
1515	Association of bovine major histocompatibility complex (BoLA) gene polymorphism with colostrum and milk microbiota of dairy cows during the first week of lactation. <i>Microbiome</i> , 2018, 6, 203.	4.9	38
1516	Estrogen-mediated gut microbiome alterations influence sexual dimorphism in metabolic syndrome in mice. <i>Microbiome</i> , 2018, 6, 205.	4.9	145
1517	Multiple Strategies for Light-Harvesting, Photoprotection, and Carbon Flow in High Latitude Microbial Mats. <i>Frontiers in Microbiology</i> , 2018, 9, 2881.	1.5	33
1518	Origin and Consequences of Chromosomal Inversions in the <i>virilis</i> Group of <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 3152-3166.	1.1	22
1519	Virulent Epidemic Pneumonia in Sheep Caused by the Human Pathogen <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2616.	1.5	20
1520	Microbiome Analysis of Biofilms of Silver Nanoparticle-Dispersed Silane-Based Coated Carbon Steel Using a Next-Generation Sequencing Technique. <i>Antibiotics</i> , 2018, 7, 91.	1.5	5
1521	Amplification of Near Full-length HIV-1 Proviruses for Next-Generation Sequencing. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	13
1522	Combining QTL mapping with transcriptome and metabolome profiling reveals a possible role for ABA signaling in resistance against the cabbage whitefly in cabbage. <i>PLoS ONE</i> , 2018, 13, e0206103.	1.1	13

#	ARTICLE	IF	CITATIONS
1523	Bacterial Diversity and the Geochemical Landscape in the Southwestern Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2018, 9, 2528.	1.5	39
1524	Stormwater influences phytoplankton assemblages within the diverse, but impacted Sydney Harbour estuary. <i>PLoS ONE</i> , 2018, 13, e0209857.	1.1	12
1525	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. <i>ISME Journal</i> , 2018, 12, 2706-2722.	4.4	45
1526	Harvest of the Oleaginous Microalgae <i>Scenedesmus obtusiusculus</i> by Flocculation From Culture Based on Natural Water Sources. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 200.	2.0	19
1527	Studying safe storage time of orange peel (<i>Citrus reticulata</i>) using high-throughput sequencing and conventional pure culture. <i>Food Science and Nutrition</i> , 2018, 6, 2545-2552.	1.5	6
1528	Niche Separation of Ammonia Oxidizers in Mudflat and Agricultural Soils Along the Yangtze River, China. <i>Frontiers in Microbiology</i> , 2018, 9, 3122.	1.5	3
1529	Analysis of Bacterial Community Characteristics, Abundance of Antibiotics and Antibiotic Resistance Genes Along a Pollution Gradient of Ba River in Xi'an, China. <i>Frontiers in Microbiology</i> , 2018, 9, 3191.	1.5	48
1530	Organic Farming Improves Soil Microbial Abundance and Diversity under Greenhouse Condition: A Case Study in Shanghai (Eastern China). <i>Sustainability</i> , 2018, 10, 3825.	1.6	34
1531	First evidence of the presence and activity of archaeal C3 group members in an Atlantic intertidal mudflat. <i>Scientific Reports</i> , 2018, 8, 11790.	1.6	5
1532	Microbial community composition and diversity in the Indian Ocean deep sea REY-rich muds. <i>PLoS ONE</i> , 2018, 13, e0208230.	1.1	14
1533	Microbial Diversity Analysis of Sediment from Nakdong River Estuary in the Republic of Korea Using 16S rRNA Gene Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
1534	Selection and Characterization of Anti-Dengue NS1 Single Domain Antibodies. <i>Scientific Reports</i> , 2018, 8, 18086.	1.6	19
1535	Specific recruitment of soil bacteria and fungi decomposers following a biostimulant application increased crop residues mineralization. <i>PLoS ONE</i> , 2018, 13, e0209089.	1.1	33
1536	Dynamics of Bacterial Communities Mediating the Treatment of an As-Rich Acid Mine Drainage in a Field Pilot. <i>Frontiers in Microbiology</i> , 2018, 9, 3169.	1.5	24
1537	A Metabologenomic Approach Reveals Changes in the Intestinal Environment of Mice Fed on American Diet. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4079.	1.8	41
1538	Evolutionary analysis of the Chikungunya virus epidemic in Mexico reveals intra-host mutational hotspots in the E1 protein. <i>PLoS ONE</i> , 2018, 13, e0209292.	1.1	8
1539	Effect of Quercetin Monoglycosides on Oxidative Stress and Gut Microbiota Diversity in Mice with Dextran Sodium Sulphate-Induced Colitis. <i>BioMed Research International</i> , 2018, 2018, 1-7.	0.9	60
1540	Effects of Rich-Polyphenols Extract of <i>Dendrobium loddigesii</i> on Anti-Diabetic, Anti-Inflammatory, Anti-Oxidant, and Gut Microbiota Modulation in db/db Mice. <i>Molecules</i> , 2018, 23, 3245.	1.7	70

#	ARTICLE	IF	CITATIONS
1541	Sewer Sediment Bacterial Communities Suggest Potential to Transform Persistent Organic Pollutants. <i>Water Environment Research</i> , 2018, 90, 2022-2029.	1.3	6
1542	Rock substrate rather than black stain alterations drives microbial community structure in the passage of Lascaux Cave. <i>Microbiome</i> , 2018, 6, 216.	4.9	34
1543	The ecological risks of hydrogen peroxide as a cyanocide: its effect on the community structure of bacterioplankton. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 2231-2242.	0.6	13
1544	SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. <i>MSystems</i> , 2018, 3, .	1.7	66
1545	Modulation of intestinal microbiota, morphology and mucin composition by dietary insect meal inclusion in free-range chickens. <i>BMC Veterinary Research</i> , 2018, 14, 383.	0.7	89
1546	Shifts of Hydrogen Metabolism From Methanogenesis to Propionate Production in Response to Replacement of Forage Fiber With Non-forage Fiber Sources in Diets in vitro. <i>Frontiers in Microbiology</i> , 2018, 9, 2764.	1.5	51
1547	Possible association of Firmicutes in the gut microbiota of patients with major depressive disorder. <i>Neuropsychiatric Disease and Treatment</i> , 2018, Volume 14, 3329-3337.	1.0	178
1548	A Pilot Study: Changes of Gut Microbiota in Post-surgery Colorectal Cancer Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 2777.	1.5	41
1549	<i>Toxoplasma gondii</i> -Induced Long-Term Changes in the Upper Intestinal Microflora during the Chronic Stage of Infection. <i>Scientifica</i> , 2018, 2018, 1-11.	0.6	11
1550	Treating wheat seeds with neonicotinoid insecticides does not harm the rhizosphere microbial community. <i>PLoS ONE</i> , 2018, 13, e0205200.	1.1	21
1551	Dysbiosis of the Salivary Microbiome Is Associated With Non-smoking Female Lung Cancer and Correlated With Immunocytochemistry Markers. <i>Frontiers in Oncology</i> , 2018, 8, 520.	1.3	69
1552	Gut Microbiota Is a Major Contributor to Adiposity in Pigs. <i>Frontiers in Microbiology</i> , 2018, 9, 3045.	1.5	63
1553	Comparison of the Abundance and Community Structure of N-Cycling Bacteria in Paddy Rhizosphere Soil under Different Rice Cultivation Patterns. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3772.	1.8	24
1554	The Microbiome of the Cosmopolitan Diatom <i>Leptocylinndrus</i> Reveals Significant Spatial and Temporal Variability. <i>Frontiers in Microbiology</i> , 2018, 9, 2758.	1.5	35
1555	Daily changes in phytoplankton lipidomes reveal mechanisms of energy storage in the open ocean. <i>Nature Communications</i> , 2018, 9, 5179.	5.8	63
1556	Complex mammalian-like haematopoietic system found in a colonial chordate. <i>Nature</i> , 2018, 564, 425-429.	13.7	60
1557	Gene mutation associated with <i>esl</i> mediates shifts on fungal community composition in rhizosphere soil of rice at grain-filling stage. <i>Scientific Reports</i> , 2018, 8, 17521.	1.6	2
1558	Genetic Effects on the Gut Microbiota Assemblages of Hybrid Fish From Parents With Different Feeding Habits. <i>Frontiers in Microbiology</i> , 2018, 9, 2972.	1.5	46

#	ARTICLE	IF	CITATIONS
1559	Potential of iturins as functional agents: safe, probiotic, and cytotoxic to cancer cells. <i>Food and Function</i> , 2018, 9, 5580-5587.	2.1	28
1560	The effects of dietary astaxanthin on intestinal health of juvenile tiger puffer <i>Takifugu rubripes</i> in terms of antioxidative status, inflammatory response and microbiota. <i>Aquaculture Nutrition</i> , 2018, 25, 466.	1.1	2
1561	Virus genotyping by massive parallel amplicon sequencing: adenovirus and enterovirus in the Norwegian MIDIA study. <i>Journal of Medical Virology</i> , 2019, 91, 606-614.	2.5	9
1562	Enantioselectivity in degradation and ecological risk of the chiral pesticide ethiprole. <i>Land Degradation and Development</i> , 2018, 29, 4242-4251.	1.8	25
1563	Exposure to heat-stress environment affects the physiology, circulation levels of cytokines, and microbiome in dairy cows. <i>Scientific Reports</i> , 2018, 8, 14606.	1.6	88
1564	Electrode Colonization by the Feammox Bacterium <i>Acidimicrobiaceae</i> sp. Strain A6. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	38
1565	Accounting for Bacterial Overlap Between Raw Water Communities and Contaminating Sources Improves the Accuracy of Signature-Based Microbial Source Tracking. <i>Frontiers in Microbiology</i> , 2018, 9, 2364.	1.5	16
1566	Microbiome dataset from the upper respiratory tract of patients living with HIV, HIV/TB and TB from Myanmar. <i>Data in Brief</i> , 2018, 21, 354-357.	0.5	1
1567	Rhizosphere Microbial Response to Multiple Metal(loid)s in Different Contaminated Arable Soils Indicates Crop-Specific Metal-Microbe Interactions. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
1568	Contrasting dynamics of polychlorinated biphenyl dissipation and fungal community composition in low and high organic carbon soils with biochar amendment. <i>Environmental Science and Pollution Research</i> , 2018, 25, 33432-33442.	2.7	12
1569	Divergence of Fecal Microbiota and Their Associations With Host Phylogeny in Cervinae. <i>Frontiers in Microbiology</i> , 2018, 9, 1823.	1.5	9
1570	Detection and characterization of bacterial nucleic acids in culture-negative synovial tissue and fluid samples from rheumatoid arthritis or osteoarthritis patients. <i>Scientific Reports</i> , 2018, 8, 14305.	1.6	76
1571	Comparative assessment of autochthonous bacterial and fungal communities and microbial biomarkers of polluted agricultural soils of the Terra dei Fuochi. <i>Scientific Reports</i> , 2018, 8, 14281.	1.6	45
1572	Chinese Black Truffle (<i>Tuber indicum</i>) Alters the Ectomycorrhizosphere and Endoectomycosphere Microbiome and Metabolic Profiles of the Host Tree <i>Quercus aliena</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2202.	1.5	38
1573	Mapping protein selectivity landscapes using multi-target selective screening and next-generation sequencing of combinatorial libraries. <i>Nature Communications</i> , 2018, 9, 3935.	5.8	13
1574	The impact of epidermal growth factor supernatant on pig performance and ileal microbiota ¹ . <i>Translational Animal Science</i> , 2018, 2, 184-194.	0.4	7
1575	Treatment of Dextran Sulfate Sodium-Induced Colitis with Mucosa-Associated Lymphoid Tissue Lymphoma Translocation 1 Inhibitor MI-2 Is Associated with Restoration of Gut Immune Function and the Microbiota. <i>Infection and Immunity</i> , 2018, 86, .	1.0	25
1576	Alterations in the Urinary Microbiota Are Associated With Cesarean Delivery. <i>Frontiers in Microbiology</i> , 2018, 9, 2193.	1.5	6

#	ARTICLE	IF	CITATIONS
1577	Sulfated Polysaccharide from Sea Cucumber and its Depolymerized Derivative Prevent Obesity in Association with Modification of Gut Microbiota in High-Fat Diet-Fed Mice. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1800446.	1.5	128
1578	Highly efficient genome editing via CRISPR-Cas9 in human pluripotent stem cells is achieved by transient BCL-XL overexpression. <i>Nucleic Acids Research</i> , 2018, 46, 10195-10215.	6.5	93
1579	<i>Bifidobacterium pseudocatenulatum</i> CECT 7765 supplementation improves inflammatory status in insulin-resistant obese children. <i>European Journal of Nutrition</i> , 2018, 58, 2789-2800.	1.8	35
1580	Historical DNA Metabarcoding of the Prey and Microbiome of Trematomid Fishes Using Museum Samples. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	16
1581	Molecular Alteration Analysis of Human Gut Microbial Composition in Graves' disease Patients. <i>International Journal of Biological Sciences</i> , 2018, 14, 1558-1570.	2.6	74
1582	Huang-Lian-Jie-Du-Decoction Ameliorates Hyperglycemia and Insulin Resistant in Association With Gut Microbiota Modulation. <i>Frontiers in Microbiology</i> , 2018, 9, 2380.	1.5	88
1583	Microbiome and Blood Analyte Differences Point to Community and Metabolic Signatures in Lean and Obese Horses. <i>Frontiers in Veterinary Science</i> , 2018, 5, 225.	0.9	55
1584	Binning enables efficient host genome reconstruction in cnidarian holobionts. <i>GigaScience</i> , 2018, 7, .	3.3	16
1585	Soil productivity and structure of bacterial and fungal communities in unfertilized arable soil. <i>PLoS ONE</i> , 2018, 13, e0204085.	1.1	13
1586	Alterations in gut bacterial and fungal microbiomes are associated with bacterial Keratitis, an inflammatory disease of the human eye. <i>Journal of Biosciences</i> , 2018, 43, 835-856.	0.5	47
1587	Variation of bacterial community associated with <i>Phaeodactylum tricornutum</i> in response to different inorganic nitrogen concentrations. <i>Acta Oceanologica Sinica</i> , 2018, 37, 118-128.	0.4	4
1588	Diet induced changes in the microbiota and cell composition of rabbit gut associated lymphoid tissue (GALT). <i>Scientific Reports</i> , 2018, 8, 14103.	1.6	18
1589	Bifidobacterial Dominance of the Gut in Early Life and Acquisition of Antimicrobial Resistance. <i>MSphere</i> , 2018, 3, .	1.3	71
1590	Obesity alters composition and diversity of the oral microbiota in patients with type 2 diabetes mellitus independently of glycemic control. <i>PLoS ONE</i> , 2018, 13, e0204724.	1.1	69
1591	Tong-Xie-Yao-Fang Regulates 5-HT Level in Diarrhea Predominant Irritable Bowel Syndrome Through Gut Microbiota Modulation. <i>Frontiers in Pharmacology</i> , 2018, 9, 1110.	1.6	41
1592	Taxonomic diversity of bacteria from mangrove sediments of Goa: metagenomic and functional analysis. <i>3 Biotech</i> , 2018, 8, 436.	1.1	30
1593	Effect of Different Disinfectants on Bacterial Aerosol Diversity in Poultry Houses. <i>Frontiers in Microbiology</i> , 2018, 9, 2113.	1.5	33
1594	Genetic Modulation of RNA Splicing with a CRISPR-Guided Cytidine Deaminase. <i>Molecular Cell</i> , 2018, 72, 380-394.e7.	4.5	107

#	ARTICLE	IF	CITATIONS
1595	Fluidigm2^{PURC}: Automated processing and haplotype inference for double-€barcoded ^{PCR} amplicons. <i>Applications in Plant Sciences</i> , 2018, 6, e01156.	0.8	12
1596	Bacterial Communities in the Womb During Healthy Pregnancy. <i>Frontiers in Microbiology</i> , 2018, 9, 2163.	1.5	65
1597	Biases in Prokaryotic Community Amplicon Sequencing Affected by DNA Extraction Methods in Both Saline and Non-saline Soil. <i>Frontiers in Microbiology</i> , 2018, 9, 1796.	1.5	12
1598	Genomic blueprint of a relapsing fever pathogen in 15th century Scandinavia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10422-10427.	3.3	22
1599	Long-Term Nitrogen Fertilization Elevates the Activity and Abundance of Nitrifying and Denitrifying Microbial Communities in an Upland Soil: Implications for Nitrogen Loss From Intensive Agricultural Systems. <i>Frontiers in Microbiology</i> , 2018, 9, 2424.	1.5	64
1600	Quinoa whole grain diet compromises the changes of gut microbiota and colonic colitis induced by dextran Sulfate sodium in C57BL/6 mice. <i>Scientific Reports</i> , 2018, 8, 14916.	1.6	48
1601	Alterations in the diversity and composition of mice gut microbiota by lytic or temperate gut phage treatment. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10219-10230.	1.7	19
1602	Intestinal toxicity of deoxynivalenol is limited by supplementation with <i>Lactobacillus plantarum</i> JM113 and consequentially altered gut microbiota in broiler chickens. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 74.	2.1	65
1603	Soil acidification amendments change the rhizosphere bacterial community of tobacco in a bacterial wilt affected field. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9781-9791.	1.7	83
1604	Stratification of microbial communities throughout a biological sulphate reducing up-flow anaerobic packed bed reactor, revealed through 16S metagenomics. <i>Research in Microbiology</i> , 2018, 169, 543-551.	1.0	13
1605	Protective Effect of <i>Pediococcus pentosaceus</i> LI05 Against <i>Clostridium difficile</i> Infection in a Mouse Model. <i>Frontiers in Microbiology</i> , 2018, 9, 2396.	1.5	26
1606	Australian dryland soils are acidic and nutrient-€depleted, and have unique microbial communities compared with other drylands. <i>Journal of Biogeography</i> , 2018, 45, 2803-2814.	1.4	35
1607	Functional profiling of the gut microbiomes in two different populations of the brown planthopper, <i>Nilaparvata lugens</i> . <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 1309-1314.	0.4	15
1608	The Biogeographical Distribution of Soil Bacterial Communities in the Loess Plateau as Revealed by High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2456.	1.5	35
1609	Fungal Endophytic Communities of Two Wild Rosa Varieties With Different Powdery Mildew Susceptibilities. <i>Frontiers in Microbiology</i> , 2018, 9, 2462.	1.5	18
1610	Composition and Genetic Diversity of the <i>Nicotiana tabacum</i> Microbiome in Different Topographic Areas and Growth Periods. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3421.	1.8	15
1611	Biofilm Microbiome (Re)Growth Dynamics in Drinking Water Distribution Systems Are Impacted by Chlorine Concentration. <i>Frontiers in Microbiology</i> , 2018, 9, 2519.	1.5	62
1612	Supplemental <i>Bacillus subtilis</i> DSM 32315 manipulates intestinal structure and microbial composition in broiler chickens. <i>Scientific Reports</i> , 2018, 8, 15358.	1.6	86

#	ARTICLE	IF	CITATIONS
1613	Mychonastes dominates the photosynthetic picoeukaryotes in Lake Poyang, a river-connected lake. FEMS Microbiology Ecology, 2019, 95, .	1.3	7
1614	Colon Microbiome of Pigs Fed Diet Contaminated with Commercial Purified Deoxynivalenol and Zearalenone. Toxins, 2018, 10, 347.	1.5	26
1615	Oral iron exacerbates colitis and influences the intestinal microbiome. PLoS ONE, 2018, 13, e0202460.	1.1	71
1616	Microbial community and functions associated with digestion of algal polysaccharides in the visceral tract of <i>Haliotis discus hannai</i> : Insights from metagenome and metatranscriptome analysis. PLoS ONE, 2018, 13, e0205594.	1.1	13
1617	Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows. PLoS Genetics, 2018, 14, e1007580.	1.5	198
1618	Rare haplotype load as marker for lethal mutagenesis. PLoS ONE, 2018, 13, e0204877.	1.1	8
1619	Changes in bacterial communities during two agricultural solid wastesâ€™ co-composting processes. Annals of Microbiology, 2018, 68, 743-754.	1.1	9
1620	acI Actinobacteria Assemble a Functional Actinorhodopsin with Natively Synthesized Retinal. Applied and Environmental Microbiology, 2018, 84, .	1.4	15
1621	The gut bacteria across life stages in the synanthropic fly <i>Chrysomya megacephala</i> . BMC Microbiology, 2018, 18, 131.	1.3	20
1622	Immune-suppression by OsHV-1 viral infection causes fatal bacteraemia in Pacific oysters. Nature Communications, 2018, 9, 4215.	5.8	217
1623	Response of activity, abundance, and composition of anammox bacterial community to different fertilization in a paddy soil. Biology and Fertility of Soils, 2018, 54, 977-984.	2.3	16
1624	Transcriptome-Wide Analysis of Proteinâ€™RNA and RNAâ€™RNA Interactions in Pathogenic Bacteria. Methods in Enzymology, 2018, 612, 467-488.	0.4	7
1625	The genomic basis of tumor regression in Tasmanian devils (<i>Sarcophilus harrisii</i>). Genome Biology and Evolution, 2018, 10, 3012-3025.	1.1	30
1626	Protists Within Corals: The Hidden Diversity. Frontiers in Microbiology, 2018, 9, 2043.	1.5	39
1627	Diversity and characteristics of colonization of root-associated fungi of <i>Vaccinium uliginosum</i> . Scientific Reports, 2018, 8, 15283.	1.6	27
1628	Anaerobic lignocellulolytic microbial consortium derived from termite gut: enrichment, lignocellulose degradation and community dynamics. Biotechnology for Biofuels, 2018, 11, 284.	6.2	32
1629	A distinct strain of <i>Arsenophonus</i> symbiont decreases insecticide resistance in its insect host. PLoS Genetics, 2018, 14, e1007725.	1.5	88
1630	Alterations of Gut Microbiome in the Patients With Severe Fever With Thrombocytopenia Syndrome. Frontiers in Microbiology, 2018, 9, 2315.	1.5	8

#	ARTICLE	IF	CITATIONS
1631	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. <i>Nature Genetics</i> , 2018, 50, 1744-1751.	9.4	150
1633	The gut microbiome participates in transgenerational inheritance of low-temperature responses in <i>Drosophila melanogaster</i> . <i>FEBS Letters</i> , 2018, 592, 4078-4086.	1.3	23
1634	Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. <i>Clinical Transplantation</i> , 2018, 32, e13436.	0.8	24
1635	Contribution of Host Genetics to the Variation of Microbial Composition of Cecum Lumen and Feces in Pigs. <i>Frontiers in Microbiology</i> , 2018, 9, 2626.	1.5	44
1636	Dietary supplement with a mixture of fish oil and krill oil has sex-dependent effects on obese mice gut microbiota. <i>Journal of Functional Foods</i> , 2018, 51, 47-54.	1.6	8
1637	Deciphering the bacterial composition in the rhizosphere of <i>Baphicacanthus cusia</i> (Nees) Bremek. <i>Scientific Reports</i> , 2018, 8, 15831.	1.6	15
1638	The Cloacal Microbiome of Five Wild Duck Species Varies by Species and Influenza A Virus Infection Status. <i>MSphere</i> , 2018, 3, .	1.3	28
1639	How the Devil Ray Got Its Horns: The Evolution and Development of Cephalic Lobes in Myliobatid Stingrays (Batoidea: Myliobatidae). <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	6
1640	Temperature-controlled thermophilic bacterial communities in hot springs of western Sichuan, China. <i>BMC Microbiology</i> , 2018, 18, 134.	1.3	45
1641	Oral microbiota dysbiosis and its association with Henoch-Schönlein Purpura in children. <i>International Immunopharmacology</i> , 2018, 65, 295-302.	1.7	18
1642	Toxic effects of Zearalenone on intestinal microflora and intestinal mucosal immunity in mice. <i>Food and Agricultural Immunology</i> , 2018, 29, 1002-1011.	0.7	22
1643	Dietary citric acid supplementation alleviates soybean meal-induced intestinal oxidative damage and micro-ecological imbalance in juvenile turbot, <i>Scophthalmus maximus</i> L. <i>Aquaculture Research</i> , 2018, 49, 3804-3816.	0.9	36
1644	Consistent responses of soil microbial taxonomic and functional attributes to mercury pollution across China. <i>Microbiome</i> , 2018, 6, 183.	4.9	109
1645	Isolation and characterization of microsatellite loci from <i>Oxytropis diversifolia</i> (Fabaceae). <i>Applications in Plant Sciences</i> , 2018, 6, e01168.	0.8	3
1646	Spatial Variability and Co-acclimation of Phytoplankton and Bacterioplankton Communities in the Pearl River Estuary, China. <i>Frontiers in Microbiology</i> , 2018, 9, 2503.	1.5	28
1647	Spatiotemporal variations in microbial diversity across the three domains of life in a tropical thalassohaline lake (Dziani Dzaha, Mayotte Island). <i>Molecular Ecology</i> , 2018, 27, 4775-4786.	2.0	27
1648	The response of dominant and rare taxa for fungal diversity within different root environments to the cultivation of Bt and conventional cotton varieties. <i>Microbiome</i> , 2018, 6, 184.	4.9	29
1649	Observed Antibody Space: A Resource for Data Mining Next-Generation Sequencing of Antibody Repertoires. <i>Journal of Immunology</i> , 2018, 201, 2502-2509.	0.4	165

#	ARTICLE	IF	CITATIONS
1650	Characterization of bacterial and microbial eukaryotic communities associated with an ephemeral hypoxia event in Taihu Lake, a shallow eutrophic Chinese lake. <i>Environmental Science and Pollution Research</i> , 2018, 25, 31543-31557.	2.7	20
1651	Effects of endogenous inhibitors on the evolution of antibiotic resistance genes during high solid anaerobic digestion of swine manure. <i>Bioresource Technology</i> , 2018, 270, 328-336.	4.8	30
1652	The gastric mucosal-associated microbiome in patients with gastric polyposis. <i>Scientific Reports</i> , 2018, 8, 13817.	1.6	30
1653	Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters. <i>Viruses</i> , 2018, 10, 496.	1.5	25
1654	Isolation by Miniaturized Culture Chip of an Antarctic bacterium <i>Aequorivita</i> sp. with antimicrobial and anthelmintic activity. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2018, 20, e00281.	2.1	11
1655	Cucumber (<i>Cucumis sativus</i> L.) Seedling Rhizosphere <i>Trichoderma</i> and <i>Fusarium</i> spp. Communities Altered by Vanillic Acid. <i>Frontiers in Microbiology</i> , 2018, 9, 2195.	1.5	36
1656	Insight Into the Pico- and Nano-Phytoplankton Communities in the Deepest Biosphere, the Mariana Trench. <i>Frontiers in Microbiology</i> , 2018, 9, 2289.	1.5	30
1657	Broad Bean (<i>Vicia faba</i> L.) Induces Intestinal Inflammation in Grass Carp (<i>Ctenopharyngodon idellus</i> C.) Tj ETQq1 1 0.784314 rgBT /Over in <i>Microbiology</i> , 2018, 9, 1913.	1.5	17
1658	Soil fungal taxonomic and functional community composition as affected by biochar properties. <i>Soil Biology and Biochemistry</i> , 2018, 126, 159-167.	4.2	57
1659	Intestinal probiotics restore the ecological fitness decline of <i>Bactrocera dorsalis</i> by irradiation. <i>Evolutionary Applications</i> , 2018, 11, 1946-1963.	1.5	64
1660	The Genetic Basis of Adaptation following Plastic Changes in Coloration in a Novel Environment. <i>Current Biology</i> , 2018, 28, 2970-2977.e7.	1.8	83
1661	Comparisons of gut microbiota profiles in wild-type and gelatinase B/matrix metalloproteinase-9-deficient mice in acute DSS-induced colitis. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 18.	2.9	10
1662	Venom gland transcriptomics and microRNA profiling of juvenile and adult yellow-bellied sea snake, <i>Hydrophis platurus</i> , from Playa del Coco (Guanacaste, Costa Rica). <i>Toxicon</i> , 2018, 153, 96-105.	0.8	14
1663	Alteration of the cutaneous microbiome in psoriasis and potential role in Th17 polarization. <i>Microbiome</i> , 2018, 6, 154.	4.9	190
1664	Root-Associated Microbiome of Maize Genotypes with Contrasting Phosphorus Use Efficiency. <i>Phytobiomes Journal</i> , 2018, 2, 129-137.	1.4	59
1665	Dietary Bile Salt Types Influence the Composition of Biliary Bile Acids and Gut Microbiota in Grass Carp. <i>Frontiers in Microbiology</i> , 2018, 9, 2209.	1.5	31
1666	Benthic deep-sea fungi in submarine canyons of the Mediterranean Sea. <i>Progress in Oceanography</i> , 2018, 168, 57-64.	1.5	39
1667	Effects of Transgenic Bt Rice Containing the Cry1Ab Protein on the Gastrointestinal Health of Highly Inbred Wuzhishan Pigs after Two Generations of Feeding. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 10575-10587.	2.4	1

#	ARTICLE	IF	CITATIONS
1668	Comparison of Healthy and Dandruff Scalp Microbiome Reveals the Role of Commensals in Scalp Health. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 346.	1.8	63
1669	Direct-fed microbial supplementation influences the bacteria community composition of the gastrointestinal tract of pre- and post-weaned calves. <i>Scientific Reports</i> , 2018, 8, 14147.	1.6	50
1670	Short-term impacts of anthropogenic stressors on <i>Aedes albopictus</i> mosquito vector microbiota. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	22
1671	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. <i>Scientific Reports</i> , 2018, 8, 13314.	1.6	54
1672	Long-term effects of legume mulching on soil chemical properties and bacterial community composition and structure. <i>Agriculture, Ecosystems and Environment</i> , 2018, 268, 24-33.	2.5	37
1673	Effects of extruded aquafeed on growth performance and gut microbiome of juvenile <i>Totoaba macdonaldi</i> . <i>Animal Feed Science and Technology</i> , 2018, 245, 91-103.	1.1	34
1674	Airway Microbiota Dynamics Uncover a Critical Window for Interplay of Pathogenic Bacteria and Allergy in Childhood Respiratory Disease. <i>Cell Host and Microbe</i> , 2018, 24, 341-352.e5.	5.1	146
1675	The effect of exposure to high altitude and low oxygen on intestinal microbial communities in mice. <i>PLoS ONE</i> , 2018, 13, e0203701.	1.1	44
1676	Effect of intermediate disturbance on soil microbial functional diversity depends on the amount of effective resources. <i>Environmental Microbiology</i> , 2018, 20, 3862-3875.	1.8	24
1677	The microbiota in the intestinal and respiratory tracts of naked mole-rats revealed by high-throughput sequencing. <i>BMC Microbiology</i> , 2018, 18, 89.	1.3	11
1678	EasyQC: Tool with Interactive User Interface for Efficient Next-Generation Sequencing Data Quality Control. <i>Journal of Computational Biology</i> , 2018, 25, 1301-1311.	0.8	8
1679	Plant Pathogenic Fungi and Oomycetes. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	4
1680	Abundant and Rare Microbial Biospheres Respond Differently to Environmental and Spatial Factors in Tibetan Hot Springs. <i>Frontiers in Microbiology</i> , 2018, 9, 2096.	1.5	45
1681	Investigation of Detection Limits and the Influence of DNA Extraction and Primer Choice on the Observed Microbial Communities in Drinking Water Samples Using 16S rRNA Gene Amplicon Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2140.	1.5	49
1682	From Short Reads to Chromosome-Scale Genome Assemblies. <i>Methods in Molecular Biology</i> , 2018, 1848, 151-197.	0.4	7
1683	Inherent bacterial community response to multiple heavy metals in sediment from river-lake systems in the Poyang Lake, China. <i>Ecotoxicology and Environmental Safety</i> , 2018, 165, 314-324.	2.9	72
1684	Composition of the teat canal and intramammary microbiota of dairy cows subjected to antimicrobial dry cow therapy and internal teat sealant. <i>Journal of Dairy Science</i> , 2018, 101, 10191-10205.	1.4	46
1685	Comparative Genomic Analysis of <i>Vibrio diabolicus</i> and Six Taxonomic Synonyms: A First Look at the Distribution and Diversity of the Expanded Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1893.	1.5	24

#	ARTICLE	IF	CITATIONS
1686	Multi-Year Persistence of Verotoxigenic <i>Escherichia coli</i> (VTEC) in a Closed Canadian Beef Herd: A Cohort Study. <i>Frontiers in Microbiology</i> , 2018, 9, 2040.	1.5	15
1687	PIPEBAR and OverlapPER: tools for a fast and accurate DNA barcoding analysis and paired-end assembly. <i>BMC Bioinformatics</i> , 2018, 19, 297.	1.2	10
1688	The Challenges of Genome-Wide Studies in a Unicellular Eukaryote With Two Nuclear Genomes. <i>Methods in Enzymology</i> , 2018, 612, 101-126.	0.4	3
1689	Enterobacteriaceae are essential for the modulation of colitis severity by fungi. <i>Microbiome</i> , 2018, 6, 152.	4.9	143
1690	A-GAME: improving the assembly of pooled functional metagenomics sequence data. <i>BMC Genomics</i> , 2018, 19, 44.	1.2	7
1691	Factors shaping the gut bacterial community assembly in two main Colombian malaria vectors. <i>Microbiome</i> , 2018, 6, 148.	4.9	91
1692	Repeated translocation of a gene cassette drives sex-chromosome turnover in strawberries. <i>PLoS Biology</i> , 2018, 16, e2006062.	2.6	85
1693	First genome-wide analysis of the endangered, endemic lichen <i>Cetradonia linearis</i> reveals isolation by distance and strong population structure. <i>American Journal of Botany</i> , 2018, 105, 1556-1567.	0.8	27
1694	The more important role of archaea than bacteria in nitrification of wastewater treatment plants in cold season despite their numerical relationships. <i>Water Research</i> , 2018, 145, 552-561.	5.3	59
1695	Gut microbiota mediates the anti-obesity effect of calorie restriction in mice. <i>Scientific Reports</i> , 2018, 8, 13037.	1.6	114
1696	Pigmented microbial eukaryotes fuel the deep sea carbon pool in the tropical Western Pacific Ocean. <i>Environmental Microbiology</i> , 2018, 20, 3811-3824.	1.8	15
1697	Increased salinity triggers significant changes in the functional proteins of ANAMMOX bacteria within a biofilm community. <i>Chemosphere</i> , 2018, 207, 655-664.	4.2	33
1698	Cultivar-specific response of bacterial community to cadmium contamination in the rhizosphere of rice (<i>Oryza sativa</i> L.). <i>Environmental Pollution</i> , 2018, 241, 63-73.	3.7	67
1699	High content analysis of sea buckthorn, black chokeberry, red and white currants microbiota – A pilot study. <i>Food Research International</i> , 2018, 111, 597-606.	2.9	14
1700	Starvation stress affects the interplay among shrimp gut microbiota, digestion and immune activities. <i>Fish and Shellfish Immunology</i> , 2018, 80, 191-199.	1.6	61
1701	Dynamics of soil microbial recovery from cropland to orchard along a 20-year chronosequence in a degraded karst ecosystem. <i>Science of the Total Environment</i> , 2018, 639, 1051-1059.	3.9	22
1702	Bloom of a denitrifying methanotroph, <i>Candidatus</i> <i>Methylomirabilis limnetica</i> TM , in a deep stratified lake. <i>Environmental Microbiology</i> , 2018, 20, 2598-2614.	1.8	87
1703	Ecology of sleeping: the microbial and arthropod associates of chimpanzee beds. <i>Royal Society Open Science</i> , 2018, 5, 180382.	1.1	7

#	ARTICLE	IF	CITATIONS
1704	Parental haplotype-specific single-cell transcriptomics reveal incomplete epigenetic reprogramming in human female germ cells. <i>Nature Communications</i> , 2018, 9, 1873.	5.8	46
1705	Growth of sedimentary Bathyarchaeota on lignin as an energy source. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6022-6027.	3.3	165
1706	Application of biosolids drives the diversity of antibiotic resistance genes in soil and lettuce at harvest. <i>Soil Biology and Biochemistry</i> , 2018, 122, 131-140.	4.2	67
1707	Effect of dietary ketoglutarate and allicin supplementation on the composition and diversity of the cecal microbial community in growing pigs. <i>Journal of the Science of Food and Agriculture</i> , 2018, 98, 5816-5821.	1.7	18
1708	Oral hydroxysafflor yellow A reduces obesity in mice by modulating the gut microbiota and serum metabolism. <i>Pharmacological Research</i> , 2018, 134, 40-50.	3.1	151
1709	Long-term application of lime or pig manure rather than plant residues suppressed diazotroph abundance and diversity and altered community structure in an acidic Ultisol. <i>Soil Biology and Biochemistry</i> , 2018, 123, 218-228.	4.2	107
1710	Experimentally testing the species-habitat size relationship on soil bacteria: A proof of concept. <i>Soil Biology and Biochemistry</i> , 2018, 123, 200-206.	4.2	13
1711	Fertilization shapes a well-organized community of bacterial decomposers for accelerated paddy straw degradation. <i>Scientific Reports</i> , 2018, 8, 7981.	1.6	45
1712	Draft Genome Sequences of <i>Streptomyces</i> sp. Strains MH60 and 111WW2. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
1713	Metagenomic study of bacterial microbiota in persistent endodontic infections using Next-generation sequencing. <i>International Endodontic Journal</i> , 2018, 51, 1336-1348.	2.3	51
1714	Effects of permafrost thaw-subsidence on soil bacterial communities in the southern Qinghai-Tibetan Plateau. <i>Applied Soil Ecology</i> , 2018, 128, 81-88.	2.1	33
1715	Altered gut microbiota associated with intestinal disease in grass carp (<i>Ctenopharyngodon idellus</i>). <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 71.	1.7	116
1716	Comparative analysis of the bacterial community compositions of the shrimp intestine, surrounding water and sediment. <i>Journal of Applied Microbiology</i> , 2018, 125, 792-799.	1.4	72
1717	The gut microbiome is associated with behavioural task in honey bees. <i>Insectes Sociaux</i> , 2018, 65, 419-429.	0.7	90
1718	Soil types influence the fate of antibiotic-resistant bacteria and antibiotic resistance genes following the land application of sludge composts. <i>Environment International</i> , 2018, 118, 34-43.	4.8	97
1719	Compositional shifts in the surface fungal communities of apple fruits during cold storage. <i>Postharvest Biology and Technology</i> , 2018, 144, 55-62.	2.9	47
1720	Multiple effects of secondary metabolites on amino acid cycling in white clover rhizosphere. <i>Soil Biology and Biochemistry</i> , 2018, 123, 54-63.	4.2	30
1721	Tick-Bacteria Mutualism Depends on B Vitamin Synthesis Pathways. <i>Current Biology</i> , 2018, 28, 1896-1902.e5.	1.8	246

#	ARTICLE	IF	CITATIONS
1722	Sulfated polysaccharides from pacific abalone reduce diet-induced obesity by modulating the gut microbiota. <i>Journal of Functional Foods</i> , 2018, 47, 211-219.	1.6	41
1723	Preferential feeding in <i>Naegleria fowleri</i> ; intracellular bacteria isolated from amoebae in operational drinking water distribution systems. <i>Water Research</i> , 2018, 141, 126-134.	5.3	10
1724	Outbreak of Invasive Wound Mucormycosis in a Burn Unit Due to Multiple Strains of <i>Mucor circinelloides</i> f. <i>circinelloides</i> Resolved by Whole-Genome Sequencing. <i>MBio</i> , 2018, 9, .	1.8	54
1725	Limited influence of hospital wastewater on the microbiome and resistome of wastewater in a community sewerage system. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	72
1726	Independent assessment and improvement of wheat genome sequence assemblies using Fosill jumping libraries. <i>GigaScience</i> , 2018, 7, .	3.3	12
1727	<i>Alpinia oxyphylla</i> Miq. Extract Prevents Diabetes in Mice by Modulating Gut Microbiota. <i>Journal of Diabetes Research</i> , 2018, 2018, 1-10.	1.0	35
1728	Analysis of the bacterial communities in the waterlogged wooden cultural relics of the <i>Xiaobaijiao</i> No. 1 shipwreck via high-throughput sequencing technology. <i>Holzforschung</i> , 2018, 72, 609-619.	0.9	14
1729	Effects of the Administration of Probiotics on Fecal Microbiota Diversity and Composition in Healthy Individuals. <i>Journal of Neurogastroenterology and Motility</i> , 2018, 24, 452-459.	0.8	12
1730	Extreme drought slightly decreased soil labile organic C and N contents and altered microbial community structure in a subtropical evergreen forest. <i>Forest Ecology and Management</i> , 2018, 429, 18-27.	1.4	54
1731	Mannan-oligosaccharide modulates the obesity and gut microbiota in high-fat diet-fed mice. <i>Food and Function</i> , 2018, 9, 3916-3929.	2.1	88
1732	The unexpected diversity of microbial communities associated with black corals revealed by high-throughput Illumina sequencing. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	8
1733	Molecular Characterization of the 2016 New World Screwworm (Diptera: Calliphoridae) Outbreak in the Florida Keys. <i>Journal of Medical Entomology</i> , 2018, 55, 938-946.	0.9	7
1734	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. <i>ELife</i> , 2018, 7, .	2.8	103
1735	Microbial distribution and turnover in Antarctic microbial mats highlight the relevance of heterotrophic bacteria in low-nutrient environments. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	19
1736	Ten novel microsatellite markers for the freshwater sleeper <i>Micropercops swinhonis</i> (Günther, 1873), with testing of cross-species amplification in two other fishes from suborder Gobioidae. <i>Journal of Applied Ichthyology</i> , 2018, 34, 1180-1182.	0.3	1
1737	Effect of Freeze-Thaw on a Midtemperate Soil Bacterial Community and the Correlation Network of Its Members. <i>BioMed Research International</i> , 2018, 2018, 1-13.	0.9	12
1738	Successive transitory distribution of Thaumarchaeota and partitioned distribution of Bathyarchaeota from the Pearl River estuary to the northern South China Sea. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8035-8048.	1.7	20
1739	Deciphering the factors influencing the discrepant fate of antibiotic resistance genes in sludge and water phases during municipal wastewater treatment. <i>Bioresource Technology</i> , 2018, 265, 310-319.	4.8	51

#	ARTICLE	IF	CITATIONS
1740	Pooled CRISPR interference screening enables genome-scale functional genomics study in bacteria with superior performance. <i>Nature Communications</i> , 2018, 9, 2475.	5.8	168
1741	Tannins and Bacitracin Differentially Modulate Gut Microbiota of Broiler Chickens. <i>BioMed Research International</i> , 2018, 2018, 1-11.	0.9	80
1742	Distinct biogeographic patterns of rhizobia and non-rhizobial endophytes associated with soybean nodules across China. <i>Science of the Total Environment</i> , 2018, 643, 569-578.	3.9	39
1743	Characteristics of fecal microbiota in non-alcoholic fatty liver disease patients. <i>Science China Life Sciences</i> , 2018, 61, 770-778.	2.3	46
1744	The High-Quality Genome Sequence of the Oceanic Island Endemic Species <i>Drosophila guanche</i> Reveals Signals of Adaptive Evolution in Genes Related to Flight and Genome Stability. <i>Genome Biology and Evolution</i> , 2018, 10, 1956-1969.	1.1	14
1745	Characterization of Microbial Communities in Pilot-Scale Constructed Wetlands with <i>Salicornia</i> for Treatment of Marine Aquaculture Effluents. <i>Archaea</i> , 2018, 2018, 1-12.	2.3	17
1746	Temporal and spatial distribution of ammonia-oxidizing organisms of two types of wetlands in Northeast China. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7195-7205.	1.7	19
1747	Characteristics and formation mechanism of membrane fouling in a full-scale RO wastewater reclamation process: Membrane autopsy and fouling characterization. <i>Journal of Membrane Science</i> , 2018, 563, 843-856.	4.1	87
1748	Aflatoxin B1 (AFB1) induced dysregulation of intestinal microbiota and damage of antioxidant system in pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2018, 495, 940-947.	1.7	62
1749	Predators and nutrient availability favor protozoa-resisting bacteria in aquatic systems. <i>Scientific Reports</i> , 2018, 8, 8415.	1.6	20
1750	Vertically distinct microbial communities in the Mariana and Kermadec trenches. <i>PLoS ONE</i> , 2018, 13, e0195102.	1.1	62
1751	Biofilm and planktonic bacterial communities in a drinking water distribution system supplied with untreated groundwater. <i>Archives of Microbiology</i> , 2018, 200, 1323-1331.	1.0	2
1752	Induction and Amelioration of Methotrexate-Induced Gastrointestinal Toxicity are Related to Immune Response and Gut Microbiota. <i>EBioMedicine</i> , 2018, 33, 122-133.	2.7	80
1753	Changes in rhizosphere microbial communities in potted cucumber seedlings treated with syringic acid. <i>PLoS ONE</i> , 2018, 13, e0200007.	1.1	23
1754	Complete Genome Sequences of Three Related Avian Avulavirus 1 Isolates from Poultry Farmers in Pakistan. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
1755	Pea-protein alginate encapsulation adversely affects development of clinical signs of <i>Citrobacter rodentium</i> -induced colitis in mice treated with probiotics. <i>Canadian Journal of Microbiology</i> , 2018, 64, 744-760.	0.8	5
1756	AnMBR as alternative to conventional CSTR to achieve efficient methane production from thermal hydrolyzed sludge at short HRTs. <i>Energy</i> , 2018, 159, 588-598.	4.5	32
1757	The decline of the Turtle Dove: Dietary associations with body condition and competition with other columbids analysed using high-throughput sequencing. <i>Molecular Ecology</i> , 2018, 27, 3386-3407.	2.0	32

#	ARTICLE	IF	CITATIONS
1758	Fungal community profiles in agricultural soils of a long-term field trial under different tillage, fertilization and crop rotation conditions analyzed by high-throughput ITS-amplicon sequencing. PLoS ONE, 2018, 13, e0195345.	1.1	82
1759	Alterations in the gut bacterial microbiome in fungal Keratitis patients. PLoS ONE, 2018, 13, e0199640.	1.1	65
1760	The delayed effects of antibiotics in type 2 diabetes, friend or foe?. Journal of Endocrinology, 2018, 238, 137-149.	1.2	15
1761	Resolving the rapid plant radiation of early diverging lineages in the tropical Zingiberales: Pushing the limits of genomic data. Molecular Phylogenetics and Evolution, 2018, 128, 55-68.	1.2	53
1762	Bacterial diversification through geological time. Nature Ecology and Evolution, 2018, 2, 1458-1467.	3.4	81
1763	Microbial responses to inorganic nutrient amendment overridden by warming: Consequences on soil carbon stability. Environmental Microbiology, 2018, 20, 2509-2522.	1.8	12
1764	Community dynamics and functional characteristics of naphthalene-degrading populations in contaminated surface sediments and hypoxic/anoxic groundwater. Environmental Microbiology, 2018, 20, 3543-3559.	1.8	22
1765	Toxic Cyanobacteria in Svalbard: Chemical Diversity of Microcystins Detected Using a Liquid Chromatography Mass Spectrometry Precursor Ion Screening Method. Toxins, 2018, 10, 147.	1.5	31
1766	Bioinformatics for Biomonitoring: Species Detection and Diversity Estimates Across Next-Generation Sequencing Platforms. Advances in Ecological Research, 2018, , 1-32.	1.4	3
1767	Effect of slow-release urea on the composition of ruminal bacteria and fungi communities in yak. Animal Feed Science and Technology, 2018, 244, 18-27.	1.1	20
1768	Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237.	13.7	1,370
1769	Short-chain fatty acids: microbial metabolites that alleviate stress-induced brain-gut axis alterations. Journal of Physiology, 2018, 596, 4923-4944.	1.3	460
1770	Antibiotic-Induced Dysbiosis Predicts Mortality in an Animal Model of Clostridium difficile Infection. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	18
1771	Isolation of microsatellite loci in the African tree species Staudtia kamerunensis (Myristicaceae) using high-throughput sequencing. Molecular Biology Reports, 2018, 45, 1539-1544.	1.0	4
1772	Environmental factors shaping the diversity of bacterial communities that promote rice production. BMC Microbiology, 2018, 18, 51.	1.3	50
1773	A high-fidelity Cas9 mutant delivered as a ribonucleoprotein complex enables efficient gene editing in human hematopoietic stem and progenitor cells. Nature Medicine, 2018, 24, 1216-1224.	15.2	573
1774	Free Dietary Choice and Free-Range Rearing Improve the Product Quality, Gait Score, and Microbial Richness of Chickens. Animals, 2018, 8, 84.	1.0	25
1775	Betaine Improves Intestinal Functions by Enhancing Digestive Enzymes, Ameliorating Intestinal Morphology, and Enriching Intestinal Microbiota in High-salt stressed Rats. Nutrients, 2018, 10, 907.	1.7	45

#	ARTICLE	IF	CITATIONS
1776	Intensified bioleaching of chalcopyrite by communities with enriched ferrous or sulfur oxidizers. <i>Bioresource Technology</i> , 2018, 268, 415-423.	4.8	37
1777	Metagenomic and Metatranscriptomic Analyses of Diverse Watermelon Cultivars Reveal the Role of Fruit Associated Microbiome in Carbohydrate Metabolism and Ripening of Mature Fruits. <i>Frontiers in Plant Science</i> , 2018, 9, 4.	1.7	43
1778	Application of Sodium Silicate Enhances Cucumber Resistance to Fusarium Wilt and Alters Soil Microbial Communities. <i>Frontiers in Plant Science</i> , 2018, 9, 624.	1.7	30
1779	Dramatic evolution of body length due to postembryonic changes in cell size in a newly discovered close relative of <i>Caenorhabditis elegans</i> . <i>Evolution Letters</i> , 2018, 2, 427-441.	1.6	13
1780	UGbS-Flex, a novel bioinformatics pipeline for imputation-free SNP discovery in polyploids without a reference genome: finger millet as a case study. <i>BMC Plant Biology</i> , 2018, 18, 117.	1.6	54
1781	Response of environmental variables and microbial community to sodium percarbonate addition to contaminated sediment. <i>Chemosphere</i> , 2018, 211, 500-509.	4.2	14
1782	Unraveling the characteristics of the microbial community and potential pathogens in the rhizosphere soil of <i>Rehmannia glutinosa</i> with root rot disease. <i>Applied Soil Ecology</i> , 2018, 130, 271-279.	2.1	21
1783	Assessment of Rumen Microbiota from a Large Dairy Cattle Cohort Reveals the Pan and Core Bacteriomes Contributing to Varied Phenotypes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	97
1784	Dynamics and Biodiversity of Bacterial and Yeast Communities during Fermentation of Cocoa Beans. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	66
1785	Tree species mixture inhibits soil organic carbon mineralization accompanied by decreased r-selected bacteria. <i>Plant and Soil</i> , 2018, 431, 203-216.	1.8	24
1786	Novel Insights into Selection for Antibiotic Resistance in Complex Microbial Communities. <i>MBio</i> , 2018, 9, .	1.8	110
1787	Microbiota assemblages of water, sediment, and intestine and their associations with environmental factors and shrimp physiological health. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8585-8598.	1.7	101
1788	<i>Coreopsis tinctoria</i> Modulates Lipid Metabolism by Decreasing Low-Density Lipoprotein and Improving Gut Microbiota. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 1060-1074.	1.1	9
1789	A novel locus on mouse chromosome 7 that influences survival after infection with tick-borne encephalitis virus. <i>BMC Neuroscience</i> , 2018, 19, 39.	0.8	14
1790	Effects of straw return on bacterial communities in a wheat-maize rotation system in the North China Plain. <i>PLoS ONE</i> , 2018, 13, e0198087.	1.1	28
1791	Comparison of Microbiota in Patients Treated by Surgery or Chemotherapy by 16S rRNA Sequencing Reveals Potential Biomarkers for Colorectal Cancer Therapy. <i>Frontiers in Microbiology</i> , 2018, 9, 1607.	1.5	103
1792	Profiling white wine seed vinegar bacterial diversity through viable counting, metagenomic sequencing and PCR-DGGE. <i>International Journal of Food Microbiology</i> , 2018, 286, 66-74.	2.1	16
1793	Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. <i>Scientific Reports</i> , 2018, 8, 11159.	1.6	60

#	ARTICLE	IF	CITATIONS
1794	Fucoidan alleviates dyslipidemia and modulates gut microbiota in high-fat diet-induced mice. <i>Journal of Functional Foods</i> , 2018, 48, 220-227.	1.6	55
1795	Beneficial changes of gut microbiota and metabolism in weaned rats with <i>Lactobacillus acidophilus</i> NCFM and <i>Bifidobacterium lactis</i> Bi-07 supplementation. <i>Journal of Functional Foods</i> , 2018, 48, 252-265.	1.6	28
1796	Succession of bacterioplankton community in intensive shrimp (<i>Litopenaeus vannamei</i>) aquaculture systems. <i>Aquaculture</i> , 2018, 497, 200-213.	1.7	35
1797	Response of host bacterial colonization in shrimp to developmental stage, environment and disease. <i>Molecular Ecology</i> , 2018, 27, 3686-3699.	2.0	82
1798	Contrasting Soil Bacterial Community, Diversity, and Function in Two Forests in China. <i>Frontiers in Microbiology</i> , 2018, 9, 1693.	1.5	72
1799	Chronic Rhinosinusitis: Potential Role of Microbial Dysbiosis and Recommendations for Sampling Sites. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 57.	1.8	75
1800	Ecological Restoration of Antibiotic-Disturbed Gastrointestinal Microbiota in Foregut and Hindgut of Cows. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 79.	1.8	31
1801	The Subgingival Microbiome of Periodontal Pockets With Different Probing Depths in Chronic and Aggressive Periodontitis: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 124.	1.8	73
1802	Association Between Gut Microbiota and <i>Helicobacter pylori</i> -Related Gastric Lesions in a High-Risk Population of Gastric Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 202.	1.8	106
1803	Distinct Nitrogen Provisioning From Organic Amendments in Soil as Influenced by Farming System and Water Regime. <i>Frontiers in Environmental Science</i> , 2018, 6, .	1.5	17
1804	Diversity of Immunoglobulin Light Chain Genes in Non-Teleost Ray-Finned Fish Uncovers IgL Subdivision into Five Ancient Isotypes. <i>Frontiers in Immunology</i> , 2018, 9, 1079.	2.2	5
1805	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018, 9, 31.	1.5	45
1806	Metagenomic Study Suggests That the Gut Microbiota of the Giant Panda (<i>Ailuropoda melanoleuca</i>) May Not Be Specialized for Fiber Fermentation. <i>Frontiers in Microbiology</i> , 2018, 9, 229.	1.5	70
1807	Indigenous <i>Pseudomonas</i> spp. Strains from the Olive (<i>Olea europaea</i> L.) Rhizosphere as Effective Biocontrol Agents against <i>Verticillium dahliae</i> : From the Host Roots to the Bacterial Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 277.	1.5	79
1808	Physiological and Metagenomic Characterizations of the Synergistic Relationships between Ammonia- and Nitrite-Oxidizing Bacteria in Freshwater Nitrification. <i>Frontiers in Microbiology</i> , 2018, 9, 280.	1.5	15
1809	Response of Nitrifier and Denitrifier Abundance and Microbial Community Structure to Experimental Warming in an Agricultural Ecosystem. <i>Frontiers in Microbiology</i> , 2018, 9, 474.	1.5	35
1810	Exploring Biogeochemistry and Microbial Diversity of Extant Microbialites in Mexico and Cuba. <i>Frontiers in Microbiology</i> , 2018, 9, 510.	1.5	29
1811	Gut Microbiome Associates With Lipid-Lowering Effect of Rosuvastatin in Vivo. <i>Frontiers in Microbiology</i> , 2018, 9, 530.	1.5	86

#	ARTICLE	IF	CITATIONS
1812	Inhibitory Effects of Sulfate and Nitrate Reduction on Reductive Dechlorination of PCP in a Flooded Paddy Soil. <i>Frontiers in Microbiology</i> , 2018, 9, 567.	1.5	22
1813	Stair-Step Pattern of Soil Bacterial Diversity Mainly Driven by pH and Vegetation Types Along the Elevational Gradients of Gongga Mountain, China. <i>Frontiers in Microbiology</i> , 2018, 9, 569.	1.5	90
1814	Alfalfa Intervention Alters Rumen Microbial Community Development in Hu Lambs During Early Life. <i>Frontiers in Microbiology</i> , 2018, 9, 574.	1.5	65
1815	Benthic Algal Community Structures and Their Response to Geographic Distance and Environmental Variables in the Qinghai-Tibetan Lakes With Different Salinity. <i>Frontiers in Microbiology</i> , 2018, 9, 578.	1.5	23
1816	Spatiotemporal Distribution and Assemblages of Planktonic Fungi in the Coastal Waters of the Bohai Sea. <i>Frontiers in Microbiology</i> , 2018, 9, 584.	1.5	37
1817	Depth-Resolved Distribution of Particle-Attached and Free-Living Bacterial Communities in the Water Column of the New Britain Trench. <i>Frontiers in Microbiology</i> , 2018, 9, 625.	1.5	52
1818	Partitioning of Fungal Endophyte Assemblages in Root-Parasitic Plant <i>Cynomorium songaricum</i> and Its Host <i>Nitraria tangutorum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 666.	1.5	28
1819	Continuously Monocropped Jerusalem Artichoke Changed Soil Bacterial Community Composition and Ammonia-Oxidizing and Denitrifying Bacteria Abundances. <i>Frontiers in Microbiology</i> , 2018, 9, 705.	1.5	44
1820	Variations of Bacterial Community Diversity Within the Rhizosphere of Three Phylogenetically Related Perennial Shrub Plant Species Across Environmental Gradients. <i>Frontiers in Microbiology</i> , 2018, 9, 709.	1.5	39
1821	Microbiome of Total Versus Live Bacteria in the Gut of Rex Rabbits. <i>Frontiers in Microbiology</i> , 2018, 9, 733.	1.5	30
1822	Comparative Genomics and Mutational Analysis Reveals a Novel XoxF-Utilizing Methylotroph in the Roseobacter Group Isolated From the Marine Environment. <i>Frontiers in Microbiology</i> , 2018, 9, 766.	1.5	13
1823	Agricultural Freshwater Pond Supports Diverse and Dynamic Bacterial and Viral Populations. <i>Frontiers in Microbiology</i> , 2018, 9, 792.	1.5	27
1824	Key Role of Alphaproteobacteria and Cyanobacteria in the Formation of Stromatolites of Lake Dziani Dzaha (Mayotte, Western Indian Ocean). <i>Frontiers in Microbiology</i> , 2018, 9, 796.	1.5	33
1825	Microbial Community Analyses of the Deteriorated Storeroom Objects in the Tianjin Museum Using Culture-Independent and Culture-Dependent Approaches. <i>Frontiers in Microbiology</i> , 2018, 9, 802.	1.5	32
1826	Dietary Deoxynivalenol Contamination and Oral Lipopolysaccharide Challenge Alters the Cecal Microbiota of Broiler Chickens. <i>Frontiers in Microbiology</i> , 2018, 9, 804.	1.5	49
1827	Trichoderma Biofertilizer Links to Altered Soil Chemistry, Altered Microbial Communities, and Improved Grassland Biomass. <i>Frontiers in Microbiology</i> , 2018, 9, 848.	1.5	89
1828	Oral Microbiota Community Dynamics Associated With Oral Squamous Cell Carcinoma Staging. <i>Frontiers in Microbiology</i> , 2018, 9, 862.	1.5	211
1829	Taxon-Function Decoupling as an Adaptive Signature of Lake Microbial Metacommunities Under a Chronic Polymetallic Pollution Gradient. <i>Frontiers in Microbiology</i> , 2018, 9, 869.	1.5	19

#	ARTICLE	IF	CITATIONS
1830	Taxonomic and Functional Responses of Soil Microbial Communities to Annual Removal of Aboveground Plant Biomass. <i>Frontiers in Microbiology</i> , 2018, 9, 954.	1.5	11
1831	Alpha-Ketoglutarate in Low-Protein Diets for Growing Pigs: Effects on Cecal Microbial Communities and Parameters of Microbial Metabolism. <i>Frontiers in Microbiology</i> , 2018, 9, 1057.	1.5	40
1832	Acclimation and Institutionalization of the Mouse Microbiota Following Transportation. <i>Frontiers in Microbiology</i> , 2018, 9, 1085.	1.5	55
1833	Sediment Depth-Dependent Spatial Variations of Bacterial Communities in Mud Deposits of the Eastern China Marginal Seas. <i>Frontiers in Microbiology</i> , 2018, 9, 1128.	1.5	32
1834	Dysbiosis and Ecotypes of the Salivary Microbiome Associated With Inflammatory Bowel Diseases and the Assistance in Diagnosis of Diseases Using Oral Bacterial Profiles. <i>Frontiers in Microbiology</i> , 2018, 9, 1136.	1.5	87
1835	Microbial Interactions With Dissolved Organic Matter Drive Carbon Dynamics and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 1234.	1.5	107
1836	5-Aminosalicylic Acid Alters the Gut Bacterial Microbiota in Patients With Ulcerative Colitis. <i>Frontiers in Microbiology</i> , 2018, 9, 1274.	1.5	113
1837	Diversity of Fungal Communities in Heshang Cave of Central China Revealed by Mycobiome-Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 1400.	1.5	23
1838	Nitrospira Cluster 8a Plays a Predominant Role in the Nitrification Process of a Subtropical Ultisol under Long-Term Inorganic and Organic Fertilization. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	42
1839	Vex-seq: high-throughput identification of the impact of genetic variation on pre-mRNA splicing efficiency. <i>Genome Biology</i> , 2018, 19, 71.	3.8	66
1840	<scp>eDNA</scp> metabarcoding as a new surveillance approach for coastal Arctic biodiversity. <i>Ecology and Evolution</i> , 2018, 8, 7763-7777.	0.8	154
1841	Microbial Community Dynamics and Assembly Follow Trajectories of an Early-Spring Diatom Bloom in a Semienclosed Bay. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	41
1842	Quantitative PCR Analysis of Gut Disease-Discriminatory Phyla for Determining Shrimp Disease Incidence. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	10
1843	Bacillales Members from the Olive Rhizosphere Are Effective Biological Control Agents against the Defoliating Pathotype of <i>Verticillium dahliae</i> . <i>Agriculture (Switzerland)</i> , 2018, 8, 90.	1.4	39
1844	Exposure to Formaldehyde Perturbs the Mouse Gut Microbiome. <i>Genes</i> , 2018, 9, 192.	1.0	11
1845	Ancient DNA from Giant Panda (<i>Ailuropoda melanoleuca</i>) of South-Western China Reveals Genetic Diversity Loss during the Holocene. <i>Genes</i> , 2018, 9, 198.	1.0	14
1846	Probiotic <i>Lactobacillus Paracasei</i> Expressing a Nucleic Acid-Hydrolyzing Minibody (3D8 Scfv) Enhances Probiotic Activities in Mice Intestine as Revealed by Metagenomic Analyses. <i>Genes</i> , 2018, 9, 276.	1.0	10
1847	Disentangling the drivers of functional complexity at the metagenomic level in Shark Bay microbial mat microbiomes. <i>ISME Journal</i> , 2018, 12, 2619-2639.	4.4	94

#	ARTICLE	IF	CITATIONS
1848	Effects of naturally-produced lovastatin on feed digestibility, rumen fermentation, microbiota and methane emissions in goats over a 12-week treatment period. <i>PLoS ONE</i> , 2018, 13, e0199840.	1.1	20
1849	Spatial distribution of microbial community composition along a steep slope plot of the Loess Plateau. <i>Applied Soil Ecology</i> , 2018, 130, 226-236.	2.1	22
1850	Soil aggregate size mediates the responses of microbial communities to crop rotation. <i>European Journal of Soil Biology</i> , 2018, 88, 48-56.	1.4	25
1851	Responses of fungal and bacterial community and network to organic inputs vary among different spatial habitats in soil. <i>Soil Biology and Biochemistry</i> , 2018, 125, 54-63.	4.2	142
1852	Development of outbred CD1 mouse colonies with distinct standardized gut microbiota profiles for use in complex microbiota targeted studies. <i>Scientific Reports</i> , 2018, 8, 10107.	1.6	30
1853	Optimized knock-in of point mutations in zebrafish using CRISPR/Cas9. <i>Nucleic Acids Research</i> , 2018, 46, e102-e102.	6.5	50
1854	Targeted resequencing of coding DNA sequences for SNP discovery in nonmodel species. <i>Molecular Ecology Resources</i> , 2018, 18, 1356-1373.	2.2	19
1855	toaSTR: A web application for forensic STR genotyping by massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2018, 37, 21-28.	1.6	19
1856	Seasonal changes in the diversity and composition of the litter fauna in native forests and rubber plantations. <i>Scientific Reports</i> , 2018, 8, 10232.	1.6	7
1857	Siglec-6 on Chronic Lymphocytic Leukemia Cells Is a Target for Post-Allogeneic Hematopoietic Stem Cell Transplantation Antibodies. <i>Cancer Immunology Research</i> , 2018, 6, 1008-1013.	1.6	10
1858	Effects of cover crop in an apple orchard on microbial community composition, networks, and potential genes involved with degradation of crop residues in soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 743-759.	2.3	85
1859	Bioturbation by the razor clam (<i>Sinonovacula constricta</i>) on the microbial community and enzymatic activities in the sediment of an ecological aquaculture wastewater treatment system. <i>Science of the Total Environment</i> , 2018, 643, 1098-1107.	3.9	57
1860	Disentangling the complexity of permafrost soil by using high resolution profiling of microbial community composition, key functions and respiration rates. <i>Environmental Microbiology</i> , 2018, 20, 4328-4342.	1.8	37
1861	Dietary Supplementation with a Magnesium-Rich Marine Mineral Blend Enhances the Diversity of Gastrointestinal Microbiota. <i>Marine Drugs</i> , 2018, 16, 216.	2.2	41
1862	Monitoring of the Apple Fruit Moth: Detection of Genetic Variation and Structure Applying a Novel Multiplex Set of 19 STR Markers. <i>Molecules</i> , 2018, 23, 850.	1.7	3
1863	High-Glucose or -Fructose Diet Cause Changes of the Gut Microbiota and Metabolic Disorders in Mice without Body Weight Change. <i>Nutrients</i> , 2018, 10, 761.	1.7	310
1864	Combined Use of <i>C. butyricum</i> Sx-01 and <i>L. salivarius</i> C-1-3 Improves Intestinal Health and Reduces the Amount of Lipids in Serum via Modulation of Gut Microbiota in Mice. <i>Nutrients</i> , 2018, 10, 810.	1.7	32
1865	Root exudate metabolites drive plant-soil feedbacks on growth and defense by shaping the rhizosphere microbiota. <i>Nature Communications</i> , 2018, 9, 2738.	5.8	861

#	ARTICLE	IF	CITATIONS
1866	The cecal microbiome of commercial broiler chickens varies significantly by season. <i>Poultry Science</i> , 2018, 97, 3635-3644.	1.5	26
1867	Hydrothermal chimneys host habitat-specific microbial communities: analogues for studying the possible impact of mining seafloor massive sulfide deposits. <i>Scientific Reports</i> , 2018, 8, 10386.	1.6	30
1868	Bio-cord plays a similar role as submerged macrophytes in harboring bacterial assemblages in an eco-ditch. <i>Environmental Science and Pollution Research</i> , 2018, 25, 26550-26561.	2.7	10
1869	Metabolic Biosynthesis Pathways Identified from Fecal Microbiome Associated with Prostate Cancer. <i>European Urology</i> , 2018, 74, 575-582.	0.9	117
1870	Response of antibiotic and heavy metal resistance genes to two different temperature sequences in anaerobic digestion of waste activated sludge. <i>Bioresource Technology</i> , 2018, 267, 303-310.	4.8	45
1871	Anti-CRISPR Phages Cooperate to Overcome CRISPR-Cas Immunity. <i>Cell</i> , 2018, 174, 908-916.e12.	13.5	179
1872	Dietary values of macroalgae <i>Porphyra haitanensis</i> in <i>Litopenaeus vannamei</i> under normal rearing and WSSV challenge conditions: Effect on growth, immune response and intestinal microbiota. <i>Fish and Shellfish Immunology</i> , 2018, 81, 135-149.	1.6	35
1873	Microbial community response to growing season and plant nutrient optimisation in a boreal Norway spruce forest. <i>Soil Biology and Biochemistry</i> , 2018, 125, 197-209.	4.2	64
1874	Exon-Capture-Based Phylogeny and Diversification of the Venomous Gastropods (Neogastropoda). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	3.5	46
1875	Thermal processing of food reduces gut microbiota diversity of the host and triggers adaptation of the microbiota: evidence from two vertebrates. <i>Microbiome</i> , 2018, 6, 99.	4.9	42
1876	Huddling remodels gut microbiota to reduce energy requirements in a small mammal species during cold exposure. <i>Microbiome</i> , 2018, 6, 103.	4.9	90
1877	Prevalence and Epidemiologic Profile of Oral Infection with Alpha, Beta, and Gamma Papillomaviruses in an Asian Chinese Population. <i>Journal of Infectious Diseases</i> , 2018, 218, 388-397.	1.9	43
1878	Saturated long-chain fatty acid-producing bacteria contribute to enhanced colonic motility in rats. <i>Microbiome</i> , 2018, 6, 107.	4.9	92
1879	Genomic analysis of MHC-based mate choice in the monogamous California mouse. <i>Behavioral Ecology</i> , 2018, 29, 1167-1180.	1.0	9
1880	Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. <i>Biotechnology for Biofuels</i> , 2018, 11, 200.	6.2	99
1881	Resource Availability Drives Responses of Soil Microbial Communities to Short-term Precipitation and Nitrogen Addition in a Desert Shrubland. <i>Frontiers in Microbiology</i> , 2018, 9, 186.	1.5	82
1882	The nasopharyngeal microbiota in patients with viral respiratory tract infections is enriched in bacterial pathogens. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 1725-1733.	1.3	78
1883	A microorganismsâ€™ journey between plant generations. <i>Microbiome</i> , 2018, 6, 79.	4.9	75

#	ARTICLE	IF	CITATIONS
1884	High-Fat Diet Consumption Induces Microbiota Dysbiosis and Intestinal Inflammation in Zebrafish. <i>Microbial Ecology</i> , 2018, 76, 1089-1101.	1.4	68
1885	Microbiota dynamics and volatilome profile during stink bean fermentation (Sataw-Dong) with <i>Lactobacillus plantarum</i> KJ03 as a starter culture. <i>Food Microbiology</i> , 2018, 76, 91-102.	2.1	28
1886	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. <i>Journal of General and Applied Microbiology</i> , 2018, 64, 158-166.	0.4	18
1887	<i>Plasmodium falciparum</i> genetic variation of var2csa in the Democratic Republic of the Congo. <i>Malaria Journal</i> , 2018, 17, 46.	0.8	13
1888	Host contributes to longitudinal diversity of fecal microbiota in swine selected for lean growth. <i>Microbiome</i> , 2018, 6, 4.	4.9	90
1889	Crawling-induced floor dust resuspension affects the microbiota of the infant breathing zone. <i>Microbiome</i> , 2018, 6, 25.	4.9	40
1890	Filter forensics: microbiota recovery from residential HVAC filters. <i>Microbiome</i> , 2018, 6, 22.	4.9	35
1891	A reservoir of "historical" antibiotic resistance genes in remote pristine Antarctic soils. <i>Microbiome</i> , 2018, 6, 40.	4.9	244
1892	DNA-SIP Reveals the Diversity of Chemolithoautotrophic Bacteria Inhabiting Three Different Soil Types in Typical Karst Rocky Desertification Ecosystems in Southwest China. <i>Microbial Ecology</i> , 2018, 76, 976-990.	1.4	16
1893	Disruption of bacterial balance in the gut of <i>Portunus trituberculatus</i> induced by <i>Vibrio alginolyticus</i> infection. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1891-1898.	0.6	8
1894	Exploring abundance, diversity and variation of a widespread antibiotic resistance gene in wastewater treatment plants. <i>Environment International</i> , 2018, 117, 186-195.	4.8	40
1895	Analyses of microbial community of naturally homemade soybean pastes in Liaoning Province of China by Illumina Miseq Sequencing. <i>Food Research International</i> , 2018, 111, 50-57.	2.9	45
1896	Different rearing conditions alter gut microbiota composition and host physiology in Shaoxing ducks. <i>Scientific Reports</i> , 2018, 8, 7387.	1.6	38
1897	Enhanced and Complete Removal of Phenylurea Herbicides by Combinational Transgenic Plant-Microbe Remediation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	22
1898	Unrevealing variation of microbial communities and correlation with environmental variables in a full culture-cycle of <i>Undaria pinnatifida</i> . <i>Marine Environmental Research</i> , 2018, 139, 46-56.	1.1	26
1899	Predatory flying squids are detritivores during their early planktonic life. <i>Scientific Reports</i> , 2018, 8, 3440.	1.6	26
1900	Mapping distribution of cysts of recent dinoflagellate and <i>Cochlodinium polykrikoides</i> using next-generation sequencing and morphological approaches in South Sea, Korea. <i>Scientific Reports</i> , 2018, 8, 7011.	1.6	17
1901	Microbial community analysis and biodeterioration of waterlogged archaeological wood from the Nanhai No. 1 shipwreck during storage. <i>Scientific Reports</i> , 2018, 8, 7170.	1.6	30

#	ARTICLE	IF	CITATIONS
1902	Microbial diversity and ecotoxicity of sediments 3 years after the Jiaozhou Bay oil spill. <i>AMB Express</i> , 2018, 8, 79.	1.4	19
1903	Multilevel social structure and diet shape the gut microbiota of the gelada monkey, the only grazing primate. <i>Microbiome</i> , 2018, 6, 84.	4.9	56
1904	Intestinal microbiota in growing pigs: effects of stocking density. <i>Food and Agricultural Immunology</i> , 2018, 29, 524-535.	0.7	2
1905	Progressive biogeochemical transformation of placer gold particles drives compositional changes in associated biofilm communities. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
1906	Gut microbiota profiling in Han Chinese with type 1 diabetes. <i>Diabetes Research and Clinical Practice</i> , 2018, 141, 256-263.	1.1	68
1907	Changes in the gut microbiota composition during pregnancy in patients with gestational diabetes mellitus (GDM). <i>Scientific Reports</i> , 2018, 8, 12216.	1.6	162
1908	The Microbial Composition of Bacteroidetes Species in Ulcerative Colitis Is Effectively Improved by Combination Therapy With Fecal Microbiota Transplantation and Antibiotics. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 2590-2598.	0.9	27
1909	Bacterial biogeography of adult airways in atopic asthma. <i>Microbiome</i> , 2018, 6, 104.	4.9	93
1910	Gut Microbiota in Tibetan Herdsmen Reflects the Degree of Urbanization. <i>Frontiers in Microbiology</i> , 2018, 9, 1745.	1.5	33
1911	2,3,5,4'-tetrahydroxy-stilbene-O- β -D-glucoside attenuates methionine and choline-deficient diet-induced non-alcoholic fatty liver disease. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1087-1094.	0.8	9
1912	Dietary l-arginine Supplementation Alleviates the Intestinal Injury and Modulates the Gut Microbiota in Broiler Chickens Challenged by <i>Clostridium perfringens</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1716.	1.5	64
1913	Responses of soil N-fixing bacterial communities to redroot pigweed (<i>Amaranthus retroflexus</i> L.) invasion under Cu and Cd heavy metal soil pollution. <i>Agriculture, Ecosystems and Environment</i> , 2018, 267, 15-22.	2.5	25
1914	Concentration and Community of Airborne Bacteria in Response to Cyclical Haze Events During the Fall and Midwinter in Beijing, China. <i>Frontiers in Microbiology</i> , 2018, 9, 1741.	1.5	35
1915	Effect of Sugarcane Straw and Goat Manure on Soil Nutrient Transformation and Bacterial Communities. <i>Sustainability</i> , 2018, 10, 2361.	1.6	35
1916	Diversity of Bacterial Communities in the Intestinal Tracts of Two Geographically Distant Populations of <i>Bactrocera dorsalis</i> (Diptera: Tephritidae). <i>Journal of Economic Entomology</i> , 2018, 111, 2861-2868.	0.8	20
1917	Gut microbiota alterations in moderate to severe acne vulgaris patients. <i>Journal of Dermatology</i> , 2018, 45, 1166-1171.	0.6	59
1918	Broad Phylogenetic Diversity Associated with Nitrogen Loss through Sulfur Oxidation in a Large Public Marine Aquarium. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	7
1919	Sanger and Next Generation Sequencing Approaches to Evaluate HIV-1 Virus in Blood Compartments. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 1697.	1.2	35

#	ARTICLE	IF	CITATIONS
1920	Sequence analysis of European maize inbred line F2 provides new insights into molecular and chromosomal characteristics of presence/absence variants. <i>BMC Genomics</i> , 2018, 19, 119.	1.2	27
1921	Gut microbiota composition and butyrate production in children affected by non-IgE-mediated cow's milk allergy. <i>Scientific Reports</i> , 2018, 8, 12500.	1.6	80
1922	Study of Microbiomes in Aseptically Collected Samples of Human Breast Tissue Using Needle Biopsy and the Potential Role of in situ Tissue Microbiomes for Promoting Malignancy. <i>Frontiers in Oncology</i> , 2018, 8, 318.	1.3	102
1923	Gene expression profiling reveals deep-sea coral response to the Deepwater Horizon oil spill. <i>Molecular Ecology</i> , 2018, 27, 4066-4077.	2.0	24
1924	Sulfated polysaccharide from sea cucumber modulates the gut microbiota and its metabolites in normal mice. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 502-512.	3.6	57
1925	Biogenic amines analysis and microbial contribution in traditional fermented food of Douchi. <i>Scientific Reports</i> , 2018, 8, 12567.	1.6	29
1926	Dynamics of compost microbiota during the cultivation of <i>Agaricus bisporus</i> in the presence of <i>Bacillus velezensis</i> QST713 as biocontrol agent against <i>Trichoderma aggressivum</i> . <i>Biological Control</i> , 2018, 127, 39-54.	1.4	18
1927	Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818.	8.1	208
1928	Oceanographic boundaries constrain microbial diversity gradients in the South Pacific Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8266-E8275.	3.3	96
1929	Cecal microbiome profile altered by <i>Salmonella enterica</i> , serovar Enteritidis inoculation in chicken. <i>Gut Pathogens</i> , 2018, 10, 34.	1.6	56
1930	Impacts of n-alkane concentration on soil bacterial community structure and alkane monooxygenase genes abundance during bioremediation processes. <i>Frontiers of Environmental Science and Engineering</i> , 2018, 12, 1.	3.3	18
1931	Protective effects of <i>Paederia scandens</i> extract on rheumatoid arthritis mouse model by modulating gut microbiota. <i>Journal of Ethnopharmacology</i> , 2018, 226, 97-104.	2.0	35
1932	Influence of Temperature on the Bacterial Community in Substrate and Extracellular Enzyme Activity of <i>Auricularia cornea</i> . <i>Mycobiology</i> , 2018, 46, 224-235.	0.6	7
1933	Plant host habitat and root exudates shape fungal diversity. <i>Mycorrhiza</i> , 2018, 28, 451-463.	1.3	63
1934	Yellow Canopy Syndrome in sugarcane is associated with shifts in the rhizosphere soil metagenome but not with overall soil microbial function. <i>Soil Biology and Biochemistry</i> , 2018, 125, 275-285.	4.2	9
1935	Analysis of sequencing strategies and tools for taxonomic annotation: Defining standards for progressive metagenomics. <i>Scientific Reports</i> , 2018, 8, 12034.	1.6	93
1936	Snake fungal disease alters skin bacterial and fungal diversity in an endangered rattlesnake. <i>Scientific Reports</i> , 2018, 8, 12147.	1.6	35
1937	Comparison of Fecal Collection Methods for Microbiome and Metabolomics Studies. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 301.	1.8	114

#	ARTICLE	IF	CITATIONS
1938	Microbial Biogeography Along the Gastrointestinal Tract of a Red Panda. <i>Frontiers in Microbiology</i> , 2018, 9, 1411.	1.5	26
1939	Rhizosphere Bacterial Communities Differ According to Fertilizer Regimes and Cabbage (Brassica) Tj ETQq1 1 0.784314 rgBT /Overloc 1620.	1.5	38
1940	Linking microbial co-occurrences to soil ecological processes across a woodland-grassland ecotone. <i>Ecology and Evolution</i> , 2018, 8, 8217-8230.	0.8	38
1941	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1635.	1.5	51
1942	Profiling of the TCR β repertoire in non-model species using high-throughput sequencing. <i>Scientific Reports</i> , 2018, 8, 11613.	1.6	13
1943	Bacterial diversity among the fruit bodies of ectomycorrhizal and saprophytic fungi and their corresponding hyphosphere soils. <i>Scientific Reports</i> , 2018, 8, 11672.	1.6	27
1944	Manure amendment reduced plant uptake and enhanced rhizodegradation of 2,2,4,4-tetrabrominated diphenyl ether in soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 807-817.	2.3	15
1945	Volatile Oil of <i>Amomum villosum</i> Inhibits Nonalcoholic Fatty Liver Disease via the Gut-Liver Axis. <i>BioMed Research International</i> , 2018, 2018, 1-16.	0.9	27
1946	Comparison between complete genomes of an isolate of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> from Japan and a New Zealand isolate of the pandemic lineage. <i>Scientific Reports</i> , 2018, 8, 10915.	1.6	23
1947	Improved sgRNA design in bacteria via genome-wide activity profiling. <i>Nucleic Acids Research</i> , 2018, 46, 7052-7069.	6.5	73
1948	The effect of several activated biochars on Cd immobilization and microbial community composition during in-situ remediation of heavy metal contaminated sediment. <i>Chemosphere</i> , 2018, 208, 655-664.	4.2	113
1949	Functional Relevance of Improbable Antibody Mutations for HIV Broadly Neutralizing Antibody Development. <i>Cell Host and Microbe</i> , 2018, 23, 759-765.e6.	5.1	98
1950	Intermittent Fasting Confers Protection in CNS Autoimmunity by Altering the Gut Microbiota. <i>Cell Metabolism</i> , 2018, 27, 1222-1235.e6.	7.2	352
1951	Analysis of gut microbiota revealed <i>Lactococcus garviaeae</i> could be an indicative of skin ulceration syndrome in farmed sea cucumber <i>Apostichopus japonicus</i> . <i>Fish and Shellfish Immunology</i> , 2018, 80, 148-154.	1.6	33
1952	Temporal dynamics of microbiota before and after host death. <i>ISME Journal</i> , 2018, 12, 2076-2085.	4.4	21
1953	Seasonal dynamics of the bacterioplankton community in a large, shallow, highly dynamic freshwater lake. <i>Canadian Journal of Microbiology</i> , 2018, 64, 786-797.	0.8	10
1954	<i>Eimeria tenella</i> infection perturbs the chicken gut microbiota from the onset of oocyst shedding. <i>Veterinary Parasitology</i> , 2018, 258, 30-37.	0.7	45
1955	Insights into the bacterial symbiont diversity in spiders. <i>Ecology and Evolution</i> , 2018, 8, 4899-4906.	0.8	46

#	ARTICLE	IF	CITATIONS
1956	Season, age, and sex affect the fecal mycobiota of free-ranging Tibetan macaques (<i>Macaca</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 7	0.8	24
1957	Analyzing High-Throughput Microbial Amplicon Sequence Data Using Multiple Markers. , 2018, , 121-138.		2
1958	Integrated interrogation of causes of membrane fouling in a pilot-scale anoxic-oxic membrane bioreactor treating oil refinery wastewater. <i>Science of the Total Environment</i> , 2018, 642, 77-89.	3.9	21
1959	Effects of a homogeneous polysaccharide from Sijunzi decoction on human intestinal microbes and short chain fatty acids in vitro. <i>Journal of Ethnopharmacology</i> , 2018, 224, 465-473.	2.0	69
1960	Removal of benzene, toluene, xylene and styrene by biotrickling filters and identification of their interactions. <i>PLoS ONE</i> , 2018, 13, e0189927.	1.1	30
1961	Does the biological treatment or membrane separation reduce the antibiotic resistance genes from swine wastewater through a sequencing-batch membrane bioreactor treatment process. <i>Environment International</i> , 2018, 118, 274-281.	4.8	39
1962	<i>Marteilia refringens</i> and <i>Marteilia pararefringens</i> sp. nov. are distinct parasites of bivalves and have different European distributions. <i>Parasitology</i> , 2018, 145, 1483-1492.	0.7	16
1963	16S rRNA analysis of diversity of manure microbial community in dairy farm environment. <i>PLoS ONE</i> , 2018, 13, e0190126.	1.1	47
1964	The biogeochemical vertical structure renders a meromictic volcanic lake a trap for geogenic CO ₂ (Lake Averno, Italy). <i>PLoS ONE</i> , 2018, 13, e0193914.	1.1	16
1965	Microbial community analysis in biologically active filters exhibiting efficient removal of emerging contaminants and impact of operational conditions. <i>Science of the Total Environment</i> , 2018, 640-641, 1455-1464.	3.9	23
1966	Biogeographic patterns of abundant and rare bacterioplankton in three subtropical bays resulting from selective and neutral processes. <i>ISME Journal</i> , 2018, 12, 2198-2210.	4.4	269
1967	Microbial communities and natural fermentation of corn silages prepared with farm bunker-silo in Southwest China. <i>Bioresource Technology</i> , 2018, 265, 282-290.	4.8	180
1968	Individuality and convergence of the infant gut microbiota during the first year of life. <i>Nature Communications</i> , 2018, 9, 2233.	5.8	85
1969	Effect of different types of olive oil pomace dietary supplementation on the rumen microbial community profile in Comisana ewes. <i>Scientific Reports</i> , 2018, 8, 8455.	1.6	46
1970	Putative Role of Flavobacterium, Dokdonella and Methylophilus Strains in Paracetamol Biodegradation. <i>Water, Air, and Soil Pollution</i> , 2018, 229, 1.	1.1	39
1971	HIV-1 Protease Evolvability Is Affected by Synonymous Nucleotide Recoding. <i>Journal of Virology</i> , 2018, 92, .	1.5	9
1972	Microbiome and butyrate production are altered in the gut of rats fed a glycated fish protein diet. <i>Journal of Functional Foods</i> , 2018, 47, 423-433.	1.6	56
1973	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. <i>Science</i> , 2018, 360, 1355-1358.	6.0	234

#	ARTICLE	IF	CITATIONS
1974	Dysbiosis in the Gut Bacterial Microbiome of Patients with Uveitis, an Inflammatory Disease of the Eye. <i>Indian Journal of Microbiology</i> , 2018, 58, 457-469.	1.5	118
1975	Distinct patterns and processes of abundant and rare eukaryotic plankton communities following a reservoir cyanobacterial bloom. <i>ISME Journal</i> , 2018, 12, 2263-2277.	4.4	412
1976	How does marker choice affect your diet analysis: comparing genetic markers and digestion levels for diet metabarcoding of tropical-reef piscivores. <i>Marine and Freshwater Research</i> , 2019, 70, 8.	0.7	27
1977	Modulation of intestinal microbiota and immunometabolic parameters by caloric restriction and lactic acid bacteria. <i>Food Research International</i> , 2019, 124, 188-199.	2.9	16
1978	Rhizosphere microbiota assemblage associated with wild and cultivated soybeans grown in three types of soil suspensions. <i>Archives of Agronomy and Soil Science</i> , 2019, 65, 74-87.	1.3	28
1979	Harnessing microfluidic streak plate technique to investigate the gut microbiome of <i>Reticulitermes chinensis</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00654.	1.2	16
1980	Temporal and long-term gut microbiota variation in allergic disease: A prospective study from infancy to school age. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 176-185.	2.7	67
1981	Insights into Endophytic Bacterial Community Structures of Seeds Among Various <i>Oryza sativa</i> L. Rice Genotypes. <i>Journal of Plant Growth Regulation</i> , 2019, 38, 93-102.	2.8	44
1982	High-throughput characterization of antibiotic resistome in soil amended with commercial organic fertilizers. <i>Journal of Soils and Sediments</i> , 2019, 19, 641-651.	1.5	11
1983	The Impact of Anthropogenic Disturbance on Bacterioplankton Communities During the Construction of Donghu Tunnel (Wuhan, China). <i>Microbial Ecology</i> , 2019, 77, 277-287.	1.4	17
1984	Magnesium lithospermate B improves the gut microbiome and bile acid metabolic profiles in a mouse model of diabetic nephropathy. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 507-513.	2.8	33
1985	A diet rich in C3 plants reveals the sensitivity of an alpine mammal to climate change. <i>Molecular Ecology</i> , 2019, 28, 250-265.	2.0	31
1986	Anaerobic ammonium oxidation coupled to iron reduction in constructed wetland mesocosms. <i>Science of the Total Environment</i> , 2019, 648, 984-992.	3.9	66
1987	Characterization of the bacterial community of braised chicken, a specialty poultry product in China. <i>Poultry Science</i> , 2019, 98, 1055-1063.	1.5	13
1988	Simulated Marine Heat Wave Alters Abundance and Structure of <i>Vibrio</i> Populations Associated with the Pacific Oyster Resulting in a Mass Mortality Event. <i>Microbial Ecology</i> , 2019, 77, 736-747.	1.4	116
1989	Profiling the Gut Microbiome: Practice and Potential. , 2019, , 200-217.		0
1990	The oral microbiome in oral lichen planus during a 1-year randomized clinical trial. <i>Oral Diseases</i> , 2019, 25, 327-338.	1.5	15
1991	Bacterial community and quality characteristics of the fermented potherb mustard (<i>Brassica juncea</i>) Tj ETQq1 1 0.784314 rgBT /Over 15	2.9	15

#	ARTICLE	IF	CITATIONS
1992	Bacterial Diversity in Replicated Hydrogen Sulfide-Rich Streams. <i>Microbial Ecology</i> , 2019, 77, 559-573.	1.4	12
1993	High Doses of Copper and Mercury Changed Cecal Microbiota in Female Mice. <i>Biological Trace Element Research</i> , 2019, 189, 134-144.	1.9	47
1994	Increasing aridity affects soil archaeal communities by mediating soil niches in semi-arid regions. <i>Science of the Total Environment</i> , 2019, 647, 699-707.	3.9	29
1995	Bacterial communities in natural versus pesticide-treated <i>Aphis gossypii</i> populations in North China. <i>MicrobiologyOpen</i> , 2019, 8, e00652.	1.2	17
1996	Gravel mulching effects on soil physicochemical properties and microbial community composition in the Loess Plateau, northwestern China. <i>European Journal of Soil Biology</i> , 2019, 94, 103115.	1.4	13
1997	Compositional shifts in the fungal diversity of garlic scapes during postharvest transportation and cold storage. <i>LWT - Food Science and Technology</i> , 2019, 115, 108453.	2.5	12
1998	Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019, 3, 1298-1308.	3.4	34
1999	Gut microbiota alterations associated with reduced bone mineral density in older adults. <i>Rheumatology</i> , 2019, 58, 2295-2304.	0.9	106
2000	Environmental filtering increases with elevation for the assembly of gut microbiota in wild pikas. <i>Microbial Biotechnology</i> , 2019, 12, 976-992.	2.0	55
2001	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal <i>Salmonella enterica</i> Serovars by Using Machine Learning. <i>MSystems</i> , 2019, 4, .	1.7	21
2002	Supplemental Plant Extracts From <i>Flos Ionicerae</i> in Combination With Baikal skullcap Attenuate Intestinal Disruption and Modulate Gut Microbiota in Laying Hens Challenged by <i>Salmonella pullorum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1681.	1.5	50
2003	Effect of dietary xylan on immune response, tight junction protein expression and bacterial community in the intestine of juvenile turbot (<i>Scophthalmus maximus</i> L.). <i>Aquaculture</i> , 2019, 512, 734361.	1.7	24
2004	Bovine mastitis is a polymicrobial disease requiring a polydiagnostic approach. <i>International Dairy Journal</i> , 2019, 99, 104539.	1.5	11
2005	Mechanistic Understanding of Predatory Bacteria-Induced Biolysis for Waste Sludge Dewaterability Improvement. <i>Water, Air, and Soil Pollution</i> , 2019, 230, 1.	1.1	10
2006	Reduced genetic potential for butyrate fermentation in the gut microbiome of infants who develop allergic sensitization. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1638-1647.e3.	1.5	95
2007	Application of organic fertilizer improves microbial community diversity and alters microbial network structure in tea (<i>Camellia sinensis</i>) plantation soils. <i>Soil and Tillage Research</i> , 2019, 195, 104356.	2.6	117
2008	Microbiota of newborn calves and their mothers reveals possible transfer routes for newborn calves' gastrointestinal microbiota. <i>PLoS ONE</i> , 2019, 14, e0220554.	1.1	61
2009	Impacts of uORF codon identity and position on translation regulation. <i>Nucleic Acids Research</i> , 2019, 47, 9358-9367.	6.5	46

#	ARTICLE	IF	CITATIONS
2010	rpoB, a promising marker for analyzing the diversity of bacterial communities by amplicon sequencing. BMC Microbiology, 2019, 19, 171.	1.3	71
2011	Changes of porcine gut microbiota in response to dietary chlorogenic acid supplementation. Applied Microbiology and Biotechnology, 2019, 103, 8157-8168.	1.7	47
2012	Dominant plant species influence nematode richness by moderating understory diversity and microbial assemblages. Soil Biology and Biochemistry, 2019, 137, 107566.	4.2	30
2013	Dynamics of Vaginal and Rectal Microbiota Over Several Menstrual Cycles in Female Cynomolgus Macaques. Frontiers in Cellular and Infection Microbiology, 2019, 9, 188.	1.8	24
2014	Feedback of airborne bacterial consortia to haze pollution with different PM2.5 levels in typical mountainous terrain of Jinan, China. Science of the Total Environment, 2019, 695, 133912.	3.9	17
2015	Development of omics-based protocols for the microbiological characterization of multi-strain formulations marketed as probiotics: the case of VSL#3. Microbial Biotechnology, 2019, 12, 1371-1386.	2.0	30
2016	Arbuscular mycorrhizal fungi shape the adaptive strategy of plants by mediating nutrient acquisition in a shrub-dominated community in the Mu Us Desert. Plant and Soil, 2019, 443, 549-564.	1.8	15
2017	Response of gut microbiota in type 2 diabetes to hypoglycemic agents. Endocrine, 2019, 66, 485-493.	1.1	59
2018	<i>Lactobacillus acidophilus</i> alleviates type 2 diabetes by regulating hepatic glucose, lipid metabolism and gut microbiota in mice. Food and Function, 2019, 10, 5804-5815.	2.1	139
2019	Evidence of Spatial Homogeneity in an Electromethanogenic Cathodic Microbial Community. Frontiers in Microbiology, 2019, 10, 1747.	1.5	19
2020	Biochar application on paddy and purple soils in southern China: soil carbon and biotic activity. Royal Society Open Science, 2019, 6, 181499.	1.1	21
2021	Diluted conventional media improve the microbial cultivability from aquarium seawater. Journal of Microbiology, 2019, 57, 759-768.	1.3	7
2022	Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes. Cell, 2019, 178, 795-806.e12.	13.5	830
2023	Comparative analysis of the gut microbial communities between two dominant amphipods from the Challenger Deep, Mariana Trench. Deep-Sea Research Part I: Oceanographic Research Papers, 2019, 151, 103081.	0.6	16
2024	Phylogenetic reconciliation reveals the natural history of glycopeptide antibiotic biosynthesis and resistance. Nature Microbiology, 2019, 4, 1862-1871.	5.9	67
2025	Comparative Analyses of Fecal Microbiota in European Mouflon (<i>Ovis orientalis musimon</i>) and Blue Sheep (<i>Pseudois nayaur</i>) Living at Low or High Altitudes. Frontiers in Microbiology, 2019, 10, 1735.	1.5	27
2026	Biogeographical patterns in soil bacterial communities across the Arctic region. FEMS Microbiology Ecology, 2019, 95, .	1.3	53
2027	Contemporary Demographic Reconstruction Methods Are Robust to Genome Assembly Quality: A Case Study in Tasmanian Devils. Molecular Biology and Evolution, 2019, 36, 2906-2921.	3.5	84

#	ARTICLE	IF	CITATIONS
2028	Bacterial community and composition in Jiang-shui and Suan-cai revealed by high-throughput sequencing of 16S rRNA. <i>International Journal of Food Microbiology</i> , 2019, 306, 108271.	2.1	61
2029	Large dataset enables prediction of repair after CRISPR-Cas9 editing in primary T cells. <i>Nature Biotechnology</i> , 2019, 37, 1034-1037.	9.4	87
2030	Following legume establishment, microbial and chemical associations facilitate improved productivity in degraded grasslands. <i>Plant and Soil</i> , 2019, 443, 273-292.	1.8	14
2031	Functional Differences in the Blooming Phytoplankton <i>Heterosigma akashiwo</i> and <i>Prorocentrum donghaiense</i> Revealed by Comparative Metaproteomics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	19
2032	Natural Farming Improves Soil Quality and Alters Microbial Diversity in a Cabbage Field in Japan. <i>Sustainability</i> , 2019, 11, 3131.	1.6	26
2033	Taking insight into the gut microbiota of three spider species: No characteristic symbiont was found corresponding to the special feeding style of spiders. <i>Ecology and Evolution</i> , 2019, 9, 8146-8156.	0.8	19
2034	Genetic Characterization and Enhanced Surveillance of Ceftriaxone-Resistant <i>Neisseria gonorrhoeae</i> Strain, Alberta, Canada, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 1660-1667.	2.0	24
2035	Long-Term Monoculture Negatively Regulates Fungal Community Composition and Abundance of Tea Orchards. <i>Agronomy</i> , 2019, 9, 466.	1.3	43
2036	Phylogeny of <i>Paullinia</i> L. (Paullinieae: Sapindaceae), a diverse genus of lianas with dynamic fruit evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106577.	1.2	15
2037	Impact of Antibiotic Gut Exposure on the Temporal Changes in Microbiome Diversity. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	35
2038	Altered diversity and composition of the gut microbiome in patients with cervical cancer. <i>AMB Express</i> , 2019, 9, 40.	1.4	55
2039	Changes in cecal microbiota community of suckling piglets infected with porcine epidemic diarrhea virus. <i>PLoS ONE</i> , 2019, 14, e0219868.	1.1	26
2040	Molecular characterization of alterations in the intestinal microbiota of patients with grade 3 hypertension. <i>International Journal of Molecular Medicine</i> , 2019, 44, 513-522.	1.8	30
2041	Effects of different concentrations and types of Cu and Pb on soil N-fixing bacterial communities in the wheat rhizosphere. <i>Applied Soil Ecology</i> , 2019, 144, 51-59.	2.1	29
2042	Stick or leave – Pushing methanogens to biofilm formation for ex situ biomethanation. <i>Bioresource Technology</i> , 2019, 291, 121784.	4.8	33
2043	Cyanobacterial bloom mitigation by sanguinarine and its effects on aquatic microbial community structure. <i>Environmental Pollution</i> , 2019, 253, 497-506.	3.7	13
2044	More than the eye can see: Genomic insights into the drivers of genetic differentiation in Royal/Macaroni penguins across the Southern Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106563.	1.2	21
2045	Crypt- and Mucosa-Associated Core Microbiotas in Humans and Their Alteration in Colon Cancer Patients. <i>MBio</i> , 2019, 10, .	1.8	94

#	ARTICLE	IF	CITATIONS
2046	Soil microbiome mediated nutrients decline during forest degradation process. <i>Soil Ecology Letters</i> , 2019, 1, 59-71.	2.4	29
2047	Novel production of natural bacteriocin via internalization of dextran nanoparticles into probiotics. <i>Biomaterials</i> , 2019, 218, 119360.	5.7	23
2048	Zooming in on Butyrate-Producing Clostridial Consortia in the Fermented Grains of Baijiu via Gene Sequence-Guided Microbial Isolation. <i>Frontiers in Microbiology</i> , 2019, 10, 1397.	1.5	37
2049	Effects of dietary multi-strain probiotics supplementation in a low fishmeal diet on growth performance, nutrient utilization, proximate composition, immune parameters, and gut microbiota of juvenile olive flounder (<i>Paralichthys olivaceus</i>). <i>Fish and Shellfish Immunology</i> , 2019, 93, 258-268.	1.6	58
2050	Dysbiosis of the gut microbiome is associated with CKD5 and correlated with clinical indices of the disease: a caseâ€“controlled study. <i>Journal of Translational Medicine</i> , 2019, 17, 228.	1.8	29
2051	Glutamic acid supplementation reduces body fat weight in finishing pigs when provided solely or in combination with arginine and it is associated with colonic propionate and butyrate concentrations. <i>Food and Function</i> , 2019, 10, 4693-4704.	2.1	28
2052	Detection of low-density <i>Plasmodium falciparum</i> infections using amplicon deep sequencing. <i>Malaria Journal</i> , 2019, 18, 219.	0.8	40
2053	Analysis of the Relationship Between the Degree of Dysbiosis in Gut Microbiota and Prognosis at Different Stages of Primary Hepatocellular Carcinoma. <i>Frontiers in Microbiology</i> , 2019, 10, 1458.	1.5	78
2054	Multiple Maize Reference Genomes Impact the Identification of Variants by Genomeâ€“Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	1.6	37
2055	Nitrogen application increases soil respiration but decreases temperature sensitivity: Combined effects of crop and soil properties in a semiarid agroecosystem. <i>Geoderma</i> , 2019, 353, 320-330.	2.3	19
2056	Acidobacteria Subgroups and Their Metabolic Potential for Carbon Degradation in Sugarcane Soil Amended With Vinasse and Nitrogen Fertilizers. <i>Frontiers in Microbiology</i> , 2019, 10, 1680.	1.5	61
2057	Comparing the Microbial Community in Four Stomach of Dairy Cattle, Yellow Cattle and Three Yak Herds in Qinghai-Tibetan Plateau. <i>Frontiers in Microbiology</i> , 2019, 10, 1547.	1.5	67
2058	In vivo evaluation of the effect of arsenite on the intestinal epithelium and associated microbiota in mice. <i>Archives of Toxicology</i> , 2019, 93, 2127-2139.	1.9	21
2059	Metagenomics and transcriptomics data from human colorectal cancer. <i>Scientific Data</i> , 2019, 6, 116.	2.4	7
2060	Petunia- and Arabidopsis-Specific Root Microbiota Responses to Phosphate Supplementation. <i>Phytobiomes Journal</i> , 2019, 3, 112-124.	1.4	37
2061	Contrasting Winter Versus Summer Microbial Communities and Metabolic Functions in a Permafrost Thaw Lake. <i>Frontiers in Microbiology</i> , 2019, 10, 1656.	1.5	65
2062	Variation in rhizosphere microbiota correlates with edaphic factor in an abandoned antimony tailing dump. <i>Environmental Pollution</i> , 2019, 253, 141-151.	3.7	56
2063	Bacterial community composition in aquatic and sediment samples with spatiotemporal dynamics in large, shallow, eutrophic Lake Chaohu, China. <i>Journal of Freshwater Ecology</i> , 2019, 34, 575-589.	0.5	32

#	ARTICLE	IF	CITATIONS
2064	Differences in soil microbial response to anthropogenic disturbances in Sanjiang and Momoge Wetlands, China. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	18
2065	Association between the cervicovaginal microbiome, BRCA1 mutation status, and risk of ovarian cancer: a case-control study. <i>Lancet Oncology</i> , The, 2019, 20, 1171-1182.	5.1	108
2066	Bacterial Communities and Virulence Associated with Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> from Different <i>Pinus</i> spp.. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3342.	1.8	17
2067	Polyhydroxyalkanoates production from methane emissions in <i>Sphagnum</i> mosses: Assessing the effect of temperature and phosphorus limitation. <i>Science of the Total Environment</i> , 2019, 688, 684-690.	3.9	15
2068	Cultivation of a versatile manganese-oxidizing aerobic granular sludge for removal of organic micropollutants from wastewater. <i>Science of the Total Environment</i> , 2019, 690, 417-425.	3.9	16
2069	Spatial heterogeneity of the planktonic protistan community in a semi-closed eutrophic bay, China. <i>Journal of Plankton Research</i> , 2019, 41, 223-239.	0.8	7
2070	Effects of mixing <i>Neolamarckia cadamba</i> leaves on fermentation quality, microbial community of high moisture alfalfa and stylo silage. <i>Microbial Biotechnology</i> , 2019, 12, 869-878.	2.0	35
2071	Biological treatment of DMSO-containing wastewater from semiconductor industry under aerobic and methanogenic conditions. <i>Chemosphere</i> , 2019, 236, 124291.	4.2	13
2072	Gut Microbiota Differs Between Parkinson's Disease Patients and Healthy Controls in Northeast China. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 171.	1.4	100
2073	Gut microbiome and serum metabolome analyses identify molecular biomarkers and altered glutamate metabolism in fibromyalgia. <i>EBioMedicine</i> , 2019, 46, 499-511.	2.7	128
2074	Response of fungal communities in different soils to biochar and chemical fertilizers under simulated rainfall conditions. <i>Science of the Total Environment</i> , 2019, 691, 654-663.	3.9	32
2075	Sulfonate-based networks between eukaryotic phytoplankton and heterotrophic bacteria in the surface ocean. <i>Nature Microbiology</i> , 2019, 4, 1706-1715.	5.9	120
2076	Development and evolution of age-dependent defenses in ant-acacias. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15596-15601.	3.3	34
2077	Cyanobacterial diversity in mat sample obtained from hypersaline desert, Rann of Kachchh. <i>3 Biotech</i> , 2019, 9, 304.	1.1	8
2078	Wheat Straw Return Influences Nitrogen-Cycling and Pathogen Associated Soil Microbiota in a Wheat-Soybean Rotation System. <i>Frontiers in Microbiology</i> , 2019, 10, 1811.	1.5	36
2079	Photovoltaic electrolysis improves nitrogen and phosphorus removals of biochar-amended constructed wetlands. <i>Ecological Engineering</i> , 2019, 138, 71-78.	1.6	20
2080	Jellyfish summer outbreaks as bacterial vectors and potential hazards for marine animals and humans health? The case of <i>Rhizostoma pulmo</i> (Scyphozoa, Cnidaria). <i>Science of the Total Environment</i> , 2019, 692, 305-318.	3.9	27
2081	Insights into the antibiotic resistance dissemination in a wastewater effluent microbiome: bacteria, viruses and vesicles matter. <i>Environmental Microbiology</i> , 2019, 21, 4582-4596.	1.8	22

#	ARTICLE	IF	CITATIONS
2082	<i>In situ</i> metaomic insights into the community compositions and ecological roles of hadal microbes in the Mariana Trench. <i>Environmental Microbiology</i> , 2019, 21, 4092-4108.	1.8	40
2083	A large-scale CRISPR screen and identification of essential genes in cellular senescence bypass. <i>Aging</i> , 2019, 11, 4011-4031.	1.4	8
2084	Detection of Microbial 16S rRNA Gene in the Serum of Patients With Gastric Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 608.	1.3	48
2085	Oxidation of ammonium by <i>Feammox</i> <i>Acidimicrobiaceae</i> sp. A6 in anaerobic microbial electrolysis cells. <i>Environmental Science: Water Research and Technology</i> , 2019, 5, 1582-1592.	1.2	12
2086	Effects of a Fermented Beverage of Changbai Mountain Fruit and Vegetables on the Composition of Gut Microbiota in Mice. <i>Plant Foods for Human Nutrition</i> , 2019, 74, 468-473.	1.4	10
2087	Cumulative impact of long-term intensive mariculture on total and active bacterial communities in the core sediments of the Ailian Bay, North China. <i>Science of the Total Environment</i> , 2019, 691, 1212-1224.	3.9	19
2088	Microbial Community Structures and Important Associations Between Soil Nutrients and the Responses of Specific Taxa to Rice-Frog Cultivation. <i>Frontiers in Microbiology</i> , 2019, 10, 1752.	1.5	31
2089	Changes in the Microbial Community Diversity of Oil Exploitation. <i>Genes</i> , 2019, 10, 556.	1.0	13
2090	Achieving stable and efficient single-stage deammonification using plug flow reactor. <i>Environmental Science and Pollution Research</i> , 2019, 26, 28031-28039.	2.7	13
2091	Draft Genome Sequences of 42 Environmental <i>Vibrio vulnificus</i> Strains Isolated from the Northern Gulf of Mexico. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
2092	Early Feeding Regime of Waste Milk, Milk, and Milk Replacer for Calves Has Different Effects on Rumen Fermentation and the Bacterial Community. <i>Animals</i> , 2019, 9, 443.	1.0	20
2093	Spatio-temporal patterns of zooplankton in a main-stem dam affected tributary: a case study in the Xiangxi River of the Three Gorges Reservoir, China. <i>Science China Life Sciences</i> , 2019, 62, 1058-1069.	2.3	22
2094	The newly proposed TACK and DPANN archaea detected in the production waters from a high-temperature petroleum reservoir. <i>International Biodeterioration and Biodegradation</i> , 2019, 143, 104729.	1.9	11
2095	A Characterization of the DNA Data Storage Channel. <i>Scientific Reports</i> , 2019, 9, 9663.	1.6	151
2096	Roux-Y Gastric Bypass and Sleeve Gastrectomy directly change gut microbiota composition independent of surgery type. <i>Scientific Reports</i> , 2019, 9, 10979.	1.6	55
2097	Terrestrial mammal surveillance using hybridization capture of environmental DNA from African waterholes. <i>Molecular Ecology Resources</i> , 2019, 19, 1486-1496.	2.2	37
2098	Rumen and Fecal Microbial Community Structure of Holstein and Jersey Dairy Cows as Affected by Breed, Diet, and Residual Feed Intake. <i>Animals</i> , 2019, 9, 498.	1.0	39
2099	Enhanced methanization of sewage sludge using an anaerobic membrane bioreactor integrated with hyperthermophilic biological hydrolysis. <i>Energy Conversion and Management</i> , 2019, 196, 846-855.	4.4	24

#	ARTICLE	IF	CITATIONS
2100	High-throughput sequencing and analysis of microbial communities in the mangrove swamps along the coast of Beibu Gulf in Guangxi, China. <i>Scientific Reports</i> , 2019, 9, 9377.	1.6	42
2101	The Diversity and Geographic Distribution of Cultivable <i>Bacillus</i> -Like Bacteria Across Black Soils of Northeast China. <i>Frontiers in Microbiology</i> , 2019, 10, 1424.	1.5	21
2102	Exploration of the key functional strains from an azo dye degradation microbial community by DGGE and high-throughput sequencing technology. <i>Environmental Science and Pollution Research</i> , 2019, 26, 24658-24671.	2.7	18
2103	Plants exhibit significant effects on the rhizospheric microbiome across contrasting soils in tropical and subtropical China. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	4
2104	The Composition and Assembly of Bacterial Communities across the Rhizosphere and Phyllosphere Compartments of <i>Phragmites Australis</i> . <i>Diversity</i> , 2019, 11, 98.	0.7	21
2105	Development and validation of a physiologically based kinetic model for starting up and operation of the biological gas desulfurization process under haloalkaline conditions. <i>Water Research X</i> , 2019, 4, 100035.	2.8	23
2107	Forest biomass, soil and biodiversity relationships originate from biogeographic affinity and direct ecological effects. <i>Oikos</i> , 2019, 128, 1653-1665.	1.2	16
2108	Biochar Induces Changes to Basic Soil Properties and Bacterial Communities of Different Soils to Varying Degrees at 25 mm Rainfall: More Effective on Acidic Soils. <i>Frontiers in Microbiology</i> , 2019, 10, 1321.	1.5	68
2109	Analysis of microbiota in cultures of the green microalga <i>Tetraselmis suecica</i> . <i>European Journal of Phycology</i> , 2019, 54, 497-508.	0.9	15
2110	Communal metabolism by <i>Methylococcaceae</i> and <i>Methylophilaceae</i> is driving rapid aerobic methane oxidation in sediments of a shallow seep near Elba, Italy. <i>Environmental Microbiology</i> , 2019, 21, 3780-3795.	1.8	28
2111	Single Cell Genomics-Based Analysis of Gene Content and Expression of Prophages in a Diffuse-Flow Deep-Sea Hydrothermal System. <i>Frontiers in Microbiology</i> , 2019, 10, 1262.	1.5	14
2112	Compositional response of <i>Phaseolus vulgaris</i> rhizomicrobiome to a changing soil environment is regulated by long-distance plant signaling. <i>Plant and Soil</i> , 2019, 442, 257-269.	1.8	4
2113	LINE-1 Evasion of Epigenetic Repression in Humans. <i>Molecular Cell</i> , 2019, 75, 590-604.e12.	4.5	106
2114	Plug-and-Play Protein Modification Using Homology-Independent Universal Genome Engineering. <i>Neuron</i> , 2019, 103, 583-597.e8.	3.8	59
2115	Changes in Endogenous and Exogenous Koala Retrovirus Subtype Expression over Time Reflect Koala Health Outcomes. <i>Journal of Virology</i> , 2019, 93, .	1.5	21
2116	Negative Plant-Soil Feedback Driven by Re-assembly of the Rhizosphere Microbiome With the Growth of <i>Panax notoginseng</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1597.	1.5	72
2117	Gut microbiota density influences host physiology and is shaped by host and microbial factors. <i>ELife</i> , 2019, 8, .	2.8	118
2118	Sodium alginate supplementation modulates gut microbiota, health parameters, growth performance and growth-related gene expression in Malaysian Mahseer <i>Tor tambroides</i> . <i>Aquaculture Nutrition</i> , 2019, 25, 1300-1317.	1.1	10

#	ARTICLE	IF	CITATIONS
2119	Disinfection of lettuce using organic acids: an ecological analysis using 16S rRNA sequencing. <i>RSC Advances</i> , 2019, 9, 17514-17520.	1.7	21
2120	The Chinese Herbal Formula Shenzhu Tiaopi Granule Results in Metabolic Improvement in Type 2 Diabetic Rats by Modulating the Gut Microbiota. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-14.	0.5	22
2121	Active eukaryotes in drinking water distribution systems of ground and surface waterworks. <i>Microbiome</i> , 2019, 7, 99.	4.9	25
2122	Host Gender and Androgen Levels Regulate Gut Bacterial Taxa in Pigs Leading to Sex-Biased Serum Metabolite Profiles. <i>Frontiers in Microbiology</i> , 2019, 10, 1359.	1.5	29
2123	Organic Soils Control Beetle Survival While Competitors Limit Aphid Population Growth. <i>Environmental Entomology</i> , 2019, 48, 1323-1330.	0.7	14
2124	Surviving onshore soil microbial communities differ among the Qing-Tibetan lakes with different salinity. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	2
2125	High Dynamic Range Externally Time-Gated Photon Counting Optical Time-Domain Reflectometry. <i>Journal of Lightwave Technology</i> , 2019, 37, 5899-5906.	2.7	11
2126	Intestinal Microbiota of Grass Carp Fed Faba Beans: A Comparative Study. <i>Microorganisms</i> , 2019, 7, 465.	1.6	20
2127	Identification and genomic characterization of grapevine Kizil Sapak virus, a novel grapevine-infecting member of the family Betaflexiviridae. <i>Archives of Virology</i> , 2019, 164, 3145-3149.	0.9	13
2128	Dietary Supplementation of Lysophospholipids Affects Feed Digestion in Lambs. <i>Animals</i> , 2019, 9, 805.	1.0	15
2129	Effects of Nutritional Deprivation and Re-Alimentation on the Feed Efficiency, Blood Biochemistry, and Rumen Microflora in Yaks (<i>Bos grunniens</i>). <i>Animals</i> , 2019, 9, 807.	1.0	35
2130	Metagenome data of bacterial diversity in pear (<i>Pyrus communis</i> L.) rhizospheres associated with <i>Phytophthora</i> infection and amino acid treatment. <i>Data in Brief</i> , 2019, 26, 104396.	0.5	5
2131	Invader-resident community similarity contribute to the invasion process and regulate biofertilizer effectiveness. <i>Journal of Cleaner Production</i> , 2019, 241, 118278.	4.6	23
2132	Preferential degradation of long-chain alkyl substituted hydrocarbons in heavy oil under methanogenic conditions. <i>Organic Geochemistry</i> , 2019, 138, 103927.	0.9	16
2133	Composition of Bacterial and Archaeal Communities in an Alkali-Surfactant-Polyacrylamide-Flooded Oil Reservoir and the Responses of Microcosms to Nutrients. <i>Frontiers in Microbiology</i> , 2019, 10, 2197.	1.5	17
2134	The central bacterial community in <i>Pericarpium Citri Reticulatae</i> "Chachiensis"™. <i>Food Research International</i> , 2019, 125, 108624.	2.9	13
2135	Effect of a Chinese medical nutrition therapy diet on gut microbiota and short chain fatty acids in the simulator of the human intestinal microbial ecosystem (SHIME). <i>Journal of Functional Foods</i> , 2019, 62, 103555.	1.6	16
2136	High-throughput sequencing revealed differences of microbial community structure and diversity between healthy and diseased <i>Caulerpa lentillifera</i> . <i>BMC Microbiology</i> , 2019, 19, 225.	1.3	18

#	ARTICLE	IF	CITATIONS
2137	High-Throughput 16S rRNA Sequencing to Assess Potentially Active Bacteria and Foodborne Pathogens: A Case Example in Ready-to-Eat Food. <i>Foods</i> , 2019, 8, 480.	1.9	14
2138	Effects of 1, 3-dioleoyl-2-palmitoylglycerol and its plant-oil formula on the toddler fecal microbiota during <i>in vitro</i> fermentation. <i>CYTA - Journal of Food</i> , 2019, 17, 850-863.	0.9	2
2139	Bacterial Community Shifts Driven by Nitrogen Pollution in River Sediments of a Highly Urbanized City. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 3794.	1.2	20
2140	Characterizing the pharmacogenome using molecular inversion probes for targeted next-generation sequencing. <i>Pharmacogenomics</i> , 2019, 20, 1005-1020.	0.6	9
2141	Analysis of the Gut Microbiome of Wild and Captive Père David's Deer. <i>Frontiers in Microbiology</i> , 2019, 10, 2331.	1.5	32
2142	Effects of Warming and Nitrogen Addition on the Soil Bacterial Community in a Subtropical Chinese Fir Plantation. <i>Forests</i> , 2019, 10, 861.	0.9	12
2143	Thermophilic solid-state fermentation of rapeseed meal and analysis of microbial community diversity. <i>LWT - Food Science and Technology</i> , 2019, 116, 108520.	2.5	17
2144	Rapid selection and identification of functional CD8+ T cell epitopes from large peptide-coding libraries. <i>Nature Communications</i> , 2019, 10, 4553.	5.8	43
2145	Complete loss of the MHC II pathway in an anglerfish, <i>Lophius piscatorius</i> . <i>Biology Letters</i> , 2019, 15, 20190594.	1.0	31
2146	Comparative Analysis of the CDR Loops of Antigen Receptors. <i>Frontiers in Immunology</i> , 2019, 10, 2454.	2.2	40
2147	Forest Soil Fungal Community Elevational Distribution Pattern and Their Ecological Assembly Processes. <i>Frontiers in Microbiology</i> , 2019, 10, 2226.	1.5	20
2148	Comparative analysis of gut microbiota among the male, female and pregnant giant pandas (<i>Ailuropoda</i>) Tj ETQq1 1 0.784314 rgBT /Ov	0.6	4
2149	Similar Shift Patterns in Gut Bacterial and Fungal Communities Across the Life Stages of <i>Bactrocera minax</i> Larvae From Two Field Populations. <i>Frontiers in Microbiology</i> , 2019, 10, 2262.	1.5	28
2150	Effect of sodium chloride reduction or partial substitution with potassium chloride on the microbiological, biochemical and sensory characteristics of semi-hard and soft cheeses. <i>Food Research International</i> , 2019, 125, 108643.	2.9	25
2151	Regulation of dietary astragalus polysaccharide (APS) supplementation on the non-specific immune response and intestinal microbiota of sea cucumber <i>Apostichopus japonicus</i> . <i>Fish and Shellfish Immunology</i> , 2019, 94, 517-524.	1.6	37
2152	Altered short chain fatty acid profiles induced by dietary fiber intervention regulate AMPK levels and intestinal homeostasis. <i>Food and Function</i> , 2019, 10, 7174-7187.	2.1	43
2153	Mystifying mass in the right ventricle. <i>European Heart Journal Cardiovascular Imaging</i> , 2020, 21, 281.	0.5	0
2154	Mucosal Exposure to Cigarette Components Induces Intestinal Inflammation and Alters Antimicrobial Response in Mice. <i>Frontiers in Immunology</i> , 2019, 10, 2289.	2.2	29

#	ARTICLE	IF	CITATIONS
2155	Efficacy of Fecal Sampling as a Gut Proxy in the Study of Chicken Gut Microbiota. <i>Frontiers in Microbiology</i> , 2019, 10, 2126.	1.5	81
2156	Anti-Biofouling Performance of an Immobilized Indigenous Quorum Quenching Bacterium <i>Bacillus cereus</i> HG10 and Its Influence on the Microbial Community in a Bioreactor. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 3777.	1.2	6
2157	Use of omic approaches for characterizing microbiota from suppressive compost to control soil-borne plant pathogens. <i>Archives of Phytopathology and Plant Protection</i> , 2019, 52, 757-775.	0.6	5
2158	Impact of polyculture ecosystems of <i>Ctenopharyngodon idellus</i> with <i>Eriocheir sinensis</i> on bacterial communities in the sediments of Dongping Lake in China: Focus on optimization of polyculture modes. <i>Aquaculture Research</i> , 2019, 50, 3700-3710.	0.9	1
2159	Host and geography together drive early adaptive radiation of Hawaiian planthoppers. <i>Molecular Ecology</i> , 2019, 28, 4513-4528.	2.0	6
2160	Edaphic and host plant factors are linked to the composition of arbuscular mycorrhizal fungal communities in the root zone of endangered <i>Ulmus chenmoui</i> Cheng in China. <i>Ecology and Evolution</i> , 2019, 9, 8900-8910.	0.8	16
2161	A collection of rumen bacteriome data from 334 mid-lactation dairy cows. <i>Scientific Data</i> , 2019, 6, 180301.	2.4	13
2162	Hot corrosion resistance of a Ti-Mo-Al-Si titanium matrix composites reinforced with in-situ TiC prepared by powder metallurgy. <i>Materials Research Express</i> , 2019, 6, 126510.	0.8	3
2163	Contrasting Biogeographic Patterns of Bacterial and Archaeal Diversity in the Top- and Subsoils of Temperate Grasslands. <i>MSystems</i> , 2019, 4, .	1.7	24
2164	China's Approaches to the South China Sea Code of Conduct Negotiation. <i>East Asian Policy</i> , 2019, 11, 77-86.	0.6	0
2165	Analysis of nifH DNA and RNA reveals a disproportionate contribution to nitrogenase activities by rare plankton-associated diazotrophs. <i>BMC Microbiology</i> , 2019, 19, 188.	1.3	16
2166	Effects of dietary supplementation of probiotic <i>Enterococcus faecium</i> on growth performance and gut microbiota in weaned piglets. <i>AMB Express</i> , 2019, 9, 33.	1.4	15
2167	Metagenomic Analyses of Microbial and Carbohydrate-Active Enzymes in the Rumen of Holstein Cows Fed Different Forage-to-Concentrate Ratios. <i>Frontiers in Microbiology</i> , 2019, 10, 649.	1.5	90
2168	Draft genome sequence data of <i>Cercospora kikuchii</i> , a causal agent of <i>Cercospora</i> leaf blight and purple seed stain of soybeans. <i>Data in Brief</i> , 2019, 27, 104693.	0.5	11
2169	Survey of bacteria associated with western corn rootworm life stages reveals no difference between insects reared in different soils. <i>Scientific Reports</i> , 2019, 9, 15332.	1.6	11
2170	Microbial Community Structure and Methane Cycling Potential along a Thermokarst Pond-Peatland Continuum. <i>Microorganisms</i> , 2019, 7, 486.	1.6	13
2171	<i>Lactobacillus helveticus</i> R0052 alleviates liver injury by modulating gut microbiome and metabolome in d-galactosamine-treated rats. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 9673-9686.	1.7	35
2172	Rapid microevolution of biofilm cells in response to antibiotics. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 34.	2.9	96

#	ARTICLE	IF	CITATIONS
2173	Deciphering Underlying Drivers of Disease Suppressiveness Against Pathogenic <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2535.	1.5	38
2174	The impact of calcium peroxide on groundwater bacterial diversity during naphthalene removal by permeable reactive barrier (PRB). <i>Environmental Science and Pollution Research</i> , 2019, 26, 35218-35226.	2.7	9
2175	Metagenomic data of the microbial community of lab-scale nitrification-anammox sequencing-batch bioreactor performing nitrogen removal from synthetic wastewater. <i>Data in Brief</i> , 2019, 27, 104722.	0.5	5
2176	Soil Nutrients Drive Function and Composition of phoC-Harboring Bacterial Community in Acidic Soils of Southern China. <i>Frontiers in Microbiology</i> , 2019, 10, 2654.	1.5	25
2177	Respiratory Dysbiosis in Canine Bacterial Pneumonia: Standard Culture vs. Microbiome Sequencing. <i>Frontiers in Veterinary Science</i> , 2019, 6, 354.	0.9	14
2178	Small pigmented eukaryotes play a major role in carbon cycling in the P&Edepleted western subtropical North Atlantic, which may be supported by mixotrophy. <i>Limnology and Oceanography</i> , 2019, 64, 2424-2440.	1.6	27
2179	Illumina-based Analysis of Endophytic Bacterial Diversity of four <i>Allium</i> species. <i>Scientific Reports</i> , 2019, 9, 15271.	1.6	19
2180	Effects of Antibiotics on Microbial Communities Responsible for Perchlorate Degradation. <i>Water, Air, and Soil Pollution</i> , 2019, 230, 1.	1.1	6
2181	Elucidating Drought Stress Tolerance in European Oaks Through Cross-Species Transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3181-3199.	0.8	22
2182	Exploring possible associations of the intestine bacterial microbiome with the pre-weaned weight gaining performance of piglets in intensive pig production. <i>Scientific Reports</i> , 2019, 9, 15534.	1.6	27
2183	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	3.8	47
2184	Regional biogeography of microbiota composition in the Chagas disease vector <i>Rhodnius pallescens</i> . <i>Parasites and Vectors</i> , 2019, 12, 504.	1.0	17
2185	The Regulation of Ruminal Short-Chain Fatty Acids on the Functions of Rumen Barriers. <i>Frontiers in Physiology</i> , 2019, 10, 1305.	1.3	33
2186	<i>Trichinella spiralis</i> infection decreases the diversity of the intestinal flora in the infected mouse. <i>Journal of Microbiology, Immunology and Infection</i> , 2021, 54, 490-500.	1.5	12
2187	Effects of rhizoma peanut cultivars (<i>Arachis glabrata</i> Benth.) on the soil bacterial diversity and predicted function in nitrogen fixation. <i>Ecology and Evolution</i> , 2019, 9, 12676-12687.	0.8	21
2188	Shen-Ling-Bai-Zhu-San alleviates functional dyspepsia in rats and modulates the composition of the gut microbiota. <i>Nutrition Research</i> , 2019, 71, 89-99.	1.3	28
2189	DNA methylation reprogramming, TE derepression, and postzygotic isolation of nascent animal species. <i>Science Advances</i> , 2019, 5, eaaw1644.	4.7	47
2190	Genome Analysis and Multiplex PCR Method for the Molecular Detection of Coresistance to Cephalosporins and Fosfomycin in <i>Salmonella enterica</i> Serovar Heidelberg. <i>Journal of Food Protection</i> , 2019, 82, 1938-1949.	0.8	11

#	ARTICLE	IF	CITATIONS
2191	Habitat filters mediate successional trajectories in bacterial communities associated with the striped shore crab. <i>Oecologia</i> , 2019, 191, 957-970.	0.9	3
2192	Metagenomics Reveals Seasonal Functional Adaptation of the Gut Microbiome to Host Feeding and Fasting in the Chinese Alligator. <i>Frontiers in Microbiology</i> , 2019, 10, 2409.	1.5	34
2193	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019, 10, 5029.	5.8	1,007
2194	Internal and External Microbial Community of the Thitarodes Moth, the Host of <i>Ophiocordyceps sinensis</i> . <i>Microorganisms</i> , 2019, 7, 517.	1.6	23
2195	Venom Diversity and Evolution in the Most Divergent Cone Snail Genus <i>Profundiconus</i> . <i>Toxins</i> , 2019, 11, 623.	1.5	16
2196	Fish diversity assessment in the headwaters of the Volga River using environmental DNA metabarcoding. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2019, 29, 1785-1800.	0.9	34
2197	Microbial Processing of Sediment-Derived Dissolved Organic Matter: Implications for Its Subsequent Biogeochemical Cycling in Overlying Seawater. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 3479-3490.	1.3	44
2198	Genetic Markers for Species Conservation and Timber Tracking: Development of Microsatellite Primers for the Tropical African Tree Species <i>Prioria balsamifera</i> and <i>Prioria oxyphylla</i> . <i>Forests</i> , 2019, 10, 1037.	0.9	2
2199	The Effect of Organic Carbon on Soil Bacterial Diversity in an Antarctic Lake Region. <i>Journal of Ocean University of China</i> , 2019, 18, 1402-1410.	0.6	1
2200	Deep sequencing of B cell receptor repertoire. <i>BMB Reports</i> , 2019, 52, 540-547.	1.1	17
2201	Modulating Polymer Dispersity with Light: Cationic Polymerization of Vinyl Ethers Using Photochromic Initiators. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 16210-16216.	7.2	33
2202	Interface-Initiated Polymerization Enables One-Pot Synthesis of Hydrophilic and Oleophobic Foams through Emulsion Templating. <i>Macromolecular Rapid Communications</i> , 2019, 40, e1900288.	2.0	22
2203	Broad-leaved forest types affect soil fungal community structure and soil organic carbon contents. <i>MicrobiologyOpen</i> , 2019, 8, e874.	1.2	15
2204	Investigation of bacterial diversity and pathogen abundances in gibel carp (<i>Carassius auratus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.2 8	1.2	8
2205	Multiple factors govern the biogeographic distribution of archaeal community in mangroves across China. <i>Estuarine, Coastal and Shelf Science</i> , 2019, 231, 106414.	0.9	7
2206	Interdomain ecological networks between plants and microbes. <i>Molecular Ecology Resources</i> , 2019, 19, 1565-1577.	2.2	64
2207	Seasonal Fish Assemblage Structure Using Environmental DNA in the Yangtze Estuary and Its Adjacent Waters. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	31
2208	Chinese Black Truffle-Associated Bacterial Communities of <i>Tuber indicum</i> From Different Geographical Regions With Nitrogen Fixing Bioactivity. <i>Frontiers in Microbiology</i> , 2019, 10, 2515.	1.5	29

#	ARTICLE	IF	CITATIONS
2209	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. <i>Frontiers in Microbiology</i> , 2019, 10, 2620.	1.5	36
2210	Taxonomical and Functional Assessment of the Endometrial Microbiota in A Context of Recurrent Reproductive Failure: A Case Report. <i>Pathogens</i> , 2019, 8, 205.	1.2	39
2211	Effects of sialylated lactulose on the mouse intestinal microbiome using Illumina high-throughput sequencing. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 9067-9076.	1.7	6
2212	Responses of antibiotics, antibiotic resistance genes, and mobile genetic elements in sewage sludge to thermal hydrolysis pre-treatment and various anaerobic digestion conditions. <i>Environment International</i> , 2019, 133, 105156.	4.8	81
2213	Fates of intracellular and extracellular antibiotic resistance genes and microbial community structures in typical swine wastewater treatment processes. <i>Environment International</i> , 2019, 133, 105183.	4.8	66
2214	Faecal microbiota and functional capacity associated with weaning weight in meat rabbits. <i>Microbial Biotechnology</i> , 2019, 12, 1441-1452.	2.0	29
2215	Effects of florfenicol feeding on diversity and composition of the intestinal microbiota of channel catfish (<i>Ictalurus punctatus</i>). <i>Aquaculture Research</i> , 2019, 50, 3663-3672.	0.9	18
2216	Deciphering bacterial community variation during soil and leaf treatments with biologicals and biofertilizers to control huanglongbing in citrus trees. <i>Journal of Phytopathology</i> , 2019, 167, 686-694.	0.5	7
2217	Polygenic selection drives the evolution of convergent transcriptomic landscapes across continents within a Nearctic sister species complex. <i>Molecular Ecology</i> , 2019, 28, 4388-4403.	2.0	38
2218	Composition and Structure of Gut Microbiome in Adolescents with Obesity and Different Breastfeeding Duration. <i>Bulletin of Experimental Biology and Medicine</i> , 2019, 167, 759-762.	0.3	15
2219	Monocropping decouples plant-bacteria interaction and strengthens phytopathogenic fungi colonization in the rhizosphere of a perennial plant species. <i>Plant and Soil</i> , 2019, 445, 549-564.	1.8	11
2220	gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffold output. <i>PLoS ONE</i> , 2019, 14, e0216885.	1.1	14
2221	Non-human Primate Papillomaviruses Share Similar Evolutionary Histories and Niche Adaptation as the Human Counterparts. <i>Frontiers in Microbiology</i> , 2019, 10, 2093.	1.5	16
2222	Community Structure Analyses of Anodic Biofilms in a Bioelectrochemical System Combined with an Aerobic Reactor. <i>Energies</i> , 2019, 12, 3643.	1.6	3
2223	Effect of the Nursing Mother on the Gut Microbiome of the Offspring During Early Mouse Development. <i>Microbial Ecology</i> , 2019, 78, 517-527.	1.4	17
2224	Large-scale biogeography and environmental regulation of methanotrophic bacteria across boreal inland waters. <i>Molecular Ecology</i> , 2019, 28, 4181-4196.	2.0	23
2225	High-throughput DNA sequencing technologies for water and wastewater analysis. <i>Science Progress</i> , 2019, 102, 351-376.	1.0	16
2226	Stochastic processes shape microeukaryotic community assembly in a subtropical river across wet and dry seasons. <i>Microbiome</i> , 2019, 7, 138.	4.9	313

#	ARTICLE	IF	CITATIONS
2227	<p>Escherichia coli from Mexico</p>. Infection and Drug Resistance, 2019, Volume 12, 2363-2377.	1.1	22
2228	Effects of intragenomic polymorphism in the SSU rRNA gene on estimating marine microeukaryotic diversity: A test for ciliates using single-cell high-throughput DNA sequencing. Limnology and Oceanography: Methods, 2019, 17, 533-543.	1.0	22
2229	Maternal Polystyrene Microplastic Exposure during Gestation and Lactation Altered Metabolic Homeostasis in the Dams and Their F1 and F2 Offspring. Environmental Science & Technology, 2019, 53, 10978-10992.	4.6	191
2230	Agarwood wound locations provide insight into the association between fungal diversity and volatile compounds in <i>Aquilaria sinensis</i> . Royal Society Open Science, 2019, 6, 190211.	1.1	11
2231	Responses of Microbial Communities and Interaction Networks to Different Management Practices in Tea Plantation Soils. Sustainability, 2019, 11, 4428.	1.6	24
2232	Community composition of rhizosphere fungi as affected by <i>Funneliformis mosseae</i> in soybean continuous cropping soil during seedling period. Chilean Journal of Agricultural Research, 2019, 79, 356-365.	0.4	11
2233	Bacterial Diversity in the Metal-Rich Terrestrial Deep Subsurface Sediments of Krishna Godavari Basin, India. Geomicrobiology Journal, 2019, 36, 917-932.	1.0	4
2234	Comparison of Two Methods to Assess the Size Structure of Phytoplankton Community Assemblages, in Liaodong Bay, China. Journal of Ocean University of China, 2019, 18, 1207-1215.	0.6	5
2235	Tyr82 Amino Acid Mutation in PB1 Polymerase Induces an Influenza Virus Mutator Phenotype. Journal of Virology, 2019, 93, .	1.5	4
2236	Dietary Supplementation With Leucine or in Combination With Arginine Decreases Body Fat Weight and Alters Gut Microbiota Composition in Finishing Pigs. Frontiers in Microbiology, 2019, 10, 1767.	1.5	25
2237	Effects of Land Transport Stress on Variations in Ruminal Microbe Diversity and Immune Functions in Different Breeds of Cattle. Animals, 2019, 9, 599.	1.0	26
2238	Bacterioplankton community in response to biological filters (clam, biofilm, and macrophytes) in an integrated aquaculture wastewater bioremediation system. Environmental Pollution, 2019, 254, 113035.	3.7	22
2239	Response of the bacterial community of <i>Propylea japonica</i> (Thunberg) to Cry2Ab protein. Environmental Pollution, 2019, 254, 113063.	3.7	29
2240	Influence of suspended mariculture on vertical distribution profiles of bacteria in sediment from Daya Bay, Southern China. Marine Pollution Bulletin, 2019, 146, 816-826.	2.3	20
2241	Composition and change in the microbiome of <i>Diaphorina citri</i> infected with <i>Candidatus Liberibacter asiaticus</i> in China. International Journal of Tropical Insect Science, 2019, 39, 283-290.	0.4	9
2242	Full-scale anaerobic reactor samples would be more suitable than lab-scale anaerobic reactor and natural samples to inoculate the wheat straw batch anaerobic digesters. Bioresource Technology, 2019, 293, 122040.	4.8	10
2243	Soil tillage and compost amendment promote bioremediation and biofertility of polluted area. Journal of Cleaner Production, 2019, 239, 118087.	4.6	38
2244	Denitrification is the main microbial N loss pathway on the Qinghai-Tibet Plateau above an elevation of 5000 m. Science of the Total Environment, 2019, 696, 133852.	3.9	21

#	ARTICLE	IF	CITATIONS
2245	Humic Acid Fertilizer Improved Soil Properties and Soil Microbial Diversity of Continuous Cropping Peanut: A Three-Year Experiment. <i>Scientific Reports</i> , 2019, 9, 12014.	1.6	110
2246	Comparison and Selection of Three-Core Cable and Single-Core Cable. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 300, 042047.	0.2	3
2247	Nitrogen-dependent bacterial community shifts in root, rhizome and rhizosphere of nutrient-efficient <i>Miscanthus x giganteus</i> from long-term field trials. <i>GCB Bioenergy</i> , 2019, 11, 1334-1347.	2.5	30
2248	Phylogeny of the Australian <i>Solanum dioicum</i> group using seven nuclear genes, with consideration of Symon's fruit and seed dispersal hypotheses. <i>PLoS ONE</i> , 2019, 14, e0207564.	1.1	15
2249	Three-Dimensional Numerical Simulation of Rock Breaking by the Tipped Hob Cutter Based on Explicit Finite Element. <i>IEEE Access</i> , 2019, 7, 86054-86063.	2.6	13
2250	Responses of phyllosphere microbiota and plant health to application of two different biocontrol agents. <i>AMB Express</i> , 2019, 9, 42.	1.4	44
2251	Gut segments outweigh the diet in shaping the intestinal microbiota composition in grass carp <i>Ctenopharyngodon idellus</i> . <i>AMB Express</i> , 2019, 9, 44.	1.4	14
2252	Variations in phyllosphere microbial community along with the development of angular leaf-spot of cucumber. <i>AMB Express</i> , 2019, 9, 76.	1.4	34
2253	A Membrane-Bound Cytochrome Enables <i>Methanosarcina acetivorans</i> To Conserve Energy from Extracellular Electron Transfer. <i>MBio</i> , 2019, 10, .	1.8	76
2254	Alterations in the Ocular Surface Fungal Microbiome in Fungal Keratitis Patients. <i>Microorganisms</i> , 2019, 7, 309.	1.6	43
2255	Different dietary protein sources in low protein diets regulate colonic microbiota and barrier function in a piglet model. <i>Food and Function</i> , 2019, 10, 6417-6428.	2.1	25
2256	Impacts of environmental factors on AHL-producing and AHL-quenching activities of aerobic granules. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 9181-9189.	1.7	9
2257	Combining Irrigation Scheme and Phosphorous Application Levels for Grain Yield and Their Impacts on Rhizosphere Microbial Communities of Two Rice Varieties in a Field Trial. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 10577-10586.	2.4	10
2258	Leaf-Associated Shifts in Bacterial and Fungal Communities in Response to Chicken Rearing Under Moso Bamboo Forests in Subtropical China. <i>Forests</i> , 2019, 10, 216.	0.9	9
2259	Analyses of artificial morel soil bacterial community structure and mineral element contents in ascocarp and the cultivated soil. <i>Canadian Journal of Microbiology</i> , 2019, 65, 738-749.	0.8	10
2260	Composition and Dynamics of Bacterial Communities in a Full-Scale Mineral Water Treatment Plant. <i>Frontiers in Microbiology</i> , 2019, 10, 1542.	1.5	2
2261	A Comparative Metagenomics Study on Gastrointestinal Microbiota in Amphibious Mudskippers and Other Vertebrate Animals. <i>Animals</i> , 2019, 9, 660.	1.0	6
2262	Dietary daidzein improved intestinal health of juvenile turbot in terms of intestinal mucosal barrier function and intestinal microbiota. <i>Fish and Shellfish Immunology</i> , 2019, 94, 132-141.	1.6	35

#	ARTICLE	IF	CITATIONS
2263	Research on mechanism of charred hawthorn on digestive through modulating "brain-gut" axis and gut flora. <i>Journal of Ethnopharmacology</i> , 2019, 245, 112166.	2.0	33
2264	An orally administered magnololide A ameliorates functional dyspepsia by modulating brain-gut peptides and gut microbiota. <i>Life Sciences</i> , 2019, 233, 116749.	2.0	22
2265	Selective enrichment of bacterial pathogens by microplastic biofilm. <i>Water Research</i> , 2019, 165, 114979.	5.3	408
2266	Characterisation of polymorphic microsatellite loci in three copper butterfly species (<i>Lycaena</i> spp.). <i>Molecular Biology Reports</i> , 2019, 46, 6585-6591.	1.0	3
2267	Antibiotic resistance in urban green spaces mirrors the pattern of industrial distribution. <i>Environment International</i> , 2019, 132, 105106.	4.8	42
2268	Soil biofilm formation enhances microbial community diversity and metabolic activity. <i>Environment International</i> , 2019, 132, 105116.	4.8	80
2269	Characterization of Distinct T Cell Receptor Repertoires in Tumor and Distant Non-tumor Tissues from Lung Cancer Patients. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 287-296.	3.0	20
2270	Organs, Cultivars, Soil, and Fruit Properties Affect Structure of Endophytic Mycobiota of Pinggu Peach Trees. <i>Microorganisms</i> , 2019, 7, 322.	1.6	21
2271	Effects of Dietary-SCFA on Microbial Protein Synthesis and Urinal Urea-N Excretion Are Related to Microbiota Diversity in Rumen. <i>Frontiers in Physiology</i> , 2019, 10, 1079.	1.3	12
2272	Effects of Two <i>Trichoderma</i> Strains on Plant Growth, Rhizosphere Soil Nutrients, and Fungal Community of <i>Pinus sylvestris</i> var. <i>mongolica</i> Annual Seedlings. <i>Forests</i> , 2019, 10, 758.	0.9	86
2273	Network Analysis Reveals Seasonal Patterns of Bacterial Community Networks in Lake Taihu under Aquaculture Conditions. <i>Water (Switzerland)</i> , 2019, 11, 1868.	1.2	13
2274	Effect of continuous sorghum cropping on the rhizosphere microbial community and the role of <i>Bacillus amyloliquefaciens</i> in altering the microbial composition. <i>Plant Growth Regulation</i> , 2019, 89, 299-308.	1.8	28
2275	Blueberry Extract Improves Obesity through Regulation of the Gut Microbiota and Bile Acids via Pathways Involving FXR and TGR5. <i>IScience</i> , 2019, 19, 676-690.	1.9	76
2276	Fungal succession during mammalian cadaver decomposition and potential forensic implications. <i>Scientific Reports</i> , 2019, 9, 12907.	1.6	30
2277	Impact of cleaning and disinfection procedures on microbial ecology and <i>Salmonella</i> antimicrobial resistance in a pig slaughterhouse. <i>Scientific Reports</i> , 2019, 9, 12947.	1.6	23
2278	Characteristics of mucosa-associated gut microbiota during treatment in Crohn's disease. <i>World Journal of Gastroenterology</i> , 2019, 25, 2204-2216.	1.4	46
2279	Can extreme MHC class I diversity be a feature of a wide geographic range? The example of <i>Seba's</i> short-tailed bat (<i>Carollia perspicillata</i>). <i>Immunogenetics</i> , 2019, 71, 575-587.	1.2	15
2280	Upper versus lower airway microbiome and metagenome in children with cystic fibrosis and their correlation with lung inflammation. <i>PLoS ONE</i> , 2019, 14, e0222323.	1.1	17

#	ARTICLE	IF	CITATIONS
2281	Targeted amplicon sequencing of 40 nuclear genes supports a single introduction and rapid radiation of Hawaiian <i>Metrosideros</i> (Myrtaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 961-974.	0.3	15
2282	Maternal pluripotency factors initiate extensive chromatin remodelling to predefine first response to inductive signals. <i>Nature Communications</i> , 2019, 10, 4269.	5.8	45
2283	Adenovirus infection is associated with altered gut microbial communities in a non-human primate. <i>Scientific Reports</i> , 2019, 9, 13410.	1.6	32
2284	Metagenome of a polluted river reveals a reservoir of metabolic and antibiotic resistance genes. <i>Environmental Microbiomes</i> , 2019, 14, 5.	2.2	44
2285	Dramatic Remodeling of the Gut Microbiome Around Parturition and Its Relationship With Host Serum Metabolic Changes in Sows. <i>Frontiers in Microbiology</i> , 2019, 10, 2123.	1.5	22
2286	Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of prakriti. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	11
2287	Field Evaluation of DNA Based Biodiversity Monitoring of Caribbean Mosquitoes. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	17
2288	Effect of acclimation on inoculum functioning and dynamics within a microbial community. <i>Biomass and Bioenergy</i> , 2019, 128, 105312.	2.9	8
2289	Arsenic mobilization in a high arsenic groundwater revealed by metagenomic and Geochip analyses. <i>Scientific Reports</i> , 2019, 9, 12972.	1.6	23
2290	The Root Endophytic Fungi Community Structure of <i>Pennisetum sinense</i> from Four Representative Provinces in China. <i>Microorganisms</i> , 2019, 7, 332.	1.6	5
2291	Improvement of Feed Efficiency in Pigs through Microbial Modulation via Fecal Microbiota Transplantation in Sows and Dietary Supplementation of Inulin in Offspring. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	33
2292	Comparative Analysis of Fecal Microbiota Composition Between Rheumatoid Arthritis and Osteoarthritis Patients. <i>Genes</i> , 2019, 10, 748.	1.0	62
2293	The fecal resistome of dairy cattle is associated with diet during nursing. <i>Nature Communications</i> , 2019, 10, 4406.	5.8	100
2294	Effects of dietary supplementation of inulin on rumen fermentation and bacterial microbiota, inflammatory response and growth performance in finishing beef steers fed high or low-concentrate diet. <i>Animal Feed Science and Technology</i> , 2019, 258, 114299.	1.1	29
2295	Metal distribution and biological diversity of crusts in paddy fields polluted with different levels of cadmium. <i>Ecotoxicology and Environmental Safety</i> , 2019, 184, 109620.	2.9	20
2296	Variation of airborne DNA mass ratio and fungal diversity in fine particles with day-night difference during an entire winter haze evolution process of Central China. <i>Science of the Total Environment</i> , 2019, 694, 133802.	3.9	10
2297	Reduction of <i>Escherichia coli</i> O157:H7, <i>Listeria monocytogenes</i> , and Naturally Present Microbe Counts on Lettuce using an Acid Mixture of Acetic and Lactic Acid. <i>Microorganisms</i> , 2019, 7, 373.	1.6	16
2298	Spatial variation of sediment bacterial community in an acid mine drainage contaminated area and surrounding river basin. <i>Journal of Environmental Management</i> , 2019, 251, 109542.	3.8	25

#	ARTICLE	IF	CITATIONS
2299	Antibiotic Exposure Disturbs the Gut Microbiota and Its Metabolic Phenotype Differently in Rats with Advanced-Stage Type 1 Diabetes and Age-Matched Controls. <i>Journal of Proteome Research</i> , 2019, 18, 3944-3954.	1.8	2
2300	A mutation in mouse KrÄ¼ppel-like factor 15 alters the gut microbiome and response to obesogenic diet. <i>PLoS ONE</i> , 2019, 14, e0222536.	1.1	3
2301	Effects of Maternal Low-Protein Diet on Microbiota Structure and Function in the Jejunum of Huzhu Bamei Suckling Piglets. <i>Animals</i> , 2019, 9, 713.	1.0	8
2302	Soft sweep development of resistance in <i>Escherichia coli</i> under fluoroquinolone stress. <i>Journal of Microbiology</i> , 2019, 57, 1056-1064.	1.3	0
2303	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. <i>Genome Biology</i> , 2019, 20, 196.	3.8	67
2304	Colonic Microbiota and Metabolites Response to Different Dietary Protein Sources in a Piglet Model. <i>Frontiers in Nutrition</i> , 2019, 6, 151.	1.6	18
2305	Responses of soil nosZ-type denitrifying microbial communities to the various land-use types of the Loess Plateau, China. <i>Soil and Tillage Research</i> , 2019, 195, 104378.	2.6	11
2306	Looks can be deceiving: the deceptive milkcaps (<i>Lactifluus</i> , <i>Russulaceae</i>) exhibit low morphological variance but harbour high genetic diversity. <i>IMA Fungus</i> , 2019, 10, 14.	1.7	13
2307	Paddy System with a Hybrid Rice Enhances Cyanobacteria Nostoc and Increases N ₂ Fixation. <i>Pedosphere</i> , 2019, 29, 374-387.	2.1	10
2308	Water stress affects the frequency of Firmicutes, Clostridiales and <i>Lysobacter</i> in rhizosphere soils of greenhouse grape. <i>Agricultural Water Management</i> , 2019, 226, 105776.	2.4	35
2309	The local environment regulates biogeographic patterns of soil fungal communities on the Loess Plateau. <i>Catena</i> , 2019, 183, 104220.	2.2	28
2310	Bacterioplankton community responses and the potential ecological thresholds along disturbance gradients. <i>Science of the Total Environment</i> , 2019, 696, 134015.	3.9	14
2311	Gingival solitary chemosensory cells are immune sentinels for periodontitis. <i>Nature Communications</i> , 2019, 10, 4496.	5.8	40
2312	Variable effects of local management on coral defenses against a thermally regulated bleaching pathogen. <i>Science Advances</i> , 2019, 5, eaay1048.	4.7	15
2313	Stable integrant-specific differences in bimodal HIV-1 expression patterns revealed by high-throughput analysis. <i>PLoS Pathogens</i> , 2019, 15, e1007903.	2.1	5
2314	Effect of Feeding Cold-Pressed Sunflower Cake on Ruminal Fermentation, Lipid Metabolism and Bacterial Community in Dairy Cows. <i>Animals</i> , 2019, 9, 755.	1.0	15
2315	Comparative analysis of midgut bacterial community under <i>Vibrio splendidus</i> infection in <i>Apostichopus japonicus</i> with hindgut as a reference. <i>Aquaculture</i> , 2019, 513, 734427.	1.7	15
2316	The pink staircase of Sully-sur-Loire castle: Even bacteria like historic stonework. <i>International Biodeterioration and Biodegradation</i> , 2019, 145, 104805.	1.9	9

#	ARTICLE	IF	CITATIONS
2317	Temporal Dynamics in Rumen Bacterial Community Composition of Finishing Steers during an Adaptation Period of Three Months. <i>Microorganisms</i> , 2019, 7, 410.	1.6	23
2318	Distinct Drivers of Core and Accessory Components of Soil Microbial Community Functional Diversity under Environmental Changes. <i>MSystems</i> , 2019, 4, .	1.7	28
2319	Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. <i>Nature Microbiology</i> , 2019, 4, 2082-2089.	5.9	56
2320	Taxonomic and Metabolic Incongruence in the Ancient Genus <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2170.	1.5	40
2321	Biodiversity of leaf litter fungi in streams along a latitudinal gradient. <i>Science of the Total Environment</i> , 2019, 661, 306-315.	3.9	53
2322	Chlorogenic acid relieves lead-induced cognitive impairments and hepato-renal damage <i>via</i> regulating the dysbiosis of the gut microbiota in mice. <i>Food and Function</i> , 2019, 10, 681-690.	2.1	51
2323	Atypical Hemolytic <i>Listeria innocua</i> Isolates Are Virulent, albeit Less than <i>Listeria monocytogenes</i> . <i>Infection and Immunity</i> , 2019, 87, .	1.0	41
2324	Biogeographic Distribution Patterns of the Archaeal Communities Across the Black Soil Zone of Northeast China. <i>Frontiers in Microbiology</i> , 2019, 10, 23.	1.5	27
2325	Microplastics induce intestinal inflammation, oxidative stress, and disorders of metabolome and microbiome in zebrafish. <i>Science of the Total Environment</i> , 2019, 662, 246-253.	3.9	525
2326	Coral microbiome diversity reflects mass coral bleaching susceptibility during the 2016 El Niño heat wave. <i>Ecology and Evolution</i> , 2019, 9, 938-956.	0.8	81
2327	Intestinal microbiota predicts lung cancer patients at risk of immune-related diarrhea. <i>Immunotherapy</i> , 2019, 11, 385-396.	1.0	40
2328	Revealing the biodiversity and the response of pathogen to a combined use of procymidone and thiamethoxam in tomatoes. <i>Food Chemistry</i> , 2019, 284, 73-79.	4.2	11
2329	Multiple interactions between tree composition and diversity and microbial diversity underly litter decomposition. <i>Geoderma</i> , 2019, 341, 161-171.	2.3	49
2330	The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. <i>GigaScience</i> , 2019, 8, .	3.3	143
2331	Linking a mutation to survival in wild mice. <i>Science</i> , 2019, 363, 499-504.	6.0	126
2332	Hadal water sampling by in situ microbial filtration and fixation (ISMIFF) apparatus. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 144, 132-137.	0.6	29
2333	Coupled effects of land use pattern and hydrological regime on composition and diversity of riverine eukaryotic community in a coastal watershed of Southeast China. <i>Science of the Total Environment</i> , 2019, 660, 787-798.	3.9	23
2334	Feasible and effective reuse of municipal sludge for vegetation restoration: physiochemical characteristics and microbial diversity. <i>Scientific Reports</i> , 2019, 9, 879.	1.6	24

#	ARTICLE	IF	CITATIONS
2335	Exercise training modifies gut microbiota with attenuated host responses to sepsis in wild-type mice. <i>FASEB Journal</i> , 2019, 33, 5772-5781.	0.2	21
2336	The Human Ocular Surface Fungal Microbiome. , 2019, 60, 451.		54
2337	Comparison of the Vaginal Microbiomes of Premenopausal and Postmenopausal Women. <i>Frontiers in Microbiology</i> , 2019, 10, 193.	1.5	89
2338	Genomic resources for the Neotropical tree genus <i>Cedrela</i> (Meliaceae) and its relatives. <i>BMC Genomics</i> , 2019, 20, 58.	1.2	15
2339	Intestinal Morphologic and Microbiota Responses to Dietary <i>Bacillus</i> spp. in a Broiler Chicken Model. <i>Frontiers in Physiology</i> , 2018, 9, 1968.	1.3	77
2340	Integrating 16S rRNA Sequencing and LC-MS-Based Metabolomics to Evaluate the Effects of Live Yeast on Rumen Function in Beef Cattle. <i>Animals</i> , 2019, 9, 28.	1.0	42
2341	Retention of Microbiota Diversity by Lactose-Free Milk in a Mouse Model of Elderly Gut Microbiota. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2098-2112.	2.4	11
2342	Exploring the Fecal Microbial Composition and Metagenomic Functional Capacities Associated With Feed Efficiency in Commercial DLY Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 52.	1.5	77
2343	Changes in rhizosphere bacterial and fungal community composition with vegetation restoration in planted forests. <i>Land Degradation and Development</i> , 2019, 30, 1147-1157.	1.8	63
2344	Allelic diversity and selection at the MHC class I and class II in a bottlenecked bird of prey, the White-tailed Eagle. <i>BMC Evolutionary Biology</i> , 2019, 19, 2.	3.2	22
2345	Unicellular Cyanobacteria Are Important Components of Phytoplankton Communities in Australia's Northern Oceanic Ecoregions. <i>Frontiers in Microbiology</i> , 2018, 9, 3356.	1.5	12
2346	Water management impacts the soil microbial communities and total arsenic and methylated arsenicals in rice grains. <i>Environmental Pollution</i> , 2019, 247, 736-744.	3.7	68
2347	A panel of eGFP reporters for single base editing by APOBEC-Cas9 editosome complexes. <i>Scientific Reports</i> , 2019, 9, 497.	1.6	38
2348	<i>Lactobacillus plantarum</i> PFM 105 Promotes Intestinal Development Through Modulation of Gut Microbiota in Weaning Piglets. <i>Frontiers in Microbiology</i> , 2019, 10, 90.	1.5	82
2349	Genomes of three bacteriophages from the deep subsurface aquifer. <i>Data in Brief</i> , 2019, 22, 488-491.	0.5	5
2350	Design of microbial consortia for the fermentation of pea-protein-enriched emulsions. <i>International Journal of Food Microbiology</i> , 2019, 293, 124-136.	2.1	51
2351	In vitro synergy of sertraline and tetracycline cannot be reproduced in pigs orally challenged with a tetracycline resistant <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2019, 19, 12.	1.3	4
2352	Detecting antibiotic resistance genes and human potential pathogenic Bacteria in fishmeal by culture-independent method. <i>Environmental Science and Pollution Research</i> , 2019, 26, 8665-8674.	2.7	10

#	ARTICLE	IF	CITATIONS
2353	The distribution of sediment bacterial community in mangroves across China was governed by geographic location and eutrophication. <i>Marine Pollution Bulletin</i> , 2019, 140, 198-203.	2.3	35
2354	Reducing plant uptake of a brominated contaminant (2,2,4,4-tetrabrominated diphenyl ether) by incorporation of maize straw into horticultural soil. <i>Science of the Total Environment</i> , 2019, 663, 29-37.	3.9	10
2355	The antimicrobial potential of <i>Streptomyces</i> from insect microbiomes. <i>Nature Communications</i> , 2019, 10, 516.	5.8	222
2356	Oral neonatal antibiotic treatment perturbs gut microbiota and aggravates central nervous system autoimmunity in Dark Agouti rats. <i>Scientific Reports</i> , 2019, 9, 918.	1.6	29
2357	Amazon forest-to-agriculture conversion alters rhizosphere microbiome composition while functions are kept. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	32
2358	New <i>de novo</i> assembly of the Atlantic bottlenose dolphin (<i>Tursiops truncatus</i>) improves genome completeness and provides haplotype phasing. <i>GigaScience</i> , 2019, 8, .	3.3	9
2359	Bacterial community composition in a polyculture system of <i>Rhopilema esculenta</i> , <i>Penaeus monodon</i> and <i>Ruditapes philippinarum</i> . <i>Aquaculture Research</i> , 2019, 50, 973-978.	0.9	3
2360	Picoeukaryotic Diversity And Activity in the Northwestern Pacific Ocean Based on rDNA and rRNA High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 3259.	1.5	11
2361	Characterization of Fungal nirK-Containing Communities and N ₂ O Emission From Fungal Denitrification in Arable Soils. <i>Frontiers in Microbiology</i> , 2019, 10, 117.	1.5	27
2362	Soil bacterial communities with an indicative function response to nutrients in wetlands of Northeastern China that have undergone natural restoration. <i>Ecological Indicators</i> , 2019, 101, 562-571.	2.6	26
2363	Organic carbon: An overlooked factor that determines the antibiotic resistome in drinking water sand filter biofilm. <i>Environment International</i> , 2019, 125, 117-124.	4.8	42
2364	Eutrophication influences methanotrophic activity, abundance and community structure in freshwater lakes. <i>Science of the Total Environment</i> , 2019, 662, 863-872.	3.9	55
2365	Impact of gut microbiota structure in heat-stressed broilers. <i>Poultry Science</i> , 2019, 98, 2405-2413.	1.5	108
2366	Key colonist pools and habitat filters mediate the composition of fiddler crab-associated bacterial communities. <i>Ecology</i> , 2019, 100, e02628.	1.5	12
2367	Llama peripheral B-cell populations producing conventional and heavy chain-only IgG subtypes are phenotypically indistinguishable but immunogenetically distinct. <i>Immunogenetics</i> , 2019, 71, 307-320.	1.2	16
2368	<i>Streptomyces pactum</i> Act12 controls tomato yellow leaf curl virus disease and alters rhizosphere microbial communities. <i>Biology and Fertility of Soils</i> , 2019, 55, 149-169.	2.3	25
2369	D- and L-Aspartate regulates growth performance, inflammation and intestinal microbial community in young pigs. <i>Food and Function</i> , 2019, 10, 1028-1037.	2.1	21
2370	Microbial biofilm formation and community structure on low-density polyethylene microparticles in lake water microcosms. <i>Environmental Pollution</i> , 2019, 252, 94-102.	3.7	126

#	ARTICLE	IF	CITATIONS
2371	Ginkgo agroforestry practices alter the fungal community structures at different soil depths in Eastern China. <i>Environmental Science and Pollution Research</i> , 2019, 26, 21253-21263.	2.7	10
2372	A systematic approach re-analyzing the effects of temperature disturbance on the microbial community of mesophilic anaerobic digestion. <i>Scientific Reports</i> , 2019, 9, 6560.	1.6	13
2373	Concurrent and long-term associations between the endometrial microbiota and endometrial transcriptome in postpartum dairy cows. <i>BMC Genomics</i> , 2019, 20, 405.	1.2	13
2374	Age-based dynamic changes of phylogenetic composition and interaction networks of health pig gut microbiome feeding in a uniformed condition. <i>BMC Veterinary Research</i> , 2019, 15, 172.	0.7	74
2375	Effect of intestinal tapeworms on the gut microbiota of the common carp, <i>Cyprinus carpio</i> . <i>Parasites and Vectors</i> , 2019, 12, 252.	1.0	22
2376	Tracing the history of LINE and SINE extinction in sigmodontine rodents. <i>Mobile DNA</i> , 2019, 10, 22.	1.3	17
2377	An experimental assay of the interactions of amino acids from orthologous sequences shaping a complex fitness landscape. <i>PLoS Genetics</i> , 2019, 15, e1008079.	1.5	71
2378	Comparison of Bacterial Populations in the Ceca of Swine at Two Different Stages and Their Functional Annotations. <i>Genes</i> , 2019, 10, 382.	1.0	13
2379	Changes in the Soil Bacterial Community in a Chronosequence of Temperate Walnut-Based Intercropping Systems. <i>Forests</i> , 2019, 10, 299.	0.9	22
2380	Parallel Molecular Evolution in Pathways, Genes, and Sites in High-Elevation Hummingbirds Revealed by Comparative Transcriptomics. <i>Genome Biology and Evolution</i> , 2019, 11, 1573-1585.	1.1	49
2381	Soil microbiome mediates positive plant diversity–productivity relationships in late successional grassland species. <i>Ecology Letters</i> , 2019, 22, 1221-1232.	3.0	54
2382	Sediment pH, not the bacterial diversity, determines <i>Escherichia coli</i> O157:H7 survival in estuarine sediments. <i>Environmental Pollution</i> , 2019, 252, 1078-1086.	3.7	15
2383	Compositional and Functional Analysis of the Microbiome in Tissue and Saliva of Oral Squamous Cell Carcinoma. <i>Frontiers in Microbiology</i> , 2019, 10, 1439.	1.5	50
2384	Variations in soil bacterial taxonomic profiles and putative functions in response to straw incorporation combined with N fertilization during the maize growing season. <i>Agriculture, Ecosystems and Environment</i> , 2019, 283, 106578.	2.5	59
2385	Sludge bio-drying followed by land application could control the spread of antibiotic resistance genes. <i>Environment International</i> , 2019, 130, 104906.	4.8	26
2386	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019, 4, 1826-1831.	5.9	149
2387	Farm-like indoor microbiota in non-farm homes protects children from asthma development. <i>Nature Medicine</i> , 2019, 25, 1089-1095.	15.2	219
2388	Salivary Microbial Dysbiosis is Associated with Systemic Inflammatory Markers and Predicted Oral Metabolites in Non-Small Cell Lung Cancer Patients. <i>Journal of Cancer</i> , 2019, 10, 1651-1662.	1.2	57

#	ARTICLE	IF	CITATIONS
2389	Aerobic cometabolism of tetrabromobisphenol A by marine bacterial consortia. <i>Environmental Science and Pollution Research</i> , 2019, 26, 23832-23841.	2.7	17
2390	Gut microbial-derived butyrate is inversely associated with IgE responses to allergens in childhood asthma. <i>Pediatric Allergy and Immunology</i> , 2019, 30, 689-697.	1.1	89
2391	Analysis of gut microbiota and the effect of lauric acid against necrotic enteritis in <i>Clostridium perfringens</i> and <i>Eimeria</i> side-by-side challenge model. <i>PLoS ONE</i> , 2019, 14, e0205784.	1.1	91
2392	Modulation of Growth Performance and Intestinal Microbiota in Chickens Fed Plant Extracts or Virginiamycin. <i>Frontiers in Microbiology</i> , 2019, 10, 1333.	1.5	47
2393	Variability of the Ability of Complex Microbial Communities to Exclude Microbes Carrying Antibiotic Resistance Genes in Rabbits. <i>Frontiers in Microbiology</i> , 2019, 10, 1503.	1.5	4
2394	Gut microbiota determines the prevention effects of <i>Luffa cylindrica</i> (L.) Roem supplementation against obesity and associated metabolic disorders induced by high-fat diet. <i>FASEB Journal</i> , 2019, 33, 10339-10352.	0.2	47
2395	Effects of dietary supplementation with lysozyme on the structure and function of the cecal microbiota in broiler chickens. <i>PLoS ONE</i> , 2019, 14, e0216748.	1.1	20
2396	Community Structure of Bacteria Associated With Drifting <i>Sargassum horneri</i> , the Causative Species of Golden Tide in the Yellow Sea. <i>Frontiers in Microbiology</i> , 2019, 10, 1192.	1.5	22
2397	Catabolism of Nucleic Acids by a Cystic Fibrosis <i>Pseudomonas aeruginosa</i> Isolate: An Adaptive Pathway to Cystic Fibrosis Sputum Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 1199.	1.5	11
2398	Modulation of Saliva Microbiota through Prebiotic Intervention in HIV-Infected Individuals. <i>Nutrients</i> , 2019, 11, 1346.	1.7	10
2399	Microbial indicators of environmental perturbations in coral reef ecosystems. <i>Microbiome</i> , 2019, 7, 94.	4.9	126
2400	Vegetation biomass and soil moisture coregulate bacterial community succession under altered precipitation regimes in a desert steppe in northwestern China. <i>Soil Biology and Biochemistry</i> , 2019, 136, 107520.	4.2	82
2401	Selection of a Microbial Community in the Course of Formation of Acid Mine Drainage. <i>Microbiology</i> , 2019, 88, 292-299.	0.5	10
2402	Archaeal community variation in the Qinhuangdao coastal aquaculture zone revealed by high-throughput sequencing. <i>PLoS ONE</i> , 2019, 14, e0218611.	1.1	8
2403	The origins and adaptation of European potatoes reconstructed from historical genomes. <i>Nature Ecology and Evolution</i> , 2019, 3, 1093-1101.	3.4	73
2404	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. <i>Nature Methods</i> , 2019, 16, 603-606.	9.0	262
2405	Exploring the persistence and spreading of antibiotic resistance from manure to biocompost, soils and vegetables. <i>Science of the Total Environment</i> , 2019, 688, 262-269.	3.9	60
2406	Effects of struvite-humic acid loaded biochar/bentonite composite amendment on Zn(II) and antibiotic resistance genes in manure-soil. <i>Chemical Engineering Journal</i> , 2019, 375, 122013.	6.6	41

#	ARTICLE	IF	CITATIONS
2407	Improved synergistic dechlorination of PCP in flooded soil microcosms with supplementary electron donors, as revealed by strengthened connections of functional microbial interactome. <i>Soil Biology and Biochemistry</i> , 2019, 136, 107515.	4.2	27
2408	Nonferrous metal (loid)s mediate bacterial diversity in an abandoned mine tailing impoundment. <i>Environmental Science and Pollution Research</i> , 2019, 26, 24806-24818.	2.7	7
2409	Changes in endophytic bacterial communities during different growth stages of cucumber (<i>Cucumis Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>)	1.7	12
2410	High-Quality Library Preparation for NGS-Based Immunoglobulin Germline Gene Inference and Repertoire Expression Analysis. <i>Frontiers in Immunology</i> , 2019, 10, 660.	2.2	55
2411	Marine microplastic-associated bacterial community succession in response to geography, exposure time, and plastic type in China's coastal seawaters. <i>Marine Pollution Bulletin</i> , 2019, 145, 278-286.	2.3	100
2412	The influence of chlorination timing and concentration on microbial communities in labyrinth channels: implications for biofilm removal. <i>Biofouling</i> , 2019, 35, 401-415.	0.8	12
2413	Antibiotic Exposure Has Sex-Dependent Effects on the Gut Microbiota and Metabolism of Short-Chain Fatty Acids and Amino Acids in Mice. <i>MSystems</i> , 2019, 4, .	1.7	42
2414	Parthenogenesis in a captive Asian water dragon (<i>Physignathus cocincinus</i>) identified with novel microsatellites. <i>PLoS ONE</i> , 2019, 14, e0217489.	1.1	11
2415	Influence of operation conditions on methane production from swine wastewater treated by a self-agitation anaerobic reactor. <i>International Biodeterioration and Biodegradation</i> , 2019, 143, 104710.	1.9	18
2416	Anthropization level of Lascaux Cave microbiome shown by regional scale comparisons of pristine and anthropized caves. <i>Molecular Ecology</i> , 2019, 28, 3383-3394.	2.0	30
2417	Biochar Amendment Stimulates Utilization of Plant-Derived Carbon by Soil Bacteria in an Intercropping System. <i>Frontiers in Microbiology</i> , 2019, 10, 1361.	1.5	40
2418	A holistic view of gallic acid-induced attenuation in colitis based on microbiome-metabolomics analysis. <i>Food and Function</i> , 2019, 10, 4046-4061.	2.1	46
2419	Behavior and gut bacteria of <i>Partamona helleri</i> under sublethal exposure to a bioinsecticide and a leaf fertilizer. <i>Chemosphere</i> , 2019, 234, 187-195.	4.2	26
2420	High microbial diversity of the nitric oxide dismutation reaction revealed by PCR amplification and analysis of the nod gene. <i>International Biodeterioration and Biodegradation</i> , 2019, 143, 104708.	1.9	10
2421	Modulation of the Caecal Gut Microbiota of Mice by Dietary Supplement Containing Resistant Starch: Impact Is Donor-Dependent. <i>Frontiers in Microbiology</i> , 2019, 10, 1234.	1.5	18
2422	Continuous cropping of soybean alters the bulk and rhizospheric soil fungal communities in a Mollisol of Northeast PR China. <i>Land Degradation and Development</i> , 2019, 30, 1725-1738.	1.8	41
2423	Yogurt improves insulin resistance and liver fat in obese women with nonalcoholic fatty liver disease and metabolic syndrome: a randomized controlled trial. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 1611-1619.	2.2	65
2424	Phosphorus mediates soil prokaryote distribution pattern along a small-scale elevation gradient in Noijin Kangsang Peak, Tibetan Plateau. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	17

#	ARTICLE	IF	CITATIONS
2425	Characterization of Mucosa-Associated Microbiota in Matched Cancer and Non-neoplastic Mucosa From Patients With Colorectal Cancer. <i>Frontiers in Microbiology</i> , 2019, 10, 1317.	1.5	21
2426	Probiotic <i>Lactobacillus casei</i> : Effective for Managing Childhood Diarrhea by Altering Gut Microbiota and Attenuating Fecal Inflammatory Markers. <i>Nutrients</i> , 2019, 11, 1150.	1.7	80
2427	Effect of gastrointestinal microbiome and its diversity on the expression of tumor-infiltrating lymphocytes in breast cancer. <i>Oncology Letters</i> , 2019, 17, 5050-5056.	0.8	13
2428	Application of independent immobilization in benzo[a]pyrene biodegradation by synthetic microbial consortium. <i>Environmental Science and Pollution Research</i> , 2019, 26, 21052-21058.	2.7	11
2429	Key extracellular enzymes triggered high-efficiency composting associated with bacterial community succession. <i>Bioresource Technology</i> , 2019, 288, 121576.	4.8	62
2430	Biogeochemical gold cycling selects metal-resistant bacteria that promote gold particle transformation. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	14
2431	Microhomologies are prevalent at Cas9-induced larger deletions. <i>Nucleic Acids Research</i> , 2019, 47, 7402-7417.	6.5	100
2432	Response of Fish Gut Microbiota to Toxin-Containing Cyanobacterial Extracts: A Microcosm Study on the Medaka (<i>Oryzias latipes</i>). <i>Environmental Science and Technology Letters</i> , 2019, 6, 341-347.	3.9	31
2433	Dietary probiotics have different effects on the composition of fecal microbiota in farmed raccoon dog (<i>Nyctereutes procyonoides</i>) and silver fox (<i>Vulpes vulpes fulva</i>). <i>BMC Microbiology</i> , 2019, 19, 109.	1.3	14
2434	Pharmacological restoration of gut barrier function in stressed neonates partially reverses long-term alterations associated with maternal separation. <i>Psychopharmacology</i> , 2019, 236, 1583-1596.	1.5	22
2435	Metataxonomic analysis of the bacterial diversity in table olive dressing components. <i>Food Control</i> , 2019, 105, 190-197.	2.8	9
2436	A distal enhancer maintaining <i>Hoxa1</i> expression orchestrates retinoic acid-induced early ESCs differentiation. <i>Nucleic Acids Research</i> , 2019, 47, 6737-6752.	6.5	18
2437	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019, 11, 484.	1.5	27
2438	Distinct Biogeography of Different Fungal Guilds and Their Associations With Plant Species Richness in Forest Ecosystems. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	22
2439	Surface sterilization methods impact measures of internal microbial diversity in ticks. <i>Parasites and Vectors</i> , 2019, 12, 268.	1.0	81
2440	Response of the microbial community to the methanogenic performance of biologically hydrolyzed sewage sludge with variable hydraulic retention times. <i>Bioresource Technology</i> , 2019, 288, 121581.	4.8	19
2441	Molecular characterization of methanogenic microbial communities for degrading various types of polycyclic aromatic hydrocarbon. <i>Journal of Environmental Sciences</i> , 2019, 86, 97-106.	3.2	28
2442	Ruminal microbiome-host crosstalk stimulates the development of the ruminal epithelium in a lamb model. <i>Microbiome</i> , 2019, 7, 83.	4.9	116

#	ARTICLE	IF	CITATIONS
2443	Longitudinal Gut Bacterial Colonization and Its Influencing Factors of Low Birth Weight Infants During the First 3 Months of Life. <i>Frontiers in Microbiology</i> , 2019, 10, 1105.	1.5	18
2444	Importance of Species Sorting and Immigration on the Bacterial Assembly of Different-Sized Aggregates in a Full-Scale Aerobic Granular Sludge Plant. <i>Environmental Science & Technology</i> , 2019, 53, 8291-8301.	4.6	93
2445	Fecal Microbial Communities in a Large Representative Cohort of California Dairy Cows. <i>Frontiers in Microbiology</i> , 2019, 10, 1093.	1.5	60
2446	Fast bacterial succession associated with the decomposition of <i>Quercus wutaishanica</i> litter on the Loess Plateau. <i>Biogeochemistry</i> , 2019, 144, 119-131.	1.7	17
2447	Spatial differences in bacterial communities preserved in soils archived for a decade. <i>Applied Soil Ecology</i> , 2019, 142, 64-71.	2.1	3
2448	Effects of ozone treatment on performance and microbial community composition in biofiltration systems treating ethyl acetate vapours. <i>Chemosphere</i> , 2019, 233, 67-75.	4.2	13
2449	The negative impact of cadmium on nitrogen transformation processes in a paddy soil is greater under non-flooding than flooding conditions. <i>Environment International</i> , 2019, 129, 451-460.	4.8	59
2450	Co-occurrence patterns between bacterial and fungal communities in response to a vegetation gradient in a freshwater wetland. <i>Canadian Journal of Microbiology</i> , 2019, 65, 722-737.	0.8	17
2451	Dynamic construction of gut microbiota may influence allergic diseases of infants in Southwest China. <i>BMC Microbiology</i> , 2019, 19, 123.	1.3	35
2452	The effects of chemical and organic fertilizer usage on rhizosphere soil in tea orchards. <i>PLoS ONE</i> , 2019, 14, e0217018.	1.1	188
2453	Higher Bacterial Diversity of Gut Microbiota in Different Natural Populations of Leafhopper Vector Does Not Influence WDV Transmission. <i>Frontiers in Microbiology</i> , 2019, 10, 1144.	1.5	15
2454	Mucosa-Associated Microbiota in Gastric Cancer Tissues Compared With Non-cancer Tissues. <i>Frontiers in Microbiology</i> , 2019, 10, 1261.	1.5	80
2455	Effects of rumen-protected glucose on ileal microbiota and genes involved in ileal epithelial metabolism and immune homeostasis in transition dairy cows. <i>Animal Feed Science and Technology</i> , 2019, 254, 114199.	1.1	14
2456	Oral microbial dysbiosis linked to worsened periodontal condition in rheumatoid arthritis patients. <i>Scientific Reports</i> , 2019, 9, 8379.	1.6	94
2457	GenPipes: an open-source framework for distributed and scalable genomic analyses. <i>GigaScience</i> , 2019, 8, .	3.3	121
2458	A microbial factory for defensive kahalalides in a tripartite marine symbiosis. <i>Science</i> , 2019, 364, .	6.0	74
2459	Archaeal Communities in Deep Terrestrial Subsurface Underneath the Deccan Traps, India. <i>Frontiers in Microbiology</i> , 2019, 10, 1362.	1.5	15
2460	Dynamic Alterations in the Gut Microbiota of Collagen-Induced Arthritis Rats Following the Prolonged Administration of Total Glucosides of <i>Paeny</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 204.	1.8	44

#	ARTICLE	IF	CITATIONS
2461	Individual and combined effects of ammonia-N and sulfide on the immune function and intestinal microbiota of Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2019, 92, 230-240.	1.6	31
2462	Host-microbiome interactions in response to a high-saturated fat diet and fish-oil supplementation in zebrafish adult. <i>Journal of Functional Foods</i> , 2019, 60, 103416.	1.6	10
2463	A symbiotic balancing act: arbuscular mycorrhizal specificity and specialist fungus gnat pollination in the mycoheterotrophic genus <i>Thismia</i> (Thismiaceae). <i>Annals of Botany</i> , 2019, 124, 331-342.	1.4	14
2464	Biogeography of the free-living and particle-attached bacteria in Tibetan lakes. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	35
2465	Gut dysbiosis and lack of short chain fatty acids in a Chinese cohort of patients with multiple sclerosis. <i>Neurochemistry International</i> , 2019, 129, 104468.	1.9	96
2466	Analysis of marine microbial communities colonizing various metallic materials and rust layers. <i>Biofouling</i> , 2019, 35, 429-442.	0.8	39
2467	Substrate and spatial variables are major determinants of fungal community in karst caves in Southwest China. <i>Journal of Biogeography</i> , 2019, 46, 1504-1518.	1.4	21
2468	IgA-Targeted <i>Lactobacillus jensenii</i> Modulated Gut Barrier and Microbiota in High-Fat Diet-Fed Mice. <i>Frontiers in Microbiology</i> , 2019, 10, 1179.	1.5	22
2469	Isolation of phytase-producing yeasts from rice seedlings for prospective probiotic applications. <i>3 Biotech</i> , 2019, 9, 216.	1.1	8
2470	Effect of different forage-to-concentrate ratios on ruminal bacterial structure and real-time methane production in sheep. <i>PLoS ONE</i> , 2019, 14, e0214777.	1.1	24
2471	Biogeochemistry, microbial activity, and diversity in surface and subsurface deep-sea sediments of South China Sea. <i>Limnology and Oceanography</i> , 2019, 64, 2252-2270.	1.6	33
2472	Glyphosate and glyphosate-based herbicide exposure during the peripartum period affects maternal brain plasticity, maternal behaviour and microbiome. <i>Journal of Neuroendocrinology</i> , 2019, 31, e12731.	1.2	69
2473	The roles of morphological traits, resource variation and resource partitioning associated with the dietary niche expansion in the fish-eating bat <i>Myotis pilosus</i> . <i>Molecular Ecology</i> , 2019, 28, 2944-2954.	2.0	22
2474	Endophytic Communities of Transgenic Poplar Were Determined by the Environment and Niche Rather Than by Transgenic Events. <i>Frontiers in Microbiology</i> , 2019, 10, 588.	1.5	23
2475	Leaf and Root Endospheres Harbor Lower Fungal Diversity and Less Complex Fungal Co-occurrence Patterns Than Rhizosphere. <i>Frontiers in Microbiology</i> , 2019, 10, 1015.	1.5	60
2476	Evaluating the Effect of QIIME Balanced Default Parameters on Metataxonomic Analysis Workflows With a Mock Community. <i>Frontiers in Microbiology</i> , 2019, 10, 1084.	1.5	8
2477	Paleogenome Reveals Genetic Contribution of Extinct Giant Panda to Extant Populations. <i>Current Biology</i> , 2019, 29, 1695-1700.e6.	1.8	22
2478	High-throughput sequencing analysis of bacterial community composition and quality characteristics in refrigerated pork during storage. <i>Food Microbiology</i> , 2019, 83, 86-94.	2.1	87

#	ARTICLE	IF	CITATIONS
2479	The Microbiome of Temporal Arteries. <i>Pathogens and Immunity</i> , 2019, 4, 21.	1.4	19
2480	Analysis of the Rumen Microbiota of Beef Calves Supplemented During the Suckling Phase. <i>Frontiers in Microbiology</i> , 2019, 10, 1131.	1.5	15
2481	Genome-wide reconstitution of chromatin transactions reveals that RSC preferentially disrupts H2AZ-containing nucleosomes. <i>Genome Research</i> , 2019, 29, 988-998.	2.4	21
2482	The Variation of Nasal Microbiota Caused by Low Levels of Gaseous Ammonia Exposure in Growing Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 1083.	1.5	19
2483	Bacterial community composition and diversity in Koshi River, the largest river of Nepal. <i>Ecological Indicators</i> , 2019, 104, 501-511.	2.6	32
2484	Bioturbation of blood clam <i>Tegillarca granosa</i> on benthic nutrient fluxes and microbial community in an aquaculture wastewater treatment system. <i>International Biodeterioration and Biodegradation</i> , 2019, 142, 73-82.	1.9	27
2485	Microbial production and consumption of dissolved organic matter in glacial ecosystems on the Tibetan Plateau. <i>Water Research</i> , 2019, 160, 18-28.	5.3	78
2486	Prediction of pathogenicity genes involved in adaptation to a lupin host in the fungal pathogens <i>Botrytis cinerea</i> and <i>Sclerotinia sclerotiorum</i> via comparative genomics. <i>BMC Genomics</i> , 2019, 20, 385.	1.2	11
2487	Draft Genome Sequence of <i>Chlorobium</i> sp. Strain N1, a Marine Fe(II)-Oxidizing Green Sulfur Bacterium. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
2488	Haem iron reshapes colonic luminal environment: impact on mucosal homeostasis and microbiome through aldehyde formation. <i>Microbiome</i> , 2019, 7, 72.	4.9	38
2489	Transcript and metabolic adjustments triggered by drought in <i>Ilex paraguariensis</i> leaves. <i>Planta</i> , 2019, 250, 445-462.	1.6	20
2490	Soil bacterial and fungal communities and the associated nutrient cycling responses to forest conversion after selective logging in a subtropical forest of China. <i>Forest Ecology and Management</i> , 2019, 444, 308-317.	1.4	29
2491	Predicting Growth and Carcass Traits in Swine Using Microbiome Data and Machine Learning Algorithms. <i>Scientific Reports</i> , 2019, 9, 6574.	1.6	38
2492	Characterization of 15 nuclear microsatellite markers for <i>Afzelia africana</i> (Fabaceae) and related species. <i>Applications in Plant Sciences</i> , 2019, 7, e01249.	0.8	2
2493	Resistin-like Molecule $\hat{\pm}$ Provides Vitamin-A-Dependent Antimicrobial Protection in the Skin. <i>Cell Host and Microbe</i> , 2019, 25, 777-788.e8.	5.1	60
2494	How do zinc oxide and zero valent iron nanoparticles impact the occurrence of antibiotic resistance genes in landfill leachate?. <i>Environmental Science: Nano</i> , 2019, 6, 2141-2151.	2.2	23
2495	Gut Microbiota Changes in Patients with Bipolar Depression. <i>Advanced Science</i> , 2019, 6, 1900752.	5.6	98
2496	Intra-horizon differentiation of the bacterial community and its co-occurrence network in a typical Plinthic horizon. <i>Science of the Total Environment</i> , 2019, 678, 692-701.	3.9	23

#	ARTICLE	IF	CITATIONS
2497	Gut Microbiota and Mucin Composition in Female Broiler Chickens Fed Diets including Yellow Mealworm (<i>Tenebrio molitor</i> , L.). <i>Animals</i> , 2019, 9, 213.	1.0	48
2498	Longitudinal Analysis of the Human B Cell Response to Ebola Virus Infection. <i>Cell</i> , 2019, 177, 1566-1582.e17.	13.5	153
2499	Mitigating Anticipated Effects of Systematic Errors Supports Sister-Group Relationship between Xenacoelomorpha and Ambulacraria. <i>Current Biology</i> , 2019, 29, 1818-1826.e6.	1.8	120
2500	Characteristics of the intestinal flora of specific pathogen free chickens with age. <i>Microbial Pathogenesis</i> , 2019, 132, 325-334.	1.3	44
2501	Contrasting patterns and drivers of soil fungal communities in subtropical deciduous and evergreen broadleaved forests. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5421-5433.	1.7	28
2502	A Distinct Gut Microbiota Exists Within Crohn's Disease-Related Perianal Fistulae. <i>Journal of Surgical Research</i> , 2019, 242, 118-128.	0.8	18
2503	Microbial assemblages reflect environmental heterogeneity in alpine streams. <i>Global Change Biology</i> , 2019, 25, 2576-2590.	4.2	42
2504	Growth, health, rumen fermentation, and bacterial community of Holstein calves fed <i>Lactobacillus rhamnosus</i> GG during the preweaning stage1. <i>Journal of Animal Science</i> , 2019, 97, 2598-2608.	0.2	30
2505	Gut microbiota of newborn piglets with intrauterine growth restriction have lower diversity and different taxonomic abundances. <i>Journal of Applied Microbiology</i> , 2019, 127, 354-369.	1.4	68
2506	Biogas upgrading with hydrogenotrophic methanogenic biofilms. <i>Bioresource Technology</i> , 2019, 287, 121422.	4.8	33
2507	The effect of temperature during culture enrichment on methanotrophic polyhydroxyalkanoate production. <i>International Biodeterioration and Biodegradation</i> , 2019, 140, 144-151.	1.9	23
2508	Characterization and source-tracking of antibiotic resistomes in the sediments of a peri-urban river. <i>Science of the Total Environment</i> , 2019, 679, 88-96.	3.9	41
2509	Survival of Extremotolerant Bacteria from the Mukundpura Meteorite Impact Crater. <i>Astrobiology</i> , 2019, 19, 785-796.	1.5	6
2510	Computational Analysis of AmpSeq Data for Targeted, High-Throughput Genotyping of Amplicons. <i>Frontiers in Plant Science</i> , 2019, 10, 599.	1.7	115
2511	Impact of DNA extraction methods on the observed microbial communities from the intestinal flora of the penaeid shrimp <i>Litopenaeus vannamei</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	4
2512	Engineering banana endosphere microbiome to improve <i>Fusarium</i> wilt resistance in banana. <i>Microbiome</i> , 2019, 7, 74.	4.9	70
2513	The diet of red-throated divers (<i>Gavia stellata</i>) overwintering in the German Bight (North Sea) analysed using molecular diagnostics. <i>Marine Biology</i> , 2019, 166, 1.	0.7	17
2514	High-throughput sequencing of 16S rRNA amplicons characterizes gut microbiota shift of juvenile sea cucumber <i>Apostichopus japonicus</i> feeding with three antibiotics. <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1714-1725.	0.6	16

#	ARTICLE	IF	CITATIONS
2515	Gut microbial diversity increases with social rank in the African cichlid fish, <i>Astatotilapia burtoni</i> . <i>Animal Behaviour</i> , 2019, 152, 79-91.	0.8	7
2516	Linking microbial community structure to carbon substrate chemistry in soils following aboveground and belowground litter additions. <i>Applied Soil Ecology</i> , 2019, 141, 18-25.	2.1	21
2517	Iron Corrosion via Direct Metal-Microbe Electron Transfer. <i>MBio</i> , 2019, 10, .	1.8	107
2518	Whole-Genome Sequence of <i>Acinetobacter baumannii</i> HUMV-3743, Isolated from a Human Wound Exudate. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
2519	Pakchoi Antioxidant Improvement and Differential Rhizobacterial Community Composition under Organic Fertilization. <i>Sustainability</i> , 2019, 11, 2424.	1.6	4
2520	Green manures of Indian mustard and wild rocket enhance cucumber resistance to <i>Fusarium</i> wilt through modulating rhizosphere bacterial community composition. <i>Plant and Soil</i> , 2019, 441, 283-300.	1.8	26
2521	Kappa chain maturation helps drive rapid development of an infant HIV-1 broadly neutralizing antibody lineage. <i>Nature Communications</i> , 2019, 10, 2190.	5.8	31
2522	Assessment of rumen bacteria in dairy cows with varied milk protein yield. <i>Journal of Dairy Science</i> , 2019, 102, 5031-5041.	1.4	59
2523	Characterizing Relationship of Microbial Diversity and Metabolite in Sichuan Xiaoqu. <i>Frontiers in Microbiology</i> , 2019, 10, 696.	1.5	57
2524	Inulin Can Alleviate Metabolism Disorders in <i>ob/ob</i> Mice by Partially Restoring Leptin-related Pathways Mediated by Gut Microbiota. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 64-75.	3.0	134
2525	Gut microbiome-derived phenyl sulfate contributes to albuminuria in diabetic kidney disease. <i>Nature Communications</i> , 2019, 10, 1835.	5.8	173
2526	Characterizing pre-transplant and post-transplant kidney rejection risk by B cell immune repertoire sequencing. <i>Nature Communications</i> , 2019, 10, 1906.	5.8	38
2527	Antiobesity Effects of <i>Lactobacillus plantarum</i> LMT1-48 Accompanied by Inhibition of <i>Enterobacter cloacae</i> in the Intestine of Diet-Induced Obese Mice. <i>Journal of Medicinal Food</i> , 2019, 22, 560-566.	0.8	27
2528	Complete Genome Sequence of an <i>Ehrlichia minasensis</i> Strain Isolated from Cattle. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	11
2529	Plant Stage, Not Drought Stress, Determines the Effect of Cultivars on Bacterial Community Diversity in the Rhizosphere of Broomcorn Millet (<i>Panicum miliaceum</i> L.). <i>Frontiers in Microbiology</i> , 2019, 10, 828.	1.5	31
2530	Regional and Microenvironmental Scale Characterization of the <i>Zostera muelleri</i> Seagrass Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 1011.	1.5	53
2531	Supplementation with compound polysaccharides contributes to the development and metabolic activity of young rat intestinal microbiota. <i>Food and Function</i> , 2019, 10, 2658-2675.	2.1	28
2532	Why the cFos/cJun complex is extremely conserved: An in vitro evolution exploration by combining cDNA display and proximity ligation. <i>FEBS Letters</i> , 2019, 593, 1040-1049.	1.3	0

#	ARTICLE	IF	CITATIONS
2533	Antibiotic resistance genes attenuated with salt accumulation in saline soil. <i>Journal of Hazardous Materials</i> , 2019, 374, 35-42.	6.5	56
2534	The combined effect of ozone treatment and polyethylene packaging on postharvest quality and biodiversity of <i>Toona sinensis</i> (A.Juss.) M.Roem. <i>Postharvest Biology and Technology</i> , 2019, 154, 1-10.	2.9	30
2535	Long-term N fertilization altered ¹³ C-labeled fungal community composition but not diversity in wheat rhizosphere of Chinese black soil. <i>Soil Biology and Biochemistry</i> , 2019, 135, 117-126.	4.2	21
2536	Thermal disruption of soil bacterial assemblages decreases diversity and assemblage similarity. <i>Ecosphere</i> , 2019, 10, e02598.	1.0	2
2537	Do different livestock dwellings on single grassland share similar faecal microbial communities?. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5023-5037.	1.7	4
2538	Cultivated rice rhizomicrobiome is more sensitive to environmental shifts than that of wild rice in natural environments. <i>Applied Soil Ecology</i> , 2019, 140, 68-77.	2.1	17
2539	Data on microbial community composition of sludge from high altitude wastewater treatment plants determined by 16S rRNA gene sequencing. <i>Data in Brief</i> , 2019, 23, 103739.	0.5	10
2540	Estimate of the diversity of viral and bacterial assemblage in the coastal water of Lake Baikal. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	13
2541	Correlation of the rumen fluid microbiome and the average daily gain with a dietary supplementation of <i>Allium mongolicum</i> Regel extracts in sheep1. <i>Journal of Animal Science</i> , 2019, 97, 2865-2877.	0.2	20
2542	Diversity and Succession of Microbiota during Fermentation of the Traditional Indian Food Idli. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	25
2543	MHC structuring and divergent allele advantage in a urodele amphibian: a hierarchical multi-scale approach. <i>Heredity</i> , 2019, 123, 593-607.	1.2	7
2544	Unraveling the diversity of sedimentary sulfate-reducing prokaryotes (SRP) across Tibetan saline lakes using epicPCR. <i>Microbiome</i> , 2019, 7, 71.	4.9	16
2545	Decolorization and detoxification of Direct Blue 2B by indigenous bacterial consortium. <i>Journal of Environmental Management</i> , 2019, 242, 229-237.	3.8	57
2546	Alteration of microbial community for improving flavor character of Daqu by inoculation with <i>Bacillus velezensis</i> and <i>Bacillus subtilis</i> . <i>LWT - Food Science and Technology</i> , 2019, 111, 1-8.	2.5	83
2547	The invasive tree staghorn sumac affects soil N ₂ fixing bacterial communities in north China. <i>Plant Biology</i> , 2019, 21, 951-960.	1.8	13
2548	Berberine Influences Blood Glucose via Modulating the Gut Microbiome in Grass Carp. <i>Frontiers in Microbiology</i> , 2019, 10, 1066.	1.5	49
2549	Endophytic Mycobiota of Jingbai Pear Trees in North China. <i>Forests</i> , 2019, 10, 260.	0.9	9
2550	Epiphytic bacterial community composition on the surface of the submerged macrophyte <i>Myriophyllum spicatum</i> in a low-salinity sea area of Hangzhou Bay. <i>Oceanological and Hydrobiological Studies</i> , 2019, 48, 43-55.	0.3	5

#	ARTICLE	IF	CITATIONS
2551	Association of host genetics with intestinal microbial relevant to body weight in a chicken F2 resource population. <i>Poultry Science</i> , 2019, 98, 4084-4093.	1.5	23
2552	Gut bacteria are critical for optimal muscle function: a potential link with glucose homeostasis. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 317, E158-E171.	1.8	126
2553	Heterotrophic Bacteria Dominate the Diazotrophic Community in the Eastern Indian Ocean (EIO) during Pre-Southwest Monsoon. <i>Microbial Ecology</i> , 2019, 78, 804-819.	1.4	41
2554	Reshaping the rhizosphere microbiome by bio-organic amendment to enhance crop yield in a maize-cabbage rotation system. <i>Applied Soil Ecology</i> , 2019, 142, 136-146.	2.1	76
2555	InÂvitro toxicological evaluation of ionic liquids and development of effective bioremediation process for their removal. <i>Environmental Pollution</i> , 2019, 250, 567-577.	3.7	29
2556	Fungal Community Composition and Potential Depth-Related Driving Factors Impacting Distribution Pattern and Trophic Modes from Epi- to Abyssopelagic Zones of the Western Pacific Ocean. <i>Microbial Ecology</i> , 2019, 78, 820-831.	1.4	31
2557	Ammonium influences kinetics and structure of methanotrophic consortia. <i>Waste Management</i> , 2019, 89, 345-353.	3.7	10
2558	ANCHOR: a 16S rRNA gene amplicon pipeline for microbial analysis of multiple environmental samples. <i>Environmental Microbiology</i> , 2019, 21, 2440-2468.	1.8	30
2559	Effect of a polyphenol-rich plant matrix on colonic digestion and plasma antioxidant capacity in a porcine model. <i>Journal of Functional Foods</i> , 2019, 57, 211-221.	1.6	10
2560	Archaeal biogeography and interactions with microbial community across complex subtropical coastal waters. <i>Molecular Ecology</i> , 2019, 28, 3101-3118.	2.0	23
2561	Modified Mouse Model of <i>Clostridioides difficile</i> Infection as a Platform for Probiotic Efficacy Studies. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	8
2562	High dietary fat intake lowers serum equol concentration and promotes prostate carcinogenesis in a transgenic mouse prostate model. <i>Nutrition and Metabolism</i> , 2019, 16, 24.	1.3	24
2563	Diagnosing and tracing the pathogens of infantile infectious diarrhea by amplicon sequencing. <i>Gut Pathogens</i> , 2019, 11, 12.	1.6	7
2564	Zero-valent iron sand filtration reduces concentrations of virus-like particles and modifies virome community composition in reclaimed water used for agricultural irrigation. <i>BMC Research Notes</i> , 2019, 12, 223.	0.6	13
2565	Indigenous PAH degraders along the gradient of the Yangtze Estuary of China: Relationships with pollutants and their bioremediation implications. <i>Marine Pollution Bulletin</i> , 2019, 142, 419-427.	2.3	24
2566	Environmental DNA metabarcoding to detect pathogenic <i>Leptospira</i> and associated organisms in leptospirosis-endemic areas of Japan. <i>Scientific Reports</i> , 2019, 9, 6575.	1.6	28
2567	Different gut microbiome composition in obese Guizhou minipigs between female and castrated male. <i>Folia Microbiologica</i> , 2019, 64, 889-898.	1.1	4
2568	N ₂ fixation impacted by carbon fixation via dissolved organic carbon in the changing Daya Bay, South China Sea. <i>Science of the Total Environment</i> , 2019, 674, 592-602.	3.9	13

#	ARTICLE	IF	CITATIONS
2569	Functional response of sediment bacterial community to iron-reducing bioaugmentation with <i>Shewanella decolorationis</i> S12. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4997-5005.	1.7	7
2570	Correlation of Gut Microbiome Between ASD Children and Mothers and Potential Biomarkers for Risk Assessment. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 26-38.	3.0	72
2571	Shedding Light on a Secretive Tertiary Urodelean Relict: Hynobiid Salamanders (<i>Paradactylodon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 Genes, 2019, 10, 306.	1.0	4
2572	Divergent Fine-Scale Recombination Landscapes between a Freshwater and Marine Population of Threespine Stickleback Fish. <i>Genome Biology and Evolution</i> , 2019, 11, 1552-1572.	1.1	44
2573	The Association Between the Developing Nasal Microbiota of Hospitalized Neonates and <i>Staphylococcus aureus</i> Colonization. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz062.	0.4	12
2574	Bacterial composition of biofilms formed on dairy-processing equipment. <i>Preparative Biochemistry and Biotechnology</i> , 2019, 49, 477-484.	1.0	10
2575	Characterization of gut microbiota composition and functions in patients with chronic alcohol overconsumption. <i>Gut Microbes</i> , 2019, 10, 663-675.	4.3	118
2576	Rare Plankton Subcommunities Are Far More Affected by DNA Extraction Kits Than Abundant Plankton. <i>Frontiers in Microbiology</i> , 2019, 10, 454.	1.5	24
2577	Growth of <i>Salmonella enterica</i> Serovars Typhimurium and Enteritidis in Iron-Poor Media and in Meat: Role of Catecholate and Hydroxamate Siderophore Transporters. <i>Journal of Food Protection</i> , 2019, 82, 548-560.	0.8	8
2578	An Allosteric Network for Spliceosome Activation Revealed by High-Throughput Suppressor Analysis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 212, 111-124.	1.2	3
2579	Restoration of Long-Term Monoculture Degraded Tea Orchard by Green and Goat Manures Applications System. <i>Sustainability</i> , 2019, 11, 1011.	1.6	16
2580	Metagenomic analysis of composition, function and cycling processes of microbial community in water, sediment and effluent of <i>Litopenaeus vannamei</i> farming environments under different culture modes. <i>Aquaculture</i> , 2019, 506, 280-293.	1.7	56
2581	Comparing the selective and co-selective effects of different antimicrobials in bacterial communities. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 767-773.	1.1	36
2582	Extensive allopolyploidy in the neotropical genus <i>Lachemilla</i> (<i>Rosaceae</i>) revealed by <i>PCR</i> -based target enrichment of the nuclear ribosomal <i>DNA</i> cistron and plastid phylogenomics. <i>American Journal of Botany</i> , 2019, 106, 415-437.	0.8	14
2583	Heavy metal spill influences bacterial communities in freshwater sediments. <i>Archives of Microbiology</i> , 2019, 201, 847-854.	1.0	20
2584	Vaginal Glycogen, Not Estradiol, Is Associated With Vaginal Bacterial Community Composition in Black Adolescent Women. <i>Journal of Adolescent Health</i> , 2019, 65, 130-138.	1.2	16
2585	Alterations of the Mice Gut Microbiome via <i>Schistosoma japonicum</i> Ova-Induced Granuloma. <i>Frontiers in Microbiology</i> , 2019, 10, 352.	1.5	63
2586	Response of sediment bacterial community to triclosan in subtropical freshwater benthic microcosms. <i>Environmental Pollution</i> , 2019, 248, 676-683.	3.7	13

#	ARTICLE	IF	CITATIONS
2587	Inactivation of antibiotic-resistant bacteria by chlorine dioxide in soil and shifts in community composition. <i>RSC Advances</i> , 2019, 9, 6526-6532.	1.7	12
2588	Spatiotemporal successions of shrimp gut microbial colonization: high consistency despite distinct species pool. <i>Environmental Microbiology</i> , 2019, 21, 1383-1394.	1.8	44
2589	Variation in soil fungal community structure during successive rotations of <i>Casuarina equisetifolia</i> plantations as determined by high-throughput sequencing analysis. <i>Plant Growth Regulation</i> , 2019, 87, 445-453.	1.8	12
2590	Changes in the soil microbial community are associated with the occurrence of <i>Panax quinquefolius</i> L. root rot diseases. <i>Plant and Soil</i> , 2019, 438, 143-156.	1.8	39
2591	Heavy metal exposure causes changes in the metabolic health-associated gut microbiome and metabolites. <i>Environment International</i> , 2019, 126, 454-467.	4.8	125
2592	The changes of microbial community and flavor compound in the fermentation process of Chinese rice wine using <i>Fagopyrum tataricum</i> grain as feedstock. <i>Scientific Reports</i> , 2019, 9, 3365.	1.6	48
2593	Conjunctival microbiome changes associated with fungal keratitis: metagenomic analysis. <i>International Journal of Ophthalmology</i> , 2019, 12, 194-200.	0.5	38
2594	Title is missing!. <i>Turkish Journal of Fisheries and Aquatic Sciences</i> , 2019, 19, .	0.4	9
2595	Bacterial and eukaryote microbiomes of mosquito habitats in dengue-endemic southern Taiwan. <i>Journal of Asia-Pacific Entomology</i> , 2019, 22, 471-480.	0.4	9
2596	<i>In vitro</i> and <i>in vivo</i> evaluation of an exopolysaccharide produced by <i>Lactobacillus helveticus</i> KLDS1.8701 for the alleviative effect on oxidative stress. <i>Food and Function</i> , 2019, 10, 1707-1717.	2.1	34
2597	Modulation of the intestinal microbiota of dogs by kefir as a functional dairy product. <i>Journal of Dairy Science</i> , 2019, 102, 3903-3911.	1.4	31
2598	<i>Lactobacillus gasseri</i> APC 678 Reduces Shedding of the Pathogen <i>Clostridium difficile</i> in a Murine Model. <i>Frontiers in Microbiology</i> , 2019, 10, 273.	1.5	9
2599	Salinity as a predominant factor modulating the distribution patterns of antibiotic resistance genes in ocean and river beach soils. <i>Science of the Total Environment</i> , 2019, 668, 193-203.	3.9	54
2600	<i>Bacillus pumilus</i> SE5 originated PG and LTA tuned the intestinal TLRs/MyD88 signaling and microbiota in grouper (<i>Epinephelus coioides</i>). <i>Fish and Shellfish Immunology</i> , 2019, 88, 266-271.	1.6	50
2601	Health risk of Licorice-Yuanhua combination through induction of colonic H ₂ S metabolism. <i>Journal of Ethnopharmacology</i> , 2019, 236, 136-146.	2.0	14
2602	Lack of Signal for the Impact of Conotoxin Gene Diversity on Speciation Rates in Cone Snails. <i>Systematic Biology</i> , 2019, 68, 781-796.	2.7	16
2603	Shaping of infant B cell receptor repertoires by environmental factors and infectious disease. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	58
2604	Insight into the Bacterial Endophytic Communities of Peach Cultivars Related to Crown Gall Disease Resistance. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	42

#	ARTICLE	IF	CITATIONS
2605	Mycobiome Profiles in Breast Milk from Healthy Women Depend on Mode of Delivery, Geographic Location, and Interaction with Bacteria. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	76
2606	Application of next generation sequencing for species identification in meat and poultry products: A DNA metabarcoding approach. <i>Food Control</i> , 2019, 101, 173-179.	2.8	46
2607	Consistent spatial distribution patterns of bacterial communities revealed by serial time-archived soils from long-term field experiments. <i>Soil Biology and Biochemistry</i> , 2019, 133, 137-145.	4.2	6
2608	Spatial Variability of Antarctic Surface Snow Bacterial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 461.	1.5	20
2609	Amplicon sequencing reveals different microbial communities in living poplar wetwood and sapwood. <i>Trees - Structure and Function</i> , 2019, 33, 851-865.	0.9	5
2610	Characteristics of the Intestinal Microbiota in Very Low Birth Weight Infants With Extrauterine Growth Restriction. <i>Frontiers in Pediatrics</i> , 2019, 7, 99.	0.9	17
2611	The effect of environment on the microbiome associated with the roots of a native woody plant under different climate types in China. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3899-3913.	1.7	11
2612	Soil extractable organic C and N contents, methanotrophic activity under warming and degradation in a Tibetan alpine meadow. <i>Agriculture, Ecosystems and Environment</i> , 2019, 278, 6-14.	2.5	21
2613	Study of gut bacterial diversity of <i>Bombyx mandarina</i> and <i>Bombyx mori</i> through 16S rRNA gene sequencing. <i>Journal of Asia-Pacific Entomology</i> , 2019, 22, 522-530.	0.4	10
2614	Profiling the Clostridia with butyrate-producing potential in the mud of Chinese liquor fermentation cellar. <i>International Journal of Food Microbiology</i> , 2019, 297, 41-50.	2.1	79
2615	Seasonal dynamics of bacterial communities in the surface seawater around subtropical Xiamen Island, China, as determined by 16S rRNA gene profiling. <i>Marine Pollution Bulletin</i> , 2019, 142, 135-144.	2.3	39
2616	Tick Genomes' organ engagement in lipid metabolism revealed by a combined transcriptomic and proteomic approach. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 787-797.	1.1	12
2617	Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. <i>Nature Ecology and Evolution</i> , 2019, 3, 612-619.	3.4	82
2618	Characterization of the gut microbiota of invasive <i>Agrilus mali</i> Matsumara (Coleoptera: Buprestidae) using high-throughput sequencing: uncovering plant cell-wall degrading bacteria. <i>Scientific Reports</i> , 2019, 9, 4923.	1.6	29
2619	Rearing system causes changes of behavior, microbiome, and gene expression of chickens. <i>Poultry Science</i> , 2019, 98, 3365-3376.	1.5	35
2620	Pyrosequencing Uncovers a Shift in Bacterial Communities Across Life Stages of <i>Octodonta nipae</i> (Coleoptera: Chrysomelidae). <i>Frontiers in Microbiology</i> , 2019, 10, 466.	1.5	35
2621	Bacterial community response to cadmium contamination of agricultural paddy soil. <i>Applied Soil Ecology</i> , 2019, 139, 100-106.	2.1	77
2622	The Perturbation of Infant Gut Microbiota Caused by Cesarean Delivery Is Partially Restored by Exclusive Breastfeeding. <i>Frontiers in Microbiology</i> , 2019, 10, 598.	1.5	65

#	ARTICLE	IF	CITATIONS
2623	Effects of <i>Bacillus subtilis</i> on the growth, colony maintenance, and attached bacterial community composition of colonial cyanobacteria. <i>Environmental Science and Pollution Research</i> , 2019, 26, 14977-14987.	2.7	10
2624	Microbial groups and their functions control the decomposition of coniferous litter: A comparison with broadleaved tree litters. <i>Soil Biology and Biochemistry</i> , 2019, 133, 196-207.	4.2	55
2625	Deciphering host-parasitoid interactions and parasitism rates of crop pests using DNA metabarcoding. <i>Scientific Reports</i> , 2019, 9, 3646.	1.6	47
2626	Effect of green tea and mulberry leaf powders on the gut microbiota of chicken. <i>BMC Veterinary Research</i> , 2019, 15, 77.	0.7	29
2627	Phylogenetic analyses and characteristics of the microbiomes from five mealybugs (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	0.8	8
2628	Fe(III) reduction and vivianite formation in activated sludge. <i>Separation and Purification Technology</i> , 2019, 220, 126-135.	3.9	47
2629	Microbial Engraftment and Efficacy of Fecal Microbiota Transplant for <i>Clostridium Difficile</i> in Patients With and Without Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 969-979.	0.9	38
2630	Population Genomics and Structure of the Critically Endangered Mariana Crow (<i>Corvus kubaryi</i>). <i>Genes</i> , 2019, 10, 187.	1.0	11
2631	Microbial composition changes on the surface of strawberries from the field and market by 16SrDNA sequencing. <i>Journal of Food Safety</i> , 2019, 39, e12630.	1.1	4
2632	Bioremediation of dibutyl phthalate in a simulated agricultural ecosystem by <i>Gordonia</i> sp. strain QH-11 and the microbial ecological effects in soil. <i>Science of the Total Environment</i> , 2019, 667, 691-700.	3.9	54
2633	Anaerobic Process for Bioenergy Recovery From Dairy Waste: Meta-Analysis and Enumeration of Microbial Community Related to Intermediates Production. <i>Frontiers in Microbiology</i> , 2018, 9, 3229.	1.5	42
2634	Functional Genes and Bacterial Communities During Organohalide Respiration of Chloroethenes in Microcosms of Multi-Contaminated Groundwater. <i>Frontiers in Microbiology</i> , 2019, 10, 89.	1.5	21
2635	A cascade of a denitrification bioreactor and an aerobic biofilm reactor for heavy oil refinery wastewater treatment. <i>RSC Advances</i> , 2019, 9, 7495-7504.	1.7	11
2636	Evolution of the HIV-1 Rev Response Element during Natural Infection Reveals Nucleotide Changes That Correlate with Altered Structure and Increased Activity over Time. <i>Journal of Virology</i> , 2019, 93, .	1.5	14
2637	Whole-Genome Sequencing of <i>Legionella jordanis</i> Strains NML 060502 and NML 130005, Recovered from a Lower Respiratory Tract Infection and Water, Respectively. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
2638	A census-based estimate of Earth's bacterial and archaeal diversity. <i>PLoS Biology</i> , 2019, 17, e3000106.	2.6	139
2639	Nitrogen- and phosphorus-starved <i>Triticum aestivum</i> show distinct belowground microbiome profiles. <i>PLoS ONE</i> , 2019, 14, e0210538.	1.1	26
2640	The nasal and oropharyngeal microbiomes of healthy livestock workers. <i>PLoS ONE</i> , 2019, 14, e0212949.	1.1	18

#	ARTICLE	IF	CITATIONS
2641	Succession of Composition and Function of Soil Bacterial Communities During Key Rice Growth Stages. <i>Frontiers in Microbiology</i> , 2019, 10, 421.	1.5	36
2642	Rotations with Indian Mustard and Wild Rocket Suppressed Cucumber Fusarium Wilt Disease and Changed Rhizosphere Bacterial Communities. <i>Microorganisms</i> , 2019, 7, 57.	1.6	22
2643	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. <i>MSphere</i> , 2019, 4, .	1.3	14
2645	Disordered intestinal microbes are associated with the activity of Systemic Lupus Erythematosus. <i>Clinical Science</i> , 2019, 133, 821-838.	1.8	119
2646	Solid-state fermented Chinese alcoholic beverage (baijiu) and ethanol resulted in distinct metabolic and microbiome responses. <i>FASEB Journal</i> , 2019, 33, 7274-7288.	0.2	20
2647	Bacterial community in cold and alkaline environments of Hoh Xil basin in Qinghai-Tibet Plateau and isolation of potential sources of microbiota. <i>Annals of Microbiology</i> , 2019, 69, 567-576.	1.1	8
2648	Analysis of rhizosphere bacterial and fungal communities associated with rusty root disease of <i>Panax ginseng</i> . <i>Applied Soil Ecology</i> , 2019, 138, 245-252.	2.1	31
2649	Spatial Heterogeneity of <i>Vibrio</i> spp. in Sediments of Chinese Marginal Seas. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	18
2650	Microbiome diversity in carriers of fluoroquinolone resistant <i>Escherichia coli</i> . <i>Investigative and Clinical Urology</i> , 2019, 60, 75.	1.0	3
2651	Authentication and Assessment of Contamination in Ancient DNA. <i>Methods in Molecular Biology</i> , 2019, 1963, 163-194.	0.4	23
2652	Divergent responses of bacterial activity, structure, and co-occurrence patterns to long-term unbalanced fertilization without nitrogen, phosphorus, or potassium in a cultivated vertisol. <i>Environmental Science and Pollution Research</i> , 2019, 26, 12741-12754.	2.7	19
2653	Investigating the effect of biochar and fertilizer on the composition and function of bacteria in red soil. <i>Applied Soil Ecology</i> , 2019, 139, 107-116.	2.1	54
2654	Temperate airborne grass pollen defined by spatio-temporal shifts in community composition. <i>Nature Ecology and Evolution</i> , 2019, 3, 750-754.	3.4	75
2655	Mass coral bleaching of <i>P. versipora</i> in Sydney Harbour driven by the 2015-2016 heatwave. <i>Coral Reefs</i> , 2019, 38, 815-830.	0.9	20
2656	Rhizosphere microbiota compositional changes reflect potato blackleg disease. <i>Applied Soil Ecology</i> , 2019, 140, 11-17.	2.1	9
2657	Unveiling hÅkarl: A study of the microbiota of the traditional Icelandic fermented fish. <i>Food Microbiology</i> , 2019, 82, 560-572.	2.1	41
2658	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , 2019, 364, .	6.0	576
2659	Alteration of vaginal microbiota in patients with unexplained recurrent miscarriage. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 3307-3316.	0.8	25

#	ARTICLE	IF	CITATIONS
2660	Environmental factors promote pathogen-induced skin ulceration syndrome outbreak by readjusting the hindgut microbiome of <i>Apostichopus japonicus</i> . <i>Aquaculture</i> , 2019, 507, 155-163.	1.7	28
2661	<i>APOE</i> genotype influences the gut microbiome structure and function in humans and mice: relevance for Alzheimer's disease pathophysiology. <i>FASEB Journal</i> , 2019, 33, 8221-8231.	0.2	124
2662	Effects of a gut microbiota transfer on emotional reactivity in Japanese quails (<i>Coturnix</i>). <i>Journal of Applied Microbiology</i> , 2019, 126, 1506-1515.	0.8	15
2663	Impact of Saskatoon berry powder on insulin resistance and relationship with intestinal microbiota in high fat high sucrose diet-induced obese mice. <i>Journal of Nutritional Biochemistry</i> , 2019, 69, 130-138.	1.9	25
2664	The Effect of Disease and Season to Hepatopancreas and Intestinal Mycobiota of <i>Litopenaeus vannamei</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 889.	1.5	22
2665	Artificial Light at Night Alleviates the Negative Effect of Pb on Freshwater Ecosystems. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1343.	1.8	10
2666	Characteristics of airborne opportunistic pathogenic bacteria during autumn and winter in Xi'an, China. <i>Science of the Total Environment</i> , 2019, 672, 834-845.	3.9	59
2667	Mudflat reclamation causes change in the composition of fungal communities under long-term rice cultivation. <i>Canadian Journal of Microbiology</i> , 2019, 65, 530-537.	0.8	9
2668	DMSC: A Dynamic Multi-Seeds Method for Clustering 16S rRNA Sequences Into OTUs. <i>Frontiers in Microbiology</i> , 2019, 10, 428.	1.5	12
2669	Multiple-pathway arsenic oxidation and removal from wastewater by a novel manganese-oxidizing aerobic granular sludge. <i>Water Research</i> , 2019, 157, 83-93.	5.3	56
2670	Bacterial colonization and antimicrobial resistance genes in neonatal enteral feeding tubes. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	9
2671	Shift of the microbial communities from exposed sandstone rocks to forest soils during pedogenesis. <i>International Biodeterioration and Biodegradation</i> , 2019, 140, 21-28.	1.9	19
2672	Effect of intake pattern of sulfated polysaccharides on its biological activity in high fat diet-fed mice. <i>International Journal of Biological Macromolecules</i> , 2019, 132, 9-16.	3.6	19
2673	<i>Litopenaeus vannamei</i> fed diets with different replacement levels of fish meal by fish silage: A molecular approach on intestinal microbiota. <i>Aquaculture Nutrition</i> , 2019, 25, 721-728.	1.1	10
2674	The Characteristics and Distribution of Eukaryotic Phytoplankton Community in Liaodong Bay, China. <i>Ocean Science Journal</i> , 2019, 54, 183-203.	0.6	10
2675	Specific quorum sensing molecules of ammonia oxidizers and their role during ammonium metabolism in Zhalong wetland, China. <i>Science of the Total Environment</i> , 2019, 666, 1106-1113.	3.9	25
2676	Localized production of defence chemicals by intracellular symbionts of <i>Haliclona</i> sponges. <i>Nature Microbiology</i> , 2019, 4, 1149-1159.	5.9	69
2677	Oxalotrophic bacterial assemblages in the ectomycorrhizosphere of forest trees and their effects on oxalate degradation and carbon fixation potential. <i>Chemical Geology</i> , 2019, 514, 54-64.	1.4	17

#	ARTICLE	IF	CITATIONS
2678	Variation in DNA methylation in the KvDMR1 (ICR2) region in first-trimester human pregnancies. <i>Fertility and Sterility</i> , 2019, 111, 1186-1193.	0.5	4
2679	Long-term manure application increases soil organic matter and aggregation, and alters microbial community structure and keystone taxa. <i>Soil Biology and Biochemistry</i> , 2019, 134, 187-196.	4.2	302
2680	Gut microbial dysbiosis is associated with allergen-specific IgE responses in young children with airway allergies. <i>World Allergy Organization Journal</i> , 2019, 12, 100021.	1.6	77
2681	Implicating Dysbiosis of the Gut Fungal Microbiome in Uveitis, an Inflammatory Disease of the Eye. , 2019, 60, 1384.		32
2682	Reduced protocadherin17 expression in leukemia stem cells: the clinical and biological effect in acute myeloid leukemia. <i>Journal of Translational Medicine</i> , 2019, 17, 102.	1.8	18
2683	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. <i>Frontiers in Microbiology</i> , 2019, 10, 347.	1.5	59
2684	Effects of different dietary copper sources on the growth and intestinal microbial communities of Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture Nutrition</i> , 2019, 25, 828-840.	1.1	11
2685	<i>Aedes albopictus</i> mosquitoes host a locally structured mycobiota with evidence of reduced fungal diversity in invasive populations. <i>Fungal Ecology</i> , 2019, 39, 257-266.	0.7	28
2686	Dynamic changes in fermentation profiles and bacterial community composition during sugarcane top silage fermentation: A preliminary study. <i>Bioresource Technology</i> , 2019, 285, 121315.	4.8	44
2687	Wildfire severity reduces richness and alters composition of soil fungal communities in boreal forests of western Canada. <i>Global Change Biology</i> , 2019, 25, 2310-2324.	4.2	72
2688	Comparative analysis of the rhizomicrobiome of the wild versus cultivated crop: insights from rice and soybean. <i>Archives of Microbiology</i> , 2019, 201, 879-888.	1.0	22
2689	Pre-colonization of PGPR triggers rhizosphere microbiota succession associated with crop yield enhancement. <i>Plant and Soil</i> , 2019, 439, 553-567.	1.8	58
2690	Culture dependent and independent analysis and appraisal of early stage biofilm-forming bacterial community composition in the Southern coastal seawater of India. <i>Science of the Total Environment</i> , 2019, 666, 308-320.	3.9	33
2691	Variability in the Composition of Pacific Oyster Microbiomes Across Oyster Families Exhibiting Different Levels of Susceptibility to OsHV-1 μ var Disease. <i>Frontiers in Microbiology</i> , 2019, 10, 473.	1.5	59
2692	Temperature and humidity index (THI)-induced rumen bacterial community changes in goats. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3193-3203.	1.7	31
2693	Effect of the sulfation pattern of sea cucumber-derived fucoidan oligosaccharides on modulating metabolic syndromes and gut microbiota dysbiosis caused by HFD in mice. <i>Journal of Functional Foods</i> , 2019, 55, 193-210.	1.6	38
2694	Endophytic community of Pb-Zn hyperaccumulator <i>Arabis alpina</i> and its role in host plants metal tolerance. <i>Plant and Soil</i> , 2019, 437, 397-411.	1.8	19
2695	Elevational patterns of abundant and rare bacterial diversity and composition in mountain streams in the southeast of the Tibetan Plateau. <i>Science China Earth Sciences</i> , 2019, 62, 853-862.	2.3	4

#	ARTICLE	IF	CITATIONS
2696	Xiaoyaosan improves depressive-like behavior in rats with chronic immobilization stress through modulation of the gut microbiota. <i>Biomedicine and Pharmacotherapy</i> , 2019, 112, 108621.	2.5	105
2697	Mussel polysaccharide β -D-glucan (MP-A) protects against non-alcoholic fatty liver disease via maintaining the homeostasis of gut microbiota and regulating related gut-liver axis signaling pathways. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 68-78.	3.6	40
2698	Influence of pH control on material characteristics, bacterial community composition and BNR performance of mature aerobic granules. <i>Chemical Engineering Research and Design</i> , 2019, 124, 158-166.	2.7	6
2699	Long-term application of nitrogen, not phosphate or potassium, significantly alters the diazotrophic community compositions and structures in a Mollisol in northeast China. <i>Research in Microbiology</i> , 2019, 170, 147-155.	1.0	26
2700	The Growth Rate, Immune Status, Duodenal Development, and Cecal Microbial Diversity of 24-Day-Old Offspring of SD Rats Received <i>Bacillus subtilis</i> -Cu or CuSO ₄ During Pregnancy and Lactation Periods. <i>Biological Trace Element Research</i> , 2019, 191, 435-442.	1.9	4
2701	Replacement of fishmeal by fermented soybean meal could enhance the growth performance but not significantly influence the intestinal microbiota of white shrimp <i>Litopenaeus vannamei</i> . <i>Aquaculture</i> , 2019, 504, 354-360.	1.7	50
2702	The gut microbiota is largely independent of host genetics in regulating fat deposition in chickens. <i>ISME Journal</i> , 2019, 13, 1422-1436.	4.4	146
2703	Very Low Phytoplankton Diversity in a Tropical Saline-Alkaline Lake, with Co-dominance of <i>Arthrospira fusiformis</i> (Cyanobacteria) and <i>Picocystis salinarum</i> (Chlorophyta). <i>Microbial Ecology</i> , 2019, 78, 603-617.	1.4	19
2704	Kinetic and microbial analysis of methane production from dairy wastewater anaerobic digester under ammonia and salinity stresses. <i>Journal of Cleaner Production</i> , 2019, 219, 797-808.	4.6	44
2705	Two Strains of <i>Lactobacilli</i> Effectively Decrease the Colonization of VRE in a Mouse Model. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 6.	1.8	18
2706	Root-Associated Endophytic Bacterial Community Composition of <i>Pennisetum sinense</i> from Four Representative Provinces in China. <i>Microorganisms</i> , 2019, 7, 47.	1.6	13
2707	Short-Term Effects of Different Organic Amendments on Soil Fungal Composition. <i>Sustainability</i> , 2019, 11, 198.	1.6	36
2708	Direct RNA sequencing on nanopore arrays redefines the transcriptional complexity of a viral pathogen. <i>Nature Communications</i> , 2019, 10, 754.	5.8	200
2709	Impact of Nitrogen Fertilizer on the Mycorrhizal Inoculating Potential and Fungal Community Structure in Rhizosphere of Medicinal Plant <i>Curcuma longa</i> L.. <i>Geomicrobiology Journal</i> , 2019, 36, 385-395.	1.0	3
2710	Genetic evidence for alloparental care and frequent multiple paternity in the brooding sea star (<i>Leptasterias</i> sp.). <i>Marine Biology</i> , 2019, 166, 1.	0.7	6
2711	Microbial species and biodiversity in settling dust within and between pig farms. <i>Environmental Research</i> , 2019, 171, 558-567.	3.7	49
2712	Seasonal patterns and environmental drivers of nirS- and nirK-encoding denitrifiers in sediments of Daya Bay, China. <i>Oceanologia</i> , 2019, 61, 308-320.	1.1	19
2713	Electricity generation from sweet potato-shochu waste using microbial fuel cells. <i>Journal of Bioscience and Bioengineering</i> , 2019, 128, 56-63.	1.1	22

#	ARTICLE	IF	CITATIONS
2714	Evaluation of Methods to Assess in vivo Activity of Engineered Genome-Editing Nucleases in Protoplasts. <i>Frontiers in Plant Science</i> , 2019, 10, 110.	1.7	21
2715	Dispersal of a nearshore marine fish connects marine reserves and adjacent fished areas along an open coast. <i>Molecular Ecology</i> , 2019, 28, 1611-1623.	2.0	40
2716	Altered Gut Microbiota in Chinese Children With Autism Spectrum Disorders. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 40.	1.8	114
2717	Shift in Bacterial Community Structure Drives Different Atrazine-Degrading Efficiencies. <i>Frontiers in Microbiology</i> , 2019, 10, 88.	1.5	16
2718	Impacts of Human Activities on the Composition and Abundance of Sulfate-Reducing and Sulfur-Oxidizing Microorganisms in Polluted River Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 231.	1.5	15
2719	Effect of the extraction and purification of soil DNA and pooling of PCR amplification products on the description of bacterial and archaeal communities. <i>Journal of Applied Microbiology</i> , 2019, 126, 1454-1467.	1.4	26
2720	Integrated Omic Analyses Provide Evidence that a <i>Candidatus</i> <i>Accumulibacter phosphatis</i> Strain Performs Denitrification under Microaerobic Conditions. <i>MSystems</i> , 2019, 4, .	1.7	44
2721	Contrasted ecological niches shape fungal and prokaryotic community structure in mangroves sediments. <i>Environmental Microbiology</i> , 2019, 21, 1407-1424.	1.8	38
2722	Saponin-Induced Shifts in the Rumen Microbiome and Metabolome of Young Cattle. <i>Frontiers in Microbiology</i> , 2019, 10, 356.	1.5	86
2723	Antibiotic supplement in feed can perturb the intestinal microbial composition and function in Pacific white shrimp. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3111-3122.	1.7	28
2724	Comparison of bacterial diversity in traditionally homemade paocai and Chinese spicy cabbage. <i>Food Microbiology</i> , 2019, 83, 141-149.	2.1	64
2725	Soil aggregate size modifies the impacts of fertilization on microbial communities. <i>Geoderma</i> , 2019, 343, 205-214.	2.3	39
2726	The Ovotransferrin-Derived Peptide IRW Attenuates Lipopolysaccharide-Induced Inflammatory Responses. <i>BioMed Research International</i> , 2019, 2019, 1-7.	0.9	22
2727	Dynamic Development of Fecal Microbiome During the Progression of Diabetes Mellitus in Zucker Diabetic Fatty Rats. <i>Frontiers in Microbiology</i> , 2019, 10, 232.	1.5	73
2728	Temporal and spatial succession and dynamics of soil fungal communities in restored grassland on the Loess Plateau in China. <i>Land Degradation and Development</i> , 2019, 30, 1273-1287.	1.8	39
2729	Dietary supplementation of probiotic <i>Bacillus coagulans</i> ATCC 7050, improves the growth performance, intestinal morphology, microflora, immune response, and disease confrontation of Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2019, 87, 796-808.	1.6	144
2730	The Endobiota Study: Comparison of Vaginal, Cervical and Gut Microbiota Between Women with Stage 3/4 Endometriosis and Healthy Controls. <i>Scientific Reports</i> , 2019, 9, 2204.	1.6	125
2731	Biodegradability of legacy crude oil contamination in Gulf War damaged groundwater wells in Northern Kuwait. <i>Biodegradation</i> , 2019, 30, 71-85.	1.5	9

#	ARTICLE	IF	CITATIONS
2732	The intestinal environment as an evolutionary adaptation to mouthbrooding in the <i>Astatotilapia burtoni</i> cichlid. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	8
2733	Soil bacterial community structure and extracellular enzyme activities under different land use types in a long-term reclaimed wetland. <i>Journal of Soils and Sediments</i> , 2019, 19, 2543-2557.	1.5	24
2734	Optimized DNA extraction and library preparation for minute arthropods: Application to target enrichment in chalcid wasps used for biocontrol. <i>Molecular Ecology Resources</i> , 2019, 19, 702-710.	2.2	48
2735	Baseline characterization of aerobic hydrocarbon degrading microbial communities in deep-sea sediments of the Great Australian Bight, Australia. <i>Environmental Microbiology</i> , 2019, 21, 1782-1797.	1.8	14
2736	Salinity Is a Key Determinant for Soil Microbial Communities in a Desert Ecosystem. <i>MSystems</i> , 2019, 4, .	1.7	238
2737	Oropharyngeal Microbiome in Obstructive Sleep Apnea: Decreased Diversity and Abundance. <i>Journal of Clinical Sleep Medicine</i> , 2019, 15, 1777-1788.	1.4	25
2738	Performance, Microbial Community Analysis and Fertilizer Value of Anaerobic Co-digestion of Cattle Manure with Waste Kitchen Oil. <i>Applied Engineering in Agriculture</i> , 2019, 35, 239-248.	0.3	10
2739	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) – A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3943-3952.	0.8	13
2740	Monitoring of Pathogenic Bioaerosols in Beef Slaughter Facilities Based on Air Sampling and Airflow Modeling. <i>Applied Engineering in Agriculture</i> , 2019, 35, 1015-1036.	0.3	10
2741	Comparative analysis and characterization of the gut microbiota of four farmed snakes from southern China. <i>PeerJ</i> , 2019, 7, e6658.	0.9	25
2742	SIMON: Simple methods for analyzing DNA methylation by targeted bisulfite next-generation sequencing. <i>Plant Biotechnology</i> , 2019, 36, 213-222.	0.5	2
2743	A New High Throughput Sequencing Assay for Characterizing the Diversity of Natural <i>Vibrio</i> Communities and Its Application to a Pacific Oyster Mortality Event. <i>Frontiers in Microbiology</i> , 2019, 10, 2907.	1.5	27
2744	In vitro Study of <i>Lactobacillus paracasei</i> CNCM I-1518 in Healthy and <i>Clostridioides difficile</i> Colonized Elderly Gut Microbiota. <i>Frontiers in Nutrition</i> , 2019, 6, 184.	1.6	12
2745	<i>Cutibacterium acnes</i> (<i>Propionibacterium acnes</i>) 16S rRNA Genotyping of Microbial Samples from Possessions Contributes to Owner Identification. <i>MSystems</i> , 2019, 4, .	1.7	33
2746	Draft Genome Sequence of <i>Mycolicibacterium</i> sp. Strain CH28, a Potential Degradator of Diisopropyl Ether, Isolated from Pharmaceutical Wastewater. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
2747	Changes in the gut microbiota during and after commercial helium-oxygen saturation diving in China. <i>Occupational and Environmental Medicine</i> , 2019, 76, 801-807.	1.3	7
2748	6. Practical overview of bioinformatics data mining in environmental genomics. , 2019, , 127-150.		0
2749	Assessing the Influence of Fumigation and <i>Bacillus Subtilis</i> -Based Biofungicide on the Microbiome of <i>Chrysanthemum</i> Rhizosphere. <i>Agriculture (Switzerland)</i> , 2019, 9, 255.	1.4	7

#	ARTICLE	IF	CITATIONS
2750	Distribution Patterns of nirS-Encoding and nirK-Encoding Denitrifiers in the Surface Sediment of the Pearl River Estuary. <i>Russian Journal of Marine Biology</i> , 2019, 45, 453-463.	0.2	7
2751	Comparing eDNA metabarcoding and species collection for documenting Arctic metazoan biodiversity. <i>Environmental DNA</i> , 2019, 1, 342-358.	3.1	51
2752	Beneficial effects of novel hydrolysates produced by limited enzymatic broken rice on the gut microbiota and intestinal morphology in weaned piglets. <i>Journal of Functional Foods</i> , 2019, 62, 103560.	1.6	10
2753	Targeted genotyping by sequencing: a new way to genome profile the cat. <i>Animal Genetics</i> , 2019, 50, 718-725.	0.6	5
2754	Neurogenesis and longevity signaling in young germ-free mice transplanted with the gut microbiota of old mice. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	122
2755	Correlation of homologous recombination deficiency induced mutational signatures with sensitivity to PARP inhibitors and cytotoxic agents. <i>Genome Biology</i> , 2019, 20, 240.	3.8	82
2756	Structural Characteristics and Functional Implications of PM2.5 Bacterial Communities During Fall in Beijing and Shanghai, China. <i>Frontiers in Microbiology</i> , 2019, 10, 2369.	1.5	23
2757	Indigo Naturalis Ameliorates Dextran Sulfate Sodium-Induced Colitis in Mice by Modulating the Intestinal Microbiota Community. <i>Molecules</i> , 2019, 24, 4086.	1.7	46
2758	Dynamic Changes in the Microbiome and Mucosal Immune Microenvironment of the Lower Respiratory Tract by Influenza Virus Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 2491.	1.5	36
2759	Effects of different probiotics on the gut microbiome and metabolites in the serum and caecum of weaning piglets. <i>South African Journal of Animal Sciences</i> , 2019, 49, 494.	0.2	3
2760	Effects of <i>Debaryomyces hansenii</i> treatment on intestinal mucosa microecology in mice with antibiotic-associated diarrhea. <i>PLoS ONE</i> , 2019, 14, e0224730.	1.1	12
2761	Dysbiosis of the Gut Microbiome is associated with Tumor Biomarkers in Lung Cancer. <i>International Journal of Biological Sciences</i> , 2019, 15, 2381-2392.	2.6	114
2762	Habitat filtering shapes the differential structure of microbial communities in the Xilingol grassland. <i>Scientific Reports</i> , 2019, 9, 19326.	1.6	14
2763	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> F17 and <i>Leuconostoc lactis</i> H52 supernatants delay the decay of strawberry fruits: a microbiome perspective. <i>Food and Function</i> , 2019, 10, 7767-7781.	2.1	12
2764	Water-soluble phosphorus contributes significantly to shaping the community structure of rhizospheric bacteria in rocky desertification areas. <i>Scientific Reports</i> , 2019, 9, 18408.	1.6	11
2765	Simultaneous detection and comprehensive analysis of HPV and microbiome status of a cervical liquid-based cytology sample using Nanopore MinION sequencing. <i>Scientific Reports</i> , 2019, 9, 19337.	1.6	20
2766	Dynamic Succession of Microbiota during Ensiling of Whole Plant Corn Following Inoculation with <i>Lactobacillus buchneri</i> and <i>Lactobacillus hilgardii</i> Alone or in Combination. <i>Microorganisms</i> , 2019, 7, 595.	1.6	43
2767	Elevation is Associated with Human Skin Microbiomes. <i>Microorganisms</i> , 2019, 7, 611.	1.6	19

#	ARTICLE	IF	CITATIONS
2768	Effect of Seafood (Gizzard Shad) Supplementation on the Chemical Composition and Microbial Dynamics of Radish Kimchi during Fermentation. <i>Scientific Reports</i> , 2019, 9, 17693.	1.6	15
2769	Comparison of the gut microbiota of <i>Rana amurensis</i> and <i>Rana dybowskii</i> under natural winter fasting conditions. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	11
2770	Changes of Root Endophytic Bacterial Community Along a Chronosequence of Intensively Managed Lei Bamboo (<i>Phyllostachys praecox</i>) Forests in Subtropical China. <i>Microorganisms</i> , 2019, 7, 616.	1.6	10
2771	Silicon application and related changes in soil bacterial community dynamics reduced ginseng black spot incidence in <i>Panax ginseng</i> in a short-term study. <i>BMC Microbiology</i> , 2019, 19, 263.	1.3	17
2772	Identifying the core bacterial microbiome of hydrocarbon degradation and a shift of dominant methanogenesis pathways in the oil and aqueous phases of petroleum reservoirs of different temperatures from China. <i>Biogeosciences</i> , 2019, 16, 4229-4241.	1.3	9
2773	Low-Abundance Dietzia Inhabiting a Water-Flooding Oil Reservoir and the Application Potential for Oil Recovery. <i>BioMed Research International</i> , 2019, 2019, 1-11.	0.9	4
2774	Parameters Governing the Community Structure and Element Turnover in Kermadec Volcanic Ash and Hydrothermal Fluids as Monitored by Inorganic Electron Donor Consumption, Autotrophic CO ₂ Fixation and 16S Tags of the Transcriptome in Incubation Experiments. <i>Frontiers in Microbiology</i> , 2019, 10, 2296.	1.5	14
2775	Annual Protist Community Dynamics in a Freshwater Ecosystem Undergoing Contrasted Climatic Conditions: The Saint-Charles River (Canada). <i>Frontiers in Microbiology</i> , 2019, 10, 2359.	1.5	36
2776	Integrated Space-Time Dataset Reveals High Diversity and Distinct Community Structure of Ciliates in Mesopelagic Waters of the Northern South China Sea. <i>Frontiers in Microbiology</i> , 2019, 10, 2178.	1.5	20
2777	A Phage-Assisted Continuous Selection Approach for Deep Mutational Scanning of Protein-Protein Interactions. <i>ACS Chemical Biology</i> , 2019, 14, 2757-2767.	1.6	23
2778	Soluble Fiber and Insoluble Fiber Regulate Colonic Microbiota and Barrier Function in a Piglet Model. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	40
2779	Enhancing anaerobic digestion of dairy and swine wastewater by adding trace elements: evaluation in batch and continuous experiments. <i>Water Science and Technology</i> , 2019, 80, 1662-1672.	1.2	12
2780	Methanogenic Activity and Microbial Community Structure in Response to Different Mineralization Pathways of Ferrihydrite in Paddy Soil. <i>Frontiers in Earth Science</i> , 2019, 7, .	0.8	5
2781	Effects of Sphaeropsis Blight on Rhizosphere Soil Bacterial Community Structure and Soil Physicochemical Properties of <i>Pinus sylvestris</i> var. <i>mongolica</i> in Zhanggutai, China. <i>Forests</i> , 2019, 10, 954.	0.9	4
2782	Diet and irradiation effects on the bacterial community composition and structure in the gut of domesticated teneral and mature Queensland fruit fly, <i>Bactrocera tryoni</i> (Diptera: Tephritidae). <i>BMC Microbiology</i> , 2019, 19, 281.	1.3	26
2783	High-throughput sequencing of CD4+ T cell repertoire reveals disease-specific signatures in IgG4-related disease. <i>Arthritis Research and Therapy</i> , 2019, 21, 295.	1.6	11
2784	AlleleProfileR: A versatile tool to identify and profile sequence variants in edited genomes. <i>PLoS ONE</i> , 2019, 14, e0226694.	1.1	5
2785	Characterization of vaginal microbiota in women with preterm labor with intra-amniotic inflammation. <i>Scientific Reports</i> , 2019, 9, 18963.	1.6	15

#	ARTICLE	IF	CITATIONS
2786	Systematic processing of ribosomal RNA gene amplicon sequencing data. <i>GigaScience</i> , 2019, 8, .	3.3	49
2787	Impact of Tilapia hepcidin 2-3 dietary supplementation on the gut microbiota profile and immunomodulation in the grouper (<i>Epinephelus lanceolatus</i>). <i>Scientific Reports</i> , 2019, 9, 19047.	1.6	23
2788	Microbiota composition of the dorsal patch of reproductive male <i>Leptoncyteris yerbabuenae</i> . <i>PLoS ONE</i> , 2019, 14, e0226239.	1.1	13
2789	Regulation of photoprotection gene expression in <i>Chlamydomonas</i> by a putative E3 ubiquitin ligase complex and a homolog of CONSTANS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17556-17562.	3.3	44
2790	Increased performance of DNA metabarcoding of macroinvertebrates by taxonomic sorting. <i>PLoS ONE</i> , 2019, 14, e0226527.	1.1	28
2791	Hyperdiverse archaea near life limits at the polyextreme geothermal Dallol area. <i>Nature Ecology and Evolution</i> , 2019, 3, 1552-1561.	3.4	62
2792	Succession in arbuscular mycorrhizal fungi can be attributed to a chronosequence of <i>Cunninghamia lanceolata</i> . <i>Scientific Reports</i> , 2019, 9, 18057.	1.6	21
2793	Characterization of the cecal microbiome composition of Wenchang chickens before and after fattening. <i>PLoS ONE</i> , 2019, 14, e0225692.	1.1	25
2794	Environmental DNA Sequencing Reveals a Highly Complex Eukaryote Community in Sansha Yongle Blue Hole, Xisha, South China Sea. <i>Microorganisms</i> , 2019, 7, 624.	1.6	9
2795	Charting the Complexity of the Marine Microbiome through Single-Cell Genomics. <i>Cell</i> , 2019, 179, 1623-1635.e11.	13.5	158
2796	A Plant Growth-Promoting Microbial Soil Amendment Dynamically Alters the Strawberry Root Bacterial Microbiome. <i>Scientific Reports</i> , 2019, 9, 17677.	1.6	50
2797	Targeted selection of HIV-specific antibody mutations by engineering B cell maturation. <i>Science</i> , 2019, 366, .	6.0	118
2798	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019, 10, .	1.8	50
2799	Enrichment of <i>Marinobacter</i> sp. and Halophilic Homoacetogens at the Biocathode of Microbial Electrosynthesis System Inoculated With Red Sea Brine Pool. <i>Frontiers in Microbiology</i> , 2019, 10, 2563.	1.5	24
2800	Effect of supplementation of nicotinamide and sodium butyrate on the growth performance, liver mitochondrial function and gut microbiota of broilers at high stocking density. <i>Food and Function</i> , 2019, 10, 7081-7090.	2.1	15
2801	An integrated metabolomics and 16S rRNA gene sequencing approach exploring the molecular pathways and potential targets behind the effects of <i>Radix Scrophulariae</i> . <i>RSC Advances</i> , 2019, 9, 33354-33367.	1.7	3
2802	Influence of oxygen exposure on fermentation process and sensory qualities of Sichuan pickle (paocai). <i>RSC Advances</i> , 2019, 9, 38520-38530.	1.7	20
2803	Metagenomic insights into the structure and function of intestinal microbiota of the farmed Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2019, 499, 109-118.	1.7	69

#	ARTICLE	IF	CITATIONS
2804	Plant growth promoting bacteria increases biomass, effective constituent, and modifies rhizosphere bacterial communities of <i>Panax ginseng</i> . <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 2019, 69, 135-146.	0.3	4
2805	Submicron magnetite-enhanced tribromophenol removal and methanogenesis under microaerobic condition. <i>Journal of Chemical Technology and Biotechnology</i> , 2019, 94, 730-738.	1.6	7
2806	Evaluation of the bacterial diversity of Spanish-type chorizo during the ripening process using high-throughput sequencing and physicochemical characterization. <i>Meat Science</i> , 2019, 150, 7-13.	2.7	46
2807	Turning pig manure into biochar can effectively mitigate antibiotic resistance genes as organic fertilizer. <i>Science of the Total Environment</i> , 2019, 649, 902-908.	3.9	83
2808	Seed mucilage interacts with soil microbial community and physiochemical processes to affect seedling emergence on desert sand dunes. <i>Plant, Cell and Environment</i> , 2019, 42, 591-605.	2.8	18
2809	Karst rocky desertification progress: Soil calcium as a possible driving force. <i>Science of the Total Environment</i> , 2019, 649, 1250-1259.	3.9	72
2810	Impacts of Mo application on biological nitrogen fixation and diazotrophic communities in a flooded rice-soil system. <i>Science of the Total Environment</i> , 2019, 649, 686-694.	3.9	49
2811	Tree Diversity Determines the Diversity of the Taxonomic and Functional Structure of the Fungal Community in Forest Litter in Southern China. <i>Forest Science</i> , 2019, 65, 40-47.	0.5	2
2812	Characterization of the vaginal microbiome during cytolytic vaginosis using high-throughput sequencing. <i>Journal of Clinical Laboratory Analysis</i> , 2019, 33, e22653.	0.9	17
2813	Genomic insights into <i>Candidatus Amarolinea aalborgensis</i> gen. nov., sp. nov., associated with settleability problems in wastewater treatment plants. <i>Systematic and Applied Microbiology</i> , 2019, 42, 77-84.	1.2	58
2814	Effects of dietary lysozyme levels on growth performance, intestinal morphology, immunity response and microbiota community of growing pigs. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 1643-1650.	1.7	34
2815	Changes of microbial community and metabolite in kimchi inoculated with different microbial community starters. <i>Food Chemistry</i> , 2019, 274, 558-565.	4.2	58
2816	Dysbiosis of the gut microbiome is associated with thyroid cancer and thyroid nodules and correlated with clinical index of thyroid function. <i>Endocrine</i> , 2019, 64, 564-574.	1.1	78
2817	<i>Thiothrix eikelboomii</i> interferes oxygen transfer in activated sludge. <i>Water Research</i> , 2019, 151, 134-143.	5.3	63
2818	Effects of <i>Saccharomyces Cerevisiae</i> Fermentation Products on the Microbial Community throughout the Gastrointestinal Tract of Calves. <i>Animals</i> , 2019, 9, 4.	1.0	9
2819	Comparison of the gut microbiota of obese individuals from different geographic origins. <i>New Microbes and New Infections</i> , 2019, 27, 40-47.	0.8	12
2820	Multiple forms of selection shape reproductive isolation in a primate hybrid zone. <i>Molecular Ecology</i> , 2019, 28, 1056-1069.	2.0	24
2821	Addition of algicidal bacterium CZBC1 and molasses to inhibit cyanobacteria and improve microbial communities, water quality and shrimp performance in culture systems. <i>Aquaculture</i> , 2019, 502, 303-311.	1.7	24

#	ARTICLE	IF	CITATIONS
2822	Which animal type contributes the most to the emission of antibiotic resistance genes in large-scale swine farms in China?. <i>Science of the Total Environment</i> , 2019, 658, 152-159.	3.9	50
2823	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648.	6.5	70
2824	The Influence of Bt Maize Cultivation on Communities of Arbuscular Mycorrhizal Fungi Revealed by MiSeq Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 3275.	1.5	15
2825	Determination of microbiological characteristics in the digestive tract of different ruminant species. <i>MicrobiologyOpen</i> , 2019, 8, e00769.	1.2	17
2826	Large-scale mapping of microbial diversity in artisanal Brazilian cheeses. <i>Food Microbiology</i> , 2019, 80, 40-49.	2.1	83
2827	Spruce and beech as local determinants of forest fungal community structure in litter, humus and mineral soil. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	24
2828	Microbial communities in swine lungs and their association with lung lesions. <i>Microbial Biotechnology</i> , 2019, 12, 289-304.	2.0	24
2829	Diet composition and gut microbiome of 0-group European plaice <i>Pleuronectes platessa</i> L. - Strong homogeneity and subtle spatial and temporal differences. <i>Journal of Sea Research</i> , 2019, 144, 67-77.	0.6	4
2830	Rhizosphere fungal community structure succession of Xinjiang continuously cropped cotton. <i>Fungal Biology</i> , 2019, 123, 42-50.	1.1	7
2831	Biodiversity and dynamics of cyanobacterial communities during blooms in temperate lake (Harsha) Tj ETQq1 1 0.784314 rgBT /Overl	2.2	15
2832	Microtopographic differences in soil properties and microbial community composition at the field scale. <i>Soil Biology and Biochemistry</i> , 2019, 131, 71-80.	4.2	32
2833	Biofilter scaling procedures for organics removal: A potential alternative to piloting. <i>Water Research</i> , 2019, 151, 87-97.	5.3	13
2834	Biodiversity of the microbiota in <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae). <i>Journal of Applied Microbiology</i> , 2019, 126, 1199-1208.	1.4	35
2835	Compound polysaccharides ameliorate experimental colitis by modulating gut microbiota composition and function. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2019, 34, 1554-1562.	1.4	46
2836	Research on the hydrolysis of human urine using biological activated carbon and its application in bioregenerative life support system. <i>Acta Astronautica</i> , 2019, 155, 191-199.	1.7	4
2837	Effect of in situ sediment remediation combining oyster shells and bottom microporous aeration on nitrogen removal and microbiota. <i>Aquaculture Research</i> , 2019, 50, 331-341.	0.9	7
2838	Fertilisation practice changes rhizosphere microbial community structure in the agroecosystem. <i>Annals of Applied Biology</i> , 2019, 174, 123-132.	1.3	16
2839	Competition among Nasal Bacteria Suggests a Role for Siderophore-Mediated Interactions in Shaping the Human Nasal Microbiota. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	57

#	ARTICLE	IF	CITATIONS
2840	Gut microbiota dysbiosis correlates with a low-dose PCB126-induced dyslipidemia and non-alcoholic fatty liver disease. <i>Science of the Total Environment</i> , 2019, 653, 274-282.	3.9	65
2841	Lateral variations and vertical structure of the microbial methane cycle in the sediment of Lake Onego (Russia). <i>Inland Waters</i> , 2019, 9, 205-226.	1.1	8
2842	Geochemistry Shapes Bacterial Communities and their Metabolic Potentials in Tertiary Coalbed. <i>Geomicrobiology Journal</i> , 2019, 36, 179-187.	1.0	14
2843	Genomic insights into the metabolism of <i>Candidatus</i> <i>DeFluviicoccus seviourii</i> [™] , a member of <i>DeFluviicoccus</i> cluster III abundant in industrial activated sludge. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	17
2844	Diazotrophic microbial community and abundance in acidic subtropical natural and re-vegetated forest soils revealed by high-throughput sequencing of nifH gene. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 995-1005.	1.7	35
2845	Additional reduction of antibiotic resistance genes and human bacterial pathogens via thermophilic aerobic digestion of anaerobically digested sludge. <i>Bioresource Technology</i> , 2019, 273, 259-268.	4.8	33
2846	<i>Spartina alterniflora</i> invasion alters soil bacterial communities and enhances soil N ₂ O emissions by stimulating soil denitrification in mangrove wetland. <i>Science of the Total Environment</i> , 2019, 653, 231-240.	3.9	126
2847	Environmental and spatial variables determine the taxonomic but not functional structure patterns of microbial communities in alpine grasslands. <i>Science of the Total Environment</i> , 2019, 654, 960-968.	3.9	11
2848	Chikungunya Virus Fidelity Variants Exhibit Differential Attenuation and Population Diversity in Cell Culture and Adult Mice. <i>Journal of Virology</i> , 2019, 93, .	1.5	22
2849	Cooperation of lactic acid bacteria regulated by the AI-2/LuxS system involve in the biopreservation of refrigerated shrimp. <i>Food Research International</i> , 2019, 120, 679-687.	2.9	36
2850	Response of freshwater sediment archaeal community to metal spill. <i>Chemosphere</i> , 2019, 217, 584-590.	4.2	26
2851	Revegetated shrub species recruit different soil fungal assemblages in a desert ecosystem. <i>Plant and Soil</i> , 2019, 435, 81-93.	1.8	7
2852	Effects of the biological nitrification inhibitor 1,9-decanediol on nitrification and ammonia oxidizers in three agricultural soils. <i>Soil Biology and Biochemistry</i> , 2019, 129, 48-59.	4.2	61
2853	Experimental Evaluation of Coevolution in a Self-Assembling Particle. <i>Biochemistry</i> , 2019, 58, 1527-1538.	1.2	19
2854	Construction and next-generation sequencing analysis of a large phage-displayed VNAR single-domain antibody library from six naïve nurse sharks. <i>Antibody Therapeutics</i> , 2019, 2, 1-11.	1.2	53
2855	An Improved Genome Assembly for <i>Drosophila navojoa</i> , the Basal Species in the <i>mojavensis</i> Cluster. <i>Journal of Heredity</i> , 2019, 110, 118-123.	1.0	7
2856	Elevational patterns and hierarchical determinants of biodiversity across microbial taxonomic scales. <i>Molecular Ecology</i> , 2019, 28, 86-99.	2.0	34
2857	Selective colonization ability of human fecal microbes in different mouse gut environments. <i>ISME Journal</i> , 2019, 13, 805-823.	4.4	39

#	ARTICLE	IF	CITATIONS
2858	Functional analysis of the <i>TM6</i> MADS-box gene in the octoploid strawberry by CRISPR/Cas9-directed mutagenesis. <i>Journal of Experimental Botany</i> , 2019, 70, 885-895.	2.4	93
2859	Mixotrophic acidophiles increase cadmium soluble fraction and phytoextraction efficiency from cadmium contaminated soils. <i>Science of the Total Environment</i> , 2019, 655, 347-355.	3.9	30
2860	Gut and Whole-Body Microbiota of the Honey Bee Separate Thriving and Non-thriving Hives. <i>Microbial Ecology</i> , 2019, 78, 195-205.	1.4	39
2861	Genes regulating gland development in the cotton plant. <i>Plant Biotechnology Journal</i> , 2019, 17, 1142-1153.	4.1	42
2862	Altered fecal microbiota composition in the Flinders sensitive line rat model of depression. <i>Psychopharmacology</i> , 2019, 236, 1445-1457.	1.5	44
2863	Comparison of chemical composition and airborne bacterial community structure in PM2.5 during haze and non-haze days in the winter in Guilin, China. <i>Science of the Total Environment</i> , 2019, 655, 202-210.	3.9	60
2864	Targeted panel sequencing in adult patients with left ventricular non-compaction reveals a large genetic heterogeneity. <i>Clinical Genetics</i> , 2019, 95, 356-367.	1.0	56
2865	Evidence for positive selection of hepatitis A virus antigenic variants in vaccinated men-having-sex-with men patients: Implications for immunization policies. <i>EBioMedicine</i> , 2019, 39, 348-357.	2.7	22
2866	SPG-56 from Sweet potato Zhongshu-1 delayed growth of tumor xenografts in nude mice by modulating gut microbiota. <i>Journal of Functional Foods</i> , 2019, 52, 291-301.	1.6	0
2867	Silage fermentation and bacterial community of bur clover, annual ryegrass and their mixtures prepared with microbial inoculant and chemical additive. <i>Animal Feed Science and Technology</i> , 2019, 247, 285-293.	1.1	91
2868	Shelf-life and microbial community dynamics of super-chilled beef imported from Australia to China. <i>Food Research International</i> , 2019, 120, 784-792.	2.9	50
2869	Bacterial communities in prepared foods available at supermarkets in Beijing, China. <i>Food Research International</i> , 2019, 120, 668-678.	2.9	15
2870	Influence of microbial communities on the chemical and sensory features of Falanghina sweet passito wines. <i>Food Research International</i> , 2019, 120, 740-747.	2.9	22
2871	Profiles of bacterial assemblages from microplastics of tropical coastal environments. <i>Science of the Total Environment</i> , 2019, 655, 313-320.	3.9	130
2872	Genotype-free estimation of allele frequencies reduces bias and improves demographic inference from RADSeq data. <i>Molecular Ecology Resources</i> , 2019, 19, 586-596.	2.2	33
2873	Study of bacterial and fungal community structures in traditional koumiss from Inner Mongolia. <i>Journal of Dairy Science</i> , 2019, 102, 1972-1984.	1.4	34
2874	Analysis of the community composition and bacterial diversity of the rhizosphere microbiome across different plant taxa. <i>MicrobiologyOpen</i> , 2019, 8, e00762.	1.2	41
2875	Strain-specific changes in the gut microbiota profiles of the white shrimp <i>Litopenaeus vannamei</i> in response to cold stress. <i>Aquaculture</i> , 2019, 503, 357-366.	1.7	48

#	ARTICLE	IF	CITATIONS
2876	The cover crop determines the AMF community composition in soil and in roots of maize after a ten-year continuous crop rotation. <i>Science of the Total Environment</i> , 2019, 660, 913-922.	3.9	76
2877	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. <i>Canadian Journal of Microbiology</i> , 2019, 65, 353-364.	0.8	8
2878	Investigating responses of soil bacterial community composition to hardwood biochar amendment using high-throughput PCR sequencing. <i>Applied Soil Ecology</i> , 2019, 136, 80-85.	2.1	33
2879	Aqueous raw and ripe Pu-erh tea extracts alleviate obesity and alter cecal microbiota composition and function in diet-induced obese rats. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1823-1835.	1.7	31
2880	<i>Bacillus amyloliquefaciens</i> B1408 suppresses <i>Fusarium</i> wilt in cucumber by regulating the rhizosphere microbial community. <i>Applied Soil Ecology</i> , 2019, 136, 55-66.	2.1	76
2881	Linking Exoproteome Function and Structure to Anammox Biofilm Development. <i>Environmental Science & Technology</i> , 2019, 53, 1490-1500.	4.6	77
2882	Bacterial communities involved directly or indirectly in the anaerobic degradation of cellulose. <i>Biology and Fertility of Soils</i> , 2019, 55, 201-211.	2.3	52
2883	Bacterial community and metabolome shifts in the cecum and colon of captive sika deer (<i>Cervus</i>) Tj ETQq1 1 0.784314 rgBT /Over 0.7 11	0.7	11
2884	High-throughput amplicon sequencing demonstrates extensive diversity of xylanase genes in the sediment of soda lake Dabusu. <i>Biotechnology Letters</i> , 2019, 41, 409-418.	1.1	2
2885	Impact of 36 years of nitrogen fertilization on microbial community composition and soil carbon cycling-related enzyme activities in rhizospheres and bulk soils in northeast China. <i>Applied Soil Ecology</i> , 2019, 136, 148-157.	2.1	74
2886	Alleviating effects of walnut green husk extract on disorders of lipid levels and gut bacteria flora in high fat diet-induced obesity rats. <i>Journal of Functional Foods</i> , 2019, 52, 576-586.	1.6	40
2887	Combination of ribosome display and next generation sequencing as a powerful method for identification of affibody binders against β -lactamase CTX-M15. <i>New Biotechnology</i> , 2019, 50, 60-69.	2.4	7
2888	Community dynamics of free-living and particle-attached bacteria following a reservoir <i>Microcystis</i> bloom. <i>Science of the Total Environment</i> , 2019, 660, 501-511.	3.9	107
2889	The Metabolic Response to a Low Amino Acid Diet is Independent of Diet-Induced Shifts in the Composition of the Gut Microbiome. <i>Scientific Reports</i> , 2019, 9, 67.	1.6	16
2890	Soil pH dominates elevational diversity pattern for bacteria in high elevation alkaline soils on the Tibetan Plateau. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	83
2891	Repeated Evolution Versus Common Ancestry: Sex Chromosome Evolution in the Haplochromine Cichlid <i>Pseudocrenilabrus philander</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 439-458.	1.1	26
2892	Plastome-Wide Rearrangements and Gene Losses in Carnivorous Droseraceae. <i>Genome Biology and Evolution</i> , 2019, 11, 472-485.	1.1	40
2893	The microbiomic and environmental analysis of sediments in the Indo-Pacific humpback dolphin (<i>Sousa</i>) Tj ETQq1 1 0.784314 rgBT /Over 2.7 8 2019, 26, 6957-6970.	2.7	8

#	ARTICLE	IF	CITATIONS
2894	Geographic distance and soil microbial biomass carbon drive biogeographical distribution of fungal communities in Chinese Loess Plateau soils. <i>Science of the Total Environment</i> , 2019, 660, 1058-1069.	3.9	36
2895	Plastid Genomes and Proteins Illuminate the Evolution of Eustigmatophyte Algae and Their Bacterial Endosymbionts. <i>Genome Biology and Evolution</i> , 2019, 11, 362-379.	1.1	29
2896	A roadmap for high-throughput sequencing studies of wild animal populations using noninvasive samples and hybridization capture. <i>Molecular Ecology Resources</i> , 2019, 19, 609-622.	2.2	24
2897	Modulation of fat metabolism and gut microbiota by resveratrol on high-fat diet-induced obese mice. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 97-107.	1.1	58
2898	Metataxonomic comparison between internal transcribed spacer and 26S ribosomal large subunit (LSU) rDNA gene. <i>International Journal of Food Microbiology</i> , 2019, 290, 132-140.	2.1	46
2899	Characteristics of atmospheric bacterial and fungal communities in PM2.5 following biomass burning disturbance in a rural area of North China Plain. <i>Science of the Total Environment</i> , 2019, 651, 2727-2739.	3.9	71
2900	Changes in the Microbial Community of <i>Pinus arizonica</i> Saplings After Being Colonized by the Bark Beetle <i>Dendroctonus rhizophagus</i> (Curculionidae: Scolytinae). <i>Microbial Ecology</i> , 2019, 78, 102-112.	1.4	12
2901	Phylogenetic imprint of woody plants on the soil mycobiome in natural mountain forests of eastern China. <i>ISME Journal</i> , 2019, 13, 686-697.	4.4	76
2902	The rhizomicrobiomes of wild and cultivated crops react differently to fungicides. <i>Archives of Microbiology</i> , 2019, 201, 477-486.	1.0	13
2903	Rhizosphere responses to environmental conditions in <i>Radix pseudostellariae</i> under continuous monoculture regimes. <i>Agriculture, Ecosystems and Environment</i> , 2019, 270-271, 19-31.	2.5	47
2904	Comparison of long-term ceramic membrane bioreactors without and with in-situ ozonation in wastewater treatment: Membrane fouling, effluent quality and microbial community. <i>Science of the Total Environment</i> , 2019, 652, 788-799.	3.9	47
2905	Dietary shifts influenced by livestock grazing shape the gut microbiota composition and co-occurrence networks in a local rodent species. <i>Journal of Animal Ecology</i> , 2019, 88, 302-314.	1.3	36
2906	Fate of microbial pollutants and evolution of antibiotic resistance in three types of soil amended with swine slurry. <i>Environmental Pollution</i> , 2019, 245, 353-362.	3.7	41
2907	Different responses of absorptive roots and arbuscular mycorrhizal fungi to fertilization provide diverse nutrient acquisition strategies in Chinese fir. <i>Forest Ecology and Management</i> , 2019, 433, 64-72.	1.4	45
2908	Fungi participate in driving home-field advantage of litter decomposition in a subtropical forest. <i>Plant and Soil</i> , 2019, 434, 467-480.	1.8	51
2909	Comparison between kinetics of autochthonous marine bacteria in activated sludge and granular sludge systems at different salinity and SRTs. <i>Water Research</i> , 2019, 148, 425-437.	5.3	76
2910	Effect of dietary L-tryptophan on the survival, immune response and gut microbiota of the Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 1007-1017.	1.6	32
2911	Cumulative effect of yeast extract and fructooligosaccharide supplementation on composition and metabolic activity of elderly colonic microbiota in vitro. <i>Journal of Functional Foods</i> , 2019, 52, 43-53.	1.6	12

#	ARTICLE	IF	CITATIONS
2912	Exploring biogeographic patterns of bacterioplankton communities across global estuaries. <i>MicrobiologyOpen</i> , 2019, 8, e00741.	1.2	30
2913	Prokaryotic Diversity and Distribution in Different Habitats of an Alpine Rock Glacier-Pond System. <i>Microbial Ecology</i> , 2019, 78, 70-84.	1.4	12
2914	Transcriptome analysis of grass carp provides insights into disease-related genes and novel regulation pattern of bile acid feedback in response to lithocholic acid. <i>Aquaculture</i> , 2019, 500, 613-621.	1.7	21
2915	Bacterial community changes in a glacial-fed Tibetan lake are correlated with glacial melting. <i>Science of the Total Environment</i> , 2019, 651, 2059-2067.	3.9	21
2916	Altered host-gut microbes symbiosis in severely malnourished anorexia nervosa (AN) patients undergoing enteral nutrition: An explicative factor of functional intestinal disorders?. <i>Clinical Nutrition</i> , 2019, 38, 2304-2310.	2.3	62
2917	Injury, dysbiosis, and filaggrin deficiency drive skin inflammation through keratinocyte IL-1 β release. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1426-1443.e6.	1.5	56
2918	Composition and diversity of endophytic bacterial community in seeds of super hybrid rice "Shenliangyou 5814" (Oryza sativa L.) and its parental lines. <i>Plant Growth Regulation</i> , 2019, 87, 257-266.	1.8	26
2919	Tree species identity surpasses richness in affecting soil microbial richness and community composition in subtropical forests. <i>Soil Biology and Biochemistry</i> , 2019, 130, 113-121.	4.2	111
2920	Cyanate and urea are substrates for nitrification by Thaumarchaeota in the marine environment. <i>Nature Microbiology</i> , 2019, 4, 234-243.	5.9	103
2921	Characterization of Mauritian Cynomolgus Macaque Fc γ 3R Alleles Using Long-Read Sequencing. <i>Journal of Immunology</i> , 2019, 202, 151-159.	0.4	8
2922	Fall webworm genomes yield insights into rapid adaptation of invasive species. <i>Nature Ecology and Evolution</i> , 2019, 3, 105-115.	3.4	82
2923	Fate of antibiotic resistance genes during anaerobic digestion of sewage sludge: Role of solids retention times in different configurations. <i>Bioresource Technology</i> , 2019, 274, 488-495.	4.8	50
2924	Linkages between Epithelial Microbiota and Host Transcriptome in the Ileum during High-Grain Challenges: Implications for Gut Homeostasis in Goats. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 551-561.	2.4	17
2925	The genome of the jellyfish Aurelia and the evolution of animal complexity. <i>Nature Ecology and Evolution</i> , 2019, 3, 96-104.	3.4	86
2926	Soil ameliorants alter physicochemical properties and fungal communities in saline-sodic soils of Northeast China. <i>Archives of Agronomy and Soil Science</i> , 2019, 65, 1147-1159.	1.3	7
2927	Danshen can interact with intestinal bacteria from normal and chronic renal failure rats. <i>Biomedicine and Pharmacotherapy</i> , 2019, 109, 1758-1771.	2.5	22
2928	Resuscitation of anammox bacteria after >10,000 years of dormancy. <i>ISME Journal</i> , 2019, 13, 1098-1109.	4.4	51
2929	Faecal freezing preservation period influences colonization ability for faecal microbiota transplantation. <i>Journal of Applied Microbiology</i> , 2019, 126, 973-984.	1.4	19

#	ARTICLE	IF	CITATIONS
2930	The Intestinal Microbiota of <i>Hermetia illucens</i> Larvae Is Affected by Diet and Shows a Diverse Composition in the Different Midgut Regions. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	134
2931	Changes in gut bacterial communities in canaries infected by <i>Macrorhabdus ornithogaster</i> . <i>Avian Pathology</i> , 2019, 48, 111-120.	0.8	10
2932	Endophytic bacterial communities of Jingbai Pear trees in north China analyzed with Illumina sequencing of 16S rDNA. <i>Archives of Microbiology</i> , 2019, 201, 199-208.	1.0	22
2933	Soil aggregate-associated bacterial metabolic activity and community structure in different aged tea plantations. <i>Science of the Total Environment</i> , 2019, 654, 1023-1032.	3.9	76
2934	The correlation of methanogenic communities' dynamics and process performance of anaerobic digestion of thermal hydrolyzed sludge at short hydraulic retention times. <i>Bioresource Technology</i> , 2019, 272, 180-187.	4.8	41
2935	Dibutyl phthalate contamination remodeled the fungal community in agro-environmental system. <i>Chemosphere</i> , 2019, 215, 189-198.	4.2	27
2936	Evolution of intestinal microbiota and body compartments during spontaneous hyperphagia in the Greylag goose. <i>Poultry Science</i> , 2019, 98, 1390-1402.	1.5	6
2937	Structural and functional profiles of the gut microbial community in polycystic ovary syndrome with insulin resistance (IR-PCOS): a pilot study. <i>Research in Microbiology</i> , 2019, 170, 43-52.	1.0	103
2938	Bacterial community variations in paddy soils induced by application of veterinary antibiotics in plant-soil systems. <i>Ecotoxicology and Environmental Safety</i> , 2019, 167, 44-53.	2.9	50
2939	High-production dairy cattle exhibit different rumen and fecal bacterial community and rumen metabolite profile than low-production cattle. <i>MicrobiologyOpen</i> , 2019, 8, e00673.	1.2	38
2940	Long-term application of manure over plant residues mitigates acidification, builds soil organic carbon and shifts prokaryotic diversity in acidic Ultisols. <i>Applied Soil Ecology</i> , 2019, 133, 24-33.	2.1	76
2941	Protective effects of lentinan on lipopolysaccharide induced inflammatory response in intestine of juvenile taimen (<i>Hucho taimen</i> , Pallas). <i>International Journal of Biological Macromolecules</i> , 2019, 121, 317-325.	3.6	35
2942	<i>Vibrio alginolyticus</i> infection induces coupled changes of bacterial community and metabolic phenotype in the gut of swimming crab. <i>Aquaculture</i> , 2019, 499, 251-259.	1.7	42
2943	Genetic drift shaped MHC IIB diversity of an endangered anuran species within the Italian glacial refugium. <i>Journal of Zoology</i> , 2019, 307, 61-70.	0.8	12
2944	Roux-en-Y Gastric-Bypass and sleeve gastrectomy induces specific shifts of the gut microbiota without altering the metabolism of bile acids in the intestinal lumen. <i>International Journal of Obesity</i> , 2019, 43, 428-431.	1.6	19
2945	Detecting host-parasitoid interactions in an invasive Lepidopteran using nested tagging DNA metabarcoding. <i>Molecular Ecology</i> , 2019, 28, 471-483.	2.0	57
2946	Biases from different DNA extraction methods in intestine microbiome research based on 16S rDNA sequencing: a case in the koi carp, <i>Cyprinus carpio</i> var. <i>Koi</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00626.	1.2	13
2947	Effects of redox potential on soil cadmium solubility: Insight into microbial community. <i>Journal of Environmental Sciences</i> , 2019, 75, 224-232.	3.2	87

#	ARTICLE	IF	CITATIONS
2948	Effects of <i>Spartina alterniflora</i> invasion on <i>Kandelia candel</i> rhizospheric bacterial community as determined by high-throughput sequencing analysis. <i>Journal of Soils and Sediments</i> , 2019, 19, 332-344.	1.5	19
2949	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , 2019, 20, 1032-1056.	3.2	10
2950	Annual bacterial community cycle in a seasonally ice-covered river reflects environmental and climatic conditions. <i>Limnology and Oceanography</i> , 2020, 65, S21.	1.6	59
2951	Mucosa-Associated Microbiota in the Gastrointestinal Tract of Healthy Japanese Subjects. <i>Digestion</i> , 2020, 101, 107-120.	1.2	16
2952	Effects of a formula with a probiotic <i>Bifidobacterium lactis</i> Supplement on the gut microbiota of low birth weight infants. <i>European Journal of Nutrition</i> , 2020, 59, 1493-1503.	1.8	20
2953	Variation pattern of antibiotic resistance genes and microbial community succession during swine manure composting under different aeration strategies. <i>Journal of Chemical Technology and Biotechnology</i> , 2020, 95, 466-473.	1.6	26
2954	Biocontrol of Root Diseases and Growth Promotion of the Tuberos Plant <i>Aconitum carmichaelii</i> Induced by Actinomycetes Are Related to Shifts in the Rhizosphere Microbiota. <i>Microbial Ecology</i> , 2020, 79, 134-147.	1.4	30
2955	Prominence of ileal mucosa-associated microbiota to predict postoperative endoscopic recurrence in Crohn's disease. <i>Gut</i> , 2020, 69, 462-472.	6.1	76
2956	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota \pm Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020, 70, 615-627.	2.9	65
2957	Antibiotic exposure perturbs the bacterial community in the small brown planthopper <i>Laodelphax striatellus</i> . <i>Insect Science</i> , 2020, 27, 895-907.	1.5	28
2958	Fungi participate in the dysbiosis of gut microbiota in patients with primary sclerosing cholangitis. <i>Gut</i> , 2020, 69, 92-102.	6.1	136
2959	Arabinoxylan oligosaccharides and polyunsaturated fatty acid effects on gut microbiota and metabolic markers in overweight individuals with signs of metabolic syndrome: A randomized cross-over trial. <i>Clinical Nutrition</i> , 2020, 39, 67-79.	2.3	68
2960	Effect of super absorbent polymer sodium polyacrylate on the bacterial community and associated chemistry of loessial soil. <i>Archives of Agronomy and Soil Science</i> , 2020, 66, 70-82.	1.3	5
2961	Multi-hydrolytic enzyme accumulation and microbial community structure of anaerobic co-digestion of food waste and waste-activated sludge. <i>Environmental Technology (United Kingdom)</i> , 2020, 41, 478-487.	1.2	10
2962	Microbial Diversity in High-Temperature Heavy Oil Reservoirs. <i>Geomicrobiology Journal</i> , 2020, 37, 59-66.	1.0	9
2963	Seed-Associated Fungal Diversity and the Molecular Identification of <i>Fusarium</i> with Potential Threat to Ginseng (<i>Panax ginseng</i>) in China. <i>Plant Disease</i> , 2020, 104, 330-339.	0.7	7
2964	The effects of artificial light at night on Eurasian tree sparrow (<i>Passer montanus</i>): Behavioral rhythm disruption, melatonin suppression and intestinal microbiota alterations. <i>Ecological Indicators</i> , 2020, 108, 105702.	2.6	28
2965	The diversity and biogeography of microeukaryotes in the euphotic zone of the northwestern Pacific Ocean. <i>Science of the Total Environment</i> , 2020, 698, 134289.	3.9	34

#	ARTICLE	IF	CITATIONS
2966	Psoriatic lesions are characterized by higher bacterial load and imbalance between Cutibacterium and Corynebacterium. <i>Journal of the American Academy of Dermatology</i> , 2020, 82, 955-961.	0.6	54
2967	Isolation of virulent phages infecting dominant mesophilic aerobic bacteria in cucumber pickle fermentation. <i>Food Microbiology</i> , 2020, 86, 103330.	2.1	29
2968	Biostimulation of sewage sludge solubilization and methanization by hyper-thermophilic pre-hydrolysis stage and the shifts of microbial structure profiles. <i>Science of the Total Environment</i> , 2020, 699, 134373.	3.9	10
2969	Analysis of endophytic bacterial community diversity and metabolic correlation in <i>Cinnamomum camphora</i> . <i>Archives of Microbiology</i> , 2020, 202, 181-189.	1.0	13
2970	Carboxymethyl chitosan perturbs inflammation profile and colonic microbiota balance in mice. <i>Journal of Food and Drug Analysis</i> , 2020, 28, 175-182.	0.9	11
2971	Effects of multi-year biofumigation on soil bacterial and fungal communities and strawberry yield. <i>Environmental Pollution</i> , 2020, 256, 113415.	3.7	20
2972	Relationship of tongue coating microbiome on volatile sulfur compounds in healthy and halitosis adults. <i>Journal of Breath Research</i> , 2020, 14, 016005.	1.5	39
2973	Sandy soils amended with bentonite induced changes in soil microbiota and fungistasis in maize fields. <i>Applied Soil Ecology</i> , 2020, 146, 103378.	2.1	26
2974	Data, time and money: evaluating the best compromise for inferring molecular phylogenies of non-model animal taxa. <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106660.	1.2	13
2975	Factors Contributing to Interindividual Variation in Retronasal Odor Perception from Aroma Glycosides: The Role of Odorant Sensory Detection Threshold, Oral Microbiota, and Hydrolysis in Saliva. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 10299-10309.	2.4	25
2976	Fungal community demonstrates stronger dispersal limitation and less network connectivity than bacterial community in sediments along a large river. <i>Environmental Microbiology</i> , 2020, 22, 832-849.	1.8	115
2977	Fire affects the taxonomic and functional composition of soil microbial communities, with cascading effects on grassland ecosystem functioning. <i>Global Change Biology</i> , 2020, 26, 431-442.	4.2	45
2978	Ectopic osteogenesis by type I collagen loaded with a novel synthesized PTH-related peptide in vivo. <i>Journal of Biomedical Materials Research - Part A</i> , 2020, 108, 166-177.	2.1	12
2979	Sorgoleone release from sorghum roots shapes the composition of nitrifying populations, total bacteria, and archaea and determines the level of nitrification. <i>Biology and Fertility of Soils</i> , 2020, 56, 145-166.	2.3	57
2980	Fungicide azoxystrobin induced changes on the soil microbiome. <i>Applied Soil Ecology</i> , 2020, 145, 103343.	2.1	22
2981	The effect of inulin and resistant maltodextrin on weight loss during energy restriction: a randomised, placebo-controlled, double-blinded intervention. <i>European Journal of Nutrition</i> , 2020, 59, 2507-2524.	1.8	36
2982	Paenibacillus polymyxa improves the growth, immune and antioxidant activity, intestinal health, and disease resistance in <i>Litopenaeus vannamei</i> challenged with <i>Vibrio parahaemolyticus</i> . <i>Aquaculture</i> , 2020, 518, 734563.	1.7	36
2983	Inflammation inhibition and gut microbiota regulation by TSG to combat atherosclerosis in ApoE ^{-/-} mice. <i>Journal of Ethnopharmacology</i> , 2020, 247, 112232.	2.0	35

#	ARTICLE	IF	CITATIONS
2984	Enhanced reductive dechlorination of trichloroethene with immobilized <i>Clostridium butyricum</i> in silica gel. <i>Chemosphere</i> , 2020, 238, 124596.	4.2	18
2985	Absorption of 1,3-diiolelyl-2-palmitoylglycerol and intestinal flora profiles changes in mice. <i>International Journal of Food Sciences and Nutrition</i> , 2020, 71, 296-306.	1.3	8
2986	Changes in Intestinal Microbiota of Type 2 Diabetes in Mice in Response to Dietary Supplementation With Instant Tea or Matcha. <i>Canadian Journal of Diabetes</i> , 2020, 44, 44-52.	0.4	51
2987	Impact of Sugarcaneâ€“Legume Intercropping on Diazotrophic Microbiome. <i>Sugar Tech</i> , 2020, 22, 52-64.	0.9	26
2988	A Metagenomic Study of Intestinal Microbial Diversity in Relation to Feeding Habits of Surface and Cave-Dwelling <i>Sinocyclocheilus</i> Species. <i>Microbial Ecology</i> , 2020, 79, 299-311.	1.4	22
2989	NirS-type N ₂ O-producers and nosZ II-type N ₂ O-reducers determine the N ₂ O emission potential in farmland rhizosphere soils. <i>Journal of Soils and Sediments</i> , 2020, 20, 461-471.	1.5	24
2990	Ecological Processes Shaping Bulk Soil and Rhizosphere Microbiome Assembly in a Long-Term Amazon Forest-to-Agriculture Conversion. <i>Microbial Ecology</i> , 2020, 79, 110-122.	1.4	41
2991	Dietary administration of resistant starch improved caecal barrier function by enhancing intestinal morphology and modulating microbiota composition in meat duck. <i>British Journal of Nutrition</i> , 2020, 123, 172-181.	1.2	24
2992	Source of hemolymph microbiota and their roles in the immune system of mud crab. <i>Developmental and Comparative Immunology</i> , 2020, 102, 103470.	1.0	26
2993	Severe Intestinal Dysbiosis in Rat Models of Short Bowel Syndrome with Ileocecal Resection. <i>Digestive Diseases and Sciences</i> , 2020, 65, 431-441.	1.1	12
2994	Effects of <i>Bacillus Subtilis</i> -Zinc on Rats with Congenital Zinc Deficiency. <i>Biological Trace Element Research</i> , 2020, 194, 482-492.	1.9	1
2995	Modification of Rhizosphere Bacterial Community Structure and Functional Potentials to Control <i>Pseudostellaria heterophylla</i> Replant Disease. <i>Plant Disease</i> , 2020, 104, 25-34.	0.7	20
2996	Composition of the arbuscular mycorrhizal fungal community and changes in diversity of the rhizosphere of <i>Clematis fruticosa</i> over three seasons across different elevations. <i>European Journal of Soil Science</i> , 2020, 71, 511-523.	1.8	7
2997	Dietary dl-methionyl-dl-methionine supplementation increased growth performance, antioxidant ability, the content of essential amino acids and improved the diversity of intestinal microbiota in Nile tilapia (<i>Oreochromis niloticus</i>). <i>British Journal of Nutrition</i> , 2020, 123, 72-83.	1.2	22
2998	Intake of <i>Ganoderma lucidum</i> polysaccharides reverses the disturbed gut microbiota and metabolism in type 2 diabetic rats. <i>International Journal of Biological Macromolecules</i> , 2020, 155, 890-902.	3.6	124
2999	Soil bacterial community differences along a coastal restoration chronosequence. <i>Plant Ecology</i> , 2020, 221, 795-811.	0.7	12
3000	Ambient temperature alters body size and gut microbiota of <i>Xenopus tropicalis</i> . <i>Science China Life Sciences</i> , 2020, 63, 915-925.	2.3	20
3001	Different milk replacers alter growth performance and rumen bacterial diversity of dairy bull calves. <i>Livestock Science</i> , 2020, 231, 103862.	0.6	5

#	ARTICLE	IF	CITATIONS
3002	Temperature mainly determines the temporal succession of the photosynthetic picoeukaryote community in Lake Chaohu, a highly eutrophic shallow lake. <i>Science of the Total Environment</i> , 2020, 702, 134803.	3.9	21
3003	Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications. <i>Water Research</i> , 2020, 169, 115250.	5.3	21
3004	The fungal community and its interaction with the concentration of short-chain fatty acids in the faeces of Chenghua, Yorkshire and Tibetan pigs. <i>Microbial Biotechnology</i> , 2020, 13, 509-521.	2.0	17
3005	Fungal community composition in sodic soils subjected to long-term rice cultivation. <i>Archives of Agronomy and Soil Science</i> , 2020, 66, 1410-1423.	1.3	8
3006	Exploring the accuracy of amplicon-based internal transcribed spacer markers for a fungal community. <i>Molecular Ecology Resources</i> , 2020, 20, 170-184.	2.2	49
3007	Microbial composition of Korean kefir and antimicrobial activity of <i>Acetobacter fabarum</i> DH1801. <i>Journal of Food Safety</i> , 2020, 40, e12728.	1.1	11
3008	Bacterial communities in the solid, liquid, dorsal, and ventral epithelium fractions of yak (<i>Bos</i>) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50 5	1.2	43
3009	Distribution of Protists in the Deep South China Sea Revealed by High-Throughput Sequencing. <i>Journal of Ocean University of China</i> , 2020, 19, 161-170.	0.6	3
3010	Microbial taxonomic and functional attributes consistently predict soil CO ₂ emissions across contrasting croplands. <i>Science of the Total Environment</i> , 2020, 702, 134885.	3.9	13
3011	Long-term organic fertilization improves the productivity of kiwifruit (<i>Actinidia chinensis</i> Planch.) through increasing rhizosphere microbial diversity and network complexity. <i>Applied Soil Ecology</i> , 2020, 147, 103426.	2.1	56
3012	Bacterial succession and the dynamics of flavor compounds in the Huangjiu fermented from corn. <i>Archives of Microbiology</i> , 2020, 202, 299-308.	1.0	15
3013	Development of genomic microsatellite markers for <i>Aconitum gymnantrum</i> (Ranunculaceae) by next generation sequencing (NGS). <i>Molecular Biology Reports</i> , 2020, 47, 727-729.	1.0	4
3014	Short-term impact of fire-deposited charcoal on soil microbial community abundance and composition in a subtropical plantation in China. <i>Geoderma</i> , 2020, 359, 113992.	2.3	14
3015	Chloropicrin fumigation alters the soil phosphorus and the composition of the encoding alkaline phosphatase PhoD gene microbial community. <i>Science of the Total Environment</i> , 2020, 711, 135080.	3.9	29
3016	Biodegradability of wastewater determines microbial assembly mechanisms in full-scale wastewater treatment plants. <i>Water Research</i> , 2020, 169, 115276.	5.3	109
3017	Unveiling membrane thermoregulation strategies in marine picocyanobacteria. <i>New Phytologist</i> , 2020, 225, 2396-2410.	3.5	20
3018	Oral cancer-associated tertiary lymphoid structures: gene expression profile and prognostic value. <i>Clinical and Experimental Immunology</i> , 2020, 199, 172-181.	1.1	44
3019	Microbial diversity of sediments from an inactive hydrothermal vent field, Southwest Indian Ridge. <i>Marine Life Science and Technology</i> , 2020, 2, 73-86.	1.8	19

#	ARTICLE	IF	CITATIONS
3020	Preventive antibiotic treatment of calves: emergence of dysbiosis causing propagation of obese state-associated and mobile multidrug resistance-carrying bacteria. <i>Microbial Biotechnology</i> , 2020, 13, 669-682.	2.0	18
3021	eDNA metabarcoding as a promising conservation tool for monitoring fish diversity in a coastal wetland of the Pearl River Estuary compared to bottom trawling. <i>Science of the Total Environment</i> , 2020, 702, 134704.	3.9	85
3022	Ecological processes underlying community assembly of aquatic bacteria and macroinvertebrates under contrasting climates on the Tibetan Plateau. <i>Science of the Total Environment</i> , 2020, 702, 134974.	3.9	15
3023	Geographical distribution and risk assessment of heavy metals: a case study of mine tailings pond. <i>Chemistry and Ecology</i> , 2020, 36, 1-15.	0.6	9
3024	Dietary resistant starch modifies the composition and function of caecal microbiota of broilers. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 1274-1284.	1.7	38
3025	Bacterial communities in digestive and excretory organs of cicadas. <i>Archives of Microbiology</i> , 2020, 202, 539-553.	1.0	11
3026	An Illumina approach to MHC typing of Atlantic salmon. <i>Immunogenetics</i> , 2020, 72, 89-100.	1.2	7
3027	Different toxic effects of ferulic and p-hydroxybenzoic acids on cucumber seedling growth were related to their different influences on rhizosphere microbial composition. <i>Biology and Fertility of Soils</i> , 2020, 56, 125-136.	2.3	39
3028	<i>Artemisia sphaerocephala</i> Krasch polysaccharide mediates lipid metabolism and metabolic endotoxaemia in associated with the modulation of gut microbiota in diet-induced obese mice. <i>International Journal of Biological Macromolecules</i> , 2020, 147, 1008-1017.	3.6	51
3029	Anti-obesity effect of <i>Lactobacillus rhamnosus</i> LS-8 and <i>Lactobacillus crustorum</i> MN047 on high-fat and high-fructose diet mice base on inflammatory response alleviation and gut microbiota regulation. <i>European Journal of Nutrition</i> , 2020, 59, 2709-2728.	1.8	69
3030	Bacteriome and Mycobiome in <i>Nicotiana tabacum</i> Fields Affected by Black Shank Disease. <i>Plant Disease</i> , 2020, 104, 315-319.	0.7	5
3031	Diversity and dynamics of microbial communities in brown planthopper at different developmental stages revealed by high-throughput amplicon sequencing. <i>Insect Science</i> , 2020, 27, 883-894.	1.5	28
3032	Wheat-associated microbiota and their correlation with stripe rust reaction. <i>Journal of Applied Microbiology</i> , 2020, 128, 544-555.	1.4	19
3033	Effects of dietary calcium pyruvate on gastrointestinal tract development, intestinal health and growth performance of newly weaned piglets fed low-protein diets. <i>Journal of Applied Microbiology</i> , 2020, 128, 355-365.	1.4	14
3034	Presence of diverse nitrate-dependent anaerobic methane oxidizing archaea in sewage sludge. <i>Journal of Applied Microbiology</i> , 2020, 128, 775-783.	1.4	9
3035	Porcine Epidemic Diarrhea Altered Colonic Microbiota Communities in Suckling Piglets. <i>Genes</i> , 2020, 11, 44.	1.0	7
3036	The Diversity of Associated Microorganisms in Different Organs and Rhizospheric Soil of <i>Arctium lappa</i> L.. <i>Current Microbiology</i> , 2020, 77, 746-754.	1.0	6
3037	Vertical changes in bacterial community composition down to a depth of 20m on the degraded Loess Plateau in China. <i>Land Degradation and Development</i> , 2020, 31, 1300-1313.	1.8	20

#	ARTICLE	IF	CITATIONS
3038	Dietary effect of low fish meal aquafeed on gut microbiota in olive flounder (<i>Paralichthys</i>) Tj ETQq0 0 0 rgBT /Overlock 10, Jf 50 742 T	1.2	24
3039	Altered Intestinal Microbiota Composition Associated with Enteritis in Yellow Seahorses <i>Hippocampus kuda</i> (Bleeker, 1852). <i>Current Microbiology</i> , 2020, 77, 730-737.	1.0	20
3040	A new sea surface temperature proxy based on bacterial 3-hydroxy fatty acids. <i>Organic Geochemistry</i> , 2020, 141, 103975.	0.9	13
3041	Evaluation of the Bacterial Diversity of Inner Mongolian Acidic Gruel Using Illumina MiSeq and PCR-DGGE. <i>Current Microbiology</i> , 2020, 77, 434-442.	1.0	13
3042	Exploitation of the Cooperative Behaviors of Anti-CRISPR Phages. <i>Cell Host and Microbe</i> , 2020, 27, 189-198.e6.	5.1	39
3043	Effect of time-restricted feeding on metabolic risk and circadian rhythm associated with gut microbiome in healthy males. <i>British Journal of Nutrition</i> , 2020, 123, 1216-1226.	1.2	98
3044	Microbes Associated With Black Soldier Fly (Diptera: Stratiomiidae) Degradation of Food Waste. <i>Environmental Entomology</i> , 2020, 49, 405-411.	0.7	38
3045	DNA sequencing reveals bacterial communities in midgut and other parts of the larvae of <i>Spodoptera exigua</i> Hubner (Lepidoptera: Noctuidae). <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	6
3046	Colon Cancer Prevention with Walnuts: A Longitudinal Study in Mice from the Perspective of a Gut Enterotype-like Cluster. <i>Cancer Prevention Research</i> , 2020, 13, 15-24.	0.7	3
3047	Biodegradation of skatole by <i>Burkholderia</i> sp. IDO3 and its successful bioaugmentation in activated sludge systems. <i>Environmental Research</i> , 2020, 182, 109123.	3.7	21
3048	Longitudinal analysis of the antibody repertoire of a Zika virus-infected patient revealed dynamic changes in antibody response. <i>Emerging Microbes and Infections</i> , 2020, 9, 111-123.	3.0	13
3049	Progressive Microbial Community Networks with Incremental Organic Loading Rates Underlie Higher Anaerobic Digestion Performance. <i>MSystems</i> , 2020, 5, .	1.7	15
3050	Salivary Microbiome and Cigarette Smoking: A First of Its Kind Investigation in Jordan. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 256.	1.2	41
3051	Probiotic Supplementation in a <i>Clostridium difficile</i> -Infected Gastrointestinal Model Is Associated with Restoring Metabolic Function of Microbiota. <i>Microorganisms</i> , 2020, 8, 60.	1.6	19
3052	Postnatal co-development of the microbiota and gut barrier function follows different paths in the small and large intestine in piglets. <i>FASEB Journal</i> , 2020, 34, 1430-1446.	0.2	26
3053	Insight into the microbiology of nitrogen cycle in the dairy manure composting process revealed by combining high-throughput sequencing and quantitative PCR. <i>Bioresource Technology</i> , 2020, 301, 122760.	4.8	76
3054	Chronic periodontitis induces microbiota-gut-brain axis disorders and cognitive impairment in mice. <i>Experimental Neurology</i> , 2020, 326, 113176.	2.0	34
3055	An interdependent relationship between microbial ecosystems and ferromanganese nodules from the Western Pacific Ocean. <i>Sedimentary Geology</i> , 2020, 398, 105588.	1.0	13

#	ARTICLE	IF	CITATIONS
3056	Characterization of the core microbiome in tobacco leaves during aging. <i>MicrobiologyOpen</i> , 2020, 9, e984.	1.2	38
3057	<i>Lactobacillus rhamnosus</i> from human breast milk shows therapeutic function against foodborne infection by multi-drug resistant <i>Escherichia coli</i> in mice. <i>Food and Function</i> , 2020, 11, 435-447.	2.1	24
3058	High-throughput single-cell cultivation reveals the underexplored rare biosphere in deep-sea sediments along the Southwest Indian Ridge. <i>Lab on A Chip</i> , 2020, 20, 363-372.	3.1	31
3059	Differential intestinal and oral microbiota features associated with gestational diabetes and maternal inflammation. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2020, 319, E247-E253.	1.8	44
3060	Berberine ameliorates colonic damage accompanied with the modulation of dysfunctional bacteria and functions in ulcerative colitis rats. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 1737-1749.	1.7	39
3061	Organic amendment mitigates the negative impacts of mineral fertilization on bacterial communities in Shajiang black soil. <i>Applied Soil Ecology</i> , 2020, 150, 103457.	2.1	24
3062	Enhanced nitrogen removal from low C/N wastewater using biodegradable and inert carriers: Performance and microbial shift. <i>Bioresource Technology</i> , 2020, 300, 122658.	4.8	21
3063	High rate anaerobic digestion of swine wastewater in an anaerobic membrane bioreactor. <i>Energy</i> , 2020, 193, 116783.	4.5	56
3064	Environmental antibiotics drives the genetic functions of resistome dynamics. <i>Environment International</i> , 2020, 135, 105398.	4.8	29
3065	Silver nanoparticles are lethal to the ciliate model <i>Tetrahymena</i> and safe to the pike silverside <i>Chirostoma estor</i> . <i>Experimental Parasitology</i> , 2020, 209, 107825.	0.5	9
3066	Bioturbation effect of fortified Daqu on microbial community and flavor metabolite in Chinese strong-flavor liquor brewing microecosystem. <i>Food Research International</i> , 2020, 129, 108851.	2.9	86
3067	Metagenomic analysis of viruses, bacteria and protozoa in irrigation water. <i>International Journal of Hygiene and Environmental Health</i> , 2020, 224, 113440.	2.1	29
3068	Aerobic composting as an effective cow manure management strategy for reducing the dissemination of antibiotic resistance genes: An integrated meta-omics study. <i>Journal of Hazardous Materials</i> , 2020, 386, 121895.	6.5	68
3069	Green tea polyphenols decrease weight gain, ameliorate alteration of gut microbiota, and mitigate intestinal inflammation in canines with high-fat-diet-induced obesity. <i>Journal of Nutritional Biochemistry</i> , 2020, 78, 108324.	1.9	82
3070	Microbial indicators are better predictors of wheat yield and quality than N fertilization. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	31
3071	Disordered cutaneous microbiota in systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2020, 108, 102391.	3.0	35
3072	Soil microbiotic homogenization occurred after long-term agricultural development in desert areas across northern China. <i>Land Degradation and Development</i> , 2020, 31, 1014-1025.	1.8	7
3073	Revealing the impact of global mass bleaching on coral microbiome through 16S rRNA gene-based metagenomic analysis. <i>Microbiological Research</i> , 2020, 233, 126408.	2.5	7

#	ARTICLE	IF	CITATIONS
3074	Comparative genomics reveals divergent thermal selection in warm- and cold-tolerant marine mussels. <i>Molecular Ecology</i> , 2020, 29, 519-535.	2.0	24
3075	<i>Staphylococcus epidermidis</i> Contributes to Healthy Maturation of the Nasal Microbiome by Stimulating Antimicrobial Peptide Production. <i>Cell Host and Microbe</i> , 2020, 27, 68-78.e5.	5.1	99
3076	Tossed "good luck"™ coins as vectors for anthropogenic pollution into aquatic environment. <i>Environmental Pollution</i> , 2020, 259, 113800.	3.7	4
3077	Microbial community and geochemical analyses of trans-trench sediments for understanding the roles of hadal environments. <i>ISME Journal</i> , 2020, 14, 740-756.	4.4	99
3078	Insights into protist diversity and biogeography in intertidal sediments sampled across a range of spatial scales. <i>Limnology and Oceanography</i> , 2020, 65, 1103-1115.	1.6	28
3079	Direct and indirect effects of long-term ditch-buried straw return on soil bacterial community in a rice-wheat rotation system. <i>Land Degradation and Development</i> , 2020, 31, 851-867.	1.8	24
3080	Gut butyrate-producing organisms correlate to Placenta Specific 8 protein: Importance to colorectal cancer progression. <i>Journal of Advanced Research</i> , 2020, 22, 7-20.	4.4	22
3081	Manganese/iron-supported sulfate-dependent anaerobic oxidation of methane by archaea in lake sediments. <i>Limnology and Oceanography</i> , 2020, 65, 863-875.	1.6	54
3082	Deciphering microbiomes in anaerobic reactors with superior trichloroethylene dechlorination performance at low pH conditions. <i>Environmental Pollution</i> , 2020, 257, 113567.	3.7	14
3083	Restoration-mediated secondary contact leads to introgression of alewife ecotypes separated by a colonial-era dam. <i>Evolutionary Applications</i> , 2020, 13, 652-664.	1.5	10
3084	Black Soldier Fly (<i>Hermetia illucens</i>) reared on roasted coffee by-product and <i>Schizochytrium</i> sp. as a sustainable terrestrial ingredient for aquafeeds production. <i>Aquaculture</i> , 2020, 518, 734659.	1.7	60
3085	Long-term nitrogen application decreases the abundance and copy number of predatory myxobacteria and alters the myxobacterial community structure in the soil. <i>Science of the Total Environment</i> , 2020, 708, 135114.	3.9	28
3086	Genome analysis of sponge symbiont <i>Candidatus Halichondribacter symbioticus</i> ™ shows genomic adaptation to a host-dependent lifestyle. <i>Environmental Microbiology</i> , 2020, 22, 483-498.	1.8	20
3087	Exploring microbial dynamics associated with flavours production during highland barley wine fermentation. <i>Food Research International</i> , 2020, 130, 108971.	2.9	32
3088	Effects of pesticide residues on bacterial community diversity and structure in typical greenhouse soils with increasing cultivation years in Northern China. <i>Science of the Total Environment</i> , 2020, 710, 136321.	3.9	32
3089	Evidence for niche differentiation of nitrifying communities in grassland soils after 44 years of different field fertilization scenarios. <i>Pedosphere</i> , 2020, 30, 87-97.	2.1	15
3090	Blood Loss Leads to Increase in Relative Abundance of Opportunistic Pathogens in the Gut Microbiome of Rabbits. <i>Current Microbiology</i> , 2020, 77, 415-424.	1.0	5
3091	Fungal endophytic communities of two wild <i>Rosa</i> varieties and the role of an endophytic <i>Seimatosporium</i> sp. in enhancing host plant powdery mildew resistance. <i>Plant and Soil</i> , 2020, 447, 553-564.	1.8	7

#	ARTICLE	IF	CITATIONS
3092	A novel polysaccharide isolated from <i>Flammulina velutipes</i> , characterization, macrophage immunomodulatory activities and its impact on gut microbiota in rats. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2020, 104, 735-748.	1.0	31
3093	Characteristic Microbiomes Correlate with Polyphosphate Accumulation of Marine Sponges in South China Sea Areas. <i>Microorganisms</i> , 2020, 8, 63.	1.6	7
3094	Mechanisms of water regime effects on uptake of cadmium and nitrate by two ecotypes of water spinach (<i>Ipomoea aquatica</i> Forsk.) in contaminated soil. <i>Chemosphere</i> , 2020, 246, 125798.	4.2	24
3095	Dynamic changes of total acid and bacterial communities during the traditional fermentation of Hong Qu glutinous rice wine. <i>Electronic Journal of Biotechnology</i> , 2020, 43, 23-31.	1.2	22
3096	High Diversity and Functional Complementation of Alimentary Canal Microbiota Ensure Small Brown Planthopper to Adapt Different Biogeographic Environments. <i>Frontiers in Microbiology</i> , 2020, 10, 2953.	1.5	14
3097	The therapeutic efficacy of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 [®] in infant colic: A randomised, double blind, placebo-controlled trial. <i>Alimentary Pharmacology and Therapeutics</i> , 2020, 51, 110-120.	1.9	46
3098	Enrichment of specific microbial communities by optimum applied voltages for enhanced methane production by microbial electrosynthesis in anaerobic digestion. <i>Bioresource Technology</i> , 2020, 300, 122624.	4.8	26
3099	<i>Pichia kudriavzevii</i> retards fungal decay by influencing the fungal community succession during cherry tomato fruit storage. <i>Food Microbiology</i> , 2020, 88, 103404.	2.1	35
3100	Effects of fortification of Daqu with various yeasts on microbial community structure and flavor metabolism. <i>Food Research International</i> , 2020, 129, 108837.	2.9	75
3101	Dysbiosis of gut microbiota in patients with neuromyelitis optica spectrum disorders: A cross sectional study. <i>Journal of Neuroimmunology</i> , 2020, 339, 577126.	1.1	31
3102	Differences in Fecal Microbiomes and Metabolomes of People With vs Without Irritable Bowel Syndrome and Bile Acid Malabsorption. <i>Gastroenterology</i> , 2020, 158, 1016-1028.e8.	0.6	122
3103	Nanoparticle Conjugation of Ginsenoside Rg3 Inhibits Hepatocellular Carcinoma Development and Metastasis. <i>Small</i> , 2020, 16, e1905233.	5.2	72
3104	The Bacterial Flora Associated with the Polyphagous Aphid <i>Aphis gossypii</i> Glover (Hemiptera: Aphididae) Is Strongly Affected by Host Plants. <i>Microbial Ecology</i> , 2020, 79, 971-984.	1.4	29
3105	Dominant and Subordinate Relationship Formed by Repeated Social Encounters Alters Gut Microbiota in Greater Long-Tailed Hamsters. <i>Microbial Ecology</i> , 2020, 79, 998-1010.	1.4	5
3106	Shifts in Microbial Biomass C/N/P Stoichiometry and Bacterial Community Composition in Subtropical Estuarine Tidal Marshes Along a Gradient of Freshwater to Oligohaline Water. <i>Ecosystems</i> , 2020, 23, 1265-1280.	1.6	3
3107	Therapeutic effect of n-butanol fraction of Huang-lian-jie-du Decoction on ulcerative colitis and its regulation on intestinal flora in colitis mice. <i>Biomedicine and Pharmacotherapy</i> , 2020, 121, 109638.	2.5	29
3108	Development of biological soil crust prompts convergent succession of prokaryotic communities. <i>Catena</i> , 2020, 187, 104360.	2.2	29
3109	Dynamics of a natural bacterial community under technological and environmental pressures: The case of natural whey starter for Parmigiano Reggiano cheese. <i>Food Research International</i> , 2020, 129, 108860.	2.9	27

#	ARTICLE	IF	CITATIONS
3110	Water mass-driven spatial effects and environmental heterogeneity shape microeukaryote biogeography in a subtropical, hydrographically complex ocean system - A case study of ciliates. <i>Science of the Total Environment</i> , 2020, 706, 135753.	3.9	31
3111	Responses of microbial community to different concentration of perchlorate in the Qingyi River. <i>3 Biotech</i> , 2020, 10, 21.	1.1	4
3112	Seasonal Variability of Conditionally Rare Taxa in the Water Column Bacterioplankton Community of Subtropical Reservoirs in China. <i>Microbial Ecology</i> , 2020, 80, 14-26.	1.4	54
3113	Protein Structure from Experimental Evolution. <i>Cell Systems</i> , 2020, 10, 15-24.e5.	2.9	39
3114	Biogeographical distribution of bacterial communities in saline agricultural soil. <i>Geoderma</i> , 2020, 361, 114095.	2.3	39
3115	Microbial community shifts in streams receiving treated wastewater effluent. <i>Science of the Total Environment</i> , 2020, 709, 135727.	3.9	52
3116	The role of the gut microbiome in the association between habitual anthocyanin intake and visceral abdominal fat in population-level analysis. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 340-350.	2.2	21
3117	Potential correlation between carbohydrate-active enzyme family 48 expressed by gut microbiota and the expression of intestinal epithelial AMP-activated protein kinase β . <i>Journal of Food Biochemistry</i> , 2020, 44, e13123.	1.2	2
3118	Succession of bacterioplankton communities over complete <i>Gymnodinium</i> -diatom bloom cycles. <i>Science of the Total Environment</i> , 2020, 709, 135951.	3.9	21
3119	Rare rather than abundant microbial communities drive the effects of long-term greenhouse cultivation on ecosystem functions in subtropical agricultural soils. <i>Science of the Total Environment</i> , 2020, 706, 136004.	3.9	52
3120	Effects of Seasonal Hibernation on the Similarities Between the Skin Microbiota and Gut Microbiota of an Amphibian (<i>Rana dybowskii</i>). <i>Microbial Ecology</i> , 2020, 79, 898-909.	1.4	27
3121	Evaluation of seven chemical pesticides by mixed microbial culture (PCS-1): Degradation ability, microbial community, and <i>Medicago sativa</i> phytotoxicity. <i>Journal of Hazardous Materials</i> , 2020, 389, 121834.	6.5	39
3122	The developmental transcriptome for <i>Lytechinus variegatus</i> exhibits temporally punctuated gene expression changes. <i>Developmental Biology</i> , 2020, 460, 139-154.	0.9	16
3123	Interactive effects of nitrogen fertilizer and altered precipitation on fungal communities in arid grasslands of northern China. <i>Journal of Soils and Sediments</i> , 2020, 20, 1344-1356.	1.5	10
3124	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
3125	The Gut Microbiota Composition of the Moth <i>Brithys crini</i> Reflects Insect Metamorphosis. <i>Microbial Ecology</i> , 2020, 79, 960-970.	1.4	41
3126	Changes in abundance and composition of nitrifying communities in barley (<i>Hordeum vulgare</i> L.) rhizosphere and bulk soils over the growth period following combined biochar and urea amendment. <i>Biology and Fertility of Soils</i> , 2020, 56, 169-183.	2.3	22
3127	Effect of trimethylamine N-oxide on inflammation and the gut microbiota in <i>Helicobacter pylori</i> -infected mice. <i>International Immunopharmacology</i> , 2020, 81, 106026.	1.7	14

#	ARTICLE	IF	CITATIONS
3128	Dynamics of bacterial community in litter and soil along a chronosequence of Robinia pseudoacacia plantations. <i>Science of the Total Environment</i> , 2020, 703, 135613.	3.9	40
3129	Rare microbial taxa as the major drivers of ecosystem multifunctionality in long-term fertilized soils. <i>Soil Biology and Biochemistry</i> , 2020, 141, 107686.	4.2	247
3130	Mutation of the d-hordein gene by RNA-guided Cas9 targeted editing reducing the grain size and changing grain compositions in barley. <i>Food Chemistry</i> , 2020, 311, 125892.	4.2	32
3131	Metagenomic insights unveil the dominance of undescribed Actinobacteria in pond ecosystem of an Indian shrine. <i>Meta Gene</i> , 2020, 23, 100639.	0.3	4
3132	Potential feedback mediated by soil microbiome response to warming in a glacier forefield. <i>Global Change Biology</i> , 2020, 26, 697-708.	4.2	22
3133	Microbiological evidences for gastric cardiac microflora dysbiosis inducing the progression of inflammation. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2020, 35, 1032-1041.	1.4	8
3134	A Natural High-Sugar Diet Has Different Effects on the Prokaryotic Community Structures of Lower and Higher Termites (Blattaria). <i>Environmental Entomology</i> , 2020, 49, 21-32.	0.7	4
3135	Genome sequencing as a new window into the microbial community of membrane bioreactors – A critical review. <i>Science of the Total Environment</i> , 2020, 704, 135279.	3.9	38
3136	Roles of hydroxylamine and hydrazine in the in-situ recovery of one-stage partial nitrification-anammox process: Characteristics and mechanisms. <i>Science of the Total Environment</i> , 2020, 707, 135648.	3.9	42
3137	Mitigation of antibiotic resistance in a pilot-scale system treating wastewater from high-speed railway trains. <i>Chemosphere</i> , 2020, 245, 125484.	4.2	13
3138	Host identity determines plant associated resistomes. <i>Environmental Pollution</i> , 2020, 258, 113709.	3.7	23
3139	Funneliformis mosseae alters soil fungal community dynamics and composition during litter decomposition. <i>Fungal Ecology</i> , 2020, 43, 100864.	0.7	11
3140	High abundance of Vibrio in tarball-contaminated seawater from Vagator beach, Goa, India. <i>Marine Pollution Bulletin</i> , 2020, 150, 110773.	2.3	4
3141	Nitrite accumulation stability evaluation for low-strength ammonium wastewater by adsorption and biological desorption of zeolite under different operational temperature. <i>Science of the Total Environment</i> , 2020, 704, 135260.	3.9	28
3142	Metagenomic analysis of bacterial and viral assemblages from a freshwater creek and irrigated field reveals temporal and spatial dynamics. <i>Science of the Total Environment</i> , 2020, 706, 135395.	3.9	11
3143	Exploring the genetic potential of a fosmid metagenomic library from an oil-impacted mangrove sediment for metabolism of aromatic compounds. <i>Ecotoxicology and Environmental Safety</i> , 2020, 189, 109974.	2.9	16
3144	Effects of peanut meal extracts fermented by <i>Bacillus natto</i> on the growth performance, learning and memory skills and gut microbiota modulation in mice. <i>British Journal of Nutrition</i> , 2020, 123, 383-393.	1.2	20
3145	Changes in intestinal microflora in digestive tract diseases during pregnancy. <i>Archives of Gynecology and Obstetrics</i> , 2020, 301, 243-249.	0.8	21

#	ARTICLE	IF	CITATIONS
3146	Impact of topsoil removal on soil CO ₂ emission and temperature sensitivity in Chinese Loess Plateau. <i>Science of the Total Environment</i> , 2020, 708, 135102.	3.9	20
3147	Growth performance, immunity and intestinal microbiota of swamp eel (<i>Monopterus albus</i>) fed a diet supplemented with house fly larvae (<i>Musca domestica</i>). <i>Aquaculture Nutrition</i> , 2020, 26, 693-704.	1.1	19
3148	Weak genetic structure despite strong genomic signal in lesser sandeel in the North Sea. <i>Evolutionary Applications</i> , 2020, 13, 376-387.	1.5	17
3149	<i>Fusobacterium nucleatum</i> Promotes Metastasis in Colorectal Cancer by Activating Autophagy Signaling via the Upregulation of CARD3 Expression. <i>Theranostics</i> , 2020, 10, 323-339.	4.6	115
3150	Assessing the impact of source water on tap water bacterial communities in 46 drinking water supply systems in China. <i>Water Research</i> , 2020, 172, 115469.	5.3	74
3151	Steam Explosion Pretreatment Changes Ruminal Fermentation in vitro of Corn Stover by Shifting Archaeal and Bacterial Community Structure. <i>Frontiers in Microbiology</i> , 2020, 11, 2027.	1.5	9
3152	The Interrelationship Between Microbiota and Peptides During Ripening as a Driver for Parmigiano Reggiano Cheese Quality. <i>Frontiers in Microbiology</i> , 2020, 11, 581658.	1.5	25
3153	Structure of Bacterial Communities in Phosphorus-Enriched Rhizosphere Soils. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 6387.	1.3	11
3154	Seasonality in Spatial Turnover of Bacterioplankton Along an Ecological Gradient in the East China Sea: Biogeographic Patterns, Processes and Drivers. <i>Microorganisms</i> , 2020, 8, 1484.	1.6	8
3155	The Assessment of Diet Contaminated with Aflatoxin B1 in Juvenile Turbot (<i>Scophthalmus maximus</i>) and the Evaluation of the Efficacy of Mitigation of a Yeast Cell Wall Extract. <i>Toxins</i> , 2020, 12, 597.	1.5	22
3156	Pyophage cocktail for the biocontrol of membrane fouling and its effect in aerobic microbial biofilm community during the treatment of antibiotics. <i>Bioresource Technology</i> , 2020, 318, 123965.	4.8	10
3157	Rapid recruitment of hydrogen-producing biofilms for hydrogen production in a moving bed biofilm reactor by a sequential immobilization and deoxygenation approach. <i>Bioresource Technology</i> , 2020, 317, 123979.	4.8	4
3158	Reducing bioavailability of heavy metals in contaminated soil and uptake by maize using organic-inorganic mixed fertilizer. <i>Chemosphere</i> , 2020, 261, 128122.	4.2	18
3159	Determination of the microbial communities of Guizhou Suantang, a traditional Chinese fermented sour soup, and correlation between the identified microorganisms and volatile compounds. <i>Food Research International</i> , 2020, 138, 109820.	2.9	30
3160	Sediment-associated bacterial community and predictive functionalities are influenced by choice of 16S ribosomal RNA hypervariable region(s): An amplicon-based diversity study. <i>Genomics</i> , 2020, 112, 4968-4979.	1.3	10
3161	Gut microbiota patterns associated with somatostatin in patients undergoing pancreaticoduodenectomy: a prospective study. <i>Cell Death Discovery</i> , 2020, 6, 94.	2.0	11
3162	Repair of G1 induced DNA double-strand breaks in S-G2/M by alternative NHEJ. <i>Nature Communications</i> , 2020, 11, 5239.	5.8	27
3163	Hypolipidemic effect of <i>Alisma orientale</i> (Sam.) Juzep on gut microecology and liver transcriptome in diabetic rats. <i>PLoS ONE</i> , 2020, 15, e0240616.	1.1	19

#	ARTICLE	IF	CITATIONS
3164	Interrelationships of Fiber-Associated Anaerobic Fungi and Bacterial Communities in the Rumen of Bloaty Cattle Grazing Alfalfa. <i>Microorganisms</i> , 2020, 8, 1543.	1.6	13
3165	Gut Microbiome Changes Associated With HIV Infection and Sexual Orientation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 434.	1.8	21
3166	Whole Blueberry and Isolated Polyphenol-Rich Fractions Modulate Specific Gut Microbes in an In Vitro Colon Model and in a Pilot Study in Human Consumers. <i>Nutrients</i> , 2020, 12, 2800.	1.7	30
3167	Nutrient utilization efficiency, ruminal fermentation and microbial community in Holstein bulls fed concentrate-based diets with different forage source. <i>Animal Feed Science and Technology</i> , 2020, 269, 114662.	1.1	5
3168	Are marine benthic microeukaryotes different from macrobenthos in terms of regional geographical distribution? New insights revealed by RNA metabarcoding. <i>Continental Shelf Research</i> , 2020, 209, 104255.	0.9	3
3169	Sequentially recover heavy metals from smelting wastewater using bioelectrochemical system coupled with thermoelectric generators. <i>Ecotoxicology and Environmental Safety</i> , 2020, 205, 111174.	2.9	23
3170	Fecal microbiota transplantation from mice exposed to chronic intermittent hypoxia elicits sleep disturbances in naïve mice. <i>Experimental Neurology</i> , 2020, 334, 113439.	2.0	48
3171	Light at night affects gut microbial community and negatively impacts host physiology in diurnal animals: Evidence from captive zebra finches. <i>Microbiological Research</i> , 2020, 241, 126597.	2.5	11
3172	Programmable cross-ribosome-binding sites to fine-tune the dynamic range of transcription factor-based biosensor. <i>Nucleic Acids Research</i> , 2020, 48, 10602-10613.	6.5	61
3173	Dysregulation of metabolic pathways by carnitine palmitoyl-transferase 1 plays a key role in central nervous system disorders: experimental evidence based on animal models. <i>Scientific Reports</i> , 2020, 10, 15583.	1.6	12
3174	Transposon expression in the <i>Drosophila</i> brain is driven by neighboring genes and diversifies the neural transcriptome. <i>Genome Research</i> , 2020, 30, 1559-1569.	2.4	17
3175	Obesity Impairs Short-Term and Working Memory through Gut Microbial Metabolism of Aromatic Amino Acids. <i>Cell Metabolism</i> , 2020, 32, 548-560.e7.	7.2	88
3176	High housing density increases stress hormone- or disease-associated fecal microbiota in male Brandt's voles (<i>Lasiopodomys brandtii</i>). <i>Hormones and Behavior</i> , 2020, 126, 104838.	1.0	21
3177	Anaerobic digestion performance and microbial community structures in biogas production from whiskey distillers organic by-products. <i>Bioresource Technology Reports</i> , 2020, 12, 100565.	1.5	10
3178	Soil fungal community composition differs significantly among the Antarctic, Arctic, and Tibetan Plateau. <i>Extremophiles</i> , 2020, 24, 821-829.	0.9	12
3179	Effect of modified atmosphere packaging on shelf life and bacterial community of roast duck meat. <i>Food Research International</i> , 2020, 137, 109645.	2.9	39
3180	A trophic latitudinal gradient revealed in anchovy and sardine from the Western Mediterranean Sea using a multi-proxy approach. <i>Scientific Reports</i> , 2020, 10, 17598.	1.6	27
3181	Succession of Gut Microbial Structure in Twin Giant Pandas During the Dietary Change Stage and Its Role in Polysaccharide Metabolism. <i>Frontiers in Microbiology</i> , 2020, 11, 551038.	1.5	5

#	ARTICLE	IF	CITATIONS
3182	Degradation of Veterinary Antibiotics in Swine Manure via Anaerobic Digestion. <i>Bioengineering</i> , 2020, 7, 123.	1.6	7
3183	Feasibility of Co-Treating Olive Mill Wastewater and Acid Mine Drainage. <i>Mine Water and the Environment</i> , 2020, 39, 859-880.	0.9	7
3184	Spatiotemporal Distribution of the Environmental Microbiota in Food Processing Plants as Impacted by Cleaning and Sanitizing Procedures: the Case of Slaughterhouses and Gaseous Ozone. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	24
3185	Gut Microbiota and Host Thermoregulation in Response to Ambient Temperature Fluctuations. <i>MSystems</i> , 2020, 5, .	1.7	37
3186	Rhizospheric microbiomes help Dongxiang common wild rice (<i>Oryza rufipogon</i> Griff.) rather than <i>Leersia hexandra</i> Swartz survive under cold stress. <i>Archives of Agronomy and Soil Science</i> , 2020, , 1-13.	1.3	5
3187	Changes in Gut Microorganism in Patients with Positive Immune Antibody-Associated Recurrent Abortion. <i>BioMed Research International</i> , 2020, 2020, 1-15.	0.9	6
3188	Distinctive gene and protein characteristics of extremely piezophilic <i>Colwellia</i> . <i>BMC Genomics</i> , 2020, 21, 692.	1.2	27
3189	Environmental Parameters and Substrate Type Drive Microeukaryotic Community Structure During Short-Term Experimental Colonization in Subtropical Eutrophic Freshwaters. <i>Frontiers in Microbiology</i> , 2020, 11, 555795.	1.5	8
3190	Core Mycobiome and Their Ecological Relevance in the Gut of Five Ips Bark Beetles (Coleoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 4	1.5	34
3191	Effects of phytosterols supplementation on growth performance and intestinal microflora of yellow-feather broilers. <i>Poultry Science</i> , 2020, 99, 6022-6030.	1.5	15
3192	16S rRNA metagenomic data of microbial diversity of <i>Pheidole decarinata</i> Santschi (Hymenoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 4	0.5	2
3193	Effect of <i>Lactobacillus plantarum</i> HT121 on serum lipid profile, gut microbiota, and liver transcriptome and metabolomics in a high-cholesterol diet-induced hypercholesterolemia rat model. <i>Nutrition</i> , 2020, 79-80, 110966.	1.1	18
3194	Characterisation of microbial communities for improved management of anaerobic digestion of food waste. <i>Waste Management</i> , 2020, 117, 124-135.	3.7	38
3195	Identification of African swine fever virus-like elements in the soft tick genome provides insights into the virus's evolution. <i>BMC Biology</i> , 2020, 18, 136.	1.7	28
3196	Dynamic change of the gastrointestinal bacterial ecology in cows from birth to adulthood. <i>MicrobiologyOpen</i> , 2020, 9, e1119.	1.2	14
3197	Alteration of Gut Microbiota in Patients With Epilepsy and the Potential Index as a Biomarker. <i>Frontiers in Microbiology</i> , 2020, 11, 517797.	1.5	52
3198	Molecular Analysis of the Microbial Community Developing in Continuous Culture of <i>Methylococcus</i> sp. Concept-8 on Natural Gas. <i>Microbiology</i> , 2020, 89, 551-559.	0.5	4
3199	Impact of Maize-Mushroom Intercropping on the Soil Bacterial Community Composition in Northeast China. <i>Agronomy</i> , 2020, 10, 1526.	1.3	8

#	ARTICLE	IF	CITATIONS
3200	Diversity of Eukaryotic Microorganisms in the Drainage Waters of a Coal Open-Cast Mine. <i>Microbiology</i> , 2020, 89, 641-646.	0.5	4
3201	Relationship Between the Fatty Acid Profiles and Gut Bacterial Communities of the Chinese Mitten Crab (<i>Eriocheir sinensis</i>) From Ecologically Different Habitats. <i>Frontiers in Microbiology</i> , 2020, 11, 565267.	1.5	13
3202	Genome-Wide Characterization and Comparative Analyses of Simple Sequence Repeats among Four Miniature Pig Breeds. <i>Animals</i> , 2020, 10, 1792.	1.0	4
3203	Early Inoculation of Microbial Suspension in Suckling Piglets Affects the Transmission of Maternal Microbiota and the Associated Antibiotic Resistance Genes. <i>Microorganisms</i> , 2020, 8, 1576.	1.6	3
3204	ReScan, a Multiplex Diagnostic Pipeline, Pans Human Sera for SARS-CoV-2 Antigens. <i>Cell Reports Medicine</i> , 2020, 1, 100123.	3.3	70
3205	Microbial communities associated with the camel tick, <i>Hyalomma dromedarii</i> : 16S rRNA gene-based analysis. <i>Scientific Reports</i> , 2020, 10, 17035.	1.6	18
3206	Addition of Coriander during Fermentation of Korean Soy Sauce (Gangjang) Causes Significant Shift in Microbial Composition and Reduction in Biogenic Amine Levels. <i>Foods</i> , 2020, 9, 1346.	1.9	14
3207	Effects of Dietary Supplementation with $\hat{\text{I}}^{\text{e}}$ -Selenocarrageenan on the Selenium Accumulation and Intestinal Microbiota of the Sea Cucumbers <i>Apostichopus japonicus</i> . <i>Biological Trace Element Research</i> , 2021, 199, 2753-2763.	1.9	2
3208	Metagenomic data of bacterial community from different land uses at the river basin, Kelantan. <i>Data in Brief</i> , 2020, 33, 106351.	0.5	2
3209	Enhancement of nitrogen and phosphorus removal, sludge reduction and microbial community structure in an anaerobic/anoxic/oxic process coupled with composite ferrate solution disintegration. <i>Environmental Research</i> , 2020, 190, 110006.	3.7	8
3210	Metagenomic analysis reveals enhanced biodiversity and composting efficiency of lignocellulosic waste by thermoacidophilic effective microorganism (tEM). <i>Journal of Environmental Management</i> , 2020, 276, 111252.	3.8	22
3211	Soil microbial interactions modulate the effect of <i>Artemisia ordosica</i> on herbaceous species in a desert ecosystem, northern China. <i>Soil Biology and Biochemistry</i> , 2020, 150, 108013.	4.2	17
3212	Colchicine increases intestinal permeability, suppresses inflammatory responses, and alters gut microbiota in mice. <i>Toxicology Letters</i> , 2020, 334, 66-77.	0.4	30
3213	Unveiling dynamics of size-dependent antibiotic resistome associated with microbial communities in full-scale wastewater treatment plants. <i>Water Research</i> , 2020, 187, 116450.	5.3	38
3214	<i>Lactobacillus plantarum</i> prevents obesity via modulation of gut microbiota and metabolites in high-fat feeding mice. <i>Journal of Functional Foods</i> , 2020, 73, 104103.	1.6	32
3215	Sex-dependent association of mineralocorticoid receptor gene (NR3C2) DNA methylation and schizophrenia. <i>Psychiatry Research</i> , 2020, 292, 113318.	1.7	11
3216	The intestine of artificially bred larval turbot (<i>Scophthalmus maximus</i>) contains a stable core group of microbiota. <i>Archives of Microbiology</i> , 2020, 202, 2619-2628.	1.0	5
3217	Control sulfide and methane production in sewers based on free ammonia inactivation. <i>Environment International</i> , 2020, 143, 105928.	4.8	33

#	ARTICLE	IF	CITATIONS
3218	Targeted Cell Sorting Combined With Single Cell Genomics Captures Low Abundant Microbial Dark Matter With Higher Sensitivity Than Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 1377.	1.5	25
3219	Metagenome analysis of gut microbial in both the caged and non-caged ducks. <i>Journal of Physics: Conference Series</i> , 2020, 1524, 012076.	0.3	0
3220	The differences and overlaps in the seedâ€™resident microbiome of four Leguminous and three Gramineous forages. <i>Microbial Biotechnology</i> , 2020, 13, 1461-1476.	2.0	28
3221	Metagenomic comparison of structure and function of microbial community between water, effluent and shrimp intestine of higher place <i>Litopenaeus vannamei</i> ponds. <i>Journal of Applied Microbiology</i> , 2020, 129, 243-255.	1.4	21
3222	Bulk and Active Sediment Prokaryotic Communities in the Mariana and Mussau Trenches. <i>Frontiers in Microbiology</i> , 2020, 11, 1521.	1.5	19
3223	Increased Antibody Response to Fucosylated Oligosaccharides and Fucose-Carrying Bacteroides Species in Crohnâ€™s Disease. <i>Frontiers in Microbiology</i> , 2020, 11, 1553.	1.5	10
3224	Metagenomic data on bacterial diversity profiling of high-microbial-abundance tropical marine sponges <i>Aaptos aaptos</i> and <i>Xestospongia muta</i> from waters off terengganu, South China Sea. <i>Data in Brief</i> , 2020, 31, 105971.	0.5	4
3225	Dolutegravir plus lamivudine for maintenance of HIV viral suppression in adults with and without historical resistance to lamivudine: 48-week results of a non-randomized, pilot clinical trial (ART-PRO). <i>EBioMedicine</i> , 2020, 55, 102779.	2.7	28
3226	Structural and functional characteristics of the fecal-associated microbiome in dampness-heat constitution. <i>European Journal of Integrative Medicine</i> , 2020, 37, 101166.	0.8	1
3227	Regulation of growth, intestinal microflora composition and expression of immune-related genes by dietary supplementation of <i>Streptococcus faecalis</i> in blunt snout bream (<i>Megalobrama amblycephala</i>). <i>Fish and Shellfish Immunology</i> , 2020, 105, 195-202.	1.6	9
3228	The effect of extracellular electron transfer on arsenic speciation transformation in a soil bioelectrochemical system. <i>Soil and Tillage Research</i> , 2020, 204, 104723.	2.6	4
3229	Methanotroph populations and CH4 oxidation potentials in high-Arctic peat are altered by herbivory induced vegetation change. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9
3230	Characterization of the Vaginal Microbiome in Women with Infertility and Its Potential Correlation with Hormone Stimulation during <i>In Vitro</i> Fertilization Surgery. <i>MSystems</i> , 2020, 5, .	1.7	27
3231	Bile acids regulate intestinal antigen presentation and reduce graft-versus-host disease without impairing the graft-versus-leukemia effect. <i>Haematologica</i> , 2021, 106, 2131-2146.	1.7	26
3232	Assessment of Gram- and Viability-Staining Methods for Quantifying Bacterial Community Dynamics Using Flow Cytometry. <i>Frontiers in Microbiology</i> , 2020, 11, 1469.	1.5	14
3233	Alterations in Rumen Bacterial Community and Metabolome Characteristics of Cashmere Goats in Response to Dietary Nutrient Density. <i>Animals</i> , 2020, 10, 1193.	1.0	9
3234	Multi-omic Directed Discovery of Cellulosomes, Polysaccharide Utilization Loci, and Lignocellulases from an Enriched Rumen Anaerobic Consortium. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	20
3235	Genome-wide analysis of microsatellite and sex-linked marker identification in <i>Gleditsia sinensis</i> . <i>BMC Plant Biology</i> , 2020, 20, 338.	1.6	13

#	ARTICLE	IF	CITATIONS
3236	Microbial community structure and nitrogen removal responses of an aerobic denitrification biofilm system exposed to tetracycline. <i>Aquaculture</i> , 2020, 529, 735665.	1.7	24
3237	Zebrafish (<i>Danio rerio</i>) physiological and behavioural responses to insect-based diets: a multidisciplinary approach. <i>Scientific Reports</i> , 2020, 10, 10648.	1.6	52
3238	Exploring bacteria diversity in commercialized table olive biofilms by metataxonomic and compositional data analysis. <i>Scientific Reports</i> , 2020, 10, 11381.	1.6	21
3239	Cooperation between <i>Broussonetia papyrifera</i> and Its Symbiotic Fungal Community To Improve Local Adaptation of the Host. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	7
3240	Seasonality and Community Separation of Fungi in a Municipal Wastewater Treatment Plant. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	11
3241	Effects of Paper Mulberry Silage on the Milk Production, Apparent Digestibility, Antioxidant Capacity, and Fecal Bacteria Composition in Holstein Dairy Cows. <i>Animals</i> , 2020, 10, 1152.	1.0	32
3242	Comparative analysis of the gut microbiota of <i>Apis cerana</i> in Yunnan using high-throughput sequencing. <i>Archives of Microbiology</i> , 2020, 202, 2557-2567.	1.0	8
3243	Biogeographical distribution of dissimilatory nitrate reduction to ammonium (DNRA) bacteria in wetland ecosystems around the world. <i>Journal of Soils and Sediments</i> , 2020, 20, 3769-3778.	1.5	13
3244	Maternal Linoleic Acid Overconsumption Alters Offspring Gut and Adipose Tissue Homeostasis in Young but Not Older Adult Rats. <i>Nutrients</i> , 2020, 12, 3451.	1.7	5
3245	Dietary Supplementation of $\hat{\mu}$ -Polylysine Beneficially Affects Ileal Microbiota Structure and Function in Ningxiang Pigs. <i>Frontiers in Microbiology</i> , 2020, 11, 544097.	1.5	11
3246	Data-Driven Modeling for Species-Level Taxonomic Assignment From 16S rRNA: Application to Human Microbiomes. <i>Frontiers in Microbiology</i> , 2020, 11, 570825.	1.5	12
3247	Naringin Attenuates High Fat Diet Induced Non-alcoholic Fatty Liver Disease and Gut Bacterial Dysbiosis in Mice. <i>Frontiers in Microbiology</i> , 2020, 11, 585066.	1.5	100
3248	The genomic timeline of cichlid fish diversification across continents. <i>Nature Communications</i> , 2020, 11, 5895.	5.8	41
3249	Unravelling the gut bacteriome of <i>Ips</i> (Coleoptera: Curculionidae: Scolytinae): identifying core bacterial assemblage and their ecological relevance. <i>Scientific Reports</i> , 2020, 10, 18572.	1.6	31
3250	Tibetan Sheep Adapt to Plant Phenology in Alpine Meadows by Changing Rumen Microbial Community Structure and Function. <i>Frontiers in Microbiology</i> , 2020, 11, 587558.	1.5	21
3251	Dietary supplementation of <i>Bacillus</i> sp. DU106 activates innate immunity and regulates intestinal microbiota in mice. <i>Journal of Functional Foods</i> , 2020, 75, 104247.	1.6	8
3252	Gut microbiota-specific IgA ⁺ B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020, 5, .	5.6	132
3253	Autochthonous faecal viral transfer (FVT) impacts the murine microbiome after antibiotic perturbation. <i>BMC Biology</i> , 2020, 18, 173.	1.7	43

#	ARTICLE	IF	CITATIONS
3254	High-throughput sequencing of the microbial diversity of roasted-sesame-like flavored Daqu with different characteristics. <i>3 Biotech</i> , 2020, 10, 502.	1.1	10
3255	Effects of Polysaccharides From <i>Auricularia auricula</i> on the Immuno-Stimulatory Activity and Gut Microbiota in Immunosuppressed Mice Induced by Cyclophosphamide. <i>Frontiers in Immunology</i> , 2020, 11, 595700.	2.2	29
3256	Comparative Analysis of the Fecal Microbiota of Wild and Captive Bealâ€™s Eyed Turtle (<i>Sacalia bealei</i>) by 16S rRNA Gene Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 570890.	1.5	12
3257	Differences in Gut Microbiome in Hospitalized Immunocompetent vs. Immunocompromised Children, Including Those With Sickle Cell Disease. <i>Frontiers in Pediatrics</i> , 2020, 8, 583446.	0.9	12
3258	Heritable Variation in Pea for Resistance Against a Root Rot Complex and Its Characterization by Amplicon Sequencing. <i>Frontiers in Plant Science</i> , 2020, 11, 542153.	1.7	11
3259	Different Age-Induced Changes in Rhizosphere Microbial Composition and Function of <i>Panax ginseng</i> in Transplantation Mode. <i>Frontiers in Plant Science</i> , 2020, 11, 563240.	1.7	17
3260	The Impact of Air Pollution on Intestinal Microbiome of Asthmatic Children: A Panel Study. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	20
3261	DNA methylation signatures to predict the cervicovaginal microbiome status. <i>Clinical Epigenetics</i> , 2020, 12, 180.	1.8	3
3262	Distinct Stage Changes in Early-Life Colonization and Acquisition of the Gut Microbiota and Its Correlations With Volatile Fatty Acids in Goat Kids. <i>Frontiers in Microbiology</i> , 2020, 11, 584742.	1.5	19
3263	Reducing the Number of Mismatches between Hairs and Buccal References When Analysing mtDNA Heteroplasmic Variation by Massively Parallel Sequencing. <i>Genes</i> , 2020, 11, 1355.	1.0	13
3264	Diversity, function and assembly of mangrove root-associated microbial communities at a continuous fine-scale. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 52.	2.9	68
3265	Intestine Bacterial Community Composition of Shrimp Varies Under Low- and High-Salinity Culture Conditions. <i>Frontiers in Microbiology</i> , 2020, 11, 589164.	1.5	20
3266	Diversity and connectivity of microeukaryote communities across multiple habitats from intertidal zone to deep-sea floor in the Western Pacific Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 165, 103395.	0.6	4
3267	Rhizosphere Bacterial Community Response to Continuous Cropping of Tibetan Barley. <i>Frontiers in Microbiology</i> , 2020, 11, 551444.	1.5	13
3268	A Pilot Study: Changes of Intestinal Microbiota of Patients With Non-small Cell Lung Cancer in Response to Osimertinib Therapy. <i>Frontiers in Microbiology</i> , 2020, 11, 583525.	1.5	4
3269	Zero-Valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water. <i>Frontiers in Environmental Science</i> , 2020, 8, .	1.5	7
3270	Infection of <i>Ophiocordyceps sinensis</i> Fungus Causes Dramatic Changes in the Microbiota of Its <i>Thitarodes</i> Host. <i>Frontiers in Microbiology</i> , 2020, 11, 577268.	1.5	16
3271	A Cross-Sectional Study of Dairy Cattle Metagenomes Reveals Increased Antimicrobial Resistance in Animals Farmed in a Heavy Metal Contaminated Environment. <i>Frontiers in Microbiology</i> , 2020, 11, 590325.	1.5	13

#	ARTICLE	IF	CITATIONS
3272	Dual-Function Analysis of Astaxanthin on Golden Pompano (<i>Trachinotus ovatus</i>) and Its Role in the Regulation of Gastrointestinal Immunity and Retinal Mitochondrial Dysfunction Under Hypoxia Conditions. <i>Frontiers in Physiology</i> , 2020, 11, 568462.	1.3	7
3273	<i>Phytophthora austrocedri</i> in Argentina and Co-Inhabiting <i>Phytophthoras</i> : Roles of Anthropogenic and Abiotic Factors in Species Distribution and Diversity. <i>Forests</i> , 2020, 11, 1223.	0.9	11
3274	Adjusting Organic Load as a Strategy to Direct Single-Stage Food Waste Fermentation from Anaerobic Digestion to Chain Elongation. <i>Processes</i> , 2020, 8, 1487.	1.3	15
3275	Culturing-Enriched Metabarcoding Analysis of the <i>Oryctes rhinoceros</i> Gut Microbiome. <i>Insects</i> , 2020, 11, 782.	1.0	7
3276	Similar Gut Bacterial Microbiota in Two Fruit-Feeding Moth Pests Collected from Different Host Species and Locations. <i>Insects</i> , 2020, 11, 840.	1.0	8
3277	Bioleaching of pyritic coal wastes: bioprospecting and efficiency of selected consortia. <i>Research in Microbiology</i> , 2020, 171, 260-270.	1.0	3
3278	Depthwise microbiome and isotopic profiling of a moderately saline microbial mat in a solar saltern. <i>Scientific Reports</i> , 2020, 10, 20686.	1.6	6
3279	Family matters: skin microbiome reflects the social group and spatial proximity in wild zebra finches. <i>BMC Ecology</i> , 2020, 20, 58.	3.0	15
3280	Exploring the Diversity of Active Ureolytic Bacteria in the Rumen by Comparison of cDNA and gDNA. <i>Animals</i> , 2020, 10, 2162.	1.0	1
3281	Effects of Dietary Supplementation with High Fiber (Stevia Residue) on the Fecal Flora of Pregnant Sows. <i>Animals</i> , 2020, 10, 2247.	1.0	20
3282	Provenances originate morphological and microbiome variation of <i>Tuber pseudobrumale</i> in southwestern China despite strong genetic consistency. <i>Mycological Progress</i> , 2020, 19, 1545-1558.	0.5	5
3283	Altitude influences microbial diversity and herbage fermentation in the rumen of yaks. <i>BMC Microbiology</i> , 2020, 20, 370.	1.3	57
3284	Using pollen DNA metabarcoding to profile nectar sources of urban beekeeping in Kaitaku, Tokyo. <i>BMC Research Notes</i> , 2020, 13, 515.	0.6	17
3285	Study on the Salivary Microbial Alteration of Men With Head and Neck Cancer and Its Relationship With Symptoms in Southwest China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 514943.	1.8	16
3286	Alterations in the diversity and composition of gut microbiota in weaned piglets infected with <i>Balantidioides coli</i> . <i>Veterinary Parasitology</i> , 2020, 288, 109298.	0.7	20
3287	Functional Atlas of Primary miRNA Maturation by the Microprocessor. <i>Molecular Cell</i> , 2020, 80, 892-902.e4.	4.5	26
3288	<i>Acinetobacter</i> Plasmids: Diversity and Development of Classification Strategies. <i>Frontiers in Microbiology</i> , 2020, 11, 588410.	1.5	11
3289	Engineered B cells expressing an anti-HIV antibody enable memory retention, isotype switching and clonal expansion. <i>Nature Communications</i> , 2020, 11, 5851.	5.8	42

#	ARTICLE	IF	CITATIONS
3290	Characterization of Oral Microbiome and Exploration of Potential Biomarkers in Patients with Pancreatic Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	28
3291	Composition of gut and oropharynx bacterial communities in <i>Rattus norvegicus</i> and <i>Suncus murinus</i> in China. <i>BMC Veterinary Research</i> , 2020, 16, 413.	0.7	9
3292	Temporal dynamics of <i>Pinus tabulaeformis</i> litter decomposition under nitrogen addition on the Loess Plateau of China. <i>Forest Ecology and Management</i> , 2020, 476, 118465.	1.4	10
3293	Effects of choline supplementation on liver biology, gut microbiota, and inflammation in <i>Helicobacter pylori</i> -infected mice. <i>Life Sciences</i> , 2020, 259, 118200.	2.0	15
3294	Effects of a chemical additive on the fermentation, microbial communities, and aerobic stability of corn silage with or without air stress during storage. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	20
3295	Host plants and <i>Wolbachia</i> shape the population genetics of sympatric herbivore populations. <i>Evolutionary Applications</i> , 2020, 13, 2740-2753.	1.5	13
3296	How to Count Our Microbes? The Effect of Different Quantitative Microbiome Profiling Approaches. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 403.	1.8	65
3297	Analysis of Gut Microbiome and Metabolite Characteristics in Patients with Slow Transit Constipation. <i>Digestive Diseases and Sciences</i> , 2021, 66, 3026-3035.	1.1	37
3298	Performance of an air membrane bioreactor for methanol removal under steady and transient state conditions. <i>Chemosphere</i> , 2020, 260, 127514.	4.2	5
3299	Capturing open ocean biodiversity: Comparing environmental DNA metabarcoding to the continuous plankton recorder. <i>Molecular Ecology</i> , 2021, 30, 3140-3157.	2.0	42
3300	Gut microbiota changes in patients with autism spectrum disorders. <i>Journal of Psychiatric Research</i> , 2020, 129, 149-159.	1.5	78
3301	Genomic and enzymatic evidence of acetogenesis by anaerobic methanotrophic archaea. <i>Nature Communications</i> , 2020, 11, 3941.	5.8	45
3302	Culturable diversity of bacterial endophytes associated with medicinal plants of the Western Ghats, India. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	18
3303	Age-related differences in gut microbial community composition of captive spotted seals (<i>Phoca largha</i>). <i>Marine Mammal Science</i> , 2020, 36, 1231-1240.	0.9	13
3304	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	1.7	82
3305	Assessing the impact on intestinal microbiome and clinical outcomes of antibiotherapy optimisation strategies in haematopoietic stem cell transplant recipients: study protocol for the prospective multicentre OptimBioma study. <i>BMJ Open</i> , 2020, 10, e034570.	0.8	3
3306	CDSnake: Snakemake pipeline for retrieval of annotated OTUs from paired-end reads using CD-HIT utilities. <i>BMC Bioinformatics</i> , 2020, 21, 303.	1.2	2
3307	Nutrient Removal Process and Cathodic Microbial Community Composition in Integrated Vertical-Flow Constructed Wetland " Microbial Fuel Cells Filled With Different Substrates. <i>Frontiers in Microbiology</i> , 2020, 11, 1896.	1.5	29

#	ARTICLE	IF	CITATIONS
3308	Effects of different rotation patterns on the occurrence of clubroot disease and diversity of rhizosphere microbes. <i>Journal of Integrative Agriculture</i> , 2020, 19, 2265-2273.	1.7	22
3309	Fate of integrons, antibiotic resistance genes and associated microbial community in food waste and its large-scale biotreatment systems. <i>Environment International</i> , 2020, 144, 106013.	4.8	34
3310	Optimizing dry anaerobic digestion at pilot scale for start-up strategy and long-term operation: Organic loading rate, temperature and co-digestion. <i>Bioresource Technology</i> , 2020, 316, 123828.	4.8	20
3311	Microbial catabolism of lindane in distinct layers of acidic paddy soils combinedly affected by different water managements and bioremediation strategies. <i>Science of the Total Environment</i> , 2020, 746, 140992.	3.9	13
3312	Size resolved characteristics of urban and suburban bacterial bioaerosols in Japan as assessed by 16S rRNA amplicon sequencing. <i>Scientific Reports</i> , 2020, 10, 12406.	1.6	17
3313	The Origin and Spread of Locally Adaptive Seasonal Camouflage in Snowshoe Hares. <i>American Naturalist</i> , 2020, 196, 316-332.	1.0	29
3314	Effects of Dark Septate Endophytes Strain A024 on Damping-off Biocontrol, Plant Growth and the Rhizosphere Soil Environment of <i>Pinus sylvestris</i> var. <i>mongolica</i> Annual Seedlings. <i>Plants</i> , 2020, 9, 913.	1.6	18
3315	Elevation rather than season determines the assembly and co-occurrence patterns of soil bacterial communities in forest ecosystems of Mount Gongga. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7589-7602.	1.7	28
3316	Changes in sediment microbial diversity following chronic copper-exposure induce community copper-tolerance without increasing sensitivity to arsenic. <i>Journal of Hazardous Materials</i> , 2020, 391, 122197.	6.5	13
3317	Bacterial Blight Induced Shifts in Endophytic Microbiome of Rice Leaves and the Enrichment of Specific Bacterial Strains With Pathogen Antagonism. <i>Frontiers in Plant Science</i> , 2020, 11, 963.	1.7	40
3318	Gut microbiome composition differences among breeds impact feed efficiency in swine. <i>Microbiome</i> , 2020, 8, 110.	4.9	108
3319	Taxonomic and functional profiling of the microbial communities of Arabian Sea: A metagenomics approach. <i>Genomics</i> , 2020, 112, 4361-4369.	1.3	18
3320	Metagenomic insights into the effects of nanobubble water on the composition of gut microbiota in mice. <i>Food and Function</i> , 2020, 11, 7175-7182.	2.1	10
3321	Understanding <i>Leptospirosis</i> eco-epidemiology by environmental DNA metabarcoding of irrigation water from two agro-ecological regions of Sri Lanka. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008437.	1.3	15
3322	Type I-F CRISPR-Cas Distribution and Array Dynamics in <i>Legionella pneumophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1039-1050.	0.8	12
3323	Interactions of Segmented Filamentous Bacteria (<i>Candidatus Savagella</i>) and bacterial drivers in colitis-associated colorectal cancer development. <i>PLoS ONE</i> , 2020, 15, e0236595.	1.1	5
3324	Alterations of Gut Microbiome in Tibetan Patients With Coronary Heart Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 373.	1.8	32
3325	Denitrification Potential of Paddy and Upland Soils Derived From the Same Parent Material Respond Differently to Long-Term Fertilization. <i>Frontiers in Environmental Science</i> , 2020, 8, .	1.5	5

#	ARTICLE	IF	CITATIONS
3326	Microbial Community Dynamics During the Non-filamentous Fungi Growth-Based Fermentation Process of Miang, a Traditional Fermented Tea of North Thailand and Their Product Characterizations. <i>Frontiers in Microbiology</i> , 2020, 11, 1515.	1.5	17
3327	Effects of Elevated pCO ₂ on the Survival and Growth of <i>Portunus trituberculatus</i> . <i>Frontiers in Physiology</i> , 2020, 11, 750.	1.3	17
3328	Agricultural Utilization of Unused Resources: Liquid Food Waste Material as a New Source of Plant Growth-Promoting Microbes. <i>Agronomy</i> , 2020, 10, 954.	1.3	8
3329	Alterations in Yeast Species Composition of Uninoculated Wine Ferments by the Addition of Sulphur Dioxide. <i>Fermentation</i> , 2020, 6, 62.	1.4	6
3330	The Challenges of Reconstructing Tropical Biodiversity With Sedimentary Ancient DNA: A 2200-Year-Long Metagenomic Record From Bwindi Impenetrable Forest, Uganda. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	23
3331	A Shift Pattern of Bacterial Communities Across the Life Stages of the Citrus Red Mite, <i>Panonychus citri</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1620.	1.5	7
3332	Changes in the vaginal microbiota across a gradient of urbanization. <i>Scientific Reports</i> , 2020, 10, 12487.	1.6	25
3333	Control of <i>Fusarium</i> wilt by wheat straw is associated with microbial network changes in watermelon rhizosphere. <i>Scientific Reports</i> , 2020, 10, 12736.	1.6	23
3334	The immunogenetics of sexual parasitism. <i>Science</i> , 2020, 369, 1608-1615.	6.0	46
3335	A Diverse Panel of Clinical <i>Acinetobacter baumannii</i> for Research and Development. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	39
3336	Genetic Diversity and Population Structure of Races of <i>Fusarium oxysporum</i> Causing Cotton Wilt. G3: Genes, Genomes, Genetics, 2020, 10, 3261-3269.	0.8	16
3337	Neohesperidin attenuates obesity by altering the composition of the gut microbiota in high-fat diet-fed mice. <i>FASEB Journal</i> , 2020, 34, 12053-12071.	0.2	46
3338	Melatonin Alleviates Neuroinflammation and Metabolic Disorder in DSS-Induced Depression Rats. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-17.	1.9	56
3339	Modeling host-microbiome interactions for the prediction of meat quality and carcass composition traits in swine. <i>Genetics Selection Evolution</i> , 2020, 52, 41.	1.2	14
3340	Antimicrobial Effects of Black Soldier Fly and Yellow Mealworm Fats and Their Impact on Gut Microbiota of Growing Rabbits. <i>Animals</i> , 2020, 10, 1292.	1.0	30
3341	Influence of milk microbiota on <i>Listeria monocytogenes</i> survival during cheese ripening. <i>Food Science and Nutrition</i> , 2020, 8, 5071-5076.	1.5	7
3342	Structural Variability and Functional Prediction in the Epiphytic Bacteria Assemblies of <i>Myriophyllum spicatum</i> . <i>Current Microbiology</i> , 2020, 77, 3582-3594.	1.0	8
3343	Archaeal community diversity in different types of saline-alkali soil in arid regions of Northwest China. <i>Journal of Bioscience and Bioengineering</i> , 2020, 130, 382-389.	1.1	14

#	ARTICLE	IF	CITATIONS
3344	Alterations of gut microbiota composition in neonates conceived by assisted reproductive technology and its relation to infant growth. <i>Gut Microbes</i> , 2020, 12, 1794466.	4.3	9
3345	Phylogenetic signal of host plants in the bacterial and fungal root microbiomes of cultivated angiosperms. <i>Plant Journal</i> , 2020, 104, 522-531.	2.8	19
3346	Fecal Microbiomes Distinguish Patients With Autoimmune Hepatitis From Healthy Individuals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 342.	1.8	39
3347	The Gut Microbiota of Pheasant Lineages Reflects Their Host Genetic Variation. <i>Frontiers in Genetics</i> , 2020, 11, 859.	1.1	2
3348	Consumption of Wild Rice (<i>Zizania latifolia</i>) Prevents Metabolic Associated Fatty Liver Disease through the Modulation of the Gut Microbiota in Mice Model. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5375.	1.8	8
3349	<i>Bacillus subtilis</i> biofertilizer mitigating agricultural ammonia emission and shifting soil nitrogen cycling microbiomes. <i>Environment International</i> , 2020, 144, 105989.	4.8	90
3350	Corpse decomposition increases nitrogen pollution and alters the succession of nirK-type denitrifying communities in different water types. <i>Science of the Total Environment</i> , 2020, 747, 141472.	3.9	18
3351	Agricultural pests consumed by common bat species in the United States corn belt: The importance of DNA primer choice. <i>Agriculture, Ecosystems and Environment</i> , 2020, 303, 107105.	2.5	17
3352	Comparison of cyanobacterial communities in temperate deserts: A cue for artificial inoculation of biological soil crusts. <i>Science of the Total Environment</i> , 2020, 745, 140970.	3.9	29
3353	Functional characteristic of microbial communities in large-scale biotreatment systems of food waste. <i>Science of the Total Environment</i> , 2020, 746, 141086.	3.9	37
3354	Naturally occurring SARS-CoV-2 gene deletions close to the spike S1/S2 cleavage site in the viral quasispecies of COVID19 patients. <i>Emerging Microbes and Infections</i> , 2020, 9, 1900-1911.	3.0	57
3355	Upstream Natural Pulsed Ventilation: A simple measure to control the sulfide and methane production in gravity sewer. <i>Science of the Total Environment</i> , 2020, 742, 140579.	3.9	6
3356	Gain in carbon: Deciphering the abiotic and biotic mechanisms of biochar-induced negative priming effects in contrasting soils. <i>Science of the Total Environment</i> , 2020, 746, 141057.	3.9	29
3357	Mucosal-associated invariant T cells promote inflammation and intestinal dysbiosis leading to metabolic dysfunction during obesity. <i>Nature Communications</i> , 2020, 11, 3755.	5.8	97
3358	Influence of Citrus Scion/Rootstock Genotypes on Arbuscular Mycorrhizal Community Composition under Controlled Environment Condition. <i>Plants</i> , 2020, 9, 901.	1.6	9
3359	Effects of a novel bio-organic fertilizer on the composition of rhizobacterial communities and bacterial wilt outbreak in a continuously mono-cropped tomato field. <i>Applied Soil Ecology</i> , 2020, 156, 103717.	2.1	23
3360	Effect of impact shock on extremophilic <i>Halomonas gomseomensis</i> EP-3 isolated from hypersaline sulphated lake Laguna de Peaña Hueca, Spain. <i>Planetary and Space Science</i> , 2020, 192, 105041.	0.9	2
3361	Tannins from senescent <i>Rhizophora mangle</i> mangrove leaves have a distinctive effect on prokaryotic and eukaryotic communities in a <i>Distichlis spicata</i> salt marsh soil. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9

#	ARTICLE	IF	CITATIONS
3362	The gut bacterial diversity of sheep associated with different breeds in Qinghai province. <i>BMC Veterinary Research</i> , 2020, 16, 254.	0.7	24
3363	Developmental stage-associated microbiota profile of the peach fruit fly, <i>Bactrocera zonata</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Ovele 2020, 10, 390.	1.1	5
3364	Distribution of microbiota across different intestinal tract segments of a stranded dwarf minke whale, <i>Balaenoptera acutorostrata</i> . <i>MicrobiologyOpen</i> , 2020, 9, e1108.	1.2	6
3365	Soil organic matter, nitrogen and pH driven change in bacterial community following forest conversion. <i>Forest Ecology and Management</i> , 2020, 477, 118473.	1.4	58
3366	An ambient temperature collection and stabilization strategy for canine microbiota studies. <i>Scientific Reports</i> , 2020, 10, 13383.	1.6	10
3367	Influenza vaccine-induced human bone marrow plasma cells decline within a year after vaccination. <i>Science</i> , 2020, 370, 237-241.	6.0	77
3368	Microbial Life in the Deep Subsurface Aquifer Illuminated by Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 572252.	1.5	48
3369	Lactic Acid Bacteria Adjunct Cultures Exert a Mitigation Effect against Spoilage Microbiota in Fresh Cheese. <i>Microorganisms</i> , 2020, 8, 1199.	1.6	7
3370	MYCO WELL D-ONE detection of <i>Ureaplasma</i> spp. and <i>Mycoplasma hominis</i> in sexual health patients in Wales. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2020, 39, 2427-2440.	1.3	16
3371	Anaerobic digestion of spectinomycin mycelial residues pretreated by thermal hydrolysis: removal of spectinomycin and enhancement of biogas production. <i>Environmental Science and Pollution Research</i> , 2020, 27, 39297-39307.	2.7	12
3372	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. <i>Bioresource Technology</i> , 2020, 317, 123985.	4.8	33
3373	Responses of active soil microorganisms facing to a soil biostimulant input compared to plant legacy effects. <i>Scientific Reports</i> , 2020, 10, 13727.	1.6	24
3374	Bacterial and fungal diversity in the lorandite (TlAsS ₂) mine 'Allchar' in the Republic of North Macedonia. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	11
3375	High-throughput immunogenetic typing of koalas suggests possible link between MHC alleles and cancers. <i>Immunogenetics</i> , 2020, 72, 499-506.	1.2	2
3376	Bacterial composition and community structure of the oropharynx of adults with asthma are associated with environmental factors. <i>Microbial Pathogenesis</i> , 2020, 149, 104505.	1.3	7
3377	Soil Fungal Community Composition, Not Assembly Process, Was Altered by Nitrogen Addition and Precipitation Changes at an Alpine Steppe. <i>Frontiers in Microbiology</i> , 2020, 11, 579072.	1.5	19
3378	Testing selectivity of bacterial and fungal culture media compared to original silage samples using next generation sequencing. <i>Journal of Microbiological Methods</i> , 2020, 179, 106088.	0.7	5
3379	Cyanobacteria and Algae in Clouds and Rain in the Area of puy de Dôme, Central France. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	15

#	ARTICLE	IF	CITATIONS
3380	DNA diet profiles with high-resolution animal tracking data reveal levels of prey selection relative to habitat choice in a crepuscular insectivorous bird. <i>Ecology and Evolution</i> , 2020, 10, 13044-13056.	0.8	14
3381	Influence of the flow velocity on membrane-aerated biofilm reactors: Application of a rotating disk for local flow control. <i>Biochemical Engineering Journal</i> , 2020, 164, 107771.	1.8	11
3382	Changes in serum inflammatory cytokine levels and intestinal flora in a self-healing dextran sodium sulfate-induced ulcerative colitis murine model. <i>Life Sciences</i> , 2020, 263, 118587.	2.0	52
3383	Oatmeal induced gut microbiota alteration and its relationship with improved lipid profiles: a secondary analysis of a randomized clinical trial. <i>Nutrition and Metabolism</i> , 2020, 17, 85.	1.3	10
3384	Effect of subtilisin, a protease from <i>Bacillus</i> sp., on soil biochemical parameters and microbial biodiversity. <i>European Journal of Soil Biology</i> , 2020, 101, 103244.	1.4	7
3385	The Rumen Specific Bacteriome in Dry Dairy Cows and Its Possible Relationship with Phenotypes. <i>Animals</i> , 2020, 10, 1791.	1.0	9
3386	Correlations between microbiota with physicochemical properties and volatile flavor components in black glutinous rice wine fermentation. <i>Food Research International</i> , 2020, 138, 109800.	2.9	82
3387	A genomic and historical synthesis of plague in 18th century Eurasia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28328-28335.	3.3	31
3388	Maternal and cord blood vitamin D level and the infant gut microbiota in a birth cohort study. <i>Maternal Health, Neonatology and Perinatology</i> , 2020, 6, 5.	1.0	9
3389	<i>Lactobacillus plantarum</i> L15 Alleviates Colitis by Inhibiting LPS-Mediated NF- κ B Activation and Ameliorates DSS-Induced Gut Microbiota Dysbiosis. <i>Frontiers in Immunology</i> , 2020, 11, 575173.	2.2	59
3390	Effect of Flow Configuration on Nitrifiers in Biological Activated Carbon Filters for Potable Water Production. <i>Environmental Science & Technology</i> , 2020, 54, 14646-14655.	4.6	9
3391	Compositional and Functional Comparisons of the Microbiota in the Colostrum and Mature Milk of Dairy Goats. <i>Animals</i> , 2020, 10, 1955.	1.0	9
3392	Comparative analysis of gut microbiota diversity in endangered, economical, and common freshwater mussels using 16S rRNA gene sequencing. <i>Ecology and Evolution</i> , 2020, 10, 12015-12023.	0.8	4
3393	Comparative analysis of microbial communities associated with the gill, gut, and habitat of two filter-feeding fish. <i>Aquaculture Reports</i> , 2020, 18, 100501.	0.7	24
3394	Microbial diversity in water and animal faeces: a metagenomic analysis to assess public health risk. <i>New Zealand Journal of Zoology</i> , 2021, 48, 188-201.	0.6	9
3395	Activated PI3K $\hat{\imath}$ breaches multiple B cell tolerance checkpoints and causes autoantibody production. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	33
3396	Identification of Bacteria in Two Food Waste Black Soldier Fly Larvae Rearing Residues. <i>Frontiers in Microbiology</i> , 2020, 11, 582867.	1.5	33
3397	Uncharted waters: the unintended impacts of residual chlorine on water quality and biofilms. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 34.	2.9	23

#	ARTICLE	IF	CITATIONS
3398	Koala immunogenetics and chlamydial strain type are more directly involved in chlamydial disease progression in koalas from two south east Queensland koala populations than koala retrovirus subtypes. <i>Scientific Reports</i> , 2020, 10, 15013.	1.6	15
3399	Inoculation of <i>Ensifer fredii</i> strain LP2/20 immobilized in agar results in growth promotion and alteration of bacterial community structure of Chinese kale planted soil. <i>Scientific Reports</i> , 2020, 10, 15857.	1.6	17
3400	Effects of sodium citrate on the structure and microbial community composition of an early-stage multispecies biofilm model. <i>Scientific Reports</i> , 2020, 10, 16585.	1.6	3
3401	Prebiotic effects of yeast mannan, which selectively promotes <i>Bacteroides thetaiotaomicron</i> and <i>Bacteroides ovatus</i> in a human colonic microbiota model. <i>Scientific Reports</i> , 2020, 10, 17351.	1.6	37
3402	Human milk microbiota in sub-acute lactational mastitis induces inflammation and undergoes changes in composition, diversity and load. <i>Scientific Reports</i> , 2020, 10, 18521.	1.6	17
3403	Variation of rhizosphere bacterial community diversity in the desert ephemeral plant <i>Ferula sinkiangensis</i> across environmental gradients. <i>Scientific Reports</i> , 2020, 10, 18442.	1.6	3
3404	Bacterial and Archaeal Diversity and Abundance in Shallow Subsurface Clay Sediments at Jiangnan Plain, China. <i>Frontiers in Microbiology</i> , 2020, 11, 572560.	1.5	1
3405	CDR3 sequences in IgA nephropathy are shorter and exhibit reduced diversity. <i>FEBS Open Bio</i> , 2020, 10, 2702-2711.	1.0	1
3406	Spatio-Temporal Variations in the Abundance and Community Structure of <i>Nitrospira</i> in a Tropical Bay. <i>Current Microbiology</i> , 2020, 77, 3492-3503.	1.0	2
3407	Enhancement of microbial redox cycling of iron in zero-valent iron oxidation coupling with deca-brominated diphenyl ether removal. <i>Science of the Total Environment</i> , 2020, 748, 141328.	3.9	8
3408	Gut microbiome adaptation to extreme cold winter in wild plateau pika (<i>Ochotona curzoniae</i>) on the Qinghai-Tibet Plateau. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	14
3409	Distinct disease features in chimpanzees infected with a precore HBV mutant associated with acute liver failure in humans. <i>PLoS Pathogens</i> , 2020, 16, e1008793.	2.1	4
3410	Targeted isolation based on metagenome-assembled genomes reveals a phylogenetically distinct group of thermophilic spirochetes from deep biosphere. <i>Environmental Microbiology</i> , 2021, 23, 3585-3598.	1.8	23
3411	Dietary Supplementation with Sodium Sulfate Improves Rumen Fermentation, Fiber Digestibility, and the Plasma Metabolome through Modulation of Rumen Bacterial Communities in Steers. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	15
3412	The Fungal Microbiome Is an Important Component of Vineyard Ecosystems and Correlates with Regional Distinctiveness of Wine. <i>MSphere</i> , 2020, 5, .	1.3	70
3413	Alternation of nasopharyngeal microbiota in healthy youth is associated with environmental factors: implication for respiratory diseases. <i>International Journal of Environmental Health Research</i> , 2022, 32, 952-962.	1.3	11
3414	Targeted Metagenomics for Clinical Detection and Discovery of Bacterial Tick-Borne Pathogens. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	22
3415	Sex Differences in Intestinal Microbial Composition and Function of Hainan Special Wild Boar. <i>Animals</i> , 2020, 10, 1553.	1.0	9

#	ARTICLE	IF	CITATIONS
3416	Potential Associations Among Alteration of Salivary miRNAs, Saliva Microbiome Structure, and Cognitive Impairments in Autistic Children. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6203.	1.8	23
3417	Sulfur and Methane-Oxidizing Microbial Community in a Terrestrial Mud Volcano Revealed by Metagenomics. <i>Microorganisms</i> , 2020, 8, 1333.	1.6	19
3418	Can the FLUT 2 Gene Variant Have an Effect on the Body Weight of Patients Undergoing Bariatric Surgery? Preliminary, Exploratory Study. <i>Nutrients</i> , 2020, 12, 2621.	1.7	2
3419	Alterations of the Human Gut Microbiome in Chronic Kidney Disease. <i>Advanced Science</i> , 2020, 7, 2001936.	5.6	82
3420	Altered gut microbiota correlated with systemic inflammation in children with Kawasaki disease. <i>Scientific Reports</i> , 2020, 10, 14525.	1.6	21
3421	Gut bacterial communities and their contribution to performance of specialist <i>Altica</i> flea beetles. <i>Microbial Ecology</i> , 2020, 80, 946-959.	1.4	6
3422	Microbiome of the larvae of <i>Spodoptera frugiperda</i> (J.E. Smith) (Lepidoptera: Noctuidae) from maize plants. <i>Journal of Applied Entomology</i> , 2020, 144, 764-776.	0.8	20
3423	Gut microbiota steroid sexual dimorphism and its impact on gonadal steroids: influences of obesity and menopausal status. <i>Microbiome</i> , 2020, 8, 136.	4.9	72
3424	Metagenomic Profiling and Microbial Metabolic Potential of Perdido Fold Belt (NW) and Campeche Knolls (SE) in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2020, 11, 1825.	1.5	16
3425	Is Anoxic Operation Effective to Control Nitrate Build-Up and Sludge Loss for the Combined Partial Nitrification and Anammox (CPNA) Process?. <i>Processes</i> , 2020, 8, 1053.	1.3	4
3426	Aerosol microbial community structure analysis based on two different sequencing platforms. <i>Aerobiologia</i> , 2020, 36, 617-630.	0.7	1
3427	A first phylogenomic hypothesis for Eulophidae (Hymenoptera, Chalcidoidea). <i>Journal of Natural History</i> , 2020, 54, 597-609.	0.2	12
3428	Root-associated endophytic bacterial community composition and structure of three medicinal licorices and their changes with the growing year. <i>BMC Microbiology</i> , 2020, 20, 291.	1.3	22
3429	Total Arsenic, pH, and Sulfate Are the Main Environmental Factors Affecting the Microbial Ecology of the Water and Sediments in Hulun Lake, China. <i>Frontiers in Microbiology</i> , 2020, 11, 548607.	1.5	18
3430	Human B Cell Clonal Expansion and Convergent Antibody Responses to SARS-CoV-2. <i>Cell Host and Microbe</i> , 2020, 28, 516-525.e5.	5.1	219
3431	Chronic nitrogen addition differentially affects gross nitrogen transformations in alpine and temperate grassland soils. <i>Soil Biology and Biochemistry</i> , 2020, 149, 107962.	4.2	29
3432	Bacteria Contribute to Plant Secondary Compound Degradation in a Generalist Herbivore System. <i>MBio</i> , 2020, 11, .	1.8	30
3433	Enrofloxacin Shifts Intestinal Microbiota and Metabolic Profiling and Hinders Recovery from <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Typhimurium Infection in Neonatal Chickens. <i>MSphere</i> , 2020, 5, .	1.3	18

#	ARTICLE	IF	CITATIONS
3434	Seasonal Variation in the Rhizosphere and Non-Rhizosphere Microbial Community Structures and Functions of <i>Camellia yuhsienensis</i> Hu. <i>Microorganisms</i> , 2020, 8, 1385.	1.6	23
3435	Therapeutic vaccination of koalas harbouring endogenous koala retrovirus (KoRV) improves antibody responses and reduces circulating viral load. <i>Npj Vaccines</i> , 2020, 5, 60.	2.9	10
3436	Low levels of salivary metals, oral microbiome composition and dental decay. <i>Scientific Reports</i> , 2020, 10, 14640.	1.6	14
3437	Intercropping With Turmeric or Ginger Reduce the Continuous Cropping Obstacles That Affect <i>Pogostemon cablin</i> (Patchouli). <i>Frontiers in Microbiology</i> , 2020, 11, 579719.	1.5	46
3438	Developmental, Dietary, and Geographical Impacts on Gut Microbiota of Red Swamp Crayfish (<i>Procambarus clarkii</i>). <i>Microorganisms</i> , 2020, 8, 1376.	1.6	38
3439	Nitrogen Removal for Liquid-Ammonia Mercerization Wastewater via Partial Nitritation/Anammox Based on Zeolite Sequencing Batch Reactor. <i>Water (Switzerland)</i> , 2020, 12, 2234.	1.2	5
3440	Caecal microbiota compositions from 7-day-old chicks reared in high-performance and low-performance industrial farms and systematic culturomics to select strains with anti-Campylobacter activity. <i>PLoS ONE</i> , 2020, 15, e0237541.	1.1	3
3441	Distribution and Control of Bacterial Community Composition in Marian Cove Surface Waters, King George Island, Antarctica during the Summer of 2018. <i>Microorganisms</i> , 2020, 8, 1115.	1.6	10
3442	Microbiome Diversity and Community-Level Change Points within Manure-Based Small Biogas Plants. <i>Microorganisms</i> , 2020, 8, 1169.	1.6	12
3443	Effect of Ultrasound Combined with Ozone Water Pretreatment on the Bacterial Communities and the Physicochemical Properties of Red Swamp Crayfish Meat (<i>Procambarus clarkii</i>). <i>Food and Bioprocess Technology</i> , 2020, 13, 1778-1790.	2.6	2
3444	Quercetin improves gut dysbiosis in antibiotic-treated mice. <i>Food and Function</i> , 2020, 11, 8003-8013.	2.1	74
3445	Community assembly of bacteria and archaea in coastal waters governed by contrasting mechanisms: A seasonal perspective. <i>Molecular Ecology</i> , 2020, 29, 3762-3776.	2.0	35
3446	Strain Structure and Dynamics Revealed by Targeted Deep Sequencing of the Honey Bee Gut Microbiome. <i>MSphere</i> , 2020, 5, .	1.3	19
3447	High-throughput sequencing analysis of differences in intestinal microflora between ulcerative colitis patients with different glucocorticoid response types. <i>Genes and Genomics</i> , 2020, 42, 1197-1206.	0.5	5
3448	Harnessing <i>Pseudomonas protegens</i> to Control Bacterial Panicle Blight of Rice. <i>Phytopathology</i> , 2020, 110, 1657-1667.	1.1	8
3449	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	9.4	35
3450	Distinct Effects of Milks From Various Animal Types on Infant Fecal Microbiota Through in vitro Fermentations. <i>Frontiers in Microbiology</i> , 2020, 11, 580931.	1.5	4
3451	Repertoire-scale determination of class II MHC peptide binding via yeast display improves antigen prediction. <i>Nature Communications</i> , 2020, 11, 4414.	5.8	35

#	ARTICLE	IF	CITATIONS
3452	Growth performance, nutrient digestibility, and fecal microbial composition of weaned pigs fed multi-enzyme supplemented diets. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	11
3453	Intestinal Tract Microbe Communities Associated with Horseshoe Crabs from Beibu Gulf, China. <i>Current Microbiology</i> , 2020, 77, 3330-3338.	1.0	12
3454	Acute and long-term effects of antibiotics commonly used in laboratory animal medicine on the fecal microbiota. <i>Veterinary Research</i> , 2020, 51, 116.	1.1	10
3455	Characterization of Bacterial Communities Associated with <i>Rhynchophorus ferrugineus</i> Olivier (Coleoptera: Curculionidae) and its Host <i>Phoenix sylvestris</i> . <i>Current Microbiology</i> , 2020, 77, 3321-3329.	1.0	1
3456	Glycans as Immune Checkpoints: Removal of Branched N-glycans Enhances Immune Recognition Preventing Cancer Progression. <i>Cancer Immunology Research</i> , 2020, 8, 1407-1425.	1.6	33
3457	Modulation of the Gut Microbiota Alters the Tumour-Suppressive Efficacy of Tim-3 Pathway Blockade in a Bacterial Species- and Host Factor-Dependent Manner. <i>Microorganisms</i> , 2020, 8, 1395.	1.6	11
3458	Perturbations of gut microbiota in gestational diabetes mellitus patients induce hyperglycemia in germ-free mice. <i>Journal of Developmental Origins of Health and Disease</i> , 2020, 11, 580-588.	0.7	19
3459	Environmental DNA metabarcoding reveals the presence of a small, quick-moving, nocturnal water shrew in a forest stream. <i>Conservation Genetics</i> , 2020, 21, 1079-1084.	0.8	16
3460	The Use of Bioinformatic Tools in Symbiosis and Co-Evolution Studies. , 0, , .		1
3461	Anaerobic respiration pathways and response to increased substrate availability of Arctic wetland soils. <i>Environmental Sciences: Processes and Impacts</i> , 2020, 22, 2070-2083.	1.7	6
3462	Rumen Microbiome and Metabolome of Tibetan Sheep (<i>Ovis aries</i>) Reflect Animal Age and Nutritional Requirement. <i>Frontiers in Veterinary Science</i> , 2020, 7, 609.	0.9	25
3463	Evolution of antibiotic resistance at low antibiotic concentrations including selection below the minimal selective concentration. <i>Communications Biology</i> , 2020, 3, 467.	2.0	90
3464	Discovering the indigenous microbial communities associated with the natural fermentation of sap from the cider gum <i>Eucalyptus gunnii</i> . <i>Scientific Reports</i> , 2020, 10, 14716.	1.6	13
3465	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020, 369, .	6.0	89
3466	Genomic Sequencing Reveals the Diversity of Seminal Bacteria and Relationships to Reproductive Potential in Boar Sperm. <i>Frontiers in Microbiology</i> , 2020, 11, 1873.	1.5	17
3467	High dietary starch inclusion impairs growth and antioxidant status, and alters liver organization and intestinal microbiota in largemouth bass <i>Micropterus salmoides</i> . <i>Aquaculture Nutrition</i> , 2020, 26, 1806-1821.	1.1	19
3468	Insights into the Evolutionary Origin of Mediterranean Sandfly Fever Viruses. <i>MSphere</i> , 2020, 5, .	1.3	17
3469	Effects of graphene oxide on PCR amplification for microbial community survey. <i>BMC Microbiology</i> , 2020, 20, 278.	1.3	4

#	ARTICLE	IF	CITATIONS
3470	Maternal gut microbes shape the early-life assembly of gut microbiota in passerine chicks via nests. <i>Microbiome</i> , 2020, 8, 129.	4.9	40
3471	Elucidation of Gut Microbiota in Mud Crab <i>Scylla paramamosain</i> Challenged to WSSV and <i>Aeromonas hydrophila</i> . <i>Marine Biotechnology</i> , 2020, 22, 661-672.	1.1	9
3472	Metagenomics approach to the intestinal microbiome structure and function in high fat diet-induced obesity in mice fed with conjugated linoleic acid (CLA). <i>Food and Function</i> , 2020, 11, 9729-9739.	2.1	18
3473	Comparison of bacterial communities associated with <i>Procoentrum donghaiense</i> and <i>Karenia mikimotoi</i> strains from Chinese coastal waters. <i>Marine and Freshwater Research</i> , 2020, 71, 1662.	0.7	7
3474	Long-Term Nitrogen Fertilization Impacts on Soil Bacteria, Grain Yield and Nitrogen Use Efficiency of Wheat in Semiarid Loess Plateau, China. <i>Agronomy</i> , 2020, 10, 1175.	1.3	9
3475	Characterization of Fe(III)-Reducing Enrichment Cultures and Isolation of <i>Enterobacter</i> sp. Nan-1 from the Deep-Sea Sediment, South China Sea. <i>Journal of Ocean University of China</i> , 2020, 19, 818-826.	0.6	1
3476	Shotgun metagenomics reveal a diverse assemblage of protists in a model Antarctic soil ecosystem. <i>Environmental Microbiology</i> , 2020, 22, 4620-4632.	1.8	13
3477	Microbial communities and food safety aspects of crickets (<i>Acheta domesticus</i>) reared under controlled conditions. <i>Journal of Insects As Food and Feed</i> , 2020, 6, 429-440.	2.1	17
3478	Reciprocal Interactions between Epigallocatechin-3-gallate (EGCG) and Human Gut Microbiota <i>in Vitro</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 9804-9815.	2.4	56
3479	Divergence, gene flow, and the origin of leapfrog geographic distributions: The history of colour pattern variation in <i>Phyllobates</i> poison dart frogs. <i>Molecular Ecology</i> , 2020, 29, 3702-3719.	2.0	14
3480	Diversity and Bioactivity of Endophytes From <i>Angelica sinensis</i> in China. <i>Frontiers in Microbiology</i> , 2020, 11, 1489.	1.5	11
3481	Diet of a rare herbivore based on DNA metabarcoding of feces: Selection, seasonality, and survival. <i>Ecology and Evolution</i> , 2020, 10, 7627-7643.	0.8	27
3482	Links between soil microbial communities, functioning, and plant nutrition under altered rainfall in Australian grassland. <i>Ecological Monographs</i> , 2020, 90, e01424.	2.4	26
3483	Microbiota of Four Tissue Types in American Alligators (<i>Alligator mississippiensis</i>) Following Extended Dietary Selenomethionine Exposure. <i>Bulletin of Environmental Contamination and Toxicology</i> , 2020, 105, 381-386.	1.3	1
3484	Effects of Gut Microbiome and Short-Chain Fatty Acids (SCFAs) on Finishing Weight of Meat Rabbits. <i>Frontiers in Microbiology</i> , 2020, 11, 1835.	1.5	26
3485	Insights into the microbiota of larval and postlarval Pacific white shrimp (<i>Penaeus vannamei</i>) along early developmental stages: a case in pond level. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1517-1528.	1.0	13
3486	A hyperaccumulator plant <i>Sedum alfredii</i> recruits Cd/Zn-tolerant but not Pb-tolerant endospheric bacterial communities from its rhizospheric soil. <i>Plant and Soil</i> , 2020, 455, 257-270.	1.8	12
3487	Optimizing bacteriophage engineering through an accelerated evolution platform. <i>Scientific Reports</i> , 2020, 10, 13981.	1.6	26

#	ARTICLE	IF	CITATIONS
3488	Microorganisms Associated with the Marine Sponge <i>Scopalina hapalia</i> : A Reservoir of Bioactive Molecules to Slow Down the Aging Process. <i>Microorganisms</i> , 2020, 8, 1262.	1.6	19
3489	Novel trophic interactions under climate change promote alpine plant coexistence. <i>Science</i> , 2020, 370, 1469-1473.	6.0	51
3490	Microbial Community Profiling Distinguishes Left-Sided and Right-Sided Colon Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 498502.	1.8	20
3491	Effect of Sulfate on Carbon Monoxide Conversion by a Thermophilic Syngas-Fermenting Culture Dominated by a <i>Desulfotomaculum</i> Species. <i>Frontiers in Microbiology</i> , 2020, 11, 588468.	1.5	8
3492	Impacts of Milking and Housing Environment on Milk Microbiota. <i>Animals</i> , 2020, 10, 2339.	1.0	15
3493	Divergence in Gut Bacterial Community Structure between Male and Female Stag Beetles <i>Odontolabis fallaciosa</i> (Coleoptera, Lucanidae). <i>Animals</i> , 2020, 10, 2352.	1.0	5
3494	Comparing the Bacterial Community in the Gastrointestinal Tracts Between Growth-Retarded and Normal Yaks on the Qinghai-Tibetan Plateau. <i>Frontiers in Microbiology</i> , 2020, 11, 600516.	1.5	24
3495	A network-based approach to deciphering a dynamic microbiome's response to a subtle perturbation. <i>Scientific Reports</i> , 2020, 10, 19530.	1.6	3
3496	Effects of set cathode potentials on microbial electrosynthesis system performance and biocathode methanogen function at a metatranscriptional level. <i>Scientific Reports</i> , 2020, 10, 19824.	1.6	13
3497	Predation impacts of invasive raccoons on rare native species. <i>Scientific Reports</i> , 2020, 10, 20860.	1.6	6
3498	Altered diversity and composition of gut microbiota in Wilson's disease. <i>Scientific Reports</i> , 2020, 10, 21825.	1.6	18
3499	Comparative Analysis of the Gut Microbial Communities of the Eurasian Kestrel (<i>Falco tinnunculus</i>) at Different Developmental Stages. <i>Frontiers in Microbiology</i> , 2020, 11, 592539.	1.5	15
3500	Sodium Houttuynonate and Sodium New Houttuynonate Affect the Composition of Gut Microbiota and Production of Inflammatory Factors in Mice. <i>Natural Product Communications</i> , 2020, 15, 1934578X2097251.	0.2	2
3501	Development of the equine hindgut microbiome in semi-feral and domestic conventionally-managed foals. <i>Animal Microbiome</i> , 2020, 2, 43.	1.5	5
3502	Six-Week Exercise Training With Dietary Restriction Improves Central Hemodynamics Associated With Altered Gut Microbiota in Adolescents With Obesity. <i>Frontiers in Endocrinology</i> , 2020, 11, 569085.	1.5	21
3503	Bacterial Community Characteristics and Enzyme Activities in <i>Bothriochloa ischaemum</i> Litter Over Progressive Phytoremediation Years in a Copper Tailings Dam. <i>Frontiers in Microbiology</i> , 2020, 11, 565806.	1.5	12
3504	Spent Coffee Grounds Alter Bacterial Communities in Latxa Dairy Ewes. <i>Microorganisms</i> , 2020, 8, 1961.	1.6	6
3505	Testing Different Membrane Filters for 16S rRNA Gene-Based Metabarcoding in Karstic Springs. <i>Water (Switzerland)</i> , 2020, 12, 3400.	1.2	7

#	ARTICLE	IF	CITATIONS
3506	Relative contributions of various endogenous and exogenous factors to theÂmosquito microbiota. <i>Parasites and Vectors</i> , 2020, 13, 619.	1.0	9
3507	Dietary Inulin Supplementation Modulates Short-Chain Fatty Acid Levels and Cecum Microbiota Composition and Function in Chickens Infected With Salmonella. <i>Frontiers in Microbiology</i> , 2020, 11, 584380.	1.5	16
3508	Probiotic <i>Lactobacillus rhamnosus</i> GG Promotes Mouse Gut Microbiota Diversity and T Cell Differentiation. <i>Frontiers in Microbiology</i> , 2020, 11, 607735.	1.5	34
3509	Comparative Analysis of Wheat Hay and Silage in Methane Production, Fermentation Characteristics and Microbiota Using In Vitro Rumen Cultures. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 8456.	1.3	1
3510	Effects of Oat Hay Content in Diets on Nutrient Metabolism and the Rumen Microflora in Sheep. <i>Animals</i> , 2020, 10, 2341.	1.0	21
3511	In situ Assemblies of Bacteria and Nutrient Dynamics in Response to an Ecosystem Engineer, Marine Clam <i>Scapharca subcrenata</i> , in the Sediment of an Aquaculture Bioremediation System. <i>Journal of Ocean University of China</i> , 2020, 19, 1447-1460.	0.6	6
3512	Compositional variations and the environmental responses of bacterioplankton in the Pengxi River of the Three Gorges Reservoir, China. <i>Journal of Freshwater Ecology</i> , 2020, 35, 449-467.	0.5	11
3513	<i>Bacillus coagulans</i> BC198 and <i>Lactobacillus paracasei</i> S38 in combination reduce body fat accumulation and modulate gut microbiota. <i>CYTA - Journal of Food</i> , 2020, 18, 764-775.	0.9	4
3514	A novel identified <i>Pseudomonas aeruginosa</i> , which exhibited nitrate- and nitrite-dependent methane oxidation abilities, could alleviate the disadvantages caused by nitrate supplementation in rumen fluid fermentation. <i>Microbial Biotechnology</i> , 2021, 14, 1397-1408.	2.0	5
3515	Alternation of supragingival microbiome in patients with cirrhosis of different Child-Pugh scores. <i>Oral Diseases</i> , 2022, 28, 233-242.	1.5	1
3516	Revealing the Disturbed Vaginal Microbiota Caused by Cervical Cancer Using High-Throughput Sequencing Technology. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 538336.	1.8	17
3517	A Probiotic Mixture Induces Anxiolytic- and Antidepressive-Like Effects in Fischer and Maternally Deprived Long Evans Rats. <i>Frontiers in Behavioral Neuroscience</i> , 2020, 14, 581296.	1.0	6
3518	The Limits and Avoidance of Biases in Metagenomic Analyses of Human Fecal Microbiota. <i>Microorganisms</i> , 2020, 8, 1954.	1.6	8
3519	Genomic Assemblies of Members of <i>Burkholderia</i> and Related Genera as a Resource for Natural Product Discovery. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
3520	Vitamin A Deficiency in the Early-Life Periods Alters a Diversity of the Colonic Mucosal Microbiota in Rats. <i>Frontiers in Nutrition</i> , 2020, 7, 580780.	1.6	11
3521	Monitoring and Surveillance of Aerial Mycobiota of Rice Paddy through DNA Metabarcoding and qPCR. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 372.	1.5	12
3522	Effects of Soil Tillage, Management Practices, and Mulching Film Application on Soil Health and Peanut Yield in a Continuous Cropping System. <i>Frontiers in Microbiology</i> , 2020, 11, 570924.	1.5	14
3523	Genetic Diversity, Community Assembly, and Shaping Factors of Benthic Microbial Eukaryotes in Dongshan Bay, Southeast China. <i>Frontiers in Microbiology</i> , 2020, 11, 592489.	1.5	8

#	ARTICLE	IF	CITATIONS
3524	Gut microbiota composition and metabolomic profiles of wild and captive Chinese monals (Lophophorus lhuysii). <i>Frontiers in Zoology</i> , 2020, 17, 36.	0.9	6
3525	Developmentally Regulated Novel Non-coding Anti-sense Regulators of mRNA Translation in <i>Trypanosoma brucei</i> . <i>IScience</i> , 2020, 23, 101780.	1.9	14
3526	Field H2 infusion alters bacterial and archaeal communities but not fungal communities nor nitrogen cycle gene abundance. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108018.	4.2	11
3527	Determination of fungal diversity of acidic gruel by using cultureâ€dependent and independent methods. <i>Food Science and Nutrition</i> , 2020, 8, 5832-5840.	1.5	1
3528	Cow, Goat, and Mare Milk Diets Differentially Modulated the Immune System and Gut Microbiota of Mice Colonized by Healthy Infant Feces. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 15345-15357.	2.4	15
3529	Bio-fertilizer and rotten straw amendments alter the rhizosphere bacterial community and increase oat productivity in a salineâ€alkaline environment. <i>Scientific Reports</i> , 2020, 10, 19896.	1.6	24
3530	A transmissible cancer shifts from emergence to endemism in Tasmanian devils. <i>Science</i> , 2020, 370, .	6.0	24
3531	Distinct Features of Gut Microbiota in High-Altitude Tibetan and Middle-Altitude Han Hypertensive Patients. <i>Cardiology Research and Practice</i> , 2020, 2020, 1-15.	0.5	6
3532	The Prebiotic-Like Effects of <i>Coprinus comatus</i> Polysaccharides on Gut Microbiota in Normal Mice and Those with Acute Alcoholic Liver Injury: A Comparative Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-6.	0.5	7
3533	<i>E. coli</i> NF73-1 Isolated From NASH Patients Aggravates NAFLD in Mice by Translocating Into the Liver and Stimulating M1 Polarization. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 535940.	1.8	16
3534	Intramuscular injection of tetracycline decreased gut microbial diversity in mouse. <i>Mammalian Genome</i> , 2020, 31, 295-308.	1.0	2
3535	Vaginal microbiota diversity and paucity of <i>Lactobacillus</i> species are associated with persistent hrHPV infection in HIV negative but not in HIV positive women. <i>Scientific Reports</i> , 2020, 10, 19095.	1.6	14
3536	Identification of the gut microbiota biomarkers associated with heat cycle and failure to enter oestrus in gilts. <i>Microbial Biotechnology</i> , 2021, 14, 1316-1330.	2.0	9
3537	Influence of Different Media and Conditions on Probiotics Isolation from Breast Milk. <i>IOP Conference Series: Earth and Environmental Science</i> , 2020, 545, 012014.	0.2	0
3538	Effect of transgenic cotton continuous cropping on soil bacterial community. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	8
3539	The Dynamics of Endophytic Bacterial Community Structure in Rice Roots under Different Field Management Systems. <i>Agronomy</i> , 2020, 10, 1623.	1.3	7
3540	Use of Targeted Amplicon Sequencing in Peanut to Generate Allele Information on Allotetraploid Sub-Genomes. <i>Genes</i> , 2020, 11, 1220.	1.0	3
3541	Mild heat stress changes the microbiota diversity in the respiratory tract and the cecum of layer-type pullets. <i>Poultry Science</i> , 2020, 99, 7015-7026.	1.5	19

#	ARTICLE	IF	CITATIONS
3542	Dysbiosis in the Gut Microbiota of Adolescents with Obesity. , 2020, , .		0
3543	Diversity and Structure of Bacterial Communities in the Gut of Spider: Thomisidae and Oxyopidae. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	14
3544	Screening for functional transcriptional and splicing regulatory variants with GenIE. <i>Nucleic Acids Research</i> , 2020, 48, e131-e131.	6.5	8
3545	Rapid Changes in Microbial Community Structures along a Meandering River. <i>Microorganisms</i> , 2020, 8, 1631.	1.6	13
3546	Transitions in microbial communities along two sediment cores collected from the landward walls of the New Britain trench. <i>Marine Biology</i> , 2020, 167, 1.	0.7	4
3547	Microbial response of nitrifying biofilms to cold-shock. <i>Environmental Science: Water Research and Technology</i> , 2020, 6, 3428-3439.	1.2	0
3548	The gut microbiota-related metabolite phenylacetylglutamine associates with increased risk of incident coronary artery disease. <i>Journal of Hypertension</i> , 2020, 38, 2427-2434.	0.3	52
3549	Sulfate Reduction in Underground Horizons of a Flooded Coal Mine in Kuzbass. <i>Microbiology</i> , 2020, 89, 542-550.	0.5	4
3550	Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond. <i>Environmental Microbiomes</i> , 2020, 15, 18.	2.2	16
3551	Seasonal Variation and Assessment of Fish Resources in the Yangtze Estuary Based on Environmental DNA. <i>Water (Switzerland)</i> , 2020, 12, 2874.	1.2	17
3552	Characteristics of Ammonia Removal and Nitrifying Microbial Communities in a Hybrid Biofloc-RAS for Intensive <i>Litopenaeus vannamei</i> Culture: A Pilot-Scale Study. <i>Water (Switzerland)</i> , 2020, 12, 3000.	1.2	22
3553	Microbiota Analysis of Eggshells in Different Areas and During Different Storage Time by Non-cultural Methods. <i>Current Microbiology</i> , 2020, 77, 3842-3850.	1.0	5
3554	Comparison of Anaerobic Methane Oxidation in Different Sediment Habitats of Dianchi Lake. <i>Water, Air, and Soil Pollution</i> , 2020, 231, 1.	1.1	5
3555	BIOCOM-PIPE: a new user-friendly metabarcoding pipeline for the characterization of microbial diversity from 16S, 18S and 23S rRNA gene amplicons. <i>BMC Bioinformatics</i> , 2020, 21, 492.	1.2	16
3556	Gut bacterial ClpB-like gene function is associated with decreased body weight and a characteristic microbiota profile. <i>Microbiome</i> , 2020, 8, 59.	4.9	46
3557	Thermo-TRPs and gut microbiota are involved in thermogenesis and energy metabolism during low temperature exposure of obese mice. <i>Journal of Experimental Biology</i> , 2020, 223, .	0.8	14
3558	The microbiomes of adenoid and middle ear in children with otitis media with effusion and hypertrophy from a tertiary hospital in China. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2020, 134, 110058.	0.4	12
3559	Dynamics of heavy chain junctional length biases in antibody repertoires. <i>Communications Biology</i> , 2020, 3, 207.	2.0	14

#	ARTICLE	IF	CITATIONS
3560	The response of soil and phyllosphere microbial communities to repeated application of the fungicide iprodione: accelerated biodegradation or toxicity?. FEMS Microbiology Ecology, 2020, 96, .	1.3	29
3561	Genome Sequence Resources of <i>Colletotrichum truncatum</i> , <i>C. plurivorum</i> , <i>C. musicola</i> , and <i>C. sojae</i> : Four Species Pathogenic to Soybean (<i>Glycine max</i>). Phytopathology, 2020, 110, 1497-1499.	1.1	12
3562	Contrast diversity patterns and processes of microbial community assembly in a river-lake continuum across a catchment scale in northwestern China. Environmental Microbiomes, 2020, 15, 10.	2.2	34
3563	Marine Microbial Community Composition During the Upwelling Season in the Southern Benguela. Frontiers in Marine Science, 2020, 7, .	1.2	8
3564	Potential Pathogenic Bacteria in Seminal Microbiota of Patients with Different Types of Dysspermatism. Scientific Reports, 2020, 10, 6876.	1.6	32
3565	Experimental assembly reveals ecological drift as a major driver of root nodule bacterial diversity in a woody legume crop. FEMS Microbiology Ecology, 2020, 96, .	1.3	13
3566	Metagenomic 16S rDNA amplicon data of microbial diversity of guts of fully fed tropical bed bugs, <i>Cimex hemipterus</i> (F.) (Hemiptera: Cimicidae). Data in Brief, 2020, 30, 105575.	0.5	10
3567	nirS-type denitrifying bacterial communities in relation to soil physicochemical conditions and soil depths of two montane riparian meadows in North China. Environmental Science and Pollution Research, 2020, 27, 28899-28911.	2.7	5
3568	Continental-Scale Microbiome Study Reveals Different Environmental Characteristics Determining Microbial Richness, Composition, and Quantity in Hotel Rooms. MSystems, 2020, 5, .	1.7	20
3569	Bats actively prey on mosquitoes and other deleterious insects in rice paddies: Potential impact on human health and agriculture. Pest Management Science, 2020, 76, 3759-3769.	1.7	37
3570	Endophytic bacterial and fungal microbiota in different cultivars of cassava (<i>Manihot esculenta</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	1.3	18
3571	Effect of vegetation on soil bacteria and their potential functions for ecological restoration in the Hulun Buir Sandy Land, China. Journal of Arid Land, 2020, 12, 473-494.	0.9	8
3572	Effects of Drought-Tolerant Ea-DREB2B Transgenic Sugarcane on Bacterial Communities in Soil. Frontiers in Microbiology, 2020, 11, 704.	1.5	29
3573	Administration of <i>Bifidobacterium bifidum</i> CGMCC 15068 modulates gut microbiota and metabolome in azoxymethane (AOM)/dextran sulphate sodium (DSS)-induced colitis-associated colon cancer (CAC) in mice. Applied Microbiology and Biotechnology, 2020, 104, 5915-5928.	1.7	44
3574	Mechanisms for <i>Lactobacillus rhamnosus</i> treatment of intestinal infection by drug-resistant <i>Escherichia coli</i> . Food and Function, 2020, 11, 4428-4445.	2.1	22
3575	Integrative Analysis of Fecal Metagenomics and Metabolomics in Colorectal Cancer. Cancers, 2020, 12, 1142.	1.7	53
3576	eDNA and metabarcoding for rewilding projects monitoring, a dietary approach. Mammalian Biology, 2020, 100, 411-418.	0.8	6
3577	Nitrogen and water addition regulate soil fungal diversity and co-occurrence networks. Journal of Soils and Sediments, 2020, 20, 3192-3203.	1.5	18

#	ARTICLE	IF	CITATIONS
3578	Phylogenomics, biogeography, and evolution of morphology and ecological niche of the eastern Asian "eastern North American" <i>Nyssa</i> (<i>Nyssaceae</i>). <i>Journal of Systematics and Evolution</i> , 2020, 58, 571-603.	1.6	24
3579	Contrasting Patterns in Diversity and Community Assembly of <i>Phragmites australis</i> Root-Associated Bacterial Communities from Different Seasons. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	39
3580	Biogeography of microbiome and short-chain fatty acids in the gastrointestinal tract of duck. <i>Poultry Science</i> , 2020, 99, 4016-4027.	1.5	21
3581	Stability and nuclear localization of yeast telomerase depend on protein components of RNase P/MRP. <i>Nature Communications</i> , 2020, 11, 2173.	5.8	23
3582	Co-occurrence of antibiotic, biocide, and heavy metal resistance genes in bacteria from metal and radionuclide contaminated soils at the Savannah River Site. <i>Microbial Biotechnology</i> , 2020, 13, 1179-1200.	2.0	89
3583	Gut microbiota in early pregnancy among women with Hyperglycaemia vs. Normal blood glucose. <i>BMC Pregnancy and Childbirth</i> , 2020, 20, 284.	0.9	19
3584	Reducing protein content in the diet of growing goats: implications for nitrogen balance, intestinal nutrient digestion and absorption, and rumen microbiota. <i>Animal</i> , 2020, 14, 2063-2073.	1.3	8
3585	Long-term fertilization alters soil properties and fungal community composition in fluvo-aquic soil of the North China Plain. <i>Scientific Reports</i> , 2020, 10, 7198.	1.6	48
3586	Endophytic fungal community in grape is correlated to foliar age and domestication. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	17
3587	NIPT Technique Based on the Use of Long Chimeric DNA Reads. <i>Genes</i> , 2020, 11, 590.	1.0	2
3588	Analysis of Fungal Composition in Mine-Contaminated Soils in Hechi City. <i>Current Microbiology</i> , 2020, 77, 2685-2693.	1.0	8
3589	Changes in colonic microbiotas in rat after long-term exposure to low dose of okadaic acid. <i>Chemosphere</i> , 2020, 254, 126874.	4.2	14
3590	Comparison of microbial communities and amino acid metabolites in different traditional fermentation starters used during the fermentation of Hong Qu glutinous rice wine. <i>Food Research International</i> , 2020, 136, 109329.	2.9	30
3591	A High-Throughput Screen for Transcription Activation Domains Reveals Their Sequence Features and Permits Prediction by Deep Learning. <i>Molecular Cell</i> , 2020, 78, 890-902.e6.	4.5	70
3592	Administration of probiotic <i>Bacillus licheniformis</i> induces growth, immune and antioxidant enzyme activities, gut microbiota assembly and resistance to <i>Vibrio parahaemolyticus</i> in <i>Litopenaeus vannamei</i> . <i>Aquaculture Nutrition</i> , 2020, 26, 1604-1622.	1.1	27
3593	A Novel Screening Approach for the Dissection of Cellular Regulatory Networks of NF- κ B Using Arrayed CRISPR gRNA Libraries. <i>SLAS Discovery</i> , 2020, 25, 618-633.	1.4	4
3594	Breast-Milk Microbiota Linked to Celiac Disease Development in Children: A Pilot Study From the PreventCD Cohort. <i>Frontiers in Microbiology</i> , 2020, 11, 1335.	1.5	24
3595	Inactivation of specific spoilage organism (<i>Pseudomonas</i>) of sturgeon by curcumin-mediated photodynamic inactivation. <i>Photodiagnosis and Photodynamic Therapy</i> , 2020, 31, 101827.	1.3	14

#	ARTICLE	IF	CITATIONS
3596	Comparable Ecological Processes Govern the Temporal Succession of Gut Bacteria and Microeukaryotes as Shrimp Aged. <i>Microbial Ecology</i> , 2020, 80, 935-945.	1.4	23
3597	Metagenomic and metatranscriptomic insights into the complex nitrogen metabolic pathways in a single-stage bioreactor coupling partial denitrification with anammox. <i>Chemical Engineering Journal</i> , 2020, 398, 125653.	6.6	66
3598	Advanced strategy to exploit wine-making waste by manufacturing antioxidant and prebiotic fibre-enriched vesicles for intestinal health. <i>Colloids and Surfaces B: Biointerfaces</i> , 2020, 193, 111146.	2.5	14
3599	The immune function of a novel crustin with an atypical WAP domain in regulating intestinal microbiota homeostasis in <i>Litopenaeus vannamei</i> . <i>Developmental and Comparative Immunology</i> , 2020, 111, 103756.	1.0	14
3600	Folding Keratin Gene Clusters during Skin Regional Specification. <i>Developmental Cell</i> , 2020, 53, 561-576.e9.	3.1	18
3601	High-Throughput Sequencing Reveals a Potentially Novel <i>Sulfurovum</i> Species Dominating the Microbial Communities of the Seawater-Sediment Interface of a Deep-Sea Cold Seep in South China Sea. <i>Microorganisms</i> , 2020, 8, 687.	1.6	27
3602	Implications of continuous and rotational cropping practices on soil bacterial communities in pineapple cultivation. <i>European Journal of Soil Biology</i> , 2020, 97, 103172.	1.4	17
3603	Housefly (<i>Musca domestica</i> L.) associated microbiota across different life stages. <i>Scientific Reports</i> , 2020, 10, 7842.	1.6	32
3604	The probiotic <i>L. casei</i> LC-XCAL ₁ improves metabolic health in a diet-induced obesity mouse model without altering the microbiome. <i>Gut Microbes</i> , 2020, 12, 1747330.	4.3	16
3605	The marine intertidal zone shapes oyster and clam digestive bacterial microbiota. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	25
3606	Space Is More Important than Season when Shaping Soil Microbial Communities at a Large Spatial Scale. <i>MSystems</i> , 2020, 5, .	1.7	71
3607	Efficacy of 0.5% Levofloxacin and 5.0% Povidone-Iodine Eyedrops in Reducing Conjunctival Bacterial Flora: Metagenomic Analysis. <i>Journal of Ophthalmology</i> , 2020, 2020, 1-9.	0.6	11
3608	Combining a COI Mini-Barcode with Next-Generation Sequencing for Animal Origin Ingredients Identification in Processed Meat Product. <i>Journal of Food Quality</i> , 2020, 2020, 1-9.	1.4	10
3609	Composition and co-occurrence patterns of the microbiota of different niches of the bovine mammary gland: potential associations with mastitis susceptibility, udder inflammation, and teat-end hyperkeratosis. <i>Animal Microbiome</i> , 2020, 2, 11.	1.5	32
3610	Distinct Gut Microbiota and Metabolite Profiles Induced by Different Feeding Methods in Healthy Chinese Infants. <i>Frontiers in Microbiology</i> , 2020, 11, 714.	1.5	39
3611	DNA Metabarcoding as a Tool for Disentangling Food Webs in Agroecosystems. <i>Insects</i> , 2020, 11, 294.	1.0	22
3612	Soil management under tomato-wheat rotation increases the suppressive response against <i>Fusarium</i> wilt and tomato shoot growth by changing the microbial composition and chemical parameters. <i>Applied Soil Ecology</i> , 2020, 154, 103601.	2.1	27
3613	Insights into the histopathology and microbiome of Pacific white shrimp, <i>Penaeus vannamei</i> , suffering from white feces syndrome. <i>Aquaculture</i> , 2020, 527, 735447.	1.7	35

#	ARTICLE	IF	CITATIONS
3614	Insights into factors driving the transmission of antibiotic resistance from sludge compost-amended soil to vegetables under cadmium stress. <i>Science of the Total Environment</i> , 2020, 729, 138990.	3.9	30
3615	Longer persistence of quorum quenching bacteria over quorum sensing bacteria in aerobic granules. <i>Water Research</i> , 2020, 179, 115904.	5.3	21
3616	A Soluble Fiber Diet Increases <i>Bacteroides fragilis</i> Group Abundance and Immunoglobulin A Production in the Gut. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	54
3617	Immunoglobulin variable domain high-throughput sequencing reveals specific novel mutational patterns in POEMS syndrome. <i>Blood</i> , 2020, 135, 1750-1758.	0.6	29
3618	Dynamic distribution of gut microbiota in meat rabbits at different growth stages and relationship with average daily gain (ADG). <i>BMC Microbiology</i> , 2020, 20, 116.	1.3	26
3619	Microbial Community and Fermentation Dynamics of Corn Silage Prepared with Heat-Resistant Lactic Acid Bacteria in a Hot Environment. <i>Microorganisms</i> , 2020, 8, 719.	1.6	41
3620	Effect of feeding a daily oral care chew on the composition of plaque microbiota in dogs. <i>Research in Veterinary Science</i> , 2020, 132, 133-141.	0.9	6
3621	Long-term effects of gravel mulching and straw mulching on soil physicochemical properties and bacterial and fungal community composition in the Loess Plateau of China. <i>European Journal of Soil Biology</i> , 2020, 98, 103188.	1.4	32
3622	Stochastic determination of the spatial variation of potentially pathogenic bacteria communities in a large subtropical river. <i>Environmental Pollution</i> , 2020, 264, 114683.	3.7	26
3623	Prebiotics effects in vitro of polysaccharides from tea flowers on gut microbiota of healthy persons and patients with inflammatory bowel disease. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 968-976.	3.6	38
3624	Microbial functional attributes, rather than taxonomic attributes, drive top soil respiration, nitrification and denitrification processes. <i>Science of the Total Environment</i> , 2020, 734, 139479.	3.9	56
3625	Combining whole-genome shotgun sequencing and rRNA gene amplicon analyses to improve detection of microbe-microbe interaction networks in plant leaves. <i>ISME Journal</i> , 2020, 14, 2116-2130.	4.4	56
3626	Control of Hydraulic Load on Bacterioplankton Diversity in Cascade Hydropower Reservoirs, Southwest China. <i>Microbial Ecology</i> , 2020, 80, 537-545.	1.4	20
3627	The Dynamics of Interacting Bacterial and Fungal Communities of the Mouse Colon Following Antibiotics. <i>Microbial Ecology</i> , 2020, 80, 573-592.	1.4	4
3628	Microsatellite markers development for Indonesian nutmeg (<i>Myristica fragrans</i> Houtt.) and transferability to other Myristicaceae spp.. <i>Molecular Biology Reports</i> , 2020, 47, 4835-4840.	1.0	3
3629	Pervasive promoter hypermethylation of silenced TERT alleles in human cancers. <i>Cellular Oncology (Dordrecht)</i> , 2020, 43, 847-861.	2.1	14
3630	Bacterioplankton assembly and interspecies interactions follow trajectories of <i>Gymnodinium</i> diatom bloom. <i>Marine Environmental Research</i> , 2020, 160, 105010.	1.1	4
3631	Metagenomic analysis of relative abundance and diversity of bacterial microbiota in <i>Bemisia tabaci</i> infesting cotton crop in Pakistan. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104381.	1.0	6

#	ARTICLE	IF	CITATIONS
3632	Copper accumulation in agricultural soils: Risks for the food chain and soil microbial populations. <i>Science of the Total Environment</i> , 2020, 734, 139434.	3.9	58
3633	Homologous recombination DNA repair deficiency and PARP inhibition activity in primary triple negative breast cancer. <i>Nature Communications</i> , 2020, 11, 2662.	5.8	157
3634	Genomes of the dinoflagellate <i>Polarella glacialis</i> encode tandemly repeated single-exon genes with adaptive functions. <i>BMC Biology</i> , 2020, 18, 56.	1.7	64
3635	Different wheat cultivars exhibit variable responses to inoculation with arbuscular mycorrhizal fungi from organic and conventional farms. <i>PLoS ONE</i> , 2020, 15, e0233878.	1.1	29
3636	Effects of different types of zinc supplement on the growth, incidence of diarrhea, immune function, and rectal microbiota of newborn dairy calves. <i>Journal of Dairy Science</i> , 2020, 103, 6100-6113.	1.4	37
3637	Mycorrhizal nitrogen uptake of wheat is increased by earthworm activity only under no-till and straw removal conditions. <i>Applied Soil Ecology</i> , 2020, 155, 103672.	2.1	16
3638	Temporal dynamics of bacterial communities in the water and sediments of sea cucumber (<i>Apostichopus japonicus</i>) culture ponds. <i>Aquaculture</i> , 2020, 528, 735498.	1.7	29
3639	Soil microbial community responses to soil chemistry modifications in alpine meadows following human trampling. <i>Catena</i> , 2020, 194, 104717.	2.2	16
3640	Microbial Communities Associated with Methylmercury Degradation in Paddy Soils. <i>Environmental Science & Technology</i> , 2020, 54, 7952-7960.	4.6	40
3641	Grazing Management Influences Gut Microbial Diversity of Livestock in the Same Area. <i>Sustainability</i> , 2020, 12, 4160.	1.6	2
3642	Effects of long-term straw retention on soil microorganisms under a rice-wheat cropping system. <i>Archives of Microbiology</i> , 2020, 202, 1915-1927.	1.0	16
3643	Persistent organic fertilization reinforces soil-borne disease suppressiveness of rhizosphere bacterial community. <i>Plant and Soil</i> , 2020, 452, 313-328.	1.8	30
3644	The Effects of Tetracycline Residues on the Microbial Community Structure of Tobacco Soil in Pot Experiment. <i>Scientific Reports</i> , 2020, 10, 8804.	1.6	19
3645	Fucoidan isolated from <i>Ascophyllum nodosum</i> alleviates gut microbiota dysbiosis and colonic inflammation in antibiotic-treated mice. <i>Food and Function</i> , 2020, 11, 5595-5606.	2.1	36
3646	A Recent Human Immunodeficiency Virus Outbreak Among People Who Inject Drugs in Munich, Germany, Is Associated With Consumption of Synthetic Cathinones. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa192.	0.4	4
3647	Identification of the distribution of human endogenous retroviruses K (HML-2) by PCR-based target enrichment sequencing. <i>Retrovirology</i> , 2020, 17, 10.	0.9	20
3648	Variations of Gut Microbiome Profile Under Different Storage Conditions and Preservation Periods: A Multi-Dimensional Evaluation. <i>Frontiers in Microbiology</i> , 2020, 11, 972.	1.5	21
3649	Soil bacterial diversity, structure, and function of <i>Suaeda salsa</i> in rhizosphere and non-rhizosphere soils in various habitats in the Yellow River Delta, China. <i>Science of the Total Environment</i> , 2020, 740, 140144.	3.9	49

#	ARTICLE	IF	CITATIONS
3650	Can We Use Functional Genetics to Predict the Fate of Nitrogen in Estuaries?. <i>Frontiers in Microbiology</i> , 2020, 11, 1261.	1.5	19
3651	Bacterial viability and diversity in a landscape lake replenished with reclaimed water: a case study in Xi'an, China. <i>Environmental Science and Pollution Research</i> , 2020, 27, 32796-32808.	2.7	7
3652	Climate influences the alpine soil bacterial communities by regulating the vegetation and the soil properties along an altitudinal gradient in SW China. <i>Catena</i> , 2020, 195, 104727.	2.2	15
3653	Deciphering the rhizosphere microbiome of a bamboo plant in response to different chromium contamination levels. <i>Journal of Hazardous Materials</i> , 2020, 399, 123107.	6.5	32
3654	Intact Ether Lipids in Trench Sediments Related to Archaeal Community and Environmental Conditions in the Deepest Ocean. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2020, 125, e2019JG005431.	1.3	7
3655	Influence of gut microbiota on mucosal IgA antibody response to the polio vaccine. <i>Npj Vaccines</i> , 2020, 5, 47.	2.9	33
3656	Using molecular microbial ecology to define differential responses to the inoculation of barley silage. <i>Canadian Journal of Animal Science</i> , 2020, 100, 703-715.	0.7	3
3657	Host Species Determines the Composition of the Prokaryotic Microbiota in Phlebotomus Sandflies. <i>Pathogens</i> , 2020, 9, 428.	1.2	16
3658	CHANGE-seq reveals genetic and epigenetic effects on CRISPR-Cas9 genome-wide activity. <i>Nature Biotechnology</i> , 2020, 38, 1317-1327.	9.4	149
3659	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 Xiongan New Area. <i>Canadian Journal of Microbiology</i> , 2020, 66, 605-622.	0.8	10
3660	Diazotrophic communities are more responsive to maize cultivation than phosphorus fertilization in an acidic soil. <i>Plant and Soil</i> , 2020, 452, 499-512.	1.8	11
3661	Carvacrol promotes intestinal health in Pengze crucian carp, enhancing resistance to <i>Aeromonas hydrophila</i> . <i>Aquaculture Reports</i> , 2020, 17, 100325.	0.7	4
3662	Deciphering the d-/l-lactate-producing microbiota and manipulating their accumulation during solid-state fermentation of cereal vinegar. <i>Food Microbiology</i> , 2020, 92, 103559.	2.1	23
3663	Insight into the effect of oxytetracycline on the pollutant removal performance, nitrogen removal rate, microbial community and enzymatic activity of sequencing batch reactor. <i>Journal of Water Process Engineering</i> , 2020, 36, 101309.	2.6	3
3664	Deciphering the succession dynamics of dominant and rare genera in biofilm development process. <i>Science of the Total Environment</i> , 2020, 739, 139961.	3.9	11
3665	Antibiotic resistomes in drinking water sources across a large geographical scale: Multiple drivers and co-occurrence with opportunistic bacterial pathogens. <i>Water Research</i> , 2020, 183, 116088.	5.3	80
3666	Luminal microbiota related to Crohn's disease recurrence after surgery. <i>Gut Microbes</i> , 2020, 11, 1713-1728.	4.3	22
3667	Importance of <i>Deffluviitalea raffinosedens</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	1.6	13

#	ARTICLE	IF	CITATIONS
3668	Temporal dynamics of aquatic microbiota and their correlation with environmental factors during larviculture of the shrimp <i>Litopenaeus vannamei</i> . <i>Aquaculture</i> , 2020, 529, 735605.	1.7	10
3669	Organic fertilizer improves soil fertility and restores the bacterial community after 1,3-dichloropropene fumigation. <i>Science of the Total Environment</i> , 2020, 738, 140345.	3.9	57
3670	Stepping into the past to conserve the future: Archived skin swabs from extant and extirpated populations inform genetic management of an endangered amphibian. <i>Molecular Ecology</i> , 2020, 29, 2598-2611.	2.0	3
3671	Fat- δ -Shaped Microbiota Affects Lipid Metabolism, Liver Steatosis, and Intestinal Homeostasis in Mice Fed a Low-Protein Diet. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e1900835.	1.5	11
3672	Changes of water, sediment, and intestinal bacterial communities in <i>Penaeus japonicus</i> cultivation and their impacts on shrimp physiological health. <i>Aquaculture International</i> , 2020, 28, 1847-1865.	1.1	10
3673	Metagenomics analysis of rhizospheric bacterial communities of <i>Saccharum arundinaceum</i> growing on organometallic sludge of sugarcane molasses-based distillery. <i>3 Biotech</i> , 2020, 10, 316.	1.1	47
3674	Influences of Hillslope Biogeochemistry on Anaerobic Soil Organic Matter Decomposition in a Tundra Watershed. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2020, 125, e2019JG005512.	1.3	4
3675	Imprint of Trace Dissolved Oxygen on Prokaryoplankton Community Structure in an Oxygen Minimum Zone. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	9
3676	Pea (<i>Pisum sativum</i> L.) Plant Shapes Its Rhizosphere Microbiome for Nutrient Uptake and Stress Amelioration in Acidic Soils of the North-East Region of India. <i>Frontiers in Microbiology</i> , 2020, 11, 968.	1.5	21
3677	Rhizosphere Soil Fungal Communities of Aluminum-Tolerant and -Sensitive Soybean Genotypes Respond Differently to Aluminum Stress in an Acid Soil. <i>Frontiers in Microbiology</i> , 2020, 11, 1177.	1.5	23
3678	The Effects of Different Concentrate-to-Forage Ratio Diets on Rumen Bacterial Microbiota and the Structures of Holstein Cows during the Feeding Cycle. <i>Animals</i> , 2020, 10, 957.	1.0	24
3679	Intercropping with Potato-Onion Enhanced the Soil Microbial Diversity of Tomato. <i>Microorganisms</i> , 2020, 8, 834.	1.6	32
3680	Analysis of the Endophytic Bacteria Community Structure and Function of <i>Panax notoginseng</i> Based on High-Throughput Sequencing. <i>Current Microbiology</i> , 2020, 77, 2745-2750.	1.0	8
3681	Effects of biocontrol agents and compost against the <i>Phytophthora capsici</i> of zucchini and their impact on the rhizosphere microbiota. <i>Applied Soil Ecology</i> , 2020, 154, 103659.	2.1	22
3682	Bacterial profiles and volatile flavor compounds in commercial Suancai with varying salt concentration from Northeastern China. <i>Food Research International</i> , 2020, 137, 109384.	2.9	47
3683	High-throughput sequencing analysis of endophytic fungal diversity in <i>cynanchum</i> sp.. <i>South African Journal of Botany</i> , 2020, 134, 349-358.	1.2	11
3684	Spatial Variation in Bacterioplankton Communities in the Pearl River, South China: Impacts of Land Use and Physicochemical Factors. <i>Microorganisms</i> , 2020, 8, 814.	1.6	11
3685	Patterns of Bacterial Community Composition and Diversity Following the Embryonic Development Stages of <i>Macrobrachium rosenbergii</i> . <i>Aquaculture Reports</i> , 2020, 17, 100372.	0.7	6

#	ARTICLE	IF	CITATIONS
3686	Human milk microbiota development during lactation and its relation to maternal geographic location and gestational hypertensive status. <i>Gut Microbes</i> , 2020, 11, 1438-1449.	4.3	26
3687	The role of root community attributes in predicting soil fungal and bacterial community patterns. <i>New Phytologist</i> , 2020, 228, 1070-1082.	3.5	47
3688	Validating the Cyc2 Neutrophilic Iron Oxidation Pathway Using Meta-omics of <i>Zetaproteobacteria</i> Iron Mats at Marine Hydrothermal Vents. <i>MSystems</i> , 2020, 5, .	1.7	65
3689	A prospective longitudinal study on the microbiota composition in amyotrophic lateral sclerosis. <i>BMC Medicine</i> , 2020, 18, 153.	2.3	78
3690	Soil fungal taxonomic diversity along an elevation gradient on the semi-arid Xinglong Mountain, Northwest China. <i>Archives of Microbiology</i> , 2020, 202, 2291-2302.	1.0	5
3691	Light inhibition of carbon mineralization associated with iron redox processes in calcareous paddy soil. <i>Journal of Soils and Sediments</i> , 2020, 20, 3171-3180.	1.5	1
3692	Change of rhizospheric bacterial community of the ancient wild tea along elevational gradients in Ailao mountain, China. <i>Scientific Reports</i> , 2020, 10, 9203.	1.6	19
3693	Chemical Composition of Milk and Rumen Microbiome Diversity of Yak, Impacting by Herbage Grown at Different Phenological Periods on the Qinghai-Tibet Plateau. <i>Animals</i> , 2020, 10, 1030.	1.0	26
3694	Alterations in intestinal microbiota by alginate oligosaccharide improve intestinal barrier integrity in weaned pigs. <i>Journal of Functional Foods</i> , 2020, 71, 104040.	1.6	18
3695	Genomic Insights into Two Novel Fe(II)-Oxidizing <i>Zetaproteobacteria</i> Isolates Reveal Lifestyle Adaption to Coastal Marine Sediments. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	4
3696	A novel apidaecin Api-PR19 synergizes with the gut microbial community to maintain intestinal health and promote growth performance of broilers. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 61.	2.1	11
3697	Spontaneous Tumor Regression in Tasmanian Devils Associated with <i>RASL11A</i> Activation. <i>Genetics</i> , 2020, 215, 1143-1152.	1.2	22
3698	The legacy of trace metal deposition from historical anthropogenic river management: A regional driver of offshore sedimentary microbial diversity. <i>Journal of Hazardous Materials</i> , 2020, 400, 123164.	6.5	7
3699	Temporal patterns in the interaction between photosynthetic picoeukaryotes and their attached fungi in Lake Chaohu. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	7
3700	Yeast and bacterial inoculation practices influence the microbial communities of barrel-fermented Chardonnay wines. <i>Australian Journal of Grape and Wine Research</i> , 2020, 26, 279-289.	1.0	1
3701	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. <i>Microbiome</i> , 2020, 8, 84.	4.9	47
3702	Profiling the mid-adult cecal microbiota associated with host healthy by using herbal formula Kang Shuai Lao Pian treated mid-adult mice. <i>Chinese Journal of Natural Medicines</i> , 2020, 18, 90-102.	0.7	4
3703	Nondigestible Carbohydrates Affect Metabolic Health and Gut Microbiota in Overweight Adults after Weight Loss. <i>Journal of Nutrition</i> , 2020, 150, 1859-1870.	1.3	16

#	ARTICLE	IF	CITATIONS
3704	The saprotrophic <i>Pleurotus ostreatus</i> species complex: late Eocene origin in East Asia, multiple dispersal, and complex speciation. <i>IMA Fungus</i> , 2020, 11, 10.	1.7	17
3705	<i>Rehmannia glutinosa</i> Replant Issues: Root Exudate-Rhizobiome Interactions Clearly Influence Replant Success. <i>Frontiers in Microbiology</i> , 2020, 11, 1413.	1.5	14
3706	Effect of <i>Rhizophora apiculata</i> plantation for improving water quality, growth, and health of mud crab. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6813-6824.	1.7	7
3707	Eutrophication as a driver of microbial community structure in lake sediments. <i>Environmental Microbiology</i> , 2020, 22, 3446-3462.	1.8	51
3708	Impact of Chemical and Alternative Fungicides Applied to Grapevine cv Nebbiolo on Microbial Ecology and Chemical-Physical Grape Characteristics at Harvest. <i>Frontiers in Plant Science</i> , 2020, 11, 700.	1.7	34
3709	Changes in Soil Properties and Bacterial Community Composition with Biochar Amendment after Six Years. <i>Agronomy</i> , 2020, 10, 746.	1.3	30
3710	Effects of dietary rumen-protected Lys levels on rumen fermentation and bacterial community composition in Holstein heifers. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6623-6634.	1.7	18
3711	Study of kefir drinks produced by backslopping method using kefir grains from Bosnia and Herzegovina: Microbial dynamics and volatilome profile. <i>Food Research International</i> , 2020, 137, 109369.	2.9	33
3712	Analysis of Marine Planktonic Cyanobacterial Assemblages From Mooriganga Estuary, Indian Sundarbans Using Molecular Approaches. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
3713	Genome Size, rDNA Copy, and qPCR Assays for Symbiodiniaceae. <i>Frontiers in Microbiology</i> , 2020, 11, 847.	1.5	29
3714	Modulation of Gut Microbiota, Short-Chain Fatty Acid Production, and Inflammatory Cytokine Expression in the Cecum of Porcine Deltacoronavirus-Infected Chicks. <i>Frontiers in Microbiology</i> , 2020, 11, 897.	1.5	17
3715	Comparison of Meconium Microbiome in Dizygotic and Monozygotic Twins Born by Caesarean Section (CS). <i>Frontiers in Microbiology</i> , 2020, 11, 1139.	1.5	9
3716	Underlying Mechanism of Wild <i>Radix pseudostellariae</i> in Tolerance to Disease Under the Natural Forest Cover. <i>Frontiers in Microbiology</i> , 2020, 11, 1142.	1.5	12
3717	Isolation and Comparative Genomic Analysis of Reuterin-Producing <i>Lactobacillus reuteri</i> From the Chicken Gastrointestinal Tract. <i>Frontiers in Microbiology</i> , 2020, 11, 1166.	1.5	18
3718	Contrasting Community Composition of Active Microbial Eukaryotes in Melt Ponds and Sea Water of the Arctic Ocean Revealed by High Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 1170.	1.5	13
3719	Determination of Plasmid pSN1216-29 Host Range and the Similarity in Oligonucleotide Composition Between Plasmid and Host Chromosomes. <i>Frontiers in Microbiology</i> , 2020, 11, 1187.	1.5	4
3720	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. <i>Frontiers in Plant Science</i> , 2020, 11, 601.	1.7	54
3721	Rhizospheric Organic Acids as Biostimulants: Monitoring Feedbacks on Soil Microorganisms and Biochemical Properties. <i>Frontiers in Plant Science</i> , 2020, 11, 633.	1.7	93

#	ARTICLE	IF	CITATIONS
3722	Effective Treatment of Acid Mine Drainage with Microbial Fuel Cells: An Emphasis on Typical Energy Substrates. <i>Minerals (Basel, Switzerland)</i> , 2020, 10, 443.	0.8	24
3723	Effect of Litter Treatment on <i>Campylobacter jejuni</i> in Broilers and on Cecal Microbiota. <i>Pathogens</i> , 2020, 9, 333.	1.2	3
3724	Adaptive Variations of Sediment Microbial Communities and Indication of Fecal-Associated Bacteria to Nutrients in a Regulated Urban River. <i>Water (Switzerland)</i> , 2020, 12, 1344.	1.2	6
3725	Shifts in Composition and Activity of Oral Biofilms After Fluoride Exposure. <i>Microbial Ecology</i> , 2020, 80, 729-738.	1.4	7
3726	Effects of Short-Term Application of Chemical and Organic Fertilizers on Bacterial Diversity of Cornfield Soil in a Karst Area. <i>Journal of Soil Science and Plant Nutrition</i> , 2020, 20, 2048-2058.	1.7	17
3727	Bacterial Communities Associated with the Pine Wilt Disease Insect Vector <i>Monochamus alternatus</i> (Coleoptera: Cerambycidae) during the Larvae and Pupae Stages. <i>Insects</i> , 2020, 11, 376.	1.0	17
3728	Influence of Resistance-Inducing Chemical Elicitors against Pine Wilt Disease on the Rhizosphere Microbiome. <i>Microorganisms</i> , 2020, 8, 884.	1.6	22
3729	The day-to-day stability of the ruminal and fecal microbiota in lactating dairy cows. <i>MicrobiologyOpen</i> , 2020, 9, e990.	1.2	30
3730	The potential role of the gut microbiota in modulating renal function in experimental diabetic nephropathy murine models established in same environment. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165764.	1.8	46
3731	Dynamic change of bacterial community during dairy manure composting process revealed by high-throughput sequencing and advanced bioinformatics tools. <i>Bioresource Technology</i> , 2020, 306, 123091.	4.8	93
3732	Microbiota Composition and Evenness Predict Survival Rate of Oysters Confronted to Pacific Oyster Mortality Syndrome. <i>Frontiers in Microbiology</i> , 2020, 11, 311.	1.5	57
3733	Data on community structure and diversity of the intestinal bacteria in elver and fingerling stages of wild Indonesian shortfin eel (<i>Anguilla bicolor bicolor</i>). <i>Data in Brief</i> , 2020, 29, 105299.	0.5	2
3734	Characteristics of the urinary microbiome in kidney stone patients with hypertension. <i>Journal of Translational Medicine</i> , 2020, 18, 130.	1.8	28
3735	Comparative analysis and gut bacterial community assemblages of grass carp and crucian carp in new lineages from the Dongting Lake area. <i>MicrobiologyOpen</i> , 2020, 9, e996.	1.2	15
3736	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	5.8	133
3737	Diversity and biogeography of picoplankton communities from the Straits of Malacca to the South China Sea. <i>Oceanological and Hydrobiological Studies</i> , 2020, 49, 23-33.	0.3	2
3738	Differences in Gut Microbial Diversity are Driven by Drug Use and Drug Cessation by Either Compulsory Detention or Methadone Maintenance Treatment. <i>Microorganisms</i> , 2020, 8, 411.	1.6	11
3739	Soil fungal community is more sensitive to nitrogen deposition than increased rainfall in a mixed deciduous forest of China. <i>Soil Ecology Letters</i> , 2020, 2, 20-32.	2.4	23

#	ARTICLE	IF	CITATIONS
3740	Rhizosphere fungal communities of wild and cultivated soybeans grown in three different soil suspensions. <i>Applied Soil Ecology</i> , 2020, 153, 103586.	2.1	7
3741	Total alkaloids of <i>Sophora alopecuroides</i> L. ameliorated murine colitis by regulating bile acid metabolism and gut microbiota. <i>Journal of Ethnopharmacology</i> , 2020, 255, 112775.	2.0	22
3742	Dietary garcinol supplementation improves diarrhea and intestinal barrier function associated with its modulation of gut microbiota in weaned piglets. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 12.	2.1	31
3743	Dynamic alterations in early intestinal development, microbiota and metabolome induced by in ovo feeding of L-arginine in a layer chick model. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 19.	2.1	30
3744	Impact of process temperature and organic loading rate on cellulolytic / hydrolytic biofilm microbiomes during biomethanation of ryegrass silage revealed by genome-centered metagenomics and metatranscriptomics. <i>Environmental Microbiomes</i> , 2020, 15, 7.	2.2	13
3745	Calcium propionate supplementation alters the ruminal bacterial and archaeal communities in pre- and postweaning calves. <i>Journal of Dairy Science</i> , 2020, 103, 3204-3218.	1.4	13
3746	Growth and health status of Pacific white shrimp, <i>Litopenaeus vannamei</i> , exposed to chronic water born cobalt. <i>Fish and Shellfish Immunology</i> , 2020, 100, 137-145.	1.6	30
3747	Soil protist communities in burrowing and casting hotspots of different earthworm species. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107774.	4.2	13
3748	Determinants of Eurasian otter (<i>Lutra lutra</i>) diet in a seasonally changing reservoir. <i>Hydrobiologia</i> , 2020, 847, 1803-1816.	1.0	10
3749	Effects of Dazomet Fumigation on Soil Phosphorus and the Composition of <i>phoD</i> -Harboring Microbial Communities. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 5049-5058.	2.4	18
3750	Consequences of Domestication on Gut Microbiome: A Comparative Study Between Wild Gaur and Domestic Mithun. <i>Frontiers in Microbiology</i> , 2020, 11, 133.	1.5	19
3751	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , 2020, 579, 567-574.	13.7	691
3752	Distinct fungal successional trajectories following wildfire between soil horizons in a cold-temperate forest. <i>New Phytologist</i> , 2020, 227, 572-587.	3.5	41
3753	Midgut microbiota diversity of potato tuber moth associated with potato tissue consumed. <i>BMC Microbiology</i> , 2020, 20, 58.	1.3	14
3754	Probiotic Mixture of <i>Lactobacillus plantarum</i> Strains Improves Lipid Metabolism and Gut Microbiota Structure in High Fat Diet-Fed Mice. <i>Frontiers in Microbiology</i> , 2020, 11, 512.	1.5	95
3755	Response of Bacterial Community Structure to Different Biochar Addition Dosages in Karst Yellow Soil Planted with Ryegrass and Daylily. <i>Sustainability</i> , 2020, 12, 2124.	1.6	8
3756	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 406-419.	1.7	59
3757	Simultaneous nitrogen and carbon removal in a packed A/O reactor: effect of C/N ratio on microbial community structure. <i>Bioprocess and Biosystems Engineering</i> , 2020, 43, 1241-1252.	1.7	17

#	ARTICLE	IF	CITATIONS
3758	Beneficial effects of LRP6-CRISPR on prevention of alcohol-related liver injury surpassed fecal microbiota transplant in a rat model. <i>Gut Microbes</i> , 2020, 11, 1015-1029.	4.3	29
3759	Richness of sputum microbiome in acute exacerbations of eosinophilic chronic obstructive pulmonary disease. <i>Chinese Medical Journal</i> , 2020, 133, 542-551.	0.9	13
3760	Long-lasting effects of antibiotics on bacterial communities of adult flies. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	10
3761	Combined signature of rumen microbiome and metabolome in dairy cows with different feed intake levels. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	21
3762	Disentangling the assembly mechanisms of ant cuticular bacterial communities of two Amazonian ant species sharing a common arboreal nest. <i>Molecular Ecology</i> , 2020, 29, 1372-1385.	2.0	15
3763	Effects of shade stress on turfgrasses morphophysiology and rhizosphere soil bacterial communities. <i>BMC Plant Biology</i> , 2020, 20, 92.	1.6	23
3764	Intestinal flora imbalance affects bile acid metabolism and is associated with gallstone formation. <i>BMC Gastroenterology</i> , 2020, 20, 59.	0.8	45
3765	Dual-locus DNA metabarcoding reveals southern hairy-nosed wombats (<i>Lasiorhinus latifrons</i> Owen) have a summer diet dominated by toxic invasive plants. <i>PLoS ONE</i> , 2020, 15, e0229390.	1.1	9
3766	Petroleum Depletion Property and Microbial Community Shift After Bioremediation Using <i>Bacillus halotolerans</i> T-04 and <i>Bacillus cereus</i> 1-1. <i>Frontiers in Microbiology</i> , 2020, 11, 353.	1.5	16
3767	Effects of Different Fertilizers on Rhizosphere Bacterial Communities of Winter Wheat in the North China Plain. <i>Agronomy</i> , 2020, 10, 93.	1.3	24
3768	Soil biochemical properties and bacteria community in a repeatedly fumigated-incubated soil. <i>Biology and Fertility of Soils</i> , 2020, 56, 619-631.	2.3	6
3769	Glyphosate-based herbicide affects the composition of microbes associated with Colorado potato beetle (<i>Leptinotarsa decemlineata</i>). <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	22
3770	Spatial Variation in Soil Fungal Communities across Paddy Fields in Subtropical China. <i>MSystems</i> , 2020, 5, .	1.7	56
3771	Rhizosphere Microbial Community Structure Is Selected by Habitat but Not Plant Species in Two Tropical Seagrass Beds. <i>Frontiers in Microbiology</i> , 2020, 11, 161.	1.5	33
3772	Featured Gut Microbiomes Associated With the Progression of Chronic Hepatitis B Disease. <i>Frontiers in Microbiology</i> , 2020, 11, 383.	1.5	57
3773	Soil phosphorus availability modifies the relationship between AM fungal diversity and mycorrhizal benefits to maize in an agricultural soil. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107790.	4.2	55
3774	First draft genome for the sand-hopper <i>Trinorchestia longiramus</i> . <i>Scientific Data</i> , 2020, 7, 85.	2.4	8
3775	Comparison of bacterial communities in channel catfish <i>Ictalurus punctatus</i> culture ponds of an industrial ecological purification recirculating aquaculture system. <i>Aquaculture Research</i> , 2020, 51, 2432-2442.	0.9	7

#	ARTICLE	IF	CITATIONS
3776	Deep Insights into Gut Microbiota in Four Carnivorous Coral Reef Fishes from the South China Sea. <i>Microorganisms</i> , 2020, 8, 426.	1.6	22
3777	Next-generation sequencing of the intrahepatic antibody repertoire delineates a unique B-cell response in HBV-associated acute liver failure. <i>Journal of Viral Hepatitis</i> , 2020, 27, 847-851.	1.0	5
3778	Hyena paleogenomes reveal a complex evolutionary history of cross-continental gene flow between spotted and cave hyena. <i>Science Advances</i> , 2020, 6, eaay0456.	4.7	38
3779	Gut Microbiomes of Endangered Przewalski's Horse Populations in Short- and Long-Term Captivity: Implication for Species Reintroduction Based on the Soft-Release Strategy. <i>Frontiers in Microbiology</i> , 2020, 11, 363.	1.5	13
3780	Stratified microbial structure and activity within anode biofilm during electrochemically assisted brewery wastewater treatment. <i>Biotechnology and Bioengineering</i> , 2020, 117, 2023-2031.	1.7	13
3781	Effects of temperature, diet and genotype-induced variations on the gut microbiota of abalone. <i>Aquaculture</i> , 2020, 524, 735269.	1.7	18
3782	Microbiota and metabolome responses in the cecum and serum of broiler chickens fed with plant essential oils or virginiamycin. <i>Scientific Reports</i> , 2020, 10, 5382.	1.6	41
3783	Fungal communities differentially respond to warming and drought in tropical grassland soil. <i>Molecular Ecology</i> , 2020, 29, 1550-1559.	2.0	41
3784	Critical transition of soil bacterial diversity and composition triggered by nitrogen enrichment. <i>Ecology</i> , 2020, 101, e03053.	1.5	98
3785	Co-occurrence patterns among prokaryotes across an age gradient in pit mud of Chinese strong-flavor liquor. <i>Canadian Journal of Microbiology</i> , 2020, 66, 495-504.	0.8	9
3786	Microecological Koch's postulates reveal that intestinal microbiota dysbiosis contributes to shrimp white feces syndrome. <i>Microbiome</i> , 2020, 8, 32.	4.9	126
3787	Impact of mariculture-derived microplastics on bacterial biofilm formation and their potential threat to mariculture: A case in situ study on the Sungo Bay, China. <i>Environmental Pollution</i> , 2020, 262, 114336.	3.7	63
3788	What Is in <i>Umbilicaria pustulata</i> ? A Metagenomic Approach to Reconstruct the Holo-Genome of a Lichen. <i>Genome Biology and Evolution</i> , 2020, 12, 309-324.	1.1	37
3789	Effects of a Diet Supplemented with Exogenous Catalase from <i>Penicillium notatum</i> on Intestinal Development and Microbiota in Weaned Piglets. <i>Microorganisms</i> , 2020, 8, 391.	1.6	14
3790	Cassava/peanut intercropping improves soil quality via rhizospheric microbes increased available nitrogen contents. <i>BMC Biotechnology</i> , 2020, 20, 13.	1.7	46
3791	Modulation of Gut Microbial Community and Metabolism by Dietary Glycyl-Glutamine Supplementation May Favor Weaning Transition in Piglets. <i>Frontiers in Microbiology</i> , 2019, 10, 3125.	1.5	20
3792	Agricultural Selection of Wheat Has Been Shaped by Plant-Microbe Interactions. <i>Frontiers in Microbiology</i> , 2020, 11, 132.	1.5	53
3793	Distinct Assembly Mechanisms Underlie Similar Biogeographic Patterns of Rare and Abundant Bacterioplankton in Cascade Reservoirs of a Large River. <i>Frontiers in Microbiology</i> , 2020, 11, 158.	1.5	37

#	ARTICLE	IF	CITATIONS
3794	Changes in the Solid-, Liquid-, and Epithelium-Associated Bacterial Communities in the Rumen of Hu Lambs in Response to Dietary Urea Supplementation. <i>Frontiers in Microbiology</i> , 2020, 11, 244.	1.5	35
3795	Biochanin A Inhibits Ruminal Nitrogen-Metabolizing Bacteria and Alleviates the Decomposition of Amino Acids and Urea In Vitro. <i>Animals</i> , 2020, 10, 368.	1.0	9
3796	Diversity of Intestinal Bacterial Microbiota of Indigenous and Commercial Strains of Chickens Using 16S rDNA-Based Analysis. <i>Animals</i> , 2020, 10, 391.	1.0	6
3797	Slope Position Rather Than Thinning Intensity Affects Arbuscular Mycorrhizal Fungi (AMF) Community in Chinese Fir Plantations. <i>Forests</i> , 2020, 11, 273.	0.9	12
3798	Effects of Hydraulic Retention Time and Influent Nitrate-N Concentration on Nitrogen Removal and the Microbial Community of an Aerobic Denitrification Reactor Treating Recirculating Marine Aquaculture System Effluent. <i>Water (Switzerland)</i> , 2020, 12, 650.	1.2	7
3799	Effects of mineral substrate on ectomycorrhizal fungal colonization and bacterial community structure. <i>Science of the Total Environment</i> , 2020, 721, 137663.	3.9	15
3800	Mild changes in the mucosal microbiome during terminal ileum inflammation. <i>Microbial Pathogenesis</i> , 2020, 142, 104104.	1.3	8
3801	Consumption of salt leads to ameliorate symptoms of metabolic disorder and change of gut microbiota. <i>European Journal of Nutrition</i> , 2020, 59, 3779-3790.	1.8	6
3802	Effects of the long-term application of atrazine on soil enzyme activity and bacterial community structure in farmlands in China. <i>Environmental Pollution</i> , 2020, 262, 114264.	3.7	60
3803	A comprehensive non-redundant reference transcriptome for the Atlantic silverside <i>Menidia menidia</i> . <i>Marine Genomics</i> , 2020, 53, 100738.	0.4	6
3804	The invader <i>Carpobrotus edulis</i> promotes a specific rhizosphere microbiome across globally distributed coastal ecosystems. <i>Science of the Total Environment</i> , 2020, 719, 137347.	3.9	26
3805	Rhizodegradation of Petroleum Oily Sludge-contaminated Soil Using <i>Cajanus cajan</i> Increases the Diversity of Soil Microbial Community. <i>Scientific Reports</i> , 2020, 10, 4094.	1.6	49
3806	Characterization of the Esophageal Microbiota and Prediction of the Metabolic Pathways Involved in Esophageal Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 268.	1.8	35
3807	Horizontal gene transfer and silver nanoparticles production in a new <i>Marinomonas</i> strain isolated from the Antarctic psychrophilic ciliate <i>Euplotes focardii</i> . <i>Scientific Reports</i> , 2020, 10, 10218.	1.6	22
3808	The distinct microbial community in <i>Aurelia coerulea</i> polyps versus medusae and its dynamics after exposure to $^{60}\text{Co-}\beta$ radiation. <i>Environmental Research</i> , 2020, 188, 109843.	3.7	3
3809	Dietary quinoa (<i>Chenopodium quinoa</i> Willd.) polysaccharides ameliorate high-fat diet-induced hyperlipidemia and modulate gut microbiota. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 55-65.	3.6	61
3810	A Comprehensive Multi-Omic Approach Reveals a Relatively Simple Venom in a Diet Generalist, the Northern Short-Tailed Shrew, <i>Blarina brevicauda</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 1148-1166.	1.1	12
3811	Effects of stocking density on the growth performance, physiological response and intestinal microbiota of juvenile <i>Echiura</i> worms (<i>Urechis unicinctus</i>). <i>Aquaculture Research</i> , 2020, 51, 3983-3992.	0.9	8

#	ARTICLE	IF	CITATIONS
3812	Diversity and Function of Endo-Bacteria in <i>Bursaphelenchus xylophilus</i> from <i>Pinus massoniana</i> Lamb. in Different Regions. <i>Forests</i> , 2020, 11, 487.	0.9	10
3813	The circadian disruption of night work alters gut microbiota consistent with elevated risk for future metabolic and gastrointestinal pathology. <i>Chronobiology International</i> , 2020, 37, 1067-1081.	0.9	32
3814	Gut microbiota profiles of commercial laying hens infected with tumorigenic viruses. <i>BMC Veterinary Research</i> , 2020, 16, 218.	0.7	1
3815	Behçet's Disease Under Microbiotic Surveillance? A Combined Analysis of Two Cohorts of Behçet's Disease Patients. <i>Frontiers in Immunology</i> , 2020, 11, 1192.	2.2	28
3816	In silico and empirical evaluation of twelve metabarcoding primer sets for insectivorous diet analyses. <i>Ecology and Evolution</i> , 2020, 10, 6310-6332.	0.8	28
3817	Dried fruit pomace inclusion in poultry diet: growth performance, intestinal morphology and physiology. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 63.	2.1	16
3818	The Effect of Plant Geographical Location and Developmental Stage on Root-Associated Microbiomes of <i>Gymnadenia conopsea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1257.	1.5	30
3819	Variability of Gut Microbiota Across the Life Cycle of <i>Grapholita molesta</i> (Lepidoptera: Tortricidae). <i>Frontiers in Microbiology</i> , 2020, 11, 1366.	1.5	38
3820	Diazotroph Diversity Associated With Scleractinian Corals and Its Relationships With Environmental Variables in the South China Sea. <i>Frontiers in Physiology</i> , 2020, 11, 615.	1.3	8
3821	Recent infection by <i>Wolbachia</i> alters microbial communities in wild <i>Laodelphax striatellus</i> populations. <i>Microbiome</i> , 2020, 8, 104.	4.9	43
3822	Insights into aphid prey consumption by ladybirds: Optimising field sampling methods and primer design for high throughput sequencing. <i>PLoS ONE</i> , 2020, 15, e0235054.	1.1	7
3823	Increased organic fertilizer application and reduced chemical fertilizer application affect the soil properties and bacterial communities of grape rhizosphere soil. <i>Scientific Reports</i> , 2020, 10, 9568.	1.6	77
3824	Complete mitogenome of the noble volute <i>Cymbiola nobilis</i> from the Vietnamese Island of Phú Quốc. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1661-1662.	0.2	0
3825	Effects of bird aggregation on the soil properties and microbial community diversity of urban forest fragments. <i>Science of the Total Environment</i> , 2020, 737, 140250.	3.9	4
3826	Coupling 16S rDNA Sequencing and Untargeted Mass Spectrometry for Milk Microbial Composition and Metabolites from Dairy Cows with Clinical and Subclinical Mastitis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8496-8508.	2.4	22
3827	The Beta-Diversity of <i>Siganus fuscescens</i> -Associated Microbial Communities From Different Habitats Increases With Body Weight. <i>Frontiers in Microbiology</i> , 2020, 11, 1562.	1.5	9
3828	Differential Dynamics of the Ruminal Microbiome of Jersey Cows in a Heat Stress Environment. <i>Animals</i> , 2020, 10, 1127.	1.0	21
3829	Spatiotemporal dynamics of the total and active <i>Vibrio</i> spp. populations throughout the Changjiang estuary in China. <i>Environmental Microbiology</i> , 2020, 22, 4438-4455.	1.8	22

#	ARTICLE	IF	CITATIONS
3830	Fairy rings harbor distinct soil fungal communities and high fungal diversity in a montane grassland. <i>Fungal Ecology</i> , 2020, 47, 100962.	0.7	14
3831	Dynamic distribution of gut microbiota during embryonic development in chicken. <i>Poultry Science</i> , 2020, 99, 5079-5090.	1.5	28
3832	The earliest domestic cat on the Silk Road. <i>Scientific Reports</i> , 2020, 10, 11241.	1.6	9
3833	Co-association of Two nir Denitrifiers Under the Influence of Emergent Macrophytes. <i>Microbial Ecology</i> , 2020, 80, 809-821.	1.4	13
3834	Trichoderma koningiopsis controls Fusarium oxysporum causing damping-off in Pinus massoniana seedlings by regulating active oxygen metabolism, osmotic potential, and the rhizosphere microbiome. <i>Biological Control</i> , 2020, 150, 104352.	1.4	18
3835	CuO Nanoparticles Alter the Rhizospheric Bacterial Community and Local Nitrogen Cycling for Wheat Grown in a Calcareous Soil. <i>Environmental Science & Technology</i> , 2020, 54, 8699-8709.	4.6	65
3836	Acyl homoserine lactone-mediated quorum sensing in the oral cavity: a paradigm revisited. <i>Scientific Reports</i> , 2020, 10, 9800.	1.6	34
3837	Heritability and genome-wide association of swine gut microbiome features with growth and fatness parameters. <i>Scientific Reports</i> , 2020, 10, 10134.	1.6	47
3838	Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. <i>Molecular Biology and Evolution</i> , 2020, 37, 3105-3117.	3.5	20
3839	Culturing Bacteria From Fermentation Pit Muds of Baijiu With Culturomics and Amplicon-Based Metagenomic Approaches. <i>Frontiers in Microbiology</i> , 2020, 11, 1223.	1.5	24
3840	Effects of Fermented Soybean Meal Supplementation on the Growth Performance and Cecal Microbiota Community of Broiler Chickens. <i>Animals</i> , 2020, 10, 1098.	1.0	42
3841	A novel quantitative real-time PCR diagnostic assay for fecal and nasal swab detection of an otariid lungworm, <i>Parafilaroides decorus</i> . <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 12, 85-92.	0.6	4
3842	Diversity hotspot and unique community structure of foraminifera in the world's deepest marine blue hole – Sansha Yongle Blue Hole. <i>Scientific Reports</i> , 2020, 10, 10257.	1.6	14
3843	Metagenomics analysis of fungal communities associated with postharvest diseases in pear fruits under the effect of management practices. <i>Archives of Microbiology</i> , 2020, 202, 2391-2400.	1.0	13
3844	Steel slag and biochar amendments decreased CO ₂ emissions by altering soil chemical properties and bacterial community structure over two-year in a subtropical paddy field. <i>Science of the Total Environment</i> , 2020, 740, 140403.	3.9	30
3845	Macrofaunal control of microbial community structure in continental margin sediments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15911-15922.	3.3	40
3846	Reservoirs of antimicrobial resistance genes in retail raw milk. <i>Microbiome</i> , 2020, 8, 99.	4.9	47
3847	Effects of continuous cropping of sugar beet (<i>Beta vulgaris</i> L.) on its endophytic and soil bacterial community by high-throughput sequencing. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	13

#	ARTICLE	IF	CITATIONS
3848	The Microbiome of <i>Posidonia oceanica</i> Seagrass Leaves Can Be Dominated by Planctomycetes. <i>Frontiers in Microbiology</i> , 2020, 11, 1458.	1.5	40
3849	Microbial Community Composition and Function in Sediments from the Pearl River Mouth Basin. <i>Journal of Ocean University of China</i> , 2020, 19, 941-953.	0.6	12
3850	Dynamics of airborne bacterial community during biofiltration of gases from a swine house. <i>Science of the Total Environment</i> , 2020, 740, 139898.	3.9	8
3851	Preservation of the fecal samples at ambient temperature for microbiota analysis with a cost-effective and reliable stabilizer EfficGut. <i>Science of the Total Environment</i> , 2020, 741, 140423.	3.9	11
3852	Osmotic stress induces gut microbiota community shift in fish. <i>Environmental Microbiology</i> , 2020, 22, 3784-3802.	1.8	31
3853	Fine-scale succession patterns and assembly mechanisms of bacterial community of <i>Litopenaeus vannamei</i> larvae across the developmental cycle. <i>Microbiome</i> , 2020, 8, 106.	4.9	52
3854	A novel approach for the forensic diagnosis of drowning by microbiological analysis with next-generation sequencing and unweighted UniFrac-based PCoA. <i>International Journal of Legal Medicine</i> , 2020, 134, 2149-2159.	1.2	19
3855	Invasive <i>Nicotiana glauca</i> shifts the soil microbial community composition and functioning of harsh and disturbed semiarid Mediterranean environments. <i>Biological Invasions</i> , 2020, 22, 2923-2940.	1.2	8
3856	The environmental contribution to the dissemination of carbapenem and (fluoro)quinolone resistance genes by discharged and reused wastewater effluents: The role of cellular and extracellular DNA. <i>Water Research</i> , 2020, 182, 116011.	5.3	32
3857	The colonic mucosa-associated microbiome in SIV infection: shift towards Bacteroidetes coincides with mucosal CD4+ T cell depletion and enterocyte damage. <i>Scientific Reports</i> , 2020, 10, 10887.	1.6	9
3858	Effects of dietary <i>Hermetia illucens</i> meal inclusion on cecal microbiota and small intestinal mucin dynamics and infiltration with immune cells of weaned piglets. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 64.	2.1	20
3859	Application of biofertilizer containing <i>Bacillus subtilis</i> reduced the nitrogen loss in agricultural soil. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107911.	4.2	80
3860	Comparative evaluation of peptidome and microbiota in different types of saliva samples. <i>Annals of Translational Medicine</i> , 2020, 8, 686-686.	0.7	2
3861	Successive mineral nitrogen or phosphorus fertilization alone significantly altered bacterial community rather than bacterial biomass in plantation soil. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7213-7224.	1.7	12
3862	Integrated genome-wide investigations of the housefly, a global vector of diseases reveal unique dispersal patterns and bacterial communities across farms. <i>BMC Genomics</i> , 2020, 21, 66.	1.2	13
3863	Geographical Isolation, Buried Depth, and Physicochemical Traits Drive the Variation of Species Diversity and Prokaryotic Community in Three Typical Hypersaline Environments. <i>Microorganisms</i> , 2020, 8, 120.	1.6	17
3864	Identification and Quantification of Nonviable <i>Lactobacillus pentosus</i> Cells in a Health Food Product. <i>Journal of AOAC INTERNATIONAL</i> , 2020, 103, 223-226.	0.7	0
3865	Defining endogenous barcoding sites for CRISPR/Cas9-based cell lineage tracing in zebrafish. <i>Journal of Genetics and Genomics</i> , 2020, 47, 85-91.	1.7	8

#	ARTICLE	IF	CITATIONS
3866	Testing the performance of environmental DNA metabarcoding for surveying highly diverse tropical fish communities: A case study from Lake Tanganyika. <i>Environmental DNA</i> , 2020, 2, 24-41.	3.1	38
3867	Novel 28 microsatellite loci using high-throughput sequencing for an endangered species on <i>Metasequoia glyptostroboides</i> (Cupressaceae). <i>Molecular Biology Reports</i> , 2020, 47, 2991-2996.	1.0	0
3868	Response of bacterial communities and plant-mediated soil processes to nitrogen deposition and precipitation in a desert steppe. <i>Plant and Soil</i> , 2020, 448, 277-297.	1.8	23
3869	Immune and gut bacterial successions of large yellow croaker (<i>Larimichthys crocea</i>) during <i>Pseudomonas plecoglossicida</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 99, 176-183.	1.6	20
3870	Taxonomic classification and abundance estimation using 16S and WGS—A comparison using controlled reference samples. <i>Forensic Science International: Genetics</i> , 2020, 46, 102257.	1.6	31
3871	Altered gut microbiota by azithromycin attenuates airway inflammation in allergic asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1466-1469.e8.	1.5	20
3872	Ammonia oxidizers in river sediments of the Qinghai-Tibet Plateau and their adaptations to high-elevation conditions. <i>Water Research</i> , 2020, 173, 115589.	5.3	44
3873	Urbanization drives riverine bacterial antibiotic resistome more than taxonomic community at watershed scale. <i>Environment International</i> , 2020, 137, 105524.	4.8	76
3874	Salmon Gravlox Biopreservation With Lactic Acid Bacteria: A Polyphasic Approach to Assessing the Impact on Organoleptic Properties, Microbial Ecosystem and Volatilome Composition. <i>Frontiers in Microbiology</i> , 2019, 10, 3103.	1.5	35
3875	Rhizobium Inoculation Drives the Shifting of Rhizosphere Fungal Community in a Host Genotype Dependent Manner. <i>Frontiers in Microbiology</i> , 2019, 10, 3135.	1.5	23
3876	The effect of intramammary pirlimycin hydrochloride on the fecal microbiome of early-lactation heifers. <i>Journal of Dairy Science</i> , 2020, 103, 3459-3469.	1.4	0
3877	Interaction of Oral and Toothbrush Microbiota Affects Oral Cavity Health. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 17.	1.8	17
3878	The bacteria from large-sized bioflocs are more associated with the shrimp gut microbiota in culture system. <i>Aquaculture</i> , 2020, 523, 735159.	1.7	48
3879	Effects of a blend of <i>Saccharomyces cerevisiae</i> -based direct-fed microbial and fermentation products on plasma carbonyl-metabolome and fecal bacterial community of beef steers. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 14.	2.1	12
3880	Dietary encapsulated essential oils and organic acids mixture improves gut health in broiler chickens challenged with necrotic enteritis. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 18.	2.1	86
3881	Entomopathogenic nematode-associated microbiota: from monoxenic paradigm to pathobiome. <i>Microbiome</i> , 2020, 8, 25.	4.9	49
3882	Nanoliter-scale next-generation sequencing library-mediated high-throughput 16S rRNA microbial community profiling. <i>BioTechniques</i> , 2020, 68, 204-210.	0.8	1
3883	Pollution Gradients Altered the Bacterial Community Composition and Stochastic Process of Rural Polluted Ponds. <i>Microorganisms</i> , 2020, 8, 311.	1.6	16

#	ARTICLE	IF	CITATIONS
3884	Warming exerts a stronger effect than nitrogen addition on the soil arbuscular mycorrhizal fungal community in a young subtropical <i>Cunninghamia lanceolata</i> plantation. <i>Geoderma</i> , 2020, 367, 114273.	2.3	27
3885	16S rRNA gene sequencing reveals an altered composition of the gut microbiota in chickens infected with a nephropathogenic infectious bronchitis virus. <i>Scientific Reports</i> , 2020, 10, 3556.	1.6	10
3886	Structure, Function, Diversity, and Composition of Fungal Communities in Rhizospheric Soil of <i>Coptis chinensis</i> Franch under a Successive Cropping System. <i>Plants</i> , 2020, 9, 244.	1.6	34
3887	Generating and testing ecological hypotheses at the pondscape with environmental DNA metabarcoding: A case study on a threatened amphibian. <i>Environmental DNA</i> , 2020, 2, 184-199.	3.1	13
3888	Identification of an anaerobic bacterial consortium that degrades roxarsone. <i>MicrobiologyOpen</i> , 2020, 9, e1003.	1.2	5
3889	Bacterioplankton community variation in Bohai Bay (China) is explained by joint effects of environmental and spatial factors. <i>MicrobiologyOpen</i> , 2020, 9, e997.	1.2	12
3890	<i>Nicotiana tabacum</i> seed endophytic communities share a common core structure and genotype-specific signatures in diverging cultivars. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 287-295.	1.9	35
3891	Distinct mechanisms shape soil bacterial and fungal co-occurrence networks in a mountain ecosystem. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	62
3892	Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 8.	2.9	68
3893	Novel <i>Rickettsia</i> genotypes in ticks in French Guiana, South America. <i>Scientific Reports</i> , 2020, 10, 2537.	1.6	13
3894	Contrasting microbiomes of raw and ripened Pu-erh tea associated with distinct chemical profiles. <i>LWT - Food Science and Technology</i> , 2020, 124, 109147.	2.5	11
3895	Molecular diversity and spatial distribution of benthic foraminifera of the seamounts and adjacent abyssal plains in the tropical Western Pacific Ocean. <i>Marine Micropaleontology</i> , 2020, 156, 101850.	0.5	10
3896	Differentiation strategies of soil rare and abundant microbial taxa in response to changing climatic regimes. <i>Environmental Microbiology</i> , 2020, 22, 1327-1340.	1.8	164
3897	Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. <i>Gut</i> , 2020, 69, 1218-1228.	6.1	465
3898	Sowing Methods Influence Soil Bacterial Diversity and Community Composition in a Winter Wheat-Summer Maize Rotation System on the Loess Plateau. <i>Frontiers in Microbiology</i> , 2020, 11, 192.	1.5	10
3899	Effect of inclusion of HMBi in the ration of goats on feed intake, nutrient digestibility, rumen bacteria community and blood serum parameters. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2020, 104, 987-997.	1.0	11
3900	Nitrate Stabilizes the Rhizospheric Fungal Community to Suppress <i>Fusarium</i> Wilt Disease in Cucumber. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 590-599.	1.4	17
3901	Comparative study on archaeal diversity in the sediments of two urban landscape water bodies. <i>PLoS ONE</i> , 2020, 15, e0229097.	1.1	1

#	ARTICLE	IF	CITATIONS
3902	Long-Term Effects of Multi-Drug-Resistant Tuberculosis Treatment on Gut Microbiota and Its Health Consequences. <i>Frontiers in Microbiology</i> , 2020, 11, 53.	1.5	32
3903	<i>Myzus persicae</i> (Hemiptera: Aphididae) infestation increases the risk of bacterial contamination and alters nutritional content in storage Chinese cabbage. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 3007-3012.	1.7	4
3904	Using high-throughput sequencing quantitatively to investigate soil nematode community composition in a steppe-forest ecotone. <i>Applied Soil Ecology</i> , 2020, 152, 103562.	2.1	38
3905	Rice waste biochars produced at different pyrolysis temperatures for arsenic and cadmium abatement and detoxification in sediment. <i>Chemosphere</i> , 2020, 250, 126268.	4.2	56
3906	Supplementation with nanobubble water alleviates obesity-associated markers through modulation of gut microbiota in high-fat diet fed mice. <i>Journal of Functional Foods</i> , 2020, 67, 103820.	1.6	10
3907	The effect of plant compartments on the <i>Broussonetia papyrifera</i> -associated fungal and bacterial communities. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 3627-3641.	1.7	16
3908	Dissipation of S-metolachlor and butachlor in agricultural soils and responses of bacterial communities: Insights from compound-specific isotope and biomolecular analyses. <i>Journal of Environmental Sciences</i> , 2020, 92, 163-175.	3.2	26
3909	Microbial Community and Its Association With Physicochemical Factors During Compost Bedding for Dairy Cows. <i>Frontiers in Microbiology</i> , 2020, 11, 254.	1.5	28
3910	Bioprospecting potential of microbial communities in solid waste landfills for novel enzymes through metagenomic approach. <i>World Journal of Microbiology and Biotechnology</i> , 2020, 36, 34.	1.7	25
3911	Industrial development as a key factor explaining variances in soil and grass phyllosphere microbiomes in urban green spaces. <i>Environmental Pollution</i> , 2020, 261, 114201.	3.7	19
3912	Characterization of the microbial communities and their correlations with chemical profiles in assorted vegetable Sichuan pickles. <i>Food Control</i> , 2020, 113, 107174.	2.8	55
3913	Role of microbial diversity for sustainable pyrite oxidation control in acid and metalliferous drainage prevention. <i>Journal of Hazardous Materials</i> , 2020, 393, 122338.	6.5	19
3914	Viable bacterial colonization is highly limited in the human intestine in utero. <i>Nature Medicine</i> , 2020, 26, 599-607.	15.2	180
3915	Fecal bacteria and metabolite responses to dietary lysozyme in a sow model from late gestation until lactation. <i>Scientific Reports</i> , 2020, 10, 3210.	1.6	13
3916	Bacterial community responses to tourism development in the Xixi National Wetland Park, China. <i>Science of the Total Environment</i> , 2020, 720, 137570.	3.9	40
3917	Roles of Organic Matter-Induced Heterotrophic Bacteria in Nitrification Reactors: Ammonium Removal and Bacterial Interactions. <i>ACS Sustainable Chemistry and Engineering</i> , 2020, 8, 3976-3985.	3.2	17
3918	<i>Ganoderma lucidum</i> cultivation affect microbial community structure of soil, wood segments and tree roots. <i>Scientific Reports</i> , 2020, 10, 3435.	1.6	16
3919	Draft Genome Sequences of <i>Leptospira interrogans</i> Serovar Copenhageni Strains Isolated from Patients with Weil's Disease in Brazil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0

#	ARTICLE	IF	CITATIONS
3920	Profiling the urinary microbiome in men with calcium-based kidney stones. <i>BMC Microbiology</i> , 2020, 20, 41.	1.3	42
3921	The canine oral microbiome: variation in bacterial populations across different niches. <i>BMC Microbiology</i> , 2020, 20, 42.	1.3	41
3922	Pyrodextrin enhances intestinal function through changing the intestinal microbiota composition and metabolism in early weaned piglets. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4141-4154.	1.7	18
3923	Cyanobacteria in an urban lake: hidden diversity revealed by metabarcoding. <i>Aquatic Ecology</i> , 2020, 54, 671-675.	0.7	3
3924	Assembly and shifts of the bacterial rhizobiome of field grown transgenic maize line carrying mcrY1Ab and mcrY2Ab genes at different developmental stages. <i>Plant Growth Regulation</i> , 2020, 91, 113-126.	1.8	8
3925	Distribution characteristics of fungal communities with depth in paddy fields of three soil types in China. <i>Journal of Microbiology</i> , 2020, 58, 279-287.	1.3	10
3926	Application of enhanced bioreduction for hexavalent chromium-polluted groundwater cleanup: Microcosm and microbial diversity studies. <i>Environmental Research</i> , 2020, 184, 109296.	3.7	18
3927	Amino acid and microbial community dynamics during the fermentation of Hong Qu glutinous rice wine. <i>Food Microbiology</i> , 2020, 90, 103467.	2.1	45
3928	Variations in the gut microbiota of sympatric <i>Presbytis</i> langurs and rhesus macaques living in limestone forests in southwest Guangxi, China. <i>Global Ecology and Conservation</i> , 2020, 22, e00929.	1.0	14
3929	Effects of <i>Eimeria tenella</i> infection on the barrier damage and microbiota diversity of chicken cecum. <i>Poultry Science</i> , 2020, 99, 1297-1305.	1.5	34
3930	Long-term performance and microbial community characteristics of pilot-scale anaerobic reactors for thermal hydrolyzed sludge digestion under mesophilic and thermophilic conditions. <i>Science of the Total Environment</i> , 2020, 720, 137566.	3.9	27
3931	Decoupled diversity patterns in bacteria and fungi across continental forest ecosystems. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107763.	4.2	78
3932	The Removal of Antibiotics in Relation to a Microbial Community in an Integrated Constructed Wetland for Tail Water Decontamination. <i>Wetlands</i> , 2020, 40, 993-1004.	0.7	14
3933	The first glimpse of the endometrial microbiota in early pregnancy. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, 296-305.	0.7	40
3934	The Influence of Land Use Patterns on Soil Bacterial Community Structure in the Karst Graben Basin of Yunnan Province, China. <i>Forests</i> , 2020, 11, 51.	0.9	18
3935	Bacteriophages Isolated from Stunted Children Can Regulate Gut Bacterial Communities in an Age-Specific Manner. <i>Cell Host and Microbe</i> , 2020, 27, 199-212.e5.	5.1	85
3936	Gut Microbiota Plasticity Influences the Adaptability of Wild and Domestic Animals in Co-inhabited Areas. <i>Frontiers in Microbiology</i> , 2020, 11, 125.	1.5	23
3937	The profile of antibiotic resistance genes in pig manure composting shaped by composting stage: Mesophilic-thermophilic and cooling-maturation stages. <i>Chemosphere</i> , 2020, 250, 126181.	4.2	65

#	ARTICLE	IF	CITATIONS
3938	Two-year study of biochar: Achieving excellent capability of potassium supply via alter clay mineral composition and potassium-dissolving bacteria activity. <i>Science of the Total Environment</i> , 2020, 717, 137286.	3.9	43
3939	Characterization of Microbial Communities in <i>Ixodes persulcatus</i> (Ixodida: Ixodidae), a Veterinary and Medical Important Tick Species in Northeastern China. <i>Journal of Medical Entomology</i> , 2020, 57, 1270-1276.	0.9	4
3940	Sludge retention time affects the microbial community structure: A large-scale sampling of aeration tanks throughout China. <i>Environmental Pollution</i> , 2020, 261, 114140.	3.7	35
3941	Characterization of the microbial community composition in Italian Cinta Senese sausages dry-fermented with natural extracts as alternatives to sodium nitrite. <i>Food Microbiology</i> , 2020, 89, 103417.	2.1	37
3942	Effects of dietary <i>Radix Rehmanniae Preparata</i> polysaccharides on the digestive enzymes, morphology, microbial communities and mucosal barrier function of the intestine of <i>Luciobarbus capito</i> . <i>Aquaculture Research</i> , 2020, 51, 1026-1037.	0.9	7
3943	Instances of altered gut microbiomes among Irish cricketers over periods of travel in the lead up to the 2016 World Cup: A sequencing analysis. <i>Travel Medicine and Infectious Disease</i> , 2020, 35, 101553.	1.5	11
3944	Characterization and Analysis of the Skin Microbiota in Acne: Impact of Systemic Antibiotics. <i>Journal of Clinical Medicine</i> , 2020, 9, 168.	1.0	37
3945	Characterization and Analysis of the Skin Microbiota in Rosacea: Impact of Systemic Antibiotics. <i>Journal of Clinical Medicine</i> , 2020, 9, 185.	1.0	46
3946	Water dynamics and microbial communities of bigeye tuna (<i>Thunnus obesus</i>) during simulated cold chain logistics. <i>Journal of Food Safety</i> , 2020, 40, e12766.	1.1	4
3947	Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. <i>Microbiome</i> , 2020, 8, 3.	4.9	75
3948	Addition of fructose to the maize rhizosphere increases phosphatase activity by changing bacterial community structure. <i>Soil Biology and Biochemistry</i> , 2020, 142, 107724.	4.2	30
3949	Fertilization regime has a greater effect on soil microbial community structure than crop rotation and growth stage in an agroecosystem. <i>Applied Soil Ecology</i> , 2020, 149, 103510.	2.1	82
3950	The effect of different doses of ozone treatments on the postharvest quality and biodiversity of cantaloupes. <i>Postharvest Biology and Technology</i> , 2020, 163, 111124.	2.9	35
3951	Antibiotic resistome associated with microbial communities in an integrated wastewater reclamation system. <i>Water Research</i> , 2020, 173, 115541.	5.3	53
3952	Geographic Patterns of Bacterioplankton among Lakes of the Middle and Lower Reaches of the Yangtze River Basin, China. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	25
3953	Ionic Liquid Enriches the Antibiotic Resistome, Especially Efflux Pump Genes, Before Significantly Affecting Microbial Community Structure. <i>Environmental Science & Technology</i> , 2020, 54, 4305-4315.	4.6	21
3954	Transcript specific regulation of expression influences susceptibility to multiple sclerosis. <i>European Journal of Human Genetics</i> , 2020, 28, 826-834.	1.4	10
3955	Who is eating fructose within the <i>Aedes albopictus</i> gut microbiota?. <i>Environmental Microbiology</i> , 2020, 22, 1193-1206.	1.8	22

#	ARTICLE	IF	CITATIONS
3956	The fungal community and its interaction with the concentration of short-chain fatty acids in the caecum and colon of weaned piglets. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2020, 104, 616-628.	1.0	9
3957	Absolute quantitation of microbes using 16S rRNA gene metabarcoding: A rapid normalization of relative abundances by quantitative PCR targeting a 16S rRNA gene spike-in standard. <i>MicrobiologyOpen</i> , 2020, 9, e977.	1.2	43
3958	Progesterone Receptor Gene Variants in Metastatic Estrogen Receptor Positive Breast Cancer. <i>Hormones and Cancer</i> , 2020, 11, 63-75.	4.9	13
3959	Characterization of tetracycline effects on microbial community, antibiotic resistance genes and antibiotic resistance of <i>Aeromonas</i> spp. in gut of goldfish <i>Carassius auratus</i> Linnaeus. <i>Ecotoxicology and Environmental Safety</i> , 2020, 191, 110182.	2.9	39
3960	Response of bacterial communities from Kongsfjorden (Svalbard, Arctic Ocean) to macroalgal polysaccharide amendments. <i>Marine Environmental Research</i> , 2020, 155, 104874.	1.1	26
3961	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	4.4	135
3962	The variability of bacterial communities in both the endosphere and ectosphere of different niches in Chinese chives (<i>Allium tuberosum</i>). <i>PLoS ONE</i> , 2020, 15, e0227671.	1.1	7
3963	The effect of environmental heterogeneity on the fitness of antibiotic resistance mutations in <i>Escherichia coli</i> . <i>Evolutionary Ecology</i> , 2020, 34, 379-390.	0.5	13
3964	Topical ozone therapy restores microbiome diversity in atopic dermatitis. <i>International Immunopharmacology</i> , 2020, 80, 106191.	1.7	32
3965	An RNA polymerase ribozyme that synthesizes its own ancestor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2906-2913.	3.3	81
3966	The dynamics of bacterial community in a polyculture aquaculture system of <i>Penaeus chinensis</i> , <i>Rhopilema esculenta</i> and <i>Sinonovacula constricta</i> . <i>Aquaculture Research</i> , 2020, 51, 1789-1800.	0.9	18
3967	New microsatellite markers for <i>Dacryodes edulis</i> (Burseraceae), an indigenous fruit tree species from Central Africa. <i>Molecular Biology Reports</i> , 2020, 47, 2391-2396.	1.0	6
3968	Prenatal exposure to glufosinate ammonium disturbs gut microbiome and induces behavioral abnormalities in mice. <i>Journal of Hazardous Materials</i> , 2020, 389, 122152.	6.5	25
3969	Legacy effects of 8-year nitrogen inputs on bacterial assemblage in wheat rhizosphere. <i>Biology and Fertility of Soils</i> , 2020, 56, 583-596.	2.3	35
3970	A more pronounced effect of type III resistant starch vs. type II resistant starch on ameliorating hyperlipidemia in high fat diet-fed mice is associated with its supramolecular structural characteristics. <i>Food and Function</i> , 2020, 11, 1982-1995.	2.1	45
3971	Consensify: A Method for Generating Pseudohaploid Genome Sequences from Palaeogenomic Datasets with Reduced Error Rates. <i>Genes</i> , 2020, 11, 50.	1.0	15
3972	Revealing the Variation and Stability of Bacterial Communities in Tomato Rhizosphere Microbiota. <i>Microorganisms</i> , 2020, 8, 170.	1.6	57
3973	A pregnancy complication-dependent change in SigA-targeted microbiota during third trimester. <i>Food and Function</i> , 2020, 11, 1513-1524.	2.1	23

#	ARTICLE	IF	CITATIONS
3974	CRISPR/Cas9-mediated precise genome modification by a long ssDNA template in zebrafish. <i>BMC Genomics</i> , 2020, 21, 67.	1.2	45
3975	Effects of oregano essential oil on in vitro ruminal fermentation, methane production, and ruminal microbial community. <i>Journal of Dairy Science</i> , 2020, 103, 2303-2314.	1.4	59
3976	A Human Lung-Associated <i>Streptomyces</i> sp. TR1341 Produces Various Secondary Metabolites Responsible for Virulence, Cytotoxicity and Modulation of Immune Response. <i>Frontiers in Microbiology</i> , 2019, 10, 3028.	1.5	20
3977	Chemical Profile, Antioxidative, and Gut Microbiota Modulatory Properties of Ganpu Tea: A Derivative of Pu-erh Tea. <i>Nutrients</i> , 2020, 12, 224.	1.7	37
3978	Enhancement of tribromophenol removal in a sequencing batch reactor via submicron magnetite. <i>Bioprocess and Biosystems Engineering</i> , 2020, 43, 851-861.	1.7	8
3979	Interannual climate variability and altered precipitation influence the soil microbial community structure in a Tibetan Plateau grassland. <i>Science of the Total Environment</i> , 2020, 714, 136794.	3.9	69
3980	Deficiency of Gankyrin in the small intestine is associated with augmented colitis accompanied by altered bacterial composition of intestinal microbiota. <i>BMC Gastroenterology</i> , 2020, 20, 12.	0.8	3
3981	Microbial Community Analysis of Digested Liquids Exhibiting Different Methane Production Potential in Methane Fermentation of Swine Feces. <i>Applied Biochemistry and Biotechnology</i> , 2020, 191, 1140-1154.	1.4	2
3982	Long-term phosphorus deficiency decreased bacterial-fungal network complexity and efficiency across three soil types in China as revealed by network analysis. <i>Applied Soil Ecology</i> , 2020, 148, 103506.	2.1	34
3983	Root tip cutting and uniconazole treatment improve the colonization rate of <i>Tuber indicum</i> on <i>Pinus armandii</i> seedlings in the greenhouse. <i>Microbial Biotechnology</i> , 2020, 13, 535-547.	2.0	10
3984	<i>Casimicrobium huifangae</i> gen. nov., sp. nov., a Ubiquitous "Most-Wanted" Core Bacterial Taxon from Municipal Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	26
3985	Trimethylamine abatement in algal-bacterial photobioreactors. <i>Environmental Science and Pollution Research</i> , 2020, 27, 9028-9037.	2.7	3
3986	Arbuscular mycorrhizal fungi biofertilizer improves American ginseng (<i>Panax quinquefolius</i> L.) growth under the continuous cropping regime. <i>Geoderma</i> , 2020, 363, 114155.	2.3	65
3987	Response of the <i>Litopenaeus vananmei</i> intestinal bacteria and antioxidant system to rearing density and exposure to <i>Vibrio parahaemolyticus</i> E1. <i>Journal of Invertebrate Pathology</i> , 2020, 170, 107326.	1.5	7
3988	Gut microbiota profiles in critically ill patients, potential biomarkers and risk variables for sepsis. <i>Gut Microbes</i> , 2020, 12, 1707610.	4.3	84
3989	Gut microbiota modulation and immunity response induced by <i>Citrobacter freundii</i> strain GC01 in grass carp (<i>Ctenopharyngodon idellus</i>). <i>Aquaculture</i> , 2020, 521, 735015.	1.7	20
3990	Gut microbiota composition after diet and probiotics in overweight breast cancer survivors: a randomized open-label pilot intervention trial. <i>Nutrition</i> , 2020, 74, 110749.	1.1	38
3991	Nitrospira bacteria in paddy soil reduced by biochar application. , 2020, 3, e20009.		4

#	ARTICLE	IF	CITATIONS
3992	Insight into the assembly of root-associated microbiome in the medicinal plant <i>Polygonum cuspidatum</i> . <i>Industrial Crops and Products</i> , 2020, 145, 112163.	2.5	38
3993	Invasion by the weed <i>Conyza canadensis</i> alters soil nutrient supply and shifts microbiota structure. <i>Soil Biology and Biochemistry</i> , 2020, 143, 107739.	4.2	58
3994	Free nitrous acid-based suppression of sulfide production in sewer sediments: In-situ effect mechanism. <i>Science of the Total Environment</i> , 2020, 715, 136871.	3.9	17
3995	Combined Application of High-Throughput Sequencing and Metabolomics Reveals Metabolically Active Microorganisms During Panxian Ham Processing. <i>Frontiers in Microbiology</i> , 2019, 10, 3012.	1.5	39
3996	The fate of cigarette butts in different environments: Decay rate, chemical changes and ecotoxicity revealed by a 5-years decomposition experiment. <i>Environmental Pollution</i> , 2020, 261, 114108.	3.7	55
3997	Maize (<i>Zea mays</i> L. Sp.) varieties significantly influence bacterial and fungal community in bulk soil, rhizosphere soil and phyllosphere. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	35
3998	Respiratory dysbiosis and population-wide temporal dynamics in canine chronic bronchitis and non-inflammatory respiratory disease. <i>PLoS ONE</i> , 2020, 15, e0228085.	1.1	6
3999	Characterization of Anaerobic Rumen Fungal Community Composition in Yak, Tibetan Sheep and Small Tail Han Sheep Grazing on the Qinghai-Tibetan Plateau. <i>Animals</i> , 2020, 10, 144.	1.0	18
4000	Gut Microbiota as Diagnostic Tools for Mirroring Disease Progression and Circulating Nephrotoxin Levels in Chronic Kidney Disease: Discovery and Validation Study. <i>International Journal of Biological Sciences</i> , 2020, 16, 420-434.	2.6	64
4001	Non-essentiality of canonical cell division genes in the planctomycete <i>Planctopirus limnophila</i> . <i>Scientific Reports</i> , 2020, 10, 66.	1.6	26
4002	Black soldier fly and gut health in broiler chickens: insights into the relationship between cecal microbiota and intestinal mucin composition. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 11.	2.1	56
4003	Shifts in microbial communities and networks are correlated with the soil ionome in a kiwifruit orchard under different fertilization regimes. <i>Applied Soil Ecology</i> , 2020, 149, 103517.	2.1	24
4004	“Frozen evolution” of an RNA virus suggests accidental release as a potential cause of arbovirus re-emergence. <i>PLoS Biology</i> , 2020, 18, e3000673.	2.6	15
4005	Novel Aptamers Selected on Living Cells for Specific Recognition of Triple-Negative Breast Cancer. <i>IScience</i> , 2020, 23, 100979.	1.9	19
4006	High L-Carnitine Ingestion Impairs Liver Function by Disordering Gut Bacteria Composition in Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 5707-5714.	2.4	12
4007	Influenza infection elicits an expansion of gut population of endogenous <i>Bifidobacterium animalis</i> which protects mice against infection. <i>Genome Biology</i> , 2020, 21, 99.	3.8	73
4008	Microeukaryote communities exhibit phyla-specific distance-decay patterns and an intimate link between seawater and sediment habitats in the Western Pacific Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 160, 103279.	0.6	15
4009	Analysis of the bacterial floral structure and diversity of Xuanwei ham by 16S rDNA sequencing. <i>Journal of Food Safety</i> , 2020, 40, e12800.	1.1	5

#	ARTICLE	IF	CITATIONS
4010	Plant Virus Genome Is Shaped by Specific Dinucleotide Restrictions That Influence Viral Infection. <i>MBio</i> , 2020, 11, .	1.8	12
4011	Major Metabolites and Microbial Community of Fermented Black Glutinous Rice Wine With Different Starters. <i>Frontiers in Microbiology</i> , 2020, 11, 593.	1.5	47
4012	Effects of Carbon/Nitrogen Ratio on Growth, Intestinal Microbiota and Metabolome of Shrimp (<i>Litopenaeus vannamei</i>). <i>Frontiers in Microbiology</i> , 2020, 11, 652.	1.5	32
4013	Host Plants Influence the Symbiont Diversity of Eriosomatinae (Hemiptera: Aphididae). <i>Insects</i> , 2020, 11, 217.	1.0	14
4014	Molecular characterization of gut microbial shift in SD rats after death for 30 days. <i>Archives of Microbiology</i> , 2020, 202, 1763-1773.	1.0	15
4015	Dual oxidase Duox and Toll-like receptor 3 TLR3 in the Toll pathway suppress zoonotic pathogens through regulating the intestinal bacterial community homeostasis in <i>Hermetia illucens</i> L.. <i>PLoS ONE</i> , 2020, 15, e0225873.	1.1	19
4016	Biodegradation of low molecular weight polyacrylamide under aerobic and anaerobic conditions: effect of the molecular weight. <i>Water Science and Technology</i> , 2020, 81, 301-308.	1.2	8
4017	Compared to conventional, ecological intensive management promotes beneficial proteolytic soil microbial communities for agro-ecosystem functioning under climate change-induced rain regimes. <i>Scientific Reports</i> , 2020, 10, 7296.	1.6	14
4018	In Human Autoimmunity, a Substantial Component of the B Cell Repertoire Consists of Polyclonal, Barely Mutated IgG+ve B Cells. <i>Frontiers in Immunology</i> , 2020, 11, 395.	2.2	16
4019	The effects of eight years of conservation tillage on the soil physicochemical properties and bacterial communities in a rainfed agroecosystem of the loess plateau, China. <i>Land Degradation and Development</i> , 2020, 31, 2475-2489.	1.8	16
4020	Porcine deltacoronavirus infection alters bacterial communities in the colon and feces of neonatal piglets. <i>MicrobiologyOpen</i> , 2020, 9, e1036.	1.2	16
4021	Influence of electron acceptor availability and microbial community structure on sedimentary methane oxidation in a boreal estuary. <i>Biogeochemistry</i> , 2020, 148, 291-309.	1.7	28
4022	The invasion of semiarid Mediterranean sites by <i>Nicotiana glauca</i> mediates temporary changes in mycorrhizal associations and a permanent decrease in rhizosphere activity. <i>Plant and Soil</i> , 2020, 450, 217-229.	1.8	10
4023	The oral microbiome profile and biomarker in Chinese type 2 diabetes mellitus patients. <i>Endocrine</i> , 2020, 68, 564-572.	1.1	29
4024	Effects of corn starch level on growth performance, antioxidant capacity, gut morphology and intestinal microflora of juvenile golden pompano, <i>Trachinotus ovatus</i> . <i>Aquaculture</i> , 2020, 524, 735197.	1.7	50
4025	The effect of <i>Lactobacillus plantarum</i> administration on the intestinal microbiota of whiteleg shrimp <i>Penaeus vannamei</i> . <i>Aquaculture</i> , 2020, 526, 735331.	1.7	50
4026	Investigating the composition and distribution of microplastics surface biofilms in coral areas. <i>Chemosphere</i> , 2020, 252, 126565.	4.2	88
4027	Discovering microbiota and volatile compounds of surströmming, the traditional Swedish sour herring. <i>Food Microbiology</i> , 2020, 91, 103503.	2.1	37

#	ARTICLE	IF	CITATIONS
4028	Dietary <i>Luffa cylindrica</i> (L.) Roem promotes branched-chain amino acid catabolism in the circulation system via gut microbiota in diet-induced obese mice. <i>Food Chemistry</i> , 2020, 320, 126648.	4.2	36
4029	Revealing structure and assembly for rhizophyte-endophyte diazotrophic community in mangrove ecosystem after introduced <i>Sonneratia apetala</i> and <i>Laguncularia racemosa</i> . <i>Science of the Total Environment</i> , 2020, 721, 137807.	3.9	35
4030	Structural and functional responses of bacterial and fungal communities to multiple heavy metal exposure in arid loess. <i>Science of the Total Environment</i> , 2020, 723, 138081.	3.9	89
4031	Biotransformation of Tris(2-chloroethyl) Phosphate (TCEP) in Sediment Microcosms and the Adaptation of Microbial Communities to TCEP. <i>Environmental Science & Technology</i> , 2020, 54, 5489-5497.	4.6	27
4032	Biogeography and Assembly of Microbial Communities in Wastewater Treatment Plants in China. <i>Environmental Science & Technology</i> , 2020, 54, 5884-5892.	4.6	34
4033	Gut, oral and skin microbiome of Indian patrilineal families reveal perceptible association with age. <i>Scientific Reports</i> , 2020, 10, 5685.	1.6	50
4034	Larval density affects phenotype and surrounding bacterial community without altering gut microbiota in <i>Drosophila melanogaster</i> . <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	16
4035	Plant nutrient acquisition strategies drive topsoil microbiome structure and function. <i>New Phytologist</i> , 2020, 227, 1189-1199.	3.5	96
4036	A Mediterranean Diet Intervention Reduces the Levels of Salivary Periodontopathogenic Bacteria in Overweight and Obese Subjects. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	30
4037	Tracking the Dairy Microbiota from Farm Bulk Tank to Skimmed Milk Powder. <i>MSystems</i> , 2020, 5, .	1.7	45
4038	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	1.7	81
4039	Insights into the Microbiological Safety of Wooden Cutting Boards Used for Meat Processing in Hong Kong's Wet Markets: A Focus on Food-Contact Surfaces, Cross-Contamination and the Efficacy of Traditional Hygiene Practices. <i>Microorganisms</i> , 2020, 8, 579.	1.6	18
4040	Impact of feeding regimens on the composition of gut microbiota and metabolite profiles of plasma and feces from Mongolian sheep. <i>Journal of Microbiology</i> , 2020, 58, 472-482.	1.3	19
4041	The Gene Catalog and Comparative Analysis of Gut Microbiome of Big Cats Provide New Insights on Panthera Species. <i>Frontiers in Microbiology</i> , 2020, 11, 1012.	1.5	9
4042	TALEN mediated gene editing in a mouse model of Fanconi anemia. <i>Scientific Reports</i> , 2020, 10, 6997.	1.6	3
4043	Assessing Chromium Contamination in Red Soil: Monitoring the Migration of Fractions and the Change of Related Microorganisms. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 2835.	1.2	10
4044	First Gut Content Analysis of 4th Instar Midge Larvae (Diptera: Chronomidae) In Large-Scale Weirs Using a DNA Meta-Barcoding Approach. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 2856.	1.2	8
4045	Deep tillage combined with biofertilizer following soil fumigation improved chrysanthemum growth by regulating the soil microbiome. <i>MicrobiologyOpen</i> , 2020, 9, e1045.	1.2	12

#	ARTICLE	IF	CITATIONS
4046	Microbial community overlap between the phyllosphere and rhizosphere of three plants from Yongxing Island, South China Sea. <i>MicrobiologyOpen</i> , 2020, 9, e1048.	1.2	18
4047	Changes in the gut microbiota of honey bees associated with jujube flower disease. <i>Ecotoxicology and Environmental Safety</i> , 2020, 198, 110616.	2.9	6
4048	Executing multi-taxa eDNA ecological assessment via traditional metrics and interactive networks. <i>Science of the Total Environment</i> , 2020, 729, 138801.	3.9	51
4049	Microbial Diversity and Physicochemical Characteristics of the Maotai-Flavored Liquor Fermentation Process. <i>Journal of Nanoscience and Nanotechnology</i> , 2020, 20, 4097-4109.	0.9	26
4050	Chinese Liquor Fermentation: Identification of Key Flavor-Producing <i>Lactobacillus</i> spp. by Quantitative Profiling with Indigenous Internal Standards. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	41
4051	Attenuated <i>Lactococcus lactis</i> and Surface Bacteria as Tools for Conditioning the Microbiota and Driving the Ripening of Semisoft Caciotta Cheese. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	13
4052	Comparison of the ruminal and fecal microbiotas in beef calves supplemented or not with concentrate. <i>PLoS ONE</i> , 2020, 15, e0231533.	1.1	56
4053	Salivary Microbiota Shifts under Sustained Consumption of Oolong Tea in Healthy Adults. <i>Nutrients</i> , 2020, 12, 966.	1.7	7
4054	Distinct lung microbial community states in patients with pulmonary tuberculosis. <i>Science China Life Sciences</i> , 2020, 63, 1522-1533.	2.3	18
4055	Metagenome sequencing to unveil the resistome in a deep subtropical lake on the Yunnan-Guizhou Plateau, China. <i>Environmental Pollution</i> , 2020, 263, 114470.	3.7	47
4056	Comparative analysis of the total and active bacterial communities in the surface sediment of Lake Taihu. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	8
4057	Convergent evolution of seasonal camouflage in response to reduced snow cover across the snowshoe hare range*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 2033-2045.	1.1	19
4058	Antimicrobial peptide and sequence variation along a latitudinal gradient in two anurans. <i>BMC Genetics</i> , 2020, 21, 38.	2.7	6
4059	Closely Located but Totally Distinct: Highly Contrasting Prokaryotic Diversity Patterns in Raised Bogs and Eutrophic Fens. <i>Microorganisms</i> , 2020, 8, 484.	1.6	25
4060	Simulated nitrogen deposition decreases soil microbial diversity in a semiarid grassland, with little mediation of this effect by mowing. <i>Pedobiologia</i> , 2020, 80, 150644.	0.5	14
4061	Analysis of endophytic and rhizosphere bacterial diversity and function in the endangered plant <i>Paeonia ludlowii</i> . <i>Archives of Microbiology</i> , 2020, 202, 1717-1728.	1.0	19
4062	Variation in soil microbial communities: elucidating relationships with vegetation and soil properties, and testing sampling effectiveness. <i>Plant Ecology</i> , 2020, 221, 837-851.	0.7	13
4063	Biotransformation of the herbicide nicosulfuron residues in soil and seven sulfonylurea herbicides by <i>Bacillus subtilis</i> YB1: A climate chamber study. <i>Environmental Pollution</i> , 2020, 263, 114492.	3.7	23

#	ARTICLE	IF	CITATIONS
4064	Increased arsenic mobilization in the rice rhizosphere is mediated by iron-reducing bacteria. <i>Environmental Pollution</i> , 2020, 263, 114561.	3.7	35
4065	Gut microbiota suggests dependency of Arunachal Macaque (<i>Macaca munzala</i>) on anthropogenic food in Western Arunachal Pradesh, Northeastern India: Preliminary findings. <i>Global Ecology and Conservation</i> , 2020, 22, e01030.	1.0	4
4066	<i>Alienimonas chondri</i> sp. nov., a novel planctomycete isolated from the biofilm of the red alga <i>Chondrus crispus</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126083.	1.2	17
4067	Different community assembly mechanisms underlie similar biogeography of bacteria and microeukaryotes in Tibetan lakes. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	43
4068	Revegetation of urban green space rewilds soil microbiotas with implications for human health and urban design. <i>Restoration Ecology</i> , 2020, 28, S322.	1.4	43
4069	The pH-based ecological coherence of active canonical methanotrophs in paddy soils. <i>Biogeosciences</i> , 2020, 17, 1451-1462.	1.3	22
4070	Spatial Patterns of Soil Fungal Communities Are Driven by Dissolved Organic Matter (DOM) Quality in Semi-Arid Regions. <i>Microbial Ecology</i> , 2021, 82, 202-214.	1.4	18
4071	Identifying Potential Polymicrobial Pathogens: Moving Beyond Differential Abundance to Driver Taxa. <i>Microbial Ecology</i> , 2020, 80, 447-458.	1.4	26
4072	The effect of antibiotic cocktails on host immune status is dynamic and does not always correspond to changes in gut microbiota. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4995-5009.	1.7	17
4073	Comparison of the Rhizosphere Soil Microbial Community Structure and Diversity Between Powdery Mildew-Infected and Noninfected Strawberry Plants in a Greenhouse by High-Throughput Sequencing Technology. <i>Current Microbiology</i> , 2020, 77, 1724-1736.	1.0	18
4074	High heterogeneity of bacterioplankton community shaped by spatially structured environmental factors in West Lake, a typical urban lake in eastern China. <i>Environmental Science and Pollution Research</i> , 2020, 27, 42283-42293.	2.7	7
4075	DNA Methylation Analysis of the NR3C1 Gene in Patients with Schizophrenia. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1177-1185.	1.1	17
4076	Interactions between social groups of colobus monkeys (<i>Colobus vellerosus</i>) explain similarities in their gut microbiomes. <i>Animal Behaviour</i> , 2020, 163, 17-31.	0.8	30
4077	Effects of protein restriction on performance, ruminal fermentation and microbial community in Holstein bulls fed high-concentrate diets. <i>Animal Feed Science and Technology</i> , 2020, 264, 114479.	1.1	9
4078	A meta-analysis of microbial community structures and associated metabolic potential of municipal wastewater treatment plants in global scope. <i>Environmental Pollution</i> , 2020, 263, 114598.	3.7	33
4079	Fecal-associated microbiome differences between traditional Chinese medicine qi-deficiency and balanced constitutions. <i>Journal of Traditional Chinese Medical Sciences</i> , 2020, 7, 104-113.	0.1	0
4080	Biodegradation of weathered crude oil in seawater with frazil ice. <i>Marine Pollution Bulletin</i> , 2020, 154, 111090.	2.3	10
4081	Probiotics and fructo-oligosaccharide intervention modulate the microbiota-gut brain axis to improve autism spectrum reducing also the hyper-serotonergic state and the dopamine metabolism disorder. <i>Pharmacological Research</i> , 2020, 157, 104784.	3.1	135

#	ARTICLE	IF	CITATIONS
4082	Mulching practices alter the bacterial-fungal community and network in favor of soil quality in a semiarid orchard system. <i>Science of the Total Environment</i> , 2020, 725, 138527.	3.9	70
4083	Microbes changed their carbon use strategy to regulate the priming effect in an 11-year nitrogen addition experiment in grassland. <i>Science of the Total Environment</i> , 2020, 727, 138645.	3.9	29
4084	Biogeography and emerging significance of Actinobacteria in Australia and Northern Antarctica soils. <i>Soil Biology and Biochemistry</i> , 2020, 146, 107805.	4.2	54
4085	Host-microbiota interaction helps to explain the bottom-up effects of climate change on a small rodent species. <i>ISME Journal</i> , 2020, 14, 1795-1808.	4.4	29
4086	Gut metagenomic and short chain fatty acids signature in hypertension: a cross-sectional study. <i>Scientific Reports</i> , 2020, 10, 6436.	1.6	115
4087	Comparative analyses of the V4 and V9 regions of 18S rDNA for the extant eukaryotic community using the Illumina platform. <i>Scientific Reports</i> , 2020, 10, 6519.	1.6	51
4088	Effects of dietary grape pomace on the intestinal microbiota and growth performance of weaned piglets. <i>Archives of Animal Nutrition</i> , 2020, 74, 296-308.	0.9	16
4089	Temporal changes in microbial communities attached to forages with different lignocellulosic compositions in cattle rumen. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	32
4090	Environmental DNA analysis shows high potential as a tool for estimating intraspecific genetic diversity in a wild fish population. <i>Molecular Ecology Resources</i> , 2020, 20, 1248-1258.	2.2	29
4091	Hybridization ddRAD sequencing for population genomics of nonmodel plants using highly degraded historical specimen DNA. <i>Molecular Ecology Resources</i> , 2020, 20, 1228-1247.	2.2	19
4092	Multiple invasions of a generalist herbivore—Secondary contact between two divergent lineages of <i>Nezara viridula</i> Linnaeus in Australia. <i>Evolutionary Applications</i> , 2020, 13, 2113-2129.	1.5	5
4093	Altered rhizoctonia assemblages in grasslands on ex-arable land support germination of mycorrhizal generalist, not specialist orchids. <i>New Phytologist</i> , 2020, 227, 1200-1212.	3.5	33
4094	Rapid Reconstitution of the Fecal Microbiome after Extended Diet-Induced Changes Indicates a Stable Gut Microbiome in Healthy Adult Dogs. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	25
4095	Depletion of <i>Blautia</i> Species in the Microbiota of Obese Children Relates to Intestinal Inflammation and Metabolic Phenotype Worsening. <i>MSystems</i> , 2020, 5, .	1.7	185
4096	Resident microbial communities inhibit growth and antibiotic-resistance evolution of <i>Escherichia coli</i> in human gut microbiome samples. <i>PLoS Biology</i> , 2020, 18, e3000465.	2.6	47
4097	Dysbiosis of saliva microbiome in patients with oral lichen planus. <i>BMC Microbiology</i> , 2020, 20, 75.	1.3	30
4098	Polysaccharide extracted from WuGuChong reduces high-fat diet-induced obesity in mice by regulating the composition of intestinal microbiota. <i>Nutrition and Metabolism</i> , 2020, 17, 27.	1.3	11
4099	A predatory myxobacterium controls cucumber <i>Fusarium</i> wilt by regulating the soil microbial community. <i>Microbiome</i> , 2020, 8, 49.	4.9	87

#	ARTICLE	IF	CITATIONS
4100	Development of 19 universal microsatellite loci for three closely related <i>Ficus</i> species (Moraceae) by high-throughput sequencing. <i>Genes and Genetic Systems</i> , 2020, 95, 21-27.	0.2	3
4101	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. <i>PLoS ONE</i> , 2020, 15, e0231237.	1.1	18
4102	Full-scale simultaneous partial nitrification, anammox, and denitrification process for treating swine wastewater. <i>Water Science and Technology</i> , 2020, 81, 456-465.	1.2	24
4103	The Relationships Between the Free-Living and Particle-Attached Bacterial Communities in Response to Elevated Eutrophication. <i>Frontiers in Microbiology</i> , 2020, 11, 423.	1.5	33
4104	Unraveling Assemblage, Functions and Stability of the Gut Microbiota of <i>Blattella germanica</i> by Antibiotic Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 487.	1.5	15
4105	Biomethane Potential Test: Influence of Inoculum and the Digestion System. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 2589.	1.3	38
4106	An Optimized Metabarcoding Method for Mimiviridae. <i>Microorganisms</i> , 2020, 8, 506.	1.6	6
4107	Mobility and potential bioavailability of antimony in contaminated soils: Short-term impact on microbial community and soil biochemical functioning. <i>Ecotoxicology and Environmental Safety</i> , 2020, 196, 110576.	2.9	29
4108	Distinct associations of sputum and oral microbiota with atopic, immunologic, and clinical features in mild asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 1016-1026.	1.5	46
4109	Molokhia leaf extract prevents gut inflammation and obesity. <i>Journal of Ethnopharmacology</i> , 2020, 257, 112866.	2.0	12
4110	Microbial Diversity and Metabolic Potential in the Stratified Sansha Yongle Blue Hole in the South China Sea. <i>Scientific Reports</i> , 2020, 10, 5949.	1.6	27
4111	Anthropogenic land use changes diversity and structure of arbuscular mycorrhizal fungal communities at 100-m scale in northeast China. <i>Archives of Agronomy and Soil Science</i> , 2021, 67, 778-792.	1.3	8
4112	A Survey of the Potential Ectomycorrhizal Fungi Associated With Nursery Seedlings of Seven Species of Exotic <i>Quercus</i> in China. <i>Journal of Sustainable Forestry</i> , 2021, 40, 357-370.	0.6	2
4113	Ultra-conserved Elements and morphology reciprocally illuminate conflicting phylogenetic hypotheses in Chalcididae (Hymenoptera, Chalcidoidea). <i>Cladistics</i> , 2021, 37, 1-35.	1.5	20
4114	Complementary DNA sequencing (cDNA): an effective approach for assessing the diversity and distribution of marine benthic ciliates along hydrographic gradients. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 208-222.	0.6	4
4115	Phylogenetic analyses confirm polyphyly of the genus <i>Campanula</i> (Campanulaceae s. str.), leading to a proposal for generic reappraisal. <i>Journal of Systematics and Evolution</i> , 2021, 59, 475-489.	1.6	6
4116	Biogeographic patterns of abundant and rare bacterial and microeukaryotic subcommunities in connected freshwater lake zones subjected to different levels of nutrient loading. <i>Journal of Applied Microbiology</i> , 2021, 130, 123-132.	1.4	6
4117	Phosphorus fertilization and intercropping interactively affect tomato and potato onion growth and rhizosphere arbuscular mycorrhizal fungal community. <i>Archives of Agronomy and Soil Science</i> , 2021, 67, 919-933.	1.3	11

#	ARTICLE	IF	CITATIONS
4118	Effects of burning and mowing on the soil microbiome of restored tallgrass prairie. <i>European Journal of Soil Science</i> , 2021, 72, 385-399.	1.8	3
4119	Synergetic responses of intestinal microbiota and epithelium to dietary inulin supplementation in pigs. <i>European Journal of Nutrition</i> , 2021, 60, 715-727.	1.8	10
4120	Dietary riboflavin deficiency induces aribo flavinosis and esophageal epithelial atrophy in association with modification of gut microbiota in rats. <i>European Journal of Nutrition</i> , 2021, 60, 807-820.	1.8	19
4121	Population-based targeted sequencing of 54 candidate genes identifies <i>PALB2</i> as a susceptibility gene for high-grade serous ovarian cancer. <i>Journal of Medical Genetics</i> , 2021, 58, 305-313.	1.5	26
4122	Microbiome Transfer Partly Overrides Lack of IL-1RI Signaling to Alter Hepatic but not Adipose Tissue Phenotype and Lipid Handling following a High-Fat Diet Challenge. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2000202.	1.5	4
4123	Glucocorticoid receptor gene (<i>NR3C1</i>) is hypermethylated in adult males with aggressive behaviour. <i>International Journal of Legal Medicine</i> , 2021, 135, 43-51.	1.2	8
4124	Diversity of endophytic bacteria and fungi in seeds of <i>Elymus nutans</i> growing in four locations of Qinghai Tibet Plateau, China. <i>Plant and Soil</i> , 2021, 459, 49-63.	1.8	19
4125	Acute and chronic improvement in postprandial glucose metabolism by a diet resembling the traditional Mediterranean dietary pattern: Can SCFAs play a role?. <i>Clinical Nutrition</i> , 2021, 40, 428-437.	2.3	43
4126	Patterns of fungal community succession triggered by C/N ratios during composting. <i>Journal of Hazardous Materials</i> , 2021, 401, 123344.	6.5	66
4127	Dietary supplementation with <i>Bacillus subtilis</i> DSM 32315 alters the intestinal microbiota and metabolites in weaned piglets. <i>Journal of Applied Microbiology</i> , 2021, 130, 217-232.	1.4	19
4128	Potential of indigenous <i>Bacillus</i> spp. as probiotic feed supplements in an extruded low-fish meal diet for juvenile olive flounder, <i>Paralichthys olivaceus</i> . <i>Journal of the World Aquaculture Society</i> , 2021, 52, 244-261.	1.2	10
4129	Effect of organic micropollutants on biofouling in a forward osmosis process integrating seawater desalination and wastewater reclamation. <i>Journal of Hazardous Materials</i> , 2021, 401, 123386.	6.5	18
4130	Post-glacial establishment of locally adapted fish populations over a steep salinity gradient. <i>Journal of Evolutionary Biology</i> , 2021, 34, 138-156.	0.8	28
4131	A novel constructed carbonate-mineralized functional bacterial consortium for high-efficiency cadmium biomineralization. <i>Journal of Hazardous Materials</i> , 2021, 401, 123269.	6.5	58
4132	Seasonal variation in the gut microbiota of rhesus macaques inhabiting limestone forests of southwest Guangxi, China. <i>Archives of Microbiology</i> , 2021, 203, 787-798.	1.0	7
4133	Root microbiome assembly of <i>Aspergillus hyperaccumulator</i> <i>Pteris vittata</i> and its efficacy in arsenic requisition. <i>Environmental Microbiology</i> , 2021, 23, 1959-1971.	1.8	25
4134	Mosquito and bacterial diversity in Phytotelmata in northern Taiwan. <i>International Journal of Tropical Insect Science</i> , 2021, 41, 969-978.	0.4	1
4135	Biogeographic patterns and co-occurrence networks of diazotrophic and arbuscular mycorrhizal fungal communities in the acidic soil ecosystem of southern China. <i>Applied Soil Ecology</i> , 2021, 158, 103798.	2.1	21

#	ARTICLE	IF	CITATIONS
4136	The fermentation properties and microbial diversity of soy sauce fermented by germinated soybean. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 2920-2929.	1.7	14
4137	Biogeography and co-occurrence patterns of bacterial generalists and specialists in three subtropical marine bays. <i>Limnology and Oceanography</i> , 2021, 66, 793-806.	1.6	36
4138	Robustness of granular activated carbon-synergized anaerobic membrane bioreactor for pilot-scale application over a wide seasonal temperature change. <i>Water Research</i> , 2021, 189, 116552.	5.3	60
4139	Characterization of <i>Bacillus cereus</i> sensu lato isolates from milk for consumption; phylogenetic identity, potential for spoilage and disease. <i>Food Microbiology</i> , 2021, 93, 103604.	2.1	14
4140	Under the Radar: Epidemiology of <i>Plasmodium ovale</i> in the Democratic Republic of the Congo. <i>Journal of Infectious Diseases</i> , 2021, 223, 1005-1014.	1.9	24
4141	Simultaneous leaching of multiple heavy metals from a soil column by extracellular polymeric substances of <i>Aspergillus tubingensis</i> F12. <i>Chemosphere</i> , 2021, 263, 127883.	4.2	17
4142	Integrating microbial metagenomics and physicochemical parameters and a new perspective on starter culture for fine cocoa fermentation. <i>Food Microbiology</i> , 2021, 93, 103608.	2.1	23
4143	Effects of substrate on the physiological characteristics and intestinal microbiota of <i>Echiura</i> worm (<i>Urechis uncinatus</i>) juveniles. <i>Aquaculture</i> , 2021, 530, 735710.	1.7	6
4144	Association of intestinal fungal communities with the body vesicular syndrome: An emerging disease of sea cucumber (<i>Apostichopus japonicus</i>). <i>Aquaculture</i> , 2021, 530, 735758.	1.7	4
4145	Do Maternal Microbes Shape Newborn Oral Microbes?. <i>Indian Journal of Microbiology</i> , 2021, 61, 16-23.	1.5	9
4146	Bioinformatic identification of key pathways, hub genes, and microbiota for therapeutic intervention in <i>Helicobacter pylori</i> infection. <i>Journal of Cellular Physiology</i> , 2021, 236, 1158-1183.	2.0	4
4147	Effects of different concentrations of coated nano zinc oxide material on fecal bacterial composition and intestinal barrier in weaned piglets. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 735-745.	1.7	15
4148	Dietary supplementation with <i>Bacillus</i> mixture modifies the intestinal ecosystem of weaned piglets in an overall beneficial way. <i>Journal of Applied Microbiology</i> , 2021, 130, 233-246.	1.4	20
4149	Community succession of the grapevine fungal microbiome in the annual growth cycle. <i>Environmental Microbiology</i> , 2021, 23, 1842-1857.	1.8	69
4150	Microbial community and transcriptional responses to increased temperatures in coral <i>Pocillopora damicornis</i> holobiont. <i>Environmental Microbiology</i> , 2021, 23, 826-843.	1.8	38
4151	Study of fermented feed by mixed strains and their effects on the survival, growth, digestive enzyme activity and intestinal flora of <i>Penaeus vannamei</i> . <i>Aquaculture</i> , 2021, 530, 735703.	1.7	27
4152	Distinction between Cr and other heavy-metal-resistant bacteria involved in C/N cycling in contaminated soils of copper producing sites. <i>Journal of Hazardous Materials</i> , 2021, 402, 123454.	6.5	67
4153	Changes in Bacterial Diversity, Composition and Interactions During the Development of the Seabird Tick <i>Ornithodoros maritimus</i> (Argasidae). <i>Microbial Ecology</i> , 2021, 81, 770-783.	1.4	10

#	ARTICLE	IF	CITATIONS
4154	Ciliate Diversity From Aquatic Environments in the Brazilian Atlantic Forest as Revealed by High-Throughput DNA Sequencing. <i>Microbial Ecology</i> , 2021, 81, 630-643.	1.4	11
4155	Shenyan Kangfu tablet alleviates diabetic kidney disease through attenuating inflammation and modulating the gut microbiota. <i>Journal of Natural Medicines</i> , 2021, 75, 84-98.	1.1	23
4156	Profiles of bacteria/phage-comediated ARGs in pig farm wastewater treatment plants in China: Association with mobile genetic elements, bacterial communities and environmental factors. <i>Journal of Hazardous Materials</i> , 2021, 404, 124149.	6.5	47
4157	Effect of balanced application of boron and phosphorus fertilizers on soil bacterial community, seed yield and phosphorus use efficiency of <i>Brassica napus</i> . <i>Science of the Total Environment</i> , 2021, 751, 141644.	3.9	10
4158	Contrasting bacterial communities and their assembly processes in karst soils under different land use. <i>Science of the Total Environment</i> , 2021, 751, 142263.	3.9	30
4159	Onshore soil microbes and endophytes respond differently to geochemical and mineralogical changes in the Aral Sea. <i>Science of the Total Environment</i> , 2021, 765, 142675.	3.9	9
4160	Assessing and modeling biocatalysis in field denitrification beds reveals key influencing factors for future constructions. <i>Water Research</i> , 2021, 188, 116467.	5.3	11
4161	Concerted and birth-and-death evolution of 26S ribosomal DNA in <i>Camellia</i> L.. <i>Annals of Botany</i> , 2021, 127, 63-73.	1.4	7
4162	Composition of soil bacterial and fungal communities in relation to vegetation composition and soil characteristics along an altitudinal gradient. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	27
4163	Changes in community structure and metabolic function of soil bacteria depending on the type restoration processing in the degraded alpine grassland ecosystems in Northern Tibet. <i>Science of the Total Environment</i> , 2021, 755, 142619.	3.9	15
4164	Association between indoor microbiome exposure and sick building syndrome (SBS) in junior high schools of Johor Bahru, Malaysia. <i>Science of the Total Environment</i> , 2021, 753, 141904.	3.9	27
4165	Community diversity and abundance of ammonia-oxidizing archaea and bacteria in shrimp pond sediment at different culture stages. <i>Journal of Applied Microbiology</i> , 2021, 130, 1442-1455.	1.4	18
4166	Effects of yeast and yeast extract on growth performance, antioxidant ability and intestinal microbiota of juvenile Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2021, 530, 735941.	1.7	31
4167	Temporal succession of water microbiomes and resistomes during carcass decomposition in a fish model. <i>Journal of Hazardous Materials</i> , 2021, 403, 123795.	6.5	26
4168	Identification of microbial strategies for labile substrate utilization at phylogenetic classification using a microcosm approach. <i>Soil Biology and Biochemistry</i> , 2021, 153, 107970.	4.2	45
4169	Effects of chicken farming on soil organic carbon fractions and fungal communities in a Lei bamboo (<i>Phyllostachys praecox</i>) forest in subtropical China. <i>Forest Ecology and Management</i> , 2021, 479, 118603.	1.4	19
4170	Diversity and Abundance of Denitrifying Bacteria in the Sediment of a Eutrophic Estuary. <i>Geomicrobiology Journal</i> , 2021, 38, 199-209.	1.0	9
4171	Comprehensive benefit evaluation of conservation tillage based on BP neural network in the Loess Plateau. <i>Soil and Tillage Research</i> , 2021, 205, 104784.	2.6	23

#	ARTICLE	IF	CITATIONS
4172	Functional Genomics Platform, A Cloud-Based Platform for Studying Microbial Life at Scale. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 940-952.	1.9	18
4173	Genetic diversity in natural populations of the endangered Neotropical orchid <i>Telipogon peruvianus</i> . Plant Species Biology, 2021, 36, 6-16.	0.6	7
4174	Effect of different glucogenic to lipogenic nutrient ratios on rumen fermentation and bacterial community <i>in vitro</i> . Journal of Applied Microbiology, 2021, 130, 1868-1882.	1.4	6
4175	Organic and inorganic model soil fractions instigate the formation of distinct microbial biofilms for enhanced biodegradation of benzo[a]pyrene. Journal of Hazardous Materials, 2021, 404, 124071.	6.5	21
4176	Effects of chicken farming on soil properties and root-associated bacterial communities in a bamboo (<i>Phyllostachys praecox</i>) ecosystem. Applied Soil Ecology, 2021, 157, 103725.	2.1	11
4177	Airborne bacterial communities over the Tibetan and Mongolian Plateaus: variations and their possible sources. Atmospheric Research, 2021, 247, 105215.	1.8	11
4178	Hydroxyapatite as a passivator for safe wheat production and its impacts on soil microbial communities in a Cd-contaminated alkaline soil. Journal of Hazardous Materials, 2021, 404, 124005.	6.5	62
4179	dbGuide: a database of functionally validated guide RNAs for genome editing in human and mouse cells. Nucleic Acids Research, 2021, 49, D871-D876.	6.5	20
4180	In-feed antibiotic use changed the behaviors of oxytetracycline, sulfamerazine, and ciprofloxacin and related antibiotic resistance genes during swine manure composting. Journal of Hazardous Materials, 2021, 402, 123710.	6.5	48
4181	Chemotaxis-selective colonization of mangrove rhizosphere microbes on nine different microplastics. Science of the Total Environment, 2021, 752, 142223.	3.9	69
4182	The microbial community, its biochemical potential, and the antimicrobial resistance of <i>Enterococcus</i> spp. in Arctic lakes under natural and anthropogenic impact (West Spitsbergen). Science of the Total Environment, 2021, 763, 142998.	3.9	6
4183	<i>Monascus purpureus</i> M-32 improves growth performance, immune response, intestinal morphology, microbiota and disease resistance in <i>Litopenaeus vannamei</i> . Aquaculture, 2021, 530, 735947.	1.7	17
4184	Soil microbial communities and their relationships to soil properties at different depths in an alpine meadow and desert grassland in the Qilian mountain range of China. Journal of Arid Environments, 2021, 184, 104316.	1.2	28
4185	Microbial diversity reveals the partial denitrification-anammox process serves as a new pathway in the first mainstream anammox plant. Science of the Total Environment, 2021, 764, 142917.	3.9	31
4186	Distinguishing Between the Impacts of Heat and Drought Stress on the Root Microbiome of <i>Sorghum bicolor</i> . Phytobiomes Journal, 2021, 5, 166-176.	1.4	28
4187	Comparative diversity analysis of halophiles at two polar saltern systems in Indramayu, West Java, Indonesia. Letters in Applied Microbiology, 2021, 72, 157-166.	1.0	1
4188	The impact of the endophytic bacterial community on mulberry tree growth in the Three Gorges Reservoir ecosystem, China. Environmental Microbiology, 2021, 23, 1858-1875.	1.8	7
4189	Exploring core microbiota responsible for the production of volatile flavor compounds during the traditional fermentation of Koumiss. LWT - Food Science and Technology, 2021, 135, 110049.	2.5	26

#	ARTICLE	IF	CITATIONS
4190	Effect of abattoir, livestock species and storage temperature on bacterial community dynamics and sensory properties of vacuum packaged red meat. <i>Food Microbiology</i> , 2021, 94, 103648.	2.1	39
4191	Characterization of a New Nepovirus Infecting Grapevine. <i>Plant Disease</i> , 2021, 105, 1432-1439.	0.7	8
4192	Using environmental DNA for biomonitoring of freshwater fish communities: Comparison with established gillnet surveys in a boreal hydroelectric impoundment. <i>Environmental DNA</i> , 2021, 3, 105-120.	3.1	50
4193	Pinewood Nematode Alters the Endophytic and Rhizospheric Microbial Communities of <i>Pinus massoniana</i> . <i>Microbial Ecology</i> , 2021, 81, 807-817.	1.4	16
4194	Diet of the European bison (<i>Bison bonasus</i>) in a forest habitat estimated by DNA barcoding. <i>Mammal Research</i> , 2021, 66, 123-136.	0.6	10
4195	Money spider dietary choice in pre- and post-harvest cereal crops using metabarcoding. <i>Ecological Entomology</i> , 2021, 46, 249-261.	1.1	32
4196	Compositional changes of sedimentary microbes in the Yangtze River Estuary and their roles in the biochemical cycle. <i>Science of the Total Environment</i> , 2021, 760, 143383.	3.9	25
4197	Influence of the cold bottom water on taxonomic and functional composition and complexity of microbial communities in the southern Yellow Sea during the summer. <i>Science of the Total Environment</i> , 2021, 759, 143496.	3.9	12
4198	Diversity and dynamics of fungi during spontaneous fermentations and association with unique aroma profiles in wine. <i>International Journal of Food Microbiology</i> , 2021, 338, 108983.	2.1	46
4199	Rhizobacterial communities, enzyme activity, and soil properties affect rice seedling's nitrogen use. <i>Agronomy Journal</i> , 2021, 113, 633-644.	0.9	3
4200	Multiple origins of a single point mutation in the cotton bollworm tetraspanin gene confers dominant resistance to Bt cotton. <i>Pest Management Science</i> , 2021, 77, 1169-1177.	1.7	13
4201	Determination of microbial diversities and aroma characteristics of Beitang shrimp paste. <i>Food Chemistry</i> , 2021, 344, 128695.	4.2	25
4202	Deciphering of antibiotic resistance genes (ARGs) and potential abiotic indicators for the emergence of ARGs in an interconnected lake-river-reservoir system. <i>Journal of Hazardous Materials</i> , 2021, 410, 124552.	6.5	38
4203	Distinct fungal plastisphere across different river functional zones: A watershed scale study. <i>Science of the Total Environment</i> , 2021, 752, 141879.	3.9	18
4204	Survey of background microbial index in inhalable particles in Beijing. <i>Science of the Total Environment</i> , 2021, 757, 143743.	3.9	10
4205	A new strategy using nanoscale zero-valent iron to simultaneously promote remediation and safe crop production in contaminated soil. <i>Nature Nanotechnology</i> , 2021, 16, 197-205.	15.6	133
4206	Bacterial community progression during food waste composting containing high dioctyl terephthalate (DOTP) concentration. <i>Chemosphere</i> , 2021, 265, 129064.	4.2	36
4207	Microbial mechanisms related to the effects of bamboo charcoal and bamboo vinegar on the degradation of organic matter and methane emissions during composting. <i>Environmental Pollution</i> , 2021, 272, 116013.	3.7	29

#	ARTICLE	IF	CITATIONS
4208	Pre-introduction introgression contributes to parallel differentiation and contrasting hybridization outcomes between invasive and native marine mussels. <i>Journal of Evolutionary Biology</i> , 2021, 34, 175-192.	0.8	10
4209	Top-down controls on nutrient cycling and population dynamics in a model estuarine photoautotroph-heterotroph co-culture system. <i>Molecular Ecology</i> , 2021, 30, 592-607.	2.0	9
4210	Characterization of microbial communities in sediments of the South Yellow Sea. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 846-864.	0.6	8
4211	Environmental drivers of plankton protist communities along latitudinal and vertical gradients in the oldest and deepest freshwater lake. <i>Environmental Microbiology</i> , 2021, 23, 1436-1451.	1.8	22
4212	Effects of <i>Clostridium butyricum</i> on growth, digestive enzyme activity, antioxidant capacity and gut microbiota in farmed tilapia (<i>Oreochromis niloticus</i>). <i>Aquaculture Research</i> , 2021, 52, 1573-1584.	0.9	16
4213	Rhizosphere bacterial and fungal communities succession patterns related to growth of poplar fine roots. <i>Science of the Total Environment</i> , 2021, 756, 143839.	3.9	7
4214	Effects of simulated nitrogen deposition on soil microbial community diversity in coastal wetland of the Yellow River Delta. <i>Science of the Total Environment</i> , 2021, 757, 143825.	3.9	36
4215	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	1.8	42
4216	Profiling prokaryotic community in pit mud of Chinese strong-aroma type liquor by using oligotrophic culturing. <i>International Journal of Food Microbiology</i> , 2021, 337, 108951.	2.1	13
4217	The composition of antibiotic resistance genes is not affected by grazing but is determined by microorganisms in grassland soils. <i>Science of the Total Environment</i> , 2021, 761, 143205.	3.9	19
4218	Early presence of <i>Batrachochytrium dendrobatidis</i> in Mexico with a contemporary dominance of the global panzootic lineage. <i>Molecular Ecology</i> , 2021, 30, 424-437.	2.0	21
4219	Active phoD-harboring bacteria are enriched by long-term organic fertilization. <i>Soil Biology and Biochemistry</i> , 2021, 152, 108071.	4.2	27
4220	Dietary vitamin A supplementation prevents early obesogenic diet-induced microbiota, neuronal and cognitive alterations. <i>International Journal of Obesity</i> , 2021, 45, 588-598.	1.6	18
4221	The impact of cropping system, tillage and season on shaping soil fungal community in a long-term field trial. <i>European Journal of Soil Biology</i> , 2021, 102, 103253.	1.4	12
4222	Variable characteristics of microbial communities on the surface of sweet cherries under different storage conditions. <i>Postharvest Biology and Technology</i> , 2021, 173, 111408.	2.9	22
4223	Monthly distribution of ammonia-oxidizing microbes in a tropical bay. <i>Journal of Microbiology</i> , 2021, 59, 10-19.	1.3	1
4224	Microbial Community Characterizing Vermiculations from Karst Caves and Its Role in Their Formation. <i>Microbial Ecology</i> , 2021, 81, 884-896.	1.4	29
4225	Comparative study of the bacterial communities throughout the gastrointestinal tract in two beef cattle breeds. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 313-325.	1.7	14

#	ARTICLE	IF	CITATIONS
4226	Characterization of bacterial communities during persistent fog and haze events in the Qingdao coastal region. <i>Frontiers of Environmental Science and Engineering</i> , 2021, 15, 1.	3.3	3
4227	Flammulina velutipes polysaccharide improves C57BL/6 mice gut health through regulation of intestine microbial metabolic activity. <i>International Journal of Biological Macromolecules</i> , 2021, 167, 1308-1318.	3.6	21
4228	Manure application increases microbiome complexity in soil aggregate fractions: Results of an 18-year field experiment. <i>Agriculture, Ecosystems and Environment</i> , 2021, 307, 107249.	2.5	54
4229	On-farm soil resistome is modified after treating dairy calves with the antibiotic florfenicol. <i>Science of the Total Environment</i> , 2021, 750, 141694.	3.9	11
4230	Drivers and dynamics of a massive adaptive radiation in cichlid fishes. <i>Nature</i> , 2021, 589, 76-81.	13.7	151
4231	Protist taxonomic and functional diversity in soil, freshwater and marine ecosystems. <i>Environment International</i> , 2021, 146, 106262.	4.8	110
4232	Derived habitats of indoor microbes are associated with asthma symptoms in Chinese university dormitories. <i>Environmental Research</i> , 2021, 194, 110501.	3.7	18
4233	Detecting community change in Arctic marine ecosystems using the temporal dynamics of environmental DNA. <i>Environmental DNA</i> , 2021, 3, 573-590.	3.1	11
4234	Whole exome sequencing identifies the potential for genetic rescue in iconic and critically endangered Panamanian harlequin frogs. <i>Global Change Biology</i> , 2021, 27, 50-70.	4.2	15
4235	Metabolites of microbiota response to tryptophan and intestinal mucosal immunity: A therapeutic target to control intestinal inflammation. <i>Medicinal Research Reviews</i> , 2021, 41, 1061-1088.	5.0	68
4236	Environment dependent microbial co-occurrences across a cyanobacterial bloom in a freshwater lake. <i>Environmental Microbiology</i> , 2021, 23, 327-339.	1.8	6
4237	Impact of DNA extraction and sampling methods on bacterial communities monitored by 16S rDNA metabarcoding in cold-smoked salmon and processing plant surfaces. <i>Food Microbiology</i> , 2021, 95, 103705.	2.1	27
4238	Distribution of physiochemically defined soil organic carbon pools and their relationship to the soil microbial community in grasslands. <i>Pedobiologia</i> , 2021, 84, 150704.	0.5	4
4239	Microplastic pollution and its relationship with the bacterial community in coastal sediments near Guangdong Province, South China. <i>Science of the Total Environment</i> , 2021, 760, 144091.	3.9	27
4240	Genome editing in human hematopoietic stem and progenitor cells via CRISPR-Cas9-mediated homology-independent targeted integration. <i>Molecular Therapy</i> , 2021, 29, 1611-1624.	3.7	17
4241	Microbial diversity and structure in the gastrointestinal tracts of two stranded short-finned pilot whales (<i>Globicephala macrorhynchus</i>) and a pygmy sperm whale (<i>Kogia breviceps</i>). <i>Integrative Zoology</i> , 2021, 16, 324-335.	1.3	16
4242	Gut Microbiome Components Predict Response to Neoadjuvant Chemoradiotherapy in Patients with Locally Advanced Rectal Cancer: A Prospective, Longitudinal Study. <i>Clinical Cancer Research</i> , 2021, 27, 1329-1340.	3.2	82
4243	Metagenomic Approach to Bacterial Diversity and Lipolytic Enzymes™ Genes from a Steam Soil of Los Humeros Geothermal Field (Puebla, MÃ©xico). <i>Geomicrobiology Journal</i> , 2021, 38, 304-314.	1.0	0

#	ARTICLE	IF	CITATIONS
4244	Substrate Pre-loading Influences Initial Colonization of GAC Biofilter Biofilms. <i>Frontiers in Microbiology</i> , 2020, 11, 596156.	1.5	2
4245	Assessment of fungal diversity in soil rhizosphere associated with <i>Rhazya stricta</i> and some desert plants using metagenomics. <i>Archives of Microbiology</i> , 2021, 203, 1211-1219.	1.0	2
4246	Floral fungal-bacterial community structure and co-occurrence patterns in four sympatric island plant species. <i>Fungal Biology</i> , 2021, 125, 49-61.	1.1	14
4247	Control of Southern Root-knot Nematodes on Tomato and Regulation of Soil Bacterial Community by Biofumigation with <i>Zanthoxylum bungeanum</i> Seed. <i>Horticultural Plant Journal</i> , 2021, 7, 49-58.	2.3	4
4248	Effect of Gender Bias on Equine Fecal Microbiota. <i>Journal of Equine Veterinary Science</i> , 2021, 97, 103355.	0.4	8
4249	Effects of dietary four different woody forages on gut microbiota of Nile tilapia (<i>Oreochromis</i>) Tj ETQq1 1 0.784314 rgBT ₆ Overload	0.9	0
4250	The structure of plant-herbivore interaction networks varies along elevational gradients in the European Alps. <i>Journal of Biogeography</i> , 2021, 48, 465-476.	1.4	15
4251	Microbiability of meat quality and carcass composition traits in swine. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 223-236.	0.8	24
4252	Phylogenetic and geographical analysis of a retrovirus during the early stages of endogenous adaptation and exogenous spread in a new host. <i>Molecular Ecology</i> , 2021, 30, 2626-2640.	2.0	16
4253	Network-directed isolation of the cooperator <i>Pseudomonas aeruginosa</i> ZM03 enhanced the dibutyl phthalate degradation capacity of <i>Arthrobacter nicotianae</i> ZM05 under pH stress. <i>Journal of Hazardous Materials</i> , 2021, 410, 124667.	6.5	19
4254	Polyester microfiber and natural organic matter impact microbial communities, carbon-degraded enzymes, and carbon accumulation in a clayey soil. <i>Journal of Hazardous Materials</i> , 2021, 405, 124701.	6.5	67
4255	Enrichment of salt-tolerant CO ₂ -fixing communities in microbial electrosynthesis systems using porous ceramic hollow tube wrapped with carbon cloth as cathode and for CO ₂ supply. <i>Science of the Total Environment</i> , 2021, 766, 142668.	3.9	17
4256	Wide distribution of <i>Phycisphaera</i> -like planctomycetes from WD2101 soil group in peatlands and genome analysis of the first cultivated representative. <i>Environmental Microbiology</i> , 2021, 23, 1510-1526.	1.8	32
4257	Large-scale evidence for microbial response and associated carbon release after permafrost thaw. <i>Global Change Biology</i> , 2021, 27, 3218-3229.	4.2	44
4258	Rapid microbial community evolution in initial <i>Carex</i> litter decomposition stages in Bayinbuluk alpine wetland during the freeze-thaw period. <i>Ecological Indicators</i> , 2021, 121, 107180.	2.6	25
4259	Microbial Metabolism of Theaflavin-3,3'-digallate and Its Gut Microbiota Composition Modulatory Effects. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 232-245.	2.4	40
4260	Soil prokaryotic community shows no response to 20 years of simulated nitrogen deposition in an arid ecosystem in northwestern China. <i>Environmental Microbiology</i> , 2021, 23, 1222-1237.	1.8	15
4261	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. <i>Molecular Ecology</i> , 2021, 30, 1072-1085.	2.0	43

#	ARTICLE	IF	CITATIONS
4262	Viral Lysis Alters the Optical Properties and Biological Availability of Dissolved Organic Matter Derived from <i>Prochlorococcus</i> Picocyanobacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	26
4263	Thallium shifts the bacterial and fungal community structures in thallium mine waste rocks. <i>Environmental Pollution</i> , 2021, 268, 115834.	3.7	19
4264	Short-term high-dose gavage of hydroxychloroquine changes gut microbiota but not the intestinal integrity and immunological responses in mice. <i>Life Sciences</i> , 2021, 264, 118450.	2.0	20
4265	Microbiota populations and short-chain fatty acids production in cecum of immunosuppressed broilers consuming diets containing I^{13} -irradiated <i>Astragalus polysaccharides</i> . <i>Poultry Science</i> , 2021, 100, 273-282.	1.5	35
4266	Applying machine learning to predict viral assembly for adeno-associated virus capsid libraries. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 20, 276-286.	1.8	25
4267	High-throughput sequencing-based analysis of the intestinal microbiota of broiler chickens fed with compound small peptides of Chinese medicine. <i>Poultry Science</i> , 2021, 100, 100897.	1.5	12
4268	<i>Lactobacillus plantarum</i> KLD51.0344 and <i>Lactobacillus acidophilus</i> KLD51.0901 Mixture Prevents Chronic Alcoholic Liver Injury in Mice by Protecting the Intestinal Barrier and Regulating Gut Microbiota and Liver-Related Pathways. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 183-197.	2.4	77
4269	Microbial metabolic efficiency and community stability in high and low fertility soils following wheat residue addition. <i>Applied Soil Ecology</i> , 2021, 159, 103848.	2.1	14
4270	Evaluation of rhizoremediation and methane emission in diesel-contaminated soil cultivated with tall fescue (<i>Festuca arundinacea</i>). <i>Environmental Research</i> , 2021, 194, 110606.	3.7	25
4271	Isolation and characterization of twelve polymorphic microsatellite markers in the endangered <i>Hopea hainanensis</i> (Dipterocarpaceae). <i>Ecology and Evolution</i> , 2021, 11, 4-10.	0.8	4
4272	Linking bacterial diversity to floral identity in the bumble bee pollen basket. <i>Environmental DNA</i> , 2021, 3, 669-680.	3.1	8
4273	Metabarcoding assays for the detection of freshwater mussels (Unionida) with environmental DNA. <i>Environmental DNA</i> , 2021, 3, 231-247.	3.1	13
4274	eDNA metabarcoding reveals a core and secondary diets of the greater horseshoe bat with strong spatio-temporal plasticity. <i>Environmental DNA</i> , 2021, 3, 277-296.	3.1	19
4275	Effects of fenvalerate concentrations and its chiral isomers on bacterial community structure in the sediment environment of aquaculture ponds. <i>Environmental Science and Pollution Research</i> , 2021, 28, 14498-14507.	2.7	2
4276	Crab bioturbation significantly alters sediment microbial composition and function in an intertidal marsh. <i>Estuarine, Coastal and Shelf Science</i> , 2021, 249, 107116.	0.9	11
4277	Alternation of soil bacterial and fungal communities by tomato-rice rotation in Hainan Island in Southeast of China. <i>Archives of Microbiology</i> , 2021, 203, 913-925.	1.0	8
4278	Quantifying the importance of external and internal sources to the gut microbiota in juvenile and adult shrimp. <i>Aquaculture</i> , 2021, 531, 735910.	1.7	27
4279	Bathymetric gradient shapes the community composition rather than the species richness of deep-sea benthic ciliates. <i>Science of the Total Environment</i> , 2021, 755, 142623.	3.9	4

#	ARTICLE	IF	CITATIONS
4280	Diversity of bacterial symbionts associated with <i>Myzus persicae</i> (Sulzer) (Hemiptera: Aphididae: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 7	1.4	14
4281	Community assembly processes underlying the temporal dynamics of glacial stream and lake bacterial communities. <i>Science of the Total Environment</i> , 2021, 761, 143178.	3.9	22
4282	The impact of different <i>Saccharomyces cerevisiae</i> strains on microbial composition and quality of Chinese rice wine fermentations. <i>Yeast</i> , 2021, 38, 147-156.	0.8	12
4283	Sediment resuspension drives protist metacommunity structure and assembly in grass carp (<i>Ctenopharyngodon idella</i>) aquaculture ponds. <i>Science of the Total Environment</i> , 2021, 764, 142840.	3.9	19
4284	Like myovirus community shaped by dispersal and deterministic processes in the South China Sea. <i>Environmental Microbiology</i> , 2021, 23, 1038-1052.	1.8	5
4285	Association of an IGHV3-66 gene variant with Kawasaki disease. <i>Journal of Human Genetics</i> , 2021, 66, 475-489.	1.1	27
4286	The impact of heavy rain event on groundwater microbial communities in Xikuangshan, Hunan Province, P.R. China. <i>Journal of Hydrology</i> , 2021, 595, 125674.	2.3	10
4287	Biofilm and microbiome response of attached growth nitrification systems across incremental decreases to low temperatures. <i>Journal of Water Process Engineering</i> , 2021, 39, 101730.	2.6	8
4288	Zooming on dynamics of marine microbial communities in the phycosphere of <i>Akashiwo sanguinea</i> (Dinophyta) blooms. <i>Molecular Ecology</i> , 2021, 30, 207-221.	2.0	19
4289	Detection and distribution of viable pathogenic bacteria in full-scale drinking water treatment plants. <i>Journal of Hazardous Materials</i> , 2021, 406, 124335.	6.5	41
4290	Stochasticity versus determinism: Microbial community assembly patterns under specific conditions in petrochemical activated sludge. <i>Journal of Hazardous Materials</i> , 2021, 407, 124372.	6.5	32
4291	Bacterial community dynamics reveal its key bacterium, <i>Bacillus amyloliquefaciens</i> ZB, involved in soybean meal fermentation for efficient water-soluble protein production. <i>LWT - Food Science and Technology</i> , 2021, 135, 110068.	2.5	21
4292	A novel workflow to improve genotyping of multigene families in wildlife species: An experimental set-up with a known model system. <i>Molecular Ecology Resources</i> , 2021, 21, 982-998.	2.2	8
4293	Emulsion-enhanced remediation of lindane and DDT in soils. <i>Journal of Soils and Sediments</i> , 2021, 21, 469-486.	1.5	8
4294	Microbiome variations in preschool children with halitosis. <i>Oral Diseases</i> , 2021, 27, 1059-1068.	1.5	9
4295	Species detection from aquatic eDNA: Assessing the importance of capture methods. <i>Environmental DNA</i> , 2021, 3, 435-448.	3.1	17
4296	Out of the Pan-Himalaya: Evolutionary history of the Paeoniaceae revealed by phylogenomics. <i>Journal of Systematics and Evolution</i> , 2021, 59, 1170-1182.	1.6	21
4297	Metagenomic analysis of microbial community succession during the pickling process of Zhacai (preserved mustard tuber) and its correlation with Zhacai biochemical indices. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 1646-1658.	1.7	5

#	ARTICLE	IF	CITATIONS
4298	Microbial communities in rare earth mining soil after in-situ leaching mining. <i>Science of the Total Environment</i> , 2021, 755, 142521.	3.9	38
4299	Airway microbiota is associated with the severity of non- CF bronchiectasis. <i>Clinical Respiratory Journal</i> , 2021, 15, 154-162.	0.6	7
4300	Sulfate-reducing bacterial community shifts in response to acid mine drainage in the sediment of the Hengshi watershed, South China. <i>Environmental Science and Pollution Research</i> , 2021, 28, 2822-2834.	2.7	20
4301	Effects of the prebiotic inulin-type fructans on post-antibiotic reconstitution of the gut microbiome. <i>Journal of Applied Microbiology</i> , 2021, 130, 634-649.	1.4	4
4302	Diversity of bacteria associated with Hormaphidinae aphids (Hemiptera: Aphididae). <i>Insect Science</i> , 2021, 28, 165-179.	1.5	20
4303	Changes to the cervicovaginal microbiota and cervical cytokine profile following surgery for cervical intraepithelial neoplasia. <i>Scientific Reports</i> , 2021, 11, 2156.	1.6	12
4304	Patterns and Dynamics of the Soil Microbial Community with Gradual Vegetation Succession in the Yellow River Delta, China. <i>Wetlands</i> , 2021, 41, 1.	0.7	13
4305	Coumarin derivative and <i>Bacillus cereus</i> change live weight and cecal ecology in broilers. <i>AIMS Agriculture and Food</i> , 2021, 6, 360-380.	0.8	2
4306	Bacterial and Fungal Microbiome Profiling in Chilluacle Negro Chili (<i>Capsicum annuum</i> L.) Associated With Fruit Rot Disease. <i>Plant Disease</i> , 2021, 105, 2618-2627.	0.7	3
4307	Prediction of the Long-Term Effect of Iron on Methane Yield in an Anaerobic Membrane Bioreactor Using Bayesian Network Meta-Analysis. <i>Membranes</i> , 2021, 11, 100.	1.4	2
4308	Self-Crossing Leads to Weak Co-Variation of the Bacterial and Fungal Communities in the Rice Rhizosphere. <i>Microorganisms</i> , 2021, 9, 175.	1.6	9
4309	Changes in the Vaginal Microbiome during the Pregnancy to Postpartum Transition. <i>Reproductive Sciences</i> , 2021, 28, 1996-2005.	1.1	33
4310	Effects of Different Vegetation on Soil Microbial Diversity in Karst Area of Northwest Guangxi. <i>Hans Journal of Agricultural Sciences</i> , 2021, 11, 658-677.	0.0	2
4311	Metagenomics of Plant Rhizosphere and Endophytic Association: Concepts and Applications. <i>Rhizosphere Biology</i> , 2021, , 275-291.	0.4	0
4312	Niche Differentiation of Comammox Nitrospira in the Mudflat and Reclaimed Agricultural Soils Along the North Branch of Yangtze River Estuary. <i>Frontiers in Microbiology</i> , 2020, 11, 618287.	1.5	25
4313	Bioaugmentation of acetamiprid-contaminated soil with <i>Pigmentiphaga</i> sp. strain D-2 and its effect on the soil microbial community. <i>Ecotoxicology</i> , 2021, 30, 1559-1571.	1.1	7
4314	Diversity of microbes colonizing forages of varying lignocellulose properties in the sheep rumen. <i>PeerJ</i> , 2021, 9, e10463.	0.9	18
4315	Gut Microbiota and Related Metabolites Were Disturbed in Ulcerative Colitis and Partly Restored After Mesalamine Treatment. <i>Frontiers in Pharmacology</i> , 2020, 11, 620724.	1.6	21

#	ARTICLE	IF	CITATIONS
4316	Effect of aquaculture water eutrophication on color development in Biolog EcoPlates. <i>Aquaculture International</i> , 2021, 29, 373-386.	1.1	5
4317	Response of bacterial and fungal communities to high petroleum pollution in different soils. <i>Scientific Reports</i> , 2021, 11, 164.	1.6	47
4318	Effect of <i>Senecio scandens</i> ethanol extract on gut microbiota composition in mice. <i>Archives of Microbiology</i> , 2021, 203, 1477-1488.	1.0	1
4320	Investigating the microbiota of fermented fish products (Pla-ra) from different communities of northeastern Thailand. <i>PLoS ONE</i> , 2021, 16, e0245227.	1.1	21
4321	Gut microbiota dynamics in carnivorous European seabass (<i>Dicentrarchus labrax</i>) fed plant-based diets. <i>Scientific Reports</i> , 2021, 11, 447.	1.6	34
4322	Dietary Supplementation With <i>Bacillus subtilis</i> Promotes Growth and Gut Health of Weaned Piglets. <i>Frontiers in Veterinary Science</i> , 2020, 7, 600772.	0.9	15
4323	A high-throughput ultrasonic spraying inoculation method promotes colony cultivation of rare microbial species. <i>Environmental Microbiology</i> , 2021, 23, 1275-1285.	1.8	3
4324	Effect of EOR Chemical Flooding on Local Microbial Ecological Characteristics in Oilfield Mining Area. <i>IOP Conference Series: Earth and Environmental Science</i> , 0, 647, 012166.	0.2	0
4325	Specificity of assemblage, not fungal partner species, explains mycorrhizal partnerships of mycoheterotrophic <i>Burmannia</i> plants. <i>ISME Journal</i> , 2021, 15, 1614-1627.	4.4	8
4326	The bacterial composition associated with <i>Atrialum robustum</i> , a common ascidian from Xisha coral reef, China. <i>Symbiosis</i> , 2021, 83, 153-161.	1.2	2
4327	Soil Bacterial Community Responds to Land-Use Change in Riparian Ecosystems. <i>Forests</i> , 2021, 12, 157.	0.9	2
4328	Comparative analysis of bacterial and fungal endophytes responses to <i>Candidatus Liberibacter asiaticus</i> infection in leaf midribs of <i>Citrus reticulata</i> cv. Shatangju. <i>Physiological and Molecular Plant Pathology</i> , 2021, 113, 101590.	1.3	6
4330	Metagenomic Analysis of the Gut Microbiome Reveals Enrichment of Menaquinones (Vitamin K2) Pathway in Diabetes Mellitus. <i>Diabetes and Metabolism Journal</i> , 2021, 45, 77-85.	1.8	22
4331	Dissimilarity analysis of microbial communities in the rhizosphere and tissues of diseased and healthy cherry trees (<i>Cerasus pseudocerasus</i>). <i>Canadian Journal of Plant Pathology</i> , 2021, 43, 612-621.	0.8	5
4332	Association of Microbial Dysbiosis with Gallbladder Diseases Identified by Bile Microbiome Profiling. <i>Journal of Korean Medical Science</i> , 2021, 36, e189.	1.1	13
4333	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. <i>Eurosurveillance</i> , 2021, 26, .	3.9	9
4334	Effects of Mesobiliverdin IX ₁ -Enriched Microalgae Feed on Gut Health and Microbiota of Broilers. <i>Frontiers in Veterinary Science</i> , 2020, 7, 586813.	0.9	7
4335	Combining random mutagenesis, structure-guided design and next-generation sequencing to mitigate polyreactivity of an anti-IL-21R antibody. <i>MAbs</i> , 2021, 13, 1883239.	2.6	4

#	ARTICLE	IF	CITATIONS
4336	<i>Lactobacillus paracasei</i> L9 improves colitis by expanding butyrate-producing bacteria that inhibit the IL-6/STAT3 signaling pathway. Food and Function, 2021, 12, 10700-10713.	2.1	15
4337	Microbiota associated with <i>Mollitrichosiphum</i> aphids (Hemiptera: Aphididae: Greenideinae): diversity, host species specificity and phyllosymbiosis. Environmental Microbiology, 2021, 23, 2184-2198.	1.8	14
4338	Patterns of Relative and Quantitative Abundances of Marine Bacteria in Surface Waters of the Subtropical Northwest Pacific Ocean Estimated With High-Throughput Quantification Sequencing. Frontiers in Microbiology, 2020, 11, 599614.	1.5	12
4339	Alteration in the Skin Microbiome in Cutaneous Graft Versus Host Disease. Acta Dermato-Venereologica, 2021, 101, adv00374.	0.6	5
4340	Social calls influence the foraging behavior in wild big-footed myotis. Frontiers in Zoology, 2021, 18, 3.	0.9	7
4341	Dietary glycyl-glutamine supplementation ameliorates intestinal integrity, inflammatory response, and oxidative status in association with the gut microbiota in LPS-challenged piglets. Food and Function, 2021, 12, 3539-3551.	2.1	24
4342	Contribution of environmental factors on the distribution of antibiotic resistance genes in agricultural soil. European Journal of Soil Biology, 2021, 102, 103269.	1.4	14
4343	Sugarcane/peanut intercropping system improves the soil quality and increases the abundance of beneficial microbes. Journal of Basic Microbiology, 2021, 61, 165-176.	1.8	24
4344	High Taxonomic and Functional Diversity of Bacterial Communities Associated with Melon Fly, <i>Zeugodacus cucurbitae</i> (Diptera: Tephritidae). Current Microbiology, 2021, 78, 611-623.	1.0	9

4345

#	ARTICLE	IF	CITATIONS
4354	Gut microbiota alterations reveal potential gut-brain axis changes in polycystic ovary syndrome. <i>Journal of Endocrinological Investigation</i> , 2021, 44, 1727-1737.	1.8	38
4355	Metagenomic analysis of formalin-fixed paraffin-embedded tumor and normal mucosa reveals differences in the microbiome of colorectal cancer patients. <i>Scientific Reports</i> , 2021, 11, 391.	1.6	21
4356	<i>Candida albicans</i> disorder is associated with gastric carcinogenesis. <i>Theranostics</i> , 2021, 11, 4945-4956.	4.6	56
4357	Investigation of bacterial diversity in <i>Cajanus cajan</i> -planted gangue soil via high-throughput sequencing. <i>Bioengineered</i> , 2021, 12, 6981-6995.	1.4	9
4358	Blood microbiota diversity determines response of advanced colorectal cancer to chemotherapy combined with adoptive T cell immunotherapy. <i>Oncolimmunology</i> , 2021, 10, 1976953.	2.1	13
4360	Changes in the Microbiome of the Inner Surface of Clear Aligners After Different Usage Periods. <i>Current Microbiology</i> , 2021, 78, 566-575.	1.0	12
4361	Shifts in the seagrass leaf microbiome associated with wasting disease in. <i>Marine and Freshwater Research</i> , 2021, 72, 1303-1320.	0.7	2
4362	Rhizosphere microbiome dynamics in tropical seagrass under short-term inorganic nitrogen fertilization. <i>Environmental Science and Pollution Research</i> , 2021, 28, 19021-19033.	2.7	8
4363	Ancient mitochondrial genomes from Chinese cave hyenas provide insights into the evolutionary history of the genus <i>Crocota</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20202934.	1.2	9
4365	Mucosal microbiome dysbiosis associated with duodenum bulb inflammation. <i>Microbial Pathogenesis</i> , 2021, 150, 104711.	1.3	4
4366	Soil biota suppress maize growth and influence root traits under continuous monoculture. <i>Plant and Soil</i> , 2021, 461, 441-455.	1.8	7
4367	The Alteration of Intestinal Microbiota Profile and Immune Response in <i>Epinephelus coioides</i> during Pathogen Infection. <i>Life</i> , 2021, 11, 99.	1.1	16
4368	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of <i>Botryococcus</i> consortia. <i>Scientific Reports</i> , 2021, 11, 1726.	1.6	12
4369	Effect of different types of industrial wastewater on the bacterial community of urban rivers. <i>Journal of Freshwater Ecology</i> , 2021, 36, 31-48.	0.5	4
4370	<i>Bacteroides uniformis</i> combined with fiber amplifies metabolic and immune benefits in obese mice. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	81
4371	Germline IGHV3-53-encoded RBD-targeting neutralizing antibodies are commonly present in the antibody repertoires of COVID-19 patients. <i>Emerging Microbes and Infections</i> , 2021, 10, 1097-1111.	3.0	25
4372	Comparison of Blood Bacterial Communities in Periodontal Health and Periodontal Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 577485.	1.8	36
4373	Interaction of Intestinal Bacteria with Human Rotavirus during Infection in Children. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1010.	1.8	142

#	ARTICLE	IF	CITATIONS
4374	Cut microbiome analysis as a predictive marker for the gastric cancer patients. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 803-814.	1.7	38
4375	Intestinal microbiome and metabolome analyses reveal metabolic disorders in the early stage of renal transplantation. <i>Molecular Omics</i> , 2021, 17, 985-996.	1.4	2
4376	Kill and cure: genomic phylogeny and bioactivity of <i>Burkholderia gladioli</i> bacteria capable of pathogenic and beneficial lifestyles. <i>Microbial Genomics</i> , 2021, 7, .	1.0	24
4377	Diversity and composition of the <i>Panax ginseng</i> rhizosphere microbiome in various cultivation modes and ages. <i>BMC Microbiology</i> , 2021, 21, 18.	1.3	46
4378	Clonal diversity of the B cell receptor repertoire in patients with coronary in-stent restenosis and type 2 diabetes. <i>Open Life Sciences</i> , 2021, 16, 884-898.	0.6	3
4379	Effect of Two Different Sugarcane Cultivars on Rhizosphere Bacterial Communities of Sugarcane and Soybean Upon Intercropping. <i>Frontiers in Microbiology</i> , 2020, 11, 596472.	1.5	28
4380	Effect of Root Diameter on the Selection and Network Interactions of Root-Associated Bacterial Microbiomes in <i>Robinia pseudoacacia</i> L. <i>Microbial Ecology</i> , 2021, 82, 391-402.	1.4	18
4381	Impact of Long-Term Organic and Mineral Fertilization on Rhizosphere Metabolites, Root-Microbial Interactions and Plant Health of Lettuce. <i>Frontiers in Microbiology</i> , 2020, 11, 597745.	1.5	17
4382	Genetic variation among Iranian <i>Medicago polymorpha</i> L. populations based on SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1411-1424.	0.8	6
4384	Disentangling Responses of the Subsurface Microbiome to Wetland Status and Implications for Indicating Ecosystem Functions. <i>Microorganisms</i> , 2021, 9, 211.	1.6	6
4385	Development and characterization of 14 novel microsatellite markers for an invasive goby (<i>Tetraodon lineatus</i>). <i>Journal of Heredity</i> , 2021, 112, 342-347.	0.8	4
4386	Effect of commercially purified deoxynivalenol and zearalenone mycotoxins on microbial diversity of pig cecum contents. <i>Animal Bioscience</i> , 2021, 34, 243-255.	0.8	12
4387	Faecal bacterial composition in horses with and without free faecal liquid: a case control study. <i>Scientific Reports</i> , 2021, 11, 4745.	1.6	4
4388	<i>Potentilla anserina</i> L. developmental changes affect the rhizosphere prokaryotic community. <i>Scientific Reports</i> , 2021, 11, 2838.	1.6	4
4389	Changes in Intestinal Microbiota Due to the Expanded Polystyrene Diet of Mealworms (<i>Tenebrio molitor</i>). <i>Journal of Heredity</i> , 2021, 112, 342-347.	1.5	11
4390	A Uniform Computational Approach Improved on Existing Pipelines to Reveal Microbiome Biomarkers of Nonresponse to Immune Checkpoint Inhibitors. <i>Clinical Cancer Research</i> , 2021, 27, 2571-2583.	3.2	22
4392	An Oral FMT Capsule as Efficient as an Enema for Microbiota Reconstruction Following Disruption by Antibiotics, as Assessed in an In Vitro Human Gut Model. <i>Microorganisms</i> , 2021, 9, 358.	1.6	14
4393	Alterations in intestinal microbiota diversity, composition, and function in patients with sarcopenia. <i>Scientific Reports</i> , 2021, 11, 4628.	1.6	69

#	ARTICLE	IF	CITATIONS
4395	Characterization and comparison of the bacterial community between complete intensive and extensive feeding patterns in pigs. <i>AMB Express</i> , 2021, 11, 32.	1.4	3
4396	Factors Structuring the Epiphytic Archaeal and Fungal Communities in a Semi-arid Mediterranean Ecosystem. <i>Microbial Ecology</i> , 2021, 82, 638-651.	1.4	6
4397	Signatures of vaginal microbiota by 16S rRNA gene: potential bio-geographical application in Chinese Han from three regions of China. <i>International Journal of Legal Medicine</i> , 2021, 135, 1213-1224.	1.2	10
4398	Dietary Glutamic Acid Modulates Immune Responses and Gut Health of Weaned Pigs. <i>Animals</i> , 2021, 11, 504.	1.0	13
4399	Volatile aroma composition and sensory profile of Shiraz and Cabernet Sauvignon wines produced with novel <i>Metschnikowia pulcherrima</i> yeast starter cultures. <i>Australian Journal of Grape and Wine Research</i> , 2021, 27, 406-418.	1.0	11
4400	Circulating exosomes and gut microbiome induced insulin resistance in mice exposed to intermittent hypoxia: Effects of physical activity. <i>EBioMedicine</i> , 2021, 64, 103208.	2.7	35
4401	Genetic relationships between feed efficiency and gut microbiome in pig lines selected for residual feed intake. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 491-507.	0.8	19
4402	The Ubiquity and Development-Related Abundance Dynamics of Ophiocordyceps Fungi in Soft Scale Insects. <i>Microorganisms</i> , 2021, 9, 404.	1.6	5
4403	Alterations in the conjunctival surface bacterial microbiome in bacterial keratitis patients. <i>Experimental Eye Research</i> , 2021, 203, 108418.	1.2	27
4404	Quantification of Cas9 binding and cleavage across diverse guide sequences maps landscapes of target engagement. <i>Science Advances</i> , 2021, 7, .	4.7	28
4405	Patterns of Sediment Fungal Community Dependent on Farming Practices in Aquaculture Ponds. <i>Frontiers in Microbiology</i> , 2021, 12, 542064.	1.5	10
4406	Gut microbiota alterations associated with antibody-mediated rejection after kidney transplantation. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2473-2484.	1.7	12
4407	Bacterial Composition and Diversity of the Digestive Tract of <i>Odontomachus monticola</i> Emery and <i>Ectomomyrmex javanus</i> Mayr. <i>Insects</i> , 2021, 12, 176.	1.0	5
4408	Intercropping With Aromatic Plants Increased the Soil Organic Matter Content and Changed the Microbial Community in a Pear Orchard. <i>Frontiers in Microbiology</i> , 2021, 12, 616932.	1.5	22
4409	RSPO4-CRISPR alleviates liver injury and restores gut microbiota in a rat model of liver fibrosis. <i>Communications Biology</i> , 2021, 4, 230.	2.0	15
4410	Removal of roosters alters the domestic phenotype and microbial and genetic profile of hens. <i>Science China Life Sciences</i> , 2021, 64, 1964-1976.	2.3	6
4411	Cultivation and characterization of snowbound microorganisms from the South Pole. <i>Extremophiles</i> , 2021, 25, 159-172.	0.9	3
4412	Diversity of microbial community structure and their association with phthalic acid esters and physicochemical parameters in informal landfills. <i>Environmental Technology (United Kingdom)</i> , 2021, , 1-11.	1.2	2

#	ARTICLE	IF	CITATIONS
4413	The regional diversity of gut microbiome along the GI tract of male C57BL/6 mice. <i>BMC Microbiology</i> , 2021, 21, 44.	1.3	52
4414	The Gut Microbial Composition Is Species-Specific and Individual-Specific in Two Species of Estrildid Finches, the Bengalese Finch and the Zebra Finch. <i>Frontiers in Microbiology</i> , 2021, 12, 619141.	1.5	13
4415	Bacterial Diversity in Pickled Cowpea (<i>Vigna unguiculata</i> [Linn.] Walp) as Determined by Illumina MiSeq Sequencing and Culture-Dependent Methods. <i>Current Microbiology</i> , 2021, 78, 1286-1297.	1.0	14
4416	High Plasticity of the Gut Microbiome and Muscle Metabolome of Chinese Mitten Crab (<i>Eriocheir</i>) Tj ETQq1 1 0.784314 rgBT /Ove	0.9	10
4417	A latitudinal gradient of microbial diversity in continental paddy soils. <i>Global Ecology and Biogeography</i> , 2021, 30, 909-919.	2.7	17
4418	Gold particles from Kamchatka: A brief look at gold biogeochemical cycling in a distinct environment. <i>Mineralogical Magazine</i> , 2021, 85, 68-75.	0.6	1
4419	In Vivo Phage Display as a Biomarker Discovery Tool for the Complex Neural Injury Microenvironment. <i>Current Protocols</i> , 2021, 1, e67.	1.3	1
4420	Influence of Pelvic Intensity-Modulated Radiation Therapy With Concurrent Cisplatin-Based Chemotherapy of Cervical Cancer on the Vaginal Microbiome. <i>Frontiers in Oncology</i> , 2021, 11, 615439.	1.3	9
4421	User-friendly bioinformatics pipeline gDAT (graphical downstream analysis tool) for analysing rDNA sequences. <i>Molecular Ecology Resources</i> , 2021, 21, 1380-1392.	2.2	27
4422	Genomic evidence for sulfur intermediates as new biogeochemical hubs in a model aquatic microbial ecosystem. <i>Microbiome</i> , 2021, 9, 46.	4.9	32
4423	C-Type Lectin Maintains the Homeostasis of Intestinal Microbiota and Mediates Biofilm Formation by Intestinal Bacteria in Shrimp. <i>Journal of Immunology</i> , 2021, 206, 1140-1150.	0.4	22
4424	Spatial and seasonal variations of sediment bacterial communities in a river-bay system in South China. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1979-1989.	1.7	21
4425	Linderae Radix Ethanol Extract Alleviates Diet-Induced Hyperlipidemia by Regulating Bile Acid Metabolism Through gut Microbiota. <i>Frontiers in Pharmacology</i> , 2021, 12, 627920.	1.6	9
4426	Pelleting of a Total Mixed Ration Affects Growth Performance of Fattening Lambs. <i>Frontiers in Veterinary Science</i> , 2021, 8, 629016.	0.9	14
4427	Influence of Spatial Scale on Structure of Soil Bacterial Communities across an Arctic Landscape. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	6
4428	<i>Helicobacter pylori</i> infection worsens impaired glucose regulation in high-fat diet mice in association with an altered gut microbiome and metabolome. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2081-2095.	1.7	16
4429	Microbial dynamics in rearing trials of <i>Hermetia illucens</i> larvae fed coffee silverskin and microalgae. <i>Food Research International</i> , 2021, 140, 110028.	2.9	21
4430	Continuous Anaerobic Treatment of the Aqueous Phase of Hydrothermal Liquefaction from <i>Spirulina</i> Using a Horizontal-Flow Anaerobic Immobilized Biomass (HAIB) Reactor. <i>Water, Air, and Soil Pollution</i> , 2021, 232, 1.	1.1	3

#	ARTICLE	IF	CITATIONS
4431	Inhibition of <i>Batrachochytrium dendrobatidis</i> Infection by Skin Bacterial Communities in Wild Amphibian Populations. <i>Microbial Ecology</i> , 2021, 82, 666-676.	1.4	14
4432	Effect of different types of anthropogenic pollution on the bacterial community of urban rivers. <i>Water Environment Research</i> , 2021, 93, 1322-1332.	1.3	0
4433	Dynamic Alterations of Oral Microbiota Related to Halitosis in Preschool Children. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 599467.	1.8	11
4434	Dietary purslane (<i>Portulaca oleracea</i> L.) promotes the growth performance of broilers by modulation of gut microbiota. <i>AMB Express</i> , 2021, 11, 31.	1.4	11
4435	Exploration of Intrinsic Microbial Community Modulators in the Rice Endosphere Indicates a Key Role of Distinct Bacterial Taxa Across Different Cultivars. <i>Frontiers in Microbiology</i> , 2021, 12, 629852.	1.5	11
4436	Diet Diversity in Carnivorous Terebrid Snails Is Tied to the Presence and Absence of a Venom Gland. <i>Toxins</i> , 2021, 13, 108.	1.5	2
4437	Response of the microbial community to phosphate-solubilizing bacterial inoculants on <i>Ulmus chenmoui</i> Cheng in Eastern China. <i>PLoS ONE</i> , 2021, 16, e0247309.	1.1	16
4438	Effects of chitoooligosaccharides on the rebalance of gut microorganisms and their metabolites in patients with nonalcoholic fatty liver disease. <i>Journal of Functional Foods</i> , 2021, 77, 104333.	1.6	12
4439	Early-Life Stress Modulates Gut Microbiota and Peripheral and Central Inflammation in a Sex-Dependent Manner. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1899.	1.8	31
4440	Impacts of replanting American ginseng on fungal assembly and abundance in response to disease outbreaks. <i>Archives of Microbiology</i> , 2021, 203, 2157-2170.	1.0	22
4441	Dicer-like proteins influence <i>Arabidopsis</i> root microbiota independent of RNA-directed DNA methylation. <i>Microbiome</i> , 2021, 9, 57.	4.9	15
4442	Characterization of Bacterial Communities of Cold-Smoked Salmon during Storage. <i>Foods</i> , 2021, 10, 362.	1.9	19
4443	Compatible Mycorrhizal Types Contribute to a Better Design for Mixed Eucalyptus Plantations. <i>Frontiers in Plant Science</i> , 2021, 12, 616726.	1.7	2
4444	Evaluation and modulation of DNA lesion bypass in an SV40 large T antigen-based <i>in vitro</i> replication system. <i>FEBS Open Bio</i> , 2021, 11, 1054-1075.	1.0	2
4445	Gut microbiota associated with two species of domesticated honey bees from Thailand. <i>Symbiosis</i> , 2021, 83, 335-345.	1.2	4
4446	Comparison of the fermentation and bacterial community in the colon of Hu sheep fed a low-grain, non-pelleted, or pelleted high-grain diet. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2071-2080.	1.7	20
4447	Evaporation efficiency and important microorganisms under different ventilation strategies of co-bioevaporation process. <i>Environmental Technology and Innovation</i> , 2021, 21, 101374.	3.0	3
4448	Complete Genome Sequence of <i>Kinneretia</i> sp. Strain DAIF2, Isolated from a Freshwater Pond. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2

#	ARTICLE	IF	CITATIONS
4449	Improving the Inhibitory Effect of Phages against <i>Pseudomonas aeruginosa</i> Isolated from a Burn Patient Using a Combination of Phages and Antibiotics. <i>Viruses</i> , 2021, 13, 334.	1.5	25
4450	Distinct rhizomicrobiota assemblages and plant performance in lettuce grown in soils with different agricultural management histories. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
4451	Effect of Long-Term Fertilization on Ammonia-Oxidizing Microorganisms and Nitrification in Brown Soil of Northeast China. <i>Frontiers in Microbiology</i> , 2020, 11, 622454.	1.5	17
4452	Long-term warming in a Mediterranean-type grassland affects soil bacterial functional potential but not bacterial taxonomic composition. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 17.	2.9	12
4453	Ecological Specialization and Evolutionary Reticulation in Extant Hyaenidae. <i>Molecular Biology and Evolution</i> , 2021, 38, 3884-3897.	3.5	15
4454	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	2.9	53
4455	IL-17 controls central nervous system autoimmunity through the intestinal microbiome. <i>Science Immunology</i> , 2021, 6, .	5.6	67
4456	Bacterial Communities and Enzymatic Activities in Sediments of Long-Term Fish and Crab Aquaculture Ponds. <i>Microorganisms</i> , 2021, 9, 501.	1.6	16
4457	Tumor-Associated Microbiota in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 641270.	1.8	28
4458	Effects of Arginine Supplementation on Serum Metabolites and the Rumen Bacterial Community of Sika Deer (<i>Cervus nippon</i>). <i>Frontiers in Veterinary Science</i> , 2021, 8, 630686.	0.9	8
4459	Intestinal Dysbiosis in Young Cystic Fibrosis Rabbits. <i>Journal of Personalized Medicine</i> , 2021, 11, 132.	1.1	6
4460	Biogeographical Distribution and Community Assembly of Active Protistan Assemblages along an Estuary to a Basin Transect of the Northern South China Sea. <i>Microorganisms</i> , 2021, 9, 351.	1.6	6
4461	Clinical Study of Correlation for the Intestinal and Pharyngeal Microbiota in the Premature Neonates. <i>Frontiers in Pediatrics</i> , 2021, 9, 632573.	0.9	4
4462	The storage stability of <i>Bacillus subtilis</i> spore displaying cysteine protease of <i>Clonorchis sinensis</i> and its effect on improving the gut microbiota of mice. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2513-2526.	1.7	5
4463	Structural changes in the oral microbiome of the adolescent patients with moderate or severe dental fluorosis. <i>Scientific Reports</i> , 2021, 11, 2897.	1.6	9
4464	Metagenomic 16S rDNA amplicon data of microbial diversity of guts in Vietnamese humans with type 2 diabetes and nondiabetic adults. <i>Data in Brief</i> , 2021, 34, 106690.	0.5	8
4465	Effects of Tobacco Stem-Derived Biochar on Soil Properties and Bacterial Community Structure under Continuous Cropping of <i>Bletilla striata</i> . <i>Journal of Soil Science and Plant Nutrition</i> , 2021, 21, 1318-1328.	1.7	11
4467	Identification of the relationship between the gut microbiome and feed efficiency in a commercial pig cohort. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	22

#	ARTICLE	IF	CITATIONS
4468	Dynamic characteristics and co-occurrence patterns of microbial community in tobacco leaves during the 24-month aging process. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	17
4469	The Structure of Rhizosphere Fungal Communities of Wild and Domesticated Rice: Changes in Diversity and Co-occurrence Patterns. <i>Frontiers in Microbiology</i> , 2021, 12, 610823.	1.5	29
4470	Multiple Selection Criteria for Probiotic Strains with High Potential for Obesity Management. <i>Nutrients</i> , 2021, 13, 713.	1.7	19
4471	Pervasive Genomic Signatures of Local Adaptation to Altitude Across Highland Specialist Andean Hummingbird Populations. <i>Journal of Heredity</i> , 2021, 112, 229-240.	1.0	10
4472	SAMHD1 restrains aberrant nucleotide insertions at repair junctions generated by DNA end joining. <i>Nucleic Acids Research</i> , 2021, 49, 2598-2608.	6.5	15
4473	Meta-analysis methods for multiple related markers: Applications to microbiome studies with the results on multiple α -diversity indices. <i>Statistics in Medicine</i> , 2021, 40, 2859-2876.	0.8	3
4474	DNA metabarcoding of zooplankton communities: species diversity and seasonal variation revealed by 18S rRNA and COI. <i>PeerJ</i> , 2021, 9, e11057.	0.9	6
4475	Temporal shifts in cyanobacterial diversity and their relationships to different types of biological soil crust in the southeastern Tengger Desert. <i>Rhizosphere</i> , 2021, 17, 100322.	1.4	10
4476	Mineralosphere Microbiome Leading to Changed Geochemical Properties of Sedimentary Rocks from Aiqigou Mud Volcano, Northwest China. <i>Microorganisms</i> , 2021, 9, 560.	1.6	3
4477	Characterization of biliary microbiota dysbiosis in extrahepatic cholangiocarcinoma. <i>PLoS ONE</i> , 2021, 16, e0247798.	1.1	30
4478	The Rumen Bacterial Community in Dairy Cows Is Correlated to Production Traits During Freshening Period. <i>Frontiers in Microbiology</i> , 2021, 12, 630605.	1.5	13
4479	Factors influencing the biodiversity of three microbial groups within and among islands of the Baltic Sea. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	8
4480	Biofertilizer-induced response to cadmium accumulation in <i>Oryza sativa</i> L. grains involving exogenous organic matter and soil bacterial community structure. <i>Ecotoxicology and Environmental Safety</i> , 2021, 211, 111952.	2.9	13
4482	Effects of lactic acid bacteria activation methods on mud crab (<i>Scylla paramamosain</i>) hatching rate and the microbiota in larval culture. <i>Aquaculture Research</i> , 2021, 52, 3997-4002.	0.9	0
4483	Colistin-resistant <i>Klebsiella pneumoniae</i> bloodstream infection: old drug, bad bug. <i>Archives of Microbiology</i> , 2021, 203, 2999-3006.	1.0	5
4484	Antimicrobial Resistance Phenotypes and Genotypes of <i>Escherichia coli</i> Isolates from Broiler Chickens Fed Encapsulated Cinnamaldehyde and Citral. <i>Journal of Food Protection</i> , 2021, 84, 1385-1399.	0.8	8
4485	Mapping the functional landscape of the receptor binding domain of T7 bacteriophage by deep mutational scanning. <i>ELife</i> , 2021, 10, .	2.8	30
4486	Effects of rumen-protected arginine supplementation on the plasma amino acids and gut microbiota of sika deer (<i>Cervus nippon</i>). <i>Animal Feed Science and Technology</i> , 2021, 273, 114828.	1.1	3

#	ARTICLE	IF	CITATIONS
4487	Enhanced rice yields are related to pronounced shifts in soil resident bacterial community structures in response to <i>Rhodospseudomonas palustris</i> and <i>Bacillus subtilis</i> inoculation. <i>Journal of Soils and Sediments</i> , 2021, 21, 2369-2380.	1.5	10
4488	Characterization of antimicrobial-resistant Gram-negative bacteria that cause neonatal sepsis in seven low- and middle-income countries. <i>Nature Microbiology</i> , 2021, 6, 512-523.	5.9	146
4489	Large-scale functional network connectivity mediate the associations of gut microbiota with sleep quality and executive functions. <i>Human Brain Mapping</i> , 2021, 42, 3088-3101.	1.9	31
4490	Digestibility, lactation performance, plasma metabolites, ruminal fermentation, and bacterial communities in Holstein cows fed a fermented corn gluten-wheat bran mixture as a substitute for soybean meal. <i>Journal of Dairy Science</i> , 2021, 104, 2866-2880.	1.4	8
4491	<i>Pediococcus acidilactici</i> Strains Improve Constipation Symptoms and Regulate Intestinal Flora in Mice. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 655258.	1.8	16
4493	Comparative Genomics Reveals Prophylactic and Catabolic Capabilities of <i>Actinobacteria</i> within the Fungus-Farming Termite Symbiosis. <i>MSphere</i> , 2021, 6, .	1.3	17
4494	Cd accumulation characteristics of <i>Salvia tiliifolia</i> and changes of rhizospheric soil enzyme activities and bacterial communities under a Cd concentration gradient. <i>Plant and Soil</i> , 2021, 463, 225-247.	1.8	19
4495	A switch of microbial flora coupled with ontogenetic niche shift in <i>Leptinotarsa decemlineata</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 107, e21782.	0.6	3
4496	Gene replacement of β -globin with γ -globin restores hemoglobin balance in β -thalassemia-derived hematopoietic stem and progenitor cells. <i>Nature Medicine</i> , 2021, 27, 677-687.	15.2	51
4497	Species and geographic specificity between endophytic fungi and host supported by parasitic <i>Cynomorium songaricum</i> and its host <i>Nitraria tangutorum</i> distributed in desert. <i>Archives of Microbiology</i> , 2021, 203, 2511-2519.	1.0	2
4499	Three phytosterols from sweet potato inhibit MCF7-xenograft-tumor growth through modulating gut microbiota homeostasis and SCFAs secretion. <i>Food Research International</i> , 2021, 141, 110147.	2.9	16
4500	Effects of biochar additions on the soil chemical properties, bacterial community structure and rape growth in an acid purple soil. <i>Plant, Soil and Environment</i> , 2021, 67, 121-129.	1.0	18
4501	Comparison of Methods for Picking the Operational Taxonomic Units From Amplicon Sequences. <i>Frontiers in Microbiology</i> , 2021, 12, 644012.	1.5	21
4502	Fungal community diversity and fermentation characteristics in regional varieties of traditional fermentation starters for Hong Qu glutinous rice wine. <i>Food Research International</i> , 2021, 141, 110146.	2.9	20
4503	Specific Microbial Taxa and Functional Capacity Contribute to Chicken Abdominal Fat Deposition. <i>Frontiers in Microbiology</i> , 2021, 12, 643025.	1.5	28
4504	Retinitis pigmentosa is associated with shifts in the gut microbiome. <i>Scientific Reports</i> , 2021, 11, 6692.	1.6	16
4505	Evaluating domestication and ploidy effects on the assembly of the wheat bacterial microbiome. <i>PLoS ONE</i> , 2021, 16, e0248030.	1.1	28
4506	Diversity and asynchrony in soil microbial communities stabilizes ecosystem functioning. <i>ELife</i> , 2021, 10, .	2.8	100

#	ARTICLE	IF	CITATIONS
4507	Metagenomic analysis exploring taxonomic and functional diversity of bacterial communities of a Himalayan urban fresh water lake. <i>PLoS ONE</i> , 2021, 16, e0248116.	1.1	27
4508	The Diversity of the Intestinal Flora Disturbed After Feeding Intolerance Recovery in Preterm Twins. <i>Frontiers in Pediatrics</i> , 2021, 9, 648979.	0.9	4
4510	Much ado about nothing? Off-target amplification can lead to false-positive bacterial brain microbiome detection in healthy and Parkinson's disease individuals. <i>Microbiome</i> , 2021, 9, 75.	4.9	31
4511	Response of Pine Rhizosphere Microbiota to Foliar Treatment with Resistance-Inducing Bacteria against Pine Wilt Disease. <i>Microorganisms</i> , 2021, 9, 688.	1.6	9
4512	Different Expressions of Pericardial Fluid MicroRNAs in Patients With Arrhythmogenic Right Ventricular Cardiomyopathy and Ischemic Heart Disease Undergoing Ventricular Tachycardia Ablation. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 647812.	1.1	10
4513	Long-term fertilisation regimes influence the diversity and community of wheat leaf bacterial endophytes. <i>Annals of Applied Biology</i> , 2021, 179, 176-184.	1.3	6
4514	Epstein-Barr virus inactivates the transcriptome and disrupts the chromatin architecture of its host cell in the first phase of lytic reactivation. <i>Nucleic Acids Research</i> , 2021, 49, 3217-3241.	6.5	16
4516	Panoramic: A package for constructing eukaryotic pan-genomes. <i>Molecular Ecology Resources</i> , 2021, 21, 1393-1403.	2.2	4
4517	Compositional and functional profiling of the rhizosphere microbiomes of the invasive weed <i>Ageratina adenophora</i> and native plants. <i>PeerJ</i> , 2021, 9, e10844.	0.9	4
4518	Epigenetic Variability Among Saffron Crocus (<i>Crocus sativus</i> L.) Accessions Characterized by Different Phenotypes. <i>Frontiers in Plant Science</i> , 2021, 12, 642631.	1.7	15
4519	Longitudinal study of the scalp microbiome suggests coconut oil to enrich healthy scalp commensals. <i>Scientific Reports</i> , 2021, 11, 7220.	1.6	13
4520	Bacterial Community Composition and Chromophoric Dissolved Organic Matter Differs with Culture Time of <i>Skeletonema dohrnii</i> . <i>Diversity</i> , 2021, 13, 150.	0.7	4
4521	Sex-specific effects of social defeat stress on miRNA expression in the anterior BNST. <i>Behavioural Brain Research</i> , 2021, 401, 113084.	1.2	13
4522	Highly parallelized droplet cultivation and prioritization of antibiotic producers from natural microbial communities. <i>ELife</i> , 2021, 10, .	2.8	44
4523	Asterix/Gtsf1 links tRNAs and piRNA silencing of retrotransposons. <i>Cell Reports</i> , 2021, 34, 108914.	2.9	12
4524	Comprehensive identification of somatic nucleotide variants in human brain tissue. <i>Genome Biology</i> , 2021, 22, 92.	3.8	26
4525	Bioaugmentation with immobilized endophytic <i>Penicillium restrictum</i> to improve quorum quenching activity for biofouling control in an aerobic hollow-fiber membrane bioreactor treating antibiotic-containing wastewater. <i>Ecotoxicology and Environmental Safety</i> , 2021, 210, 111831.	2.9	31
4526	Fungal and metabolome diversity of the rhizosphere and endosphere of <i>Phragmites australis</i> in an AMD-polluted environment. <i>Heliyon</i> , 2021, 7, e06399.	1.4	21

#	ARTICLE	IF	CITATIONS
4527	Calorie restriction prevents age-related changes in the intestinal microbiota. <i>Aging</i> , 2021, 13, 6298-6329.	1.4	11
4528	Fasting alters the gut microbiome reducing blood pressure and body weight in metabolic syndrome patients. <i>Nature Communications</i> , 2021, 12, 1970.	5.8	108
4529	Associations Between Endometriosis and Gut Microbiota. <i>Reproductive Sciences</i> , 2021, 28, 2367-2377.	1.1	49
4530	Plastid phylogenomics resolves ambiguous relationships within the orchid family and provides a solid timeframe for biogeography and macroevolution. <i>Scientific Reports</i> , 2021, 11, 6858.	1.6	30
4531	Koala Retrovirus in Northern Australia Shows a Mixture of Stable Endogenization and Exogenous Lineage Diversification within Fragmented Koala Populations. <i>Journal of Virology</i> , 2021, 95, .	1.5	8
4532	Effects of precipitation change and nitrogen addition on the composition, diversity, and molecular ecological network of soil bacterial communities in a desert steppe. <i>PLoS ONE</i> , 2021, 16, e0248194.	1.1	26
4533	Changes in above- and below-ground biodiversity and plant functional composition mediate soil respiration response to nitrogen input. <i>Functional Ecology</i> , 2021, 35, 1171-1182.	1.7	19
4534	The lung microbiota in Korean patients with non-tuberculous mycobacterial pulmonary disease. <i>BMC Microbiology</i> , 2021, 21, 84.	1.3	4
4535	Soil Microbiome Structure and Function in Ecopiles Used to Remediate Petroleum-Contaminated Soil. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	11
4536	Holstein and Jersey Steers Differ in Rumen Microbiota and Enteric Methane Emissions Even Fed the Same Total Mixed Ration. <i>Frontiers in Microbiology</i> , 2021, 12, 601061.	1.5	18
4537	Cecal microbial transplantation attenuates hyperthyroidism-induced thermogenesis in Mongolian gerbils. <i>Microbial Biotechnology</i> , 2022, 15, 817-831.	2.0	11
4538	Monitoring the variation in the gut microbiota of captive woolly monkeys related to changes in diet during a reintroduction process. <i>Scientific Reports</i> , 2021, 11, 6522.	1.6	9
4539	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. <i>Molecular Cell</i> , 2021, 81, 983-997.e7.	4.5	27
4540	Amplicon sequencing detects mutations associated with pyrethroid resistance in <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae). <i>Pest Management Science</i> , 2021, 77, 2914-2923.	1.7	5
4541	Bacteria From the Southern Gulf of Mexico: Baseline, Diversity, Hydrocarbon-Degrading Potential and Future Applications. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11
4542	Dynamic bacterial community response to <i>Akashiwo sanguinea</i> (Dinophyceae) bloom in indoor marine microcosms. <i>Scientific Reports</i> , 2021, 11, 6983.	1.6	14
4543	Analysis of Soil Fungal and Bacterial Communities in Tianchi Volcano Crater, Northeast China. <i>Life</i> , 2021, 11, 280.	1.1	11
4544	Soil profile rather than reclamation time drives the mudflat soil microbial community in the wheat-maize rotation system of Nantong, China. <i>Journal of Soils and Sediments</i> , 2021, 21, 1672-1687.	1.5	26

#	ARTICLE	IF	CITATIONS
4545	In situ characterisation of pathogen dynamics during a Pacific oyster mortality syndrome episode. <i>Marine Environmental Research</i> , 2021, 165, 105251.	1.1	12
4546	Microbiome Reengineering by Heat Selection for Rapid Biodegradation of Trichloroethylene with Minimal Vinyl Chloride Formation. <i>Water, Air, and Soil Pollution</i> , 2021, 232, 1.	1.1	4
4548	Maize germplasm chronosequence shows crop breeding history impacts recruitment of the rhizosphere microbiome. <i>ISME Journal</i> , 2021, 15, 2454-2464.	4.4	49
4549	Collection of Environmental Variables and Bacterial Community Compositions in Marian Cove, Antarctica, during Summer 2018. <i>Data</i> , 2021, 6, 27.	1.2	0
4550	Characterization of the first cultured free-living representative of <i>Candidatus</i> <i>Izemoplasma</i> uncovers its unique biology. <i>ISME Journal</i> , 2021, 15, 2676-2691.	4.4	32
4551	Gut microbiota signatures in <i>Schistosoma japonicum</i> infection-induced liver cirrhosis patients: a case-control study. <i>Infectious Diseases of Poverty</i> , 2021, 10, 43.	1.5	12
4552	Endotoxin Acts Synergistically With <i>Clostridioides difficile</i> Toxin B to Increase Interleukin 1 β Production: A Potential Role for the Intestinal Biome in Modifying the Severity of <i>C. difficile</i> Colitis. <i>Journal of Infectious Diseases</i> , 2021, 224, 1556-1565.	1.9	1
4553	The effect of flue-curing procedure on the dynamic change of microbial diversity of tobaccos. <i>Scientific Reports</i> , 2021, 11, 5354.	1.6	13
4554	Plasma cell free DNA methylation markers for hepatocellular carcinoma surveillance in patients with cirrhosis: a case control study. <i>BMC Gastroenterology</i> , 2021, 21, 136.	0.8	15
4556	Characteristics of soil bacterial and fungal communities on interval seawater covering Linchang Island, China. <i>Archives of Microbiology</i> , 2021, 203, 2453-2461.	1.0	1
4557	Cecal Microbiota Modulates Fat Deposition in Muscovy Ducks. <i>Frontiers in Veterinary Science</i> , 2021, 8, 609348.	0.9	18
4558	Community Composition and Function of Bacteria in Activated Sludge of Municipal Wastewater Treatment Plants. <i>Water (Switzerland)</i> , 2021, 13, 852.	1.2	21
4559	Nonlinear machine learning pattern recognition and bacteria-metabolite multilayer network analysis of perturbed gastric microbiome. <i>Nature Communications</i> , 2021, 12, 1926.	5.8	22
4560	Application of DNA barcoding and metabarcoding for species identification in salmon products. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2021, 38, 754-768.	1.1	11
4561	Tooth brushing using toothpaste containing theaflavins reduces the oral pathogenic bacteria in healthy adults. <i>3 Biotech</i> , 2021, 11, 150.	1.1	9
4562	Whipworm-Associated Intestinal Microbiome Members Consistent Across Both Human and Mouse Hosts. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 637570.	1.8	13
4563	Temperature and pH define the realised niche space of arbuscular mycorrhizal fungi. <i>New Phytologist</i> , 2021, 231, 763-776.	3.5	126
4564	A Phase II Randomized Clinical Trial and Mechanistic Studies Using Improved Probiotics to Prevent Oral Mucositis Induced by Concurrent Radiotherapy and Chemotherapy in Nasopharyngeal Carcinoma. <i>Frontiers in Immunology</i> , 2021, 12, 618150.	2.2	53

#	ARTICLE	IF	CITATIONS
4565	Machine learning optimization of peptides for presentation by class II MHCs. <i>Bioinformatics</i> , 2021, 37, 3160-3167.	1.8	8
4566	Bacterial diversity and flavor profile of Zha-Chili, a traditional fermented food in China. <i>Food Research International</i> , 2021, 141, 110112.	2.9	57
4567	Complete Genome Sequence, Genome Stability and Phylogeny of the Vaccine Strain <i>Mycobacterium bovis</i> BCG SL222 Sofia. <i>Vaccines</i> , 2021, 9, 237.	2.1	5
4568	Developmental exposure to silver nanoparticles leads to long term gut dysbiosis and neurobehavioral alterations. <i>Scientific Reports</i> , 2021, 11, 6558.	1.6	22
4569	Environmental filtering affects fungal communities more than dispersal limitation in a high-elevation hyperarid basin on Qinghaiâ€“Tibet Plateau. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	6
4570	Association of exacerbation phenotype with the sputum microbiome in chronic obstructive pulmonary disease patients during the clinically stable state. <i>Journal of Translational Medicine</i> , 2021, 19, 121.	1.8	31
4571	Fungal diversity in the mycangium of an ambrosia beetle <i>Xylosandrus crassiusculus</i> (Coleoptera:) Tj ETQq0 0 0 rgBT //Overlock 10 Tf 50 5	1.2	3
4572	Diversity of <i>Weissella confusa</i> in Pozol and Its Carbohydrate Metabolism. <i>Frontiers in Microbiology</i> , 2021, 12, 629449.	1.5	6
4573	Combination of Flos Sophorae and chili pepper as a nitrite alternative improves the antioxidant, microbial communities and quality traits in Chinese sausages. <i>Food Research International</i> , 2021, 141, 110131.	2.9	20
4574	Effects of propylene glycol on in vitro ruminal fermentation, methanogenesis, and microbial community structure. <i>Journal of Dairy Science</i> , 2021, 104, 2924-2934.	1.4	9
4575	Combined LCâ€“MS/MS and 16S rDNA analysis on mice under high temperature and humidity and Herb Yinchen protection mechanism. <i>Scientific Reports</i> , 2021, 11, 5099.	1.6	3
4577	Community Composition and Co-Occurrence Patterns of Diazotrophs along a Soil Profile in Paddy Fields of Three Soil Types in China. <i>Microbial Ecology</i> , 2021, 82, 961-970.	1.4	17
4578	Spatiotemporal variation of bacterial communities in three cascade reservoirs in a southern city of China. <i>Water Science and Technology: Water Supply</i> , 2021, 21, 2532-2542.	1.0	1
4579	Early Life Intervention Using Probiotic <i>Clostridium butyricum</i> Improves Intestinal Development, Immune Response, and Gut Microbiota in Large Yellow Croaker (<i>Larimichthys crocea</i>) Larvae. <i>Frontiers in Immunology</i> , 2021, 12, 640767.	2.2	36
4580	<i>Porphyrromonas gingivalis</i> Promotes Colorectal Carcinoma by Activating the Hematopoietic <i>NLRP3</i> Inflammasome. <i>Cancer Research</i> , 2021, 81, 2745-2759.	0.4	77
4581	Aerobic post-treatment of anaerobic digested sludge with a focus on organic matter stability and the fate of antibiotic resistance genes. <i>Journal of Cleaner Production</i> , 2021, 289, 125798.	4.6	15
4582	Microbial community and metabolic function analysis of cigar tobacco leaves during fermentation. <i>MicrobiologyOpen</i> , 2021, 10, e1171.	1.2	35
4583	Effects of monobutyryn supplementation on egg production, biochemical indexes, and gut microbiota of broiler breeders. <i>Poultry Science</i> , 2021, 100, 100907.	1.5	3

#	ARTICLE	IF	CITATIONS
4584	The comprehensive changes in soil properties are continuous cropping obstacles associated with American ginseng (<i>Panax quinquefolius</i>) cultivation. <i>Scientific Reports</i> , 2021, 11, 5068.	1.6	37
4585	Prime editing in mice reveals the essentiality of a single base in driving tissue-specific gene expression. <i>Genome Biology</i> , 2021, 22, 83.	3.8	62
4586	Interactions between gut microbiota and metabolites modulate cytokine network imbalances in women with unexplained miscarriage. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 24.	2.9	37
4587	Composition and co-occurrence patterns of <i>Phragmites australis</i> rhizosphere bacterial community. <i>Aquatic Ecology</i> , 2021, 55, 695-710.	0.7	9
4588	The call for regional design code from the regional discrepancy of microbial communities in activated sludge. <i>Environmental Pollution</i> , 2021, 273, 116487.	3.7	10
4589	Soil amendments change bacterial functional genes more than taxonomic structure in a cadmium-contaminated soil. <i>Soil Biology and Biochemistry</i> , 2021, 154, 108126.	4.2	25
4590	Alpine soil microbial community structure and diversity are largely influenced by moisture content in the Zoige wetland. <i>International Journal of Environmental Science and Technology</i> , 2022, 19, 4369-4378.	1.8	9
4591	Succession of endophytic fungi and arbuscular mycorrhizal fungi associated with the growth of plant and their correlation with secondary metabolites in the roots of plants. <i>BMC Plant Biology</i> , 2021, 21, 165.	1.6	26
4592	Repulsive Guidance Molecule b Deficiency Induces Gut Microbiota Dysbiosis and Increases the Susceptibility to Intestinal Inflammation in Mice. <i>Frontiers in Microbiology</i> , 2021, 12, 648915.	1.5	12
4593	Long-term effects of maize straw return and manure on the microbial community in cinnamon soil in Northern China using 16S rRNA sequencing. <i>PLoS ONE</i> , 2021, 16, e0249884.	1.1	15
4594	Organic Electron Donors and Terminal Electron Acceptors Structure Anaerobic Microbial Communities and Interactions in a Permanently Stratified Sulfidic Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 620424.	1.5	9
4595	Middle Pleistocene genome calibrates a revised evolutionary history of extinct cave bears. <i>Current Biology</i> , 2021, 31, 1771-1779.e7.	1.8	27
4596	Patterns and drivers of microeukaryotic distribution along the North Equatorial Current from the Central Pacific Ocean to the South China Sea. <i>Marine Pollution Bulletin</i> , 2021, 165, 112091.	2.3	4
4597	The genomics of rapid climatic adaptation and parallel evolution in North American house mice. <i>PLoS Genetics</i> , 2021, 17, e1009495.	1.5	26
4598	Microbial composition and dynamic succession during the Daqu production process of Northern Jiang-flavored liquor in China. <i>3 Biotech</i> , 2021, 11, 224.	1.1	20
4599	A library preparation optimized for metagenomics of RNA viruses. <i>Molecular Ecology Resources</i> , 2021, 21, 1788-1807.	2.2	10
4600	Diurnal changes in bacterial communities in oxic surface and hypoxic middle seawater layers of the Changjiang River Estuary. <i>Acta Oceanologica Sinica</i> , 2021, 40, 92-106.	0.4	0
4601	Captivity Is Associated With Gut Mycobiome Composition in Tibetan Macaques (<i>Macaca thibetana</i>). <i>Frontiers in Microbiology</i> , 2021, 12, 665853.	1.5	16

#	ARTICLE	IF	CITATIONS
4602	Gut Structure and Microbial Communities in <i>Sirex noctilio</i> (Hymenoptera: Siricidae) and Their Predicted Contribution to Larval Nutrition. <i>Frontiers in Microbiology</i> , 2021, 12, 641141.	1.5	12
4603	Plant flavones enrich rhizosphere Oxalobacteraceae to improve maize performance under nitrogen deprivation. <i>Nature Plants</i> , 2021, 7, 481-499.	4.7	247
4604	Effects of Heat Stress on Gut-Microbial Metabolites, Gastrointestinal Peptides, Glycolipid Metabolism, and Performance of Broilers. <i>Animals</i> , 2021, 11, 1286.	1.0	30
4606	Different Responses of Bacterial and Archaeal Communities in River Sediments to Water Diversion and Seasonal Changes. <i>Microorganisms</i> , 2021, 9, 782.	1.6	12
4607	Dynamic Changes in Fecal Microbial Communities of Neonatal Dairy Calves by Aging and Diarrhea. <i>Animals</i> , 2021, 11, 1113.	1.0	36
4608	CaptureSeq: Hybridization-Based Enrichment of cpn60 Gene Fragments Reveals the Community Structures of Synthetic and Natural Microbial Ecosystems. <i>Microorganisms</i> , 2021, 9, 816.	1.6	8
4609	Dysbiosis and Intestinal Barrier Dysfunction in Pediatric Congenital Heart Disease Is Exacerbated Following Cardiopulmonary Bypass. <i>JACC Basic To Translational Science</i> , 2021, 6, 311-327.	1.9	18
4610	Influence of pore structure on biologically activated carbon performance and biofilm microbial characteristics. <i>Frontiers of Environmental Science and Engineering</i> , 2021, 15, 1.	3.3	9
4611	Novel Siphoviridae Bacteriophages Infecting <i>Bacteroides uniformis</i> Contain Diversity Generating Retroelement. <i>Microorganisms</i> , 2021, 9, 892.	1.6	7
4612	The Diversity of Root-Associated Endophytic Fungi from Four Epiphytic Orchids in China. <i>Diversity</i> , 2021, 13, 197.	0.7	5
4613	Inverse hydrogen isotope fractionation indicates heterotrophic microbial production of long-chain alkyl lipids in desolate Antarctic ponds. <i>Geobiology</i> , 2021, 19, 394-404.	1.1	10
4614	Bioaugmented Phytoremediation of Metal-Contaminated Soils and Sediments by Hemp and Giant Reed. <i>Frontiers in Microbiology</i> , 2021, 12, 645893.	1.5	28
4615	Termite mounds reduce soil microbial diversity by filtering rare microbial taxa. <i>Environmental Microbiology</i> , 2021, 23, 2659-2668.	1.8	8
4616	Oak decaying wood harbors taxonomically and functionally different bacterial communities in sapwood and heartwood. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108160.	4.2	12
4617	Root exudates increase phosphorus availability in the tomato/potato onion intercropping system. <i>Plant and Soil</i> , 2021, 464, 45-62.	1.8	19
4618	Microbial characteristics response to the soil quality of newly created farmland on the Loess Plateau. <i>Environmental Science and Pollution Research</i> , 2021, 28, 42290-42299.	2.7	5
4619	Tonsillar Microbiota: a Cross-Sectional Study of Patients with Chronic Tonsillitis or Tonsillar Hypertrophy. <i>MSystems</i> , 2021, 6, .	1.7	7
4620	Grassland fairy rings of <i>Leucocalocybe mongolica</i> represent the center of a rich soil microbial community. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 1357-1369.	0.8	8

#	ARTICLE	IF	CITATIONS
4621	Probiotic <i>Bacillus subtilis</i> 29,784 improved weight gain and enhanced gut health status of broilers under necrotic enteritis condition. <i>Poultry Science</i> , 2021, 100, 100981.	1.5	24
4622	Long-term nitrogen and sulfur deposition increased root-associated pathogen diversity and changed mutualistic fungal diversity in a boreal forest. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108163.	4.2	17
4623	Characterization of bacterial communities associated with blood-fed and starved tropical bed bugs, <i>Cimex hemipterus</i> (F.) (Hemiptera): a high throughput metabarcoding analysis. <i>Scientific Reports</i> , 2021, 11, 8465.	1.6	5
4624	Host resistance to <i>Bacillus thuringiensis</i> is linked to altered bacterial community within a specialist insect herbivore. <i>Molecular Ecology</i> , 2021, 30, 5438-5453.	2.0	23
4626	Seasonal Influence on Rumen Microbiota, Rumen Fermentation, and Enteric Methane Emissions of Holstein and Jersey Steers under the Same Total Mixed Ration. <i>Animals</i> , 2021, 11, 1184.	1.0	11
4627	Ages of weaning influence the gut microbiota diversity and function in Chongming white goats. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 3649-3658.	1.7	12
4628	Chloroplast acquisition without the gene transfer in kleptoplastic sea slugs, <i>Plakobranchus ocellatus</i> . <i>ELife</i> , 2021, 10, .	2.8	29
4629	Effects of dietary protein levels on growth performance, serum indexes, PI3K/AKT/mTOR/S6K signalling and intestinal microbiota of abalone <i>Haliotis discus hannai</i> . <i>Aquaculture Nutrition</i> , 2021, 27, 941-952.	1.1	8
4630	Comparison of 15 dinoflagellate genomes reveals extensive sequence and structural divergence in family Symbiodiniaceae and genus Symbiodinium. <i>BMC Biology</i> , 2021, 19, 73.	1.7	65
4631	Changes of fungal diversity in fine coal gasification slag amendment pig manure composting. <i>Bioresource Technology</i> , 2021, 325, 124703.	4.8	29
4632	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	30
4633	Evaluation of sublethal and transgenerational effects of sulfoxaflo on <i>Aphis gossypii</i> via life table parameters and 16S rRNA sequencing. <i>Pest Management Science</i> , 2021, 77, 3406-3418.	1.7	19
4634	Detoxification of heavy metals attributed to biological and non-biological complexes in soils around copper producing areas throughout China. <i>Journal of Cleaner Production</i> , 2021, 292, 125999.	4.6	10
4635	Prodigiosin of <i>Serratia marcescens</i> ZPG19 Alters the Gut Microbiota Composition of Kunming Mice. <i>Molecules</i> , 2021, 26, 2156.	1.7	9
4636	Biotic and abiotic factors distinctly drive contrasting biogeographic patterns between phyllosphere and soil resistomes in natural ecosystems. <i>ISME Communications</i> , 2021, 1, .	1.7	23
4637	Continuous cropping of alfalfa (<i>Medicago sativa</i> L.) reduces bacterial diversity and simplifies cooccurrence networks in aeolian sandy soil. <i>Soil Ecology Letters</i> , 2022, 4, 131-143.	2.4	13
4638	Interactions between <i>Cryptosporidium</i> , <i>Enterocytozoon</i> , <i>Giardia</i> and Intestinal Microbiota in Bactrian Camels on Qinghai-Tibet Plateau, China. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3595.	1.3	4
4639	Active Microbiome Structure and Functional Analyses of Freshwater Benthic Biofilm Samples Influenced by RNA Extraction Methods. <i>Frontiers in Microbiology</i> , 2021, 12, 588025.	1.5	2

#	ARTICLE	IF	CITATIONS
4640	Analysis of Endophyte Diversity of <i>Rheum palmatum</i> from Different Production Areas in Gansu Province of China and the Association with Secondary Metabolite. <i>Microorganisms</i> , 2021, 9, 978.	1.6	16
4641	The Effects of Microbial Inoculants on Bacterial Communities of the Rhizosphere Soil of Maize. <i>Agriculture (Switzerland)</i> , 2021, 11, 389.	1.4	4
4642	The impact of urine microbiota in patients with lower urinary tract symptoms. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 23.	1.7	24
4643	Contrasting Composition, Diversity and Predictive Metabolic Potential of the Rhizobacterial Microbiomes Associated with Native and Invasive <i>Prosopis</i> Congeners. <i>Current Microbiology</i> , 2021, 78, 2051-2060.	1.0	8
4644	Bacterial and eukaryotic community interactions might contribute to shrimp culture pond soil ecosystem at different culture stages. <i>Soil Ecology Letters</i> , 0, , 1.	2.4	2
4645	Differences in microbiota between acute and chronic perianal eczema. <i>Medicine (United States)</i> , 2021, 100, e25623.	0.4	4
4646	Tracking the changes of wetland soil bacterial community and metabolic potentials under drought and flooding conditions in experimental microcosms. <i>Journal of Soils and Sediments</i> , 2021, 21, 2404-2417.	1.5	7
4647	Virus Prevalence and Genetic Diversity Across a Wild Bumblebee Community. <i>Frontiers in Microbiology</i> , 2021, 12, 650747.	1.5	10
4648	Community composition of cecal microbiota in commercial yellow broilers with high and low feed efficiencies. <i>Poultry Science</i> , 2021, 100, 100996.	1.5	26
4649	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021, 13, 61.	3.6	63
4650	The Composition of Intestinal Microbiota From <i>Collichthys lucidus</i> and Its Interaction With Microbiota From Waters Along the Pearl River Estuary in China. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	5
4651	Thermophilic Chloroflexi Dominate in the Microbial Community Associated with Coal-Fire Gas Vents in the Kuznetsk Coal Basin, Russia. <i>Microorganisms</i> , 2021, 9, 948.	1.6	8
4652	Altered Gut Microbiota Taxonomic Compositions of Patients With Sepsis in a Pediatric Intensive Care Unit. <i>Frontiers in Pediatrics</i> , 2021, 9, 645060.	0.9	15
4654	Estimation of tuna population by the improved analytical pipeline of unique molecular identifier-assisted HaCeD-Seq (haplotype count from eDNA). <i>Scientific Reports</i> , 2021, 11, 7031.	1.6	6
4655	Rapid detection of total bacteria in foods using a poly-lysine-based lateral-flow assay. <i>Journal of Microbiological Methods</i> , 2021, 183, 106175.	0.7	2
4656	Optimization of the operational parameters for mesophilic biohydrogen production from palm oil mill effluent using enriched mixed culture. <i>Biomass Conversion and Biorefinery</i> , 2023, 13, 4915-4931.	2.9	4
4657	Gut microbiota of endangered crested ibis: Establishment, diversity, and association with reproductive output. <i>PLoS ONE</i> , 2021, 16, e0250075.	1.1	9
4658	Ursolic Acid Regulates Intestinal Microbiota and Inflammatory Cell Infiltration to Prevent Ulcerative Colitis. <i>Journal of Immunology Research</i> , 2021, 2021, 1-16.	0.9	21

#	ARTICLE	IF	CITATIONS
4659	Age-associated variation in the gut microbiota of chinstrap penguins (<i>Pygoscelis antarctica</i>) reveals differences in food metabolism. <i>MicrobiologyOpen</i> , 2021, 10, e1190.	1.2	5
4660	Comparison of complete nitrification–denitrification and partial nitrification–anammox for iron oxide wastewater treatment. <i>Journal of Cleaner Production</i> , 2021, 294, 126281.	4.6	9
4661	Soil Metabarcoding Offers a New Tool for the Investigation and Hunting of Truffles in Northern Thailand. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 293.	1.5	2
4662	Peripheral blood mononuclear cells (PBMC) microbiome is not affected by colon microbiota in healthy goats. <i>Animal Microbiome</i> , 2021, 3, 28.	1.5	8
4664	Insight into the introduction of domestic cattle and the process of Neolithization to the Spanish region Galicia by genetic evidence. <i>PLoS ONE</i> , 2021, 16, e0249537.	1.1	3
4665	Dietary Fiber Ameliorates Lipopolysaccharide-Induced Intestinal Barrier Function Damage in Piglets by Modulation of Intestinal Microbiome. <i>MSystems</i> , 2021, 6, .	1.7	26
4666	A combination of <i>Tropilaelaps mercedesae</i> and imidacloprid negatively affects survival, pollen consumption and midgut bacterial composition of honey bee. <i>Chemosphere</i> , 2021, 268, 129368.	4.2	11
4667	Diversity and abundance of soil microbial communities decline, and community compositions change with severity of post-fire logging. <i>Molecular Ecology</i> , 2021, 30, 2434-2448.	2.0	18
4668	Low-N protein engineering with data-efficient deep learning. <i>Nature Methods</i> , 2021, 18, 389-396.	9.0	212
4669	Effect of mangrove restoration on sediment properties and bacterial community. <i>Ecotoxicology</i> , 2021, 30, 1672-1679.	1.1	14
4670	Effect of Quicklime on Microbial Community in Strong Acidic Soil. <i>Journal of Soil Science and Plant Nutrition</i> , 2021, 21, 1771-1781.	1.7	8
4671	Fungal-Bacterial Cooccurrence Patterns Differ between Arbuscular Mycorrhizal Fungi and Nonmycorrhizal Fungi across Soil Niches. <i>MBio</i> , 2021, 12, .	1.8	31
4672	Characterization of the B cell receptor repertoire of patients with acute coronary syndrome. <i>Genes and Genomics</i> , 2021, , 1.	0.5	1
4673	Breast milk flora plays an important role in infantile eczema: cohort study in Northeast China. <i>Journal of Applied Microbiology</i> , 2021, 131, 2981-2993.	1.4	6
4674	Alterations of Gut Microbiota in Patients With Graves' Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663131.	1.8	20
4675	The Diversity and Dynamics of Fungi in <i>Dryocosmus kuriphilus</i> Community. <i>Insects</i> , 2021, 12, 426.	1.0	3
4676	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. <i>Nature Communications</i> , 2021, 12, 3238.	5.8	81
4677	Molecular diversity and abundance of the microbial community associated to an offshore oil field on the southeast of Brazil. <i>International Biodeterioration and Biodegradation</i> , 2021, 160, 105215.	1.9	12

#	ARTICLE	IF	CITATIONS
4678	Elevated phytohaemagglutinin-induced skin swelling response at an intermediate number of MHC class II alleles in bluethroat nestlings. <i>Journal of Avian Biology</i> , 2021, 52, .	0.6	3
4679	Live <i>Bacillus subtilis</i> natto Promotes Rumen Fermentation by Modulating Rumen Microbiota In Vitro. <i>Animals</i> , 2021, 11, 1519.	1.0	10
4681	Oral administration of <i>Moringa oleifera</i> leaf powder relieves oxidative stress, modulates mucosal immune response and cecal microbiota after exposure to heat stress in New Zealand White rabbits. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 66.	2.1	17
4682	A Seed Mucilage-Degrading Fungus From the Rhizosphere Strengthens the Plant-Soil-Microbe Continuum and Potentially Regulates Root Nutrients of a Cold Desert Shrub. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 538-546.	1.4	1
4684	16S rRNA Gene Amplicon Profiling of the New Zealand Parasitic Blowfly <i>Calliphora vicina</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
4685	Effects of plant growth promoting Rhizobacteria microbial on the growth, rhizosphere soil properties, and bacterial community of <i>Pinus sylvestris</i> var. <i>mongolica</i> seedlings. <i>Scandinavian Journal of Forest Research</i> , 2021, 36, 249-262.	0.5	17
4686	Changes in soil phosphorus availability and associated microbial properties after chicken farming in Lei bamboo (<i>Phyllostachys praecox</i>) forest ecosystems. <i>Land Degradation and Development</i> , 2021, 32, 3008-3022.	1.8	13
4687	Woody encroachment in grassland elicits complex changes in the functional structure of above- and belowground biota. <i>Ecosphere</i> , 2021, 12, e03512.	1.0	14
4688	Microscopic Colitis Patients Possess a Perturbed and Inflammatory Gut Microbiota. <i>Digestive Diseases and Sciences</i> , 2022, 67, 2433-2443.	1.1	13
4689	Effects of long-term discharge of acid mine drainage from abandoned coal mines on soil microorganisms: microbial community structure, interaction patterns, and metabolic functions. <i>Environmental Science and Pollution Research</i> , 2021, 28, 53936-53952.	2.7	16
4690	Mycorrhizal Fungal Diversity and Its Relationship with Soil Properties in <i>Camellia oleifera</i> . <i>Agriculture (Switzerland)</i> , 2021, 11, 470.	1.4	15
4691	Water flushing irremovable biofilms on support material in dynamic membrane bioreactor: Formation, composition, and microbial community. <i>Chemosphere</i> , 2021, 271, 129813.	4.2	10
4692	In vivo CRISPR base editing of PCSK9 durably lowers cholesterol in primates. <i>Nature</i> , 2021, 593, 429-434.	13.7	408
4693	<i>Bremerella alba</i> sp. nov., a novel planctomycete isolated from the surface of the macroalga <i>Fucus spiralis</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126189.	1.2	14
4694	16S rRNA Gene Amplicon Sequencing of Contaminated Coastal Sediment Collected from the Taehwa River Estuary, South Korea. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
4695	Environmental DNA metabarcoding primers for freshwater fish detection and quantification: In silico and in tanks. <i>Ecology and Evolution</i> , 2021, 11, 8281-8294.	0.8	24
4696	Variations in Soil Enzyme Activities and Microbial Communities along an Altitudinal Gradient on the Eastern Qinghai-Tibetan Plateau. <i>Forests</i> , 2021, 12, 681.	0.9	8
4697	Rhizosphere-associated nosZII microbial community of <i>Phragmites australis</i> and its influence on nitrous oxide emissions in two different regions. <i>Journal of Soils and Sediments</i> , 2021, 21, 3326-3341.	1.5	7

#	ARTICLE	IF	CITATIONS
4698	The water column of the Yamal tundra lakes as a microbial filter preventing methane emission. <i>Biogeosciences</i> , 2021, 18, 2791-2807.	1.3	10
4699	Gut microbiota contributes to the development of endometrial glands in gilts during the ovary-dependent period. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 57.	2.1	5
4700	Different Cultivation Environments Affect the Yield, Bacterial Community and Metabolites of <i>Cordyceps cicadae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 669785.	1.5	12
4701	Dietary Supplementation of Yeast Culture Into Pelleted Total Mixed Rations Improves the Growth Performance of Fattening Lambs. <i>Frontiers in Veterinary Science</i> , 2021, 8, 657816.	0.9	10
4702	The Use of Molecular Profiling to Track Equine Reinfection Rates of Cyathostomin Species Following Anthelmintic Administration. <i>Animals</i> , 2021, 11, 1345.	1.0	6
4703	Metagenomic analysis of pathogen mastitis in cow's milk from Cicurug, Sukabumi, West Java, Indonesia. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 762, 012064.	0.2	2
4704	Alterations of Serum Metabolites and Fecal Microbiota Involved in Ewe Follicular Cyst. <i>Frontiers in Microbiology</i> , 2021, 12, 675480.	1.5	4
4705	Treatment of petroleum hydrocarbon-polluted groundwater with innovative in situ sulfate-releasing biobarrier. <i>Journal of Cleaner Production</i> , 2021, 295, 126424.	4.6	14
4706	Safety and Efficacy of a Phage, λ psk3, in an in vivo Model of Carbapenem-Resistant Hypermucoviscous <i>Klebsiella pneumoniae</i> Bacteremia. <i>Frontiers in Microbiology</i> , 2021, 12, 613356.	1.5	12
4707	Alteration of vaginal microbiota in patients with recurrent miscarriage. <i>Journal of Obstetrics and Gynaecology</i> , 2022, 42, 248-255.	0.4	12
4708	Oral Microbiome Characteristics in Patients With Autoimmune Hepatitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 656674.	1.8	16
4710	Extraction and characterisation of arabinoxylan from brewers spent grain and investigation of microbiome modulation potential. <i>European Journal of Nutrition</i> , 2021, 60, 4393-4411.	1.8	24
4711	Increasing Inundation Frequencies Enhance the Stochastic Process and Network Complexity of the Soil Archaeal Community in Coastal Wetlands. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	15
4712	Sampling cores and sequencing depths affected the measurement of microbial diversity in soil quadrats. <i>Science of the Total Environment</i> , 2021, 767, 144966.	3.9	14
4713	Diversity and functional characteristics of endophytic bacteria from two grass species growing on an oil-contaminated site in the Yellow River Delta, China. <i>Science of the Total Environment</i> , 2021, 767, 144340.	3.9	14
4714	Bacterial diversity and predicted enzymatic function in a multipurpose surface water system "from wastewater effluent discharges to drinking water production. <i>Environmental Microbiomes</i> , 2021, 16, 11.	2.2	17
4715	PEPPRO: quality control and processing of nascent RNA profiling data. <i>Genome Biology</i> , 2021, 22, 155.	3.8	17
4716	Characterising Post-mortem Bacterial Translocation Under Clinical Conditions Using 16S rRNA Gene Sequencing in Two Animal Models. <i>Frontiers in Microbiology</i> , 2021, 12, 649312.	1.5	2

#	ARTICLE	IF	CITATIONS
4717	Predicting the influence of fertilization regimes on potential N fixation through their effect on free-living diazotrophic community structure in double rice cropping systems. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108220.	4.2	33
4718	Environmental DNA provides higher resolution assessment of riverine biodiversity and ecosystem function via spatio-temporal nestedness and turnover partitioning. <i>Communications Biology</i> , 2021, 4, 512.	2.0	30
4719	A comparison of microbial communities and volatile compounds in wheat Qu from different geographic locations. <i>LWT - Food Science and Technology</i> , 2021, 148, 111752.	2.5	7
4720	African and Asian leopards are highly differentiated at the genomic level. <i>Current Biology</i> , 2021, 31, 1872-1882.e5.	1.8	20
4721	Bacterial community responses to the redox profile changes of mariculture sediment. <i>Marine Pollution Bulletin</i> , 2021, 166, 112250.	2.3	4
4722	Assessment of Oral Vancomycin-Induced Alterations in Gut Bacterial Microbiota and Metabolome of Healthy Men. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 629438.	1.8	9
4723	Potential of fecal microbiota for detection and postoperative surveillance of colorectal cancer. <i>BMC Microbiology</i> , 2021, 21, 156.	1.3	10
4724	Different Associations between Tonsil Microbiome, Chronic Tonsillitis, and Intermittent Hypoxemia among Obstructive Sleep Apnea Children of Different Weight Status: A Pilot Case-Control Study. <i>Journal of Personalized Medicine</i> , 2021, 11, 486.	1.1	8
4725	Abundance alteration of nondominant species in fecal-associated microbiome of patients with SAPHO syndrome. <i>BMC Microbiology</i> , 2021, 21, 161.	1.3	0
4727	Saprotrophic fungal diversity predicts ectomycorrhizal fungal diversity along the timberline in the framework of island biogeography theory. <i>ISME Communications</i> , 2021, 1, .	1.7	16
4728	Real-time monitoring of ruminal microbiota reveals their roles in dairy goats during subacute ruminal acidosis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 45.	2.9	32
4729	Screening and Comparison of Lignin Degradation Microbial Consortia from Wooden Antiques. <i>Molecules</i> , 2021, 26, 2862.	1.7	17
4730	Characteristics of the New Xanthan-Producing Strain <i>Xanthomonas campestris</i> Døe 28: Study of the Genome, Cultivation Conditions, and Physicochemical and Rheological Properties of the Polysaccharide. <i>Applied Biochemistry and Microbiology</i> , 2021, 57, 356-365.	0.3	3
4731	Human Milk Virome Analysis: Changing Pattern Regarding Mode of Delivery, Birth Weight, and Lactational Stage. <i>Nutrients</i> , 2021, 13, 1779.	1.7	18
4732	Rumen Microbiota of Tibetan Sheep (<i>Ovis aries</i>) Adaptation to Extremely Cold Season on the Qinghai-Tibetan Plateau. <i>Frontiers in Veterinary Science</i> , 2021, 8, 673822.	0.9	18
4734	Microbiota identified from preserved <i>Anopheles</i> . <i>Malaria Journal</i> , 2021, 20, 230.	0.8	10
4735	Parasites, Drugs and Captivity: Blastocystis-Microbiome Associations in Captive Water Voles. <i>Biology</i> , 2021, 10, 457.	1.3	5
4736	Bacterial Diversity Profiling of the New Zealand Parasitic Blowfly <i>Lucilia sericata</i> Based on 16S rRNA Gene Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3

#	ARTICLE	IF	CITATIONS
4737	Habitats and seasons differentiate the assembly of bacterial communities along a trophic gradient of freshwater lakes. <i>Freshwater Biology</i> , 2021, 66, 1515-1529.	1.2	16
4738	Comparison of subgingival and gingival margin plaque microbiota from dogs with healthy gingiva and early periodontal disease.. <i>Research in Veterinary Science</i> , 2021, 136, 396-407.	0.9	5
4739	Fab-dimerized glycan-reactive antibodies are a structural category of natural antibodies. <i>Cell</i> , 2021, 184, 2955-2972.e25.	13.5	57
4740	Gut Microbiota Changes and Their Correlation with Cognitive and Neuropsychiatric Symptoms in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2021, 81, 583-595.	1.2	59
4741	Specific and conserved patterns of microbiota-structuring by maize benzoxazinoids in the field. <i>Microbiome</i> , 2021, 9, 103.	4.9	57
4742	Metformin Affects Gut Microbiome Composition and Function and Circulating Short-Chain Fatty Acids: A Randomized Trial. <i>Diabetes Care</i> , 2021, 44, 1462-1471.	4.3	77
4743	Histoplasmosis acquired in Alberta, Canada: an epidemiological and genomic study. <i>Lancet Microbe</i> , 2021, 2, e191-e197.	3.4	10
4744	How animals distribute themselves in space: energy landscapes of Antarctic avian predators. <i>Movement Ecology</i> , 2021, 9, 24.	1.3	12
4745	Kefir metabolites in a fly model for Alzheimer's disease. <i>Scientific Reports</i> , 2021, 11, 11262.	1.6	16
4746	Effect of the Aerobic Denitrifying Bacterium <i>Pseudomonas furukawii</i> ZS1 on Microbiota Compositions in Grass Carp Culture Water. <i>Water (Switzerland)</i> , 2021, 13, 1329.	1.2	11
4748	Association Between Gut Akkermansia and Metabolic Syndrome is Dose-Dependent and Affected by Microbial Interactions: A Cross-Sectional Study. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2021, Volume 14, 2177-2188.	1.1	25
4749	The Impact of Microbiome and Microbiota-Derived Sodium Butyrate on Drosophila Transcriptome and Metabolome Revealed by Multi-Omics Analysis. <i>Metabolites</i> , 2021, 11, 298.	1.3	13
4750	Temporal Bacterial Community Diversity in the <i>Nicotiana tabacum</i> Rhizosphere Over Years of Continuous Monocropping. <i>Frontiers in Microbiology</i> , 2021, 12, 641643.	1.5	14
4751	Dynamic Observation of the Effect of Maternal Caries on the Oral Microbiota of Infants Aged 12-24 Months. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 637394.	1.8	3
4752	Integrated 16S rRNA Gene Sequencing and LC-MS Analysis Revealed the Interplay Between Gut Microbiota and Plasma Metabolites in Rats With Ischemic Stroke. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 2095-2106.	1.1	19
4753	Soil microbial community dynamics indicate disruption of nitrogen cycling by pollution in vegetation buffer zones. <i>Pedobiologia</i> , 2021, 85-86, 150722.	0.5	4
4754	Coexistence of Three Dominant Bacterial Symbionts in a Social Aphid and Implications for Ecological Adaptation. <i>Insects</i> , 2021, 12, 416.	1.0	7
4755	Accelerated Evolution of Tissue-Specific Genes Mediates Divergence Amidst Gene Flow in European Green Lizards. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1

#	ARTICLE	IF	CITATIONS
4756	Effects of Pasture Grass, Silage, and Hay Diet on Equine Fecal Microbiota. <i>Animals</i> , 2021, 11, 1330.	1.0	11
4757	Influences of submerged plant collapse on diet composition, breadth, and overlap among four crane species at Poyang Lake, China. <i>Frontiers in Zoology</i> , 2021, 18, 24.	0.9	25
4759	Gut Microbiota May Not Be Fully Restored in Recovered COVID-19 Patients After 3-Month Recovery. <i>Frontiers in Nutrition</i> , 2021, 8, 638825.	1.6	33
4760	Methane-Oxidizing Activity and Phylogenetic Diversity of Aerobic Methanotrophs in the Laptev Sea Upper Sediment Horizons. <i>Microbiology</i> , 2021, 90, 314-323.	0.5	4
4761	Changes of acid and alkaline phosphatase activities in long-term chemical fertilization are driven by the similar soil properties and associated microbial community composition in acidic soil. <i>European Journal of Soil Biology</i> , 2021, 104, 103312.	1.4	27
4762	Spatial and seasonal variations in biofilm formation on microplastics in coastal waters. <i>Science of the Total Environment</i> , 2021, 770, 145303.	3.9	71
4763	BAR-Seq clonal tracking of gene-edited cells. <i>Nature Protocols</i> , 2021, 16, 2991-3025.	5.5	11
4764	Diversity, Relative Abundance, and Functional Genes of Intestinal Microbiota of Tiger Grouper (<i>Epinephelus fuscoguttatus</i>) and Asian Seabass (<i>Lateolabrax japonicus</i>) Reared in A Semi-Closed Hatchery in Dry and Wet Seasons. <i>Pertanika Journal of Science and Technology</i> , 2021, 44, .	0.1	1
4765	Experimental Infection of the Biomphalaria glabrata Vector Snail by Schistosoma mansoni Parasites Drives Snail Microbiota Dysbiosis. <i>Microorganisms</i> , 2021, 9, 1084.	1.6	22
4766	Draft Genome Sequence of Bacillus velezensis BZR 277, a Prospective Biocontrol Agent against Phytoparasitic Nematodes. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
4767	Temporal overexpression of IL-22 and Reg3 β differentially impacts the severity of experimental autoimmune encephalomyelitis. <i>Immunology</i> , 2021, 164, 73-89.	2.0	5
4768	A strain of Bacteroides thetaiotaomicron attenuates colonization of Clostridioides difficile and affects intestinal microbiota and bile acids profile in a mouse model. <i>Biomedicine and Pharmacotherapy</i> , 2021, 137, 111290.	2.5	8
4769	Effects of Manure and Chemical Fertilizer on Bacterial Community Structure and Soil Enzyme Activities in North China. <i>Agronomy</i> , 2021, 11, 1017.	1.3	18
4770	Insights into the endophytic bacterial community comparison and their potential role in the dimorphic seeds of halophyte Suaeda glauca. <i>BMC Microbiology</i> , 2021, 21, 143.	1.3	5
4771	Living in a Puddle of Mud: Isolation and Characterization of Two Novel Caulobacteraceae Strains Brevundimonas pondensis sp. nov. and Brevundimonas goettingensis sp. nov.. <i>Applied Microbiology</i> , 2021, 1, 38-59.	0.7	20
4772	Continuous MYD88 Activation Is Associated With Expansion and Then Transformation of IgM Differentiating Plasma Cells. <i>Frontiers in Immunology</i> , 2021, 12, 641692.	2.2	11
4773	Effects of Different Land Use Types on Active Autotrophic Ammonia and Nitrite Oxidizers in Cinnamon Soils. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0009221.	1.4	8
4774	Differential Impacts of Water Table and Temperature on Bacterial Communities in Pore Water From a Subalpine Peatland, Central China. <i>Frontiers in Microbiology</i> , 2021, 12, 649981.	1.5	9

#	ARTICLE	IF	CITATIONS
4775	Differences in Gut Microbiome Composition and Antibiotic Resistance Gene Distribution between Chinese and Pakistani University Students from a Common Peer Group. <i>Microorganisms</i> , 2021, 9, 1152.	1.6	8
4776	Comparative analysis of de novo genomes reveals dynamic intra-species divergence of NLRs in pepper. <i>BMC Plant Biology</i> , 2021, 21, 247.	1.6	4
4777	Soil bacterial community composition in rice–fish integrated farming systems with different planting years. <i>Scientific Reports</i> , 2021, 11, 10855.	1.6	16
4778	Differential Impact of Plant Secondary Metabolites on the Soil Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 666010.	1.5	31
4779	Effects of Flurochloridone Application on Rhizosphere Soil Fungal Community and Composition in Potato Growing Areas of the Qinghai-Tibet Plateau. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 420.	1.5	2
4780	Bigu-Style Fasting Affects Metabolic Health by Modulating Taurine, Glucose, and Cholesterol Homeostasis in Healthy Young Adults. <i>Journal of Nutrition</i> , 2021, 151, 2175-2187.	1.3	6
4781	Capturing noroviruses circulating in the population: sewage surveillance in Guangdong, China (2013–2018). <i>Water Research</i> , 2021, 196, 116990.	5.3	10
4782	Long-term nitrogen input alters plant and soil bacterial, but not fungal beta diversity in a semiarid grassland. <i>Global Change Biology</i> , 2021, 27, 3939-3950.	4.2	64
4783	High-Throughput Sequencing Reveals Bacterial Diversity in Raw Milk Production Environment and Production Chain in Tangshan City of China. <i>Food Science of Animal Resources</i> , 2021, 41, 452-467.	1.7	8
4784	A Win–Loss Interaction on FeO Between Methanogens and Acetogens From a Climate Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 638282.	1.5	7
4785	Garlic skin induces shifts in the rumen microbiome and metabolome of fattening lambs. <i>Animal</i> , 2021, 15, 100216.	1.3	14
4786	Potential of Bradyrhizobia inoculation to promote peanut growth and beneficial Rhizobacteria abundance. <i>Journal of Applied Microbiology</i> , 2021, 131, 2500-2515.	1.4	8
4787	Geographical Distribution of Iron Redox Cycling Bacterial Community in Peatlands: Distinct Assemble Mechanism Across Environmental Gradient. <i>Frontiers in Microbiology</i> , 2021, 12, 674411.	1.5	6
4788	Evolving the core microbial community in pit mud based on bioturbation of fortified <i>Daqu</i> . <i>Canadian Journal of Microbiology</i> , 2021, 67, 396-405.	0.8	10
4790	High-fiber diet mitigates maternal obesity-induced cognitive and social dysfunction in the offspring via gut-brain axis. <i>Cell Metabolism</i> , 2021, 33, 923-938.e6.	7.2	110
4791	Who’s for dinner? Bird prey diversity and choice in the great evening bat, <i>la ioc</i> . <i>Ecology and Evolution</i> , 2021, 11, 8400-8409.	0.8	12
4792	Effects of Different Storage Temperatures on the Physicochemical Properties and Bacterial Community Structure of Fresh Lamb Meat. <i>Food Science of Animal Resources</i> , 2021, 41, 509-526.	1.7	26
4793	Methane oxidation in the waters of a humic-rich boreal lake stimulated by photosynthesis, nitrite, Fe(III) and humics. <i>Biogeosciences</i> , 2021, 18, 3087-3101.	1.3	20

#	ARTICLE	IF	CITATIONS
4794	Changes of gut microbiome composition and metabolites associated with hypertensive heart failure rats. <i>BMC Microbiology</i> , 2021, 21, 141.	1.3	27
4795	Genomic Characterization of the Barnacle <i>Balanus improvisus</i> Reveals Extreme Nucleotide Diversity in Coding Regions. <i>Marine Biotechnology</i> , 2021, 23, 402-416.	1.1	6
4796	Abundance, diversity, and community composition of anammox bacteria in sediments of Xiangshan Bay, China. <i>Regional Studies in Marine Science</i> , 2021, 44, 101739.	0.4	0
4797	Contrasting Patterns of the Resident and Active Rhizosphere Bacterial Communities of <i>Phragmites Australis</i> . <i>Microbial Ecology</i> , 2022, 83, 314-327.	1.4	3
4798	Effect of Vitamin A Supplementation on Growth Performance, Serum Biochemical Parameters, Intestinal Immunity Response and Gut Microbiota in American Mink (<i>Neovison vison</i>). <i>Animals</i> , 2021, 11, 1577.	1.0	11
4799	Effects of Heat Stress on Gut Microbiome in Rats. <i>Indian Journal of Microbiology</i> , 2021, 61, 338-347.	1.5	13
4800	Monosodium Glutamate Induces Changes in Hepatic and Renal Metabolic Profiles and Gut Microbiome of Wistar Rats. <i>Nutrients</i> , 2021, 13, 1865.	1.7	13
4801	Collaborative Response of the Host and Symbiotic Lignocellulytic System to Non-Lethal Toxic Stress in <i>Coptotermes formosanus</i> Skiraki. <i>Insects</i> , 2021, 12, 510.	1.0	2
4802	<i>Saccharomyces cerevisiae</i> boulardii CNCM I-1079 supplementation in finishing male pigs helps to cope with heat stress through feeding behaviour and gut microbiota modulation. <i>British Journal of Nutrition</i> , 2021, , 1-16.	1.2	7
4803	Soil microbial community variation with time and soil depth in Eurasian Steppe (Inner Mongolia,) Tj ETQq1 1 0.784314 rgBT /Overlock 11 20	1.1	20
4804	Microbial sulfate reduction by <i>Desulfovibrio</i> is an important source of hydrogen sulfide from a large swine finishing facility. <i>Scientific Reports</i> , 2021, 11, 10720.	1.6	18
4805	Interaction Between the Intestinal Microbial Community and Transcriptome Profile in Common Carp (<i>Cyprinus carpio</i> L.). <i>Frontiers in Microbiology</i> , 2021, 12, 659602.	1.5	11
4806	Evaluation of the microbiome composition in particulate matter inside and outside of pig houses. <i>Journal of Animal Science and Technology</i> , 2021, 63, 640-650.	0.8	11
4807	Biogeographic Role of the Kuroshio Current Intrusion in the Microzooplankton Community in the Boundary Zone of the Northern South China Sea. <i>Microorganisms</i> , 2021, 9, 1104.	1.6	6
4808	Illumina Sequencing of 18S/16S rRNA Reveals Microbial Community Composition, Diversity, and Potential Pathogens in 17 Turfgrass Seeds. <i>Plant Disease</i> , 2021, 105, 1328-1338.	0.7	3
4809	Mixing of biochar, vinegar and mushroom residues regulates soil microbial community and increases cucumber yield under continuous cropping regime. <i>Applied Soil Ecology</i> , 2021, 161, 103883.	2.1	27
4810	Whole-Genome Analysis Surveillance of Influenza A Virus Resistance to Polymerase Complex Inhibitors in Eastern Spain from 2016 to 2019. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	4
4811	Short- and Branched-Chain Fatty Acids as Fecal Markers for Microbiota Activity in Vegans and Omnivores. <i>Nutrients</i> , 2021, 13, 1808.	1.7	27

#	ARTICLE	IF	CITATIONS
4812	Effects of acid drainage from abandoned coal mines on the microbial community of Shandi River sediment, Shanxi Province. <i>International Journal of Coal Science and Technology</i> , 2021, 8, 756-766.	2.7	9
4813	Bias of library preparation for virome characterization in untreated and treated wastewaters. <i>Science of the Total Environment</i> , 2021, 767, 144589.	3.9	12
4814	Soil Bacterial Characteristics Under Four Habitats with Different Vegetation Communities on the Qinghai-Tibetan Plateau. <i>Wetlands</i> , 2021, 41, 1.	0.7	8
4815	Changes of gut microbiota in pregnant sows induced by 5-Aminolevulinic acid. <i>Research in Veterinary Science</i> , 2021, 136, 57-65.	0.9	5
4816	Identification and diversity assessment of cyanobacterial communities from some mine tailing sites in Benguet Province, Philippines using isolation-dependent and isolation-independent methods. <i>Environment, Development and Sustainability</i> , 2022, 24, 1166-1187.	2.7	2
4817	Genome wide association study reveals plant loci controlling heritability of the rhizosphere microbiome. <i>ISME Journal</i> , 2021, 15, 3181-3194.	4.4	97
4818	Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. <i>PLoS Genetics</i> , 2021, 17, e1009530.	1.5	26
4819	Dietary n-3 long chain polyunsaturated fatty acids affect the serum biochemical parameters, lipid metabolism-related of gene expression and intestinal health of juvenile hybrid grouper (<i>Lateolabrax japonicus</i>). <i>Journal of Applied Microbiology</i> , 2021, 130, 1383-1395.	1.1	7
4820	Biomethane production from whole and extracted algae biomass: Long-term performance evaluation and microbial community dynamics. <i>Renewable Energy</i> , 2021, 170, 38-48.	4.3	15
4821	Defining genome architecture at base-pair resolution. <i>Nature</i> , 2021, 595, 125-129.	13.7	107
4822	Gut Microbiota Signature Among Asian Post-gestational Diabetes Women Linked to Macronutrient Intakes and Metabolic Phenotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 680622.	1.5	13
4823	Effects of different dissolved organic matter on microbial communities and arsenic mobilization in aquifers. <i>Journal of Hazardous Materials</i> , 2021, 411, 125146.	6.5	71
4824	Outbreaks of Root Rot Disease in Different Aged American Ginseng Plants Are Associated With Field Microbial Dynamics. <i>Frontiers in Microbiology</i> , 2021, 12, 676880.	1.5	19
4825	Nationality and body location alter human skin microbiome. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5241-5256.	1.7	18
4826	Effects of the dietary grain content on rumen and fecal microbiota of dairy cows. <i>Canadian Journal of Animal Science</i> , 2021, 101, 274-286.	0.7	10
4827	Diversity and Distribution of Uncultured and Cultured Gaiellales and Rubrobacterales in South China Sea Sediments. <i>Frontiers in Microbiology</i> , 2021, 12, 657072.	1.5	6
4829	Therapeutic potential of an intestinotrophic hormone, glucagon-like peptide 2, for treatment of type 2 short bowel syndrome rats with intestinal bacterial and fungal dysbiosis. <i>BMC Infectious Diseases</i> , 2021, 21, 583.	1.3	8
4832	Correlations Between Intestinal Microbial Community and Hematological Profile in Native Tibetans and Han Immigrants. <i>Frontiers in Microbiology</i> , 2021, 12, 615416.	1.5	8

#	ARTICLE	IF	CITATIONS
4833	Gut Bacterial Diversity in Different Life Cycle Stages of <i>Adelphocoris suturalis</i> (Hemiptera: Miridae). <i>Frontiers in Microbiology</i> , 2021, 12, 670383.	1.5	22
4834	Host Phylogeny and Diet Shape Gut Microbial Communities Within Bamboo-Feeding Insects. <i>Frontiers in Microbiology</i> , 2021, 12, 633075.	1.5	27
4835	Printing Microbial Dark Matter: Using Single Cell Dispensing and Genomics to Investigate the Patescibacteria/Candidate Phyla Radiation. <i>Frontiers in Microbiology</i> , 2021, 12, 635506.	1.5	14
4836	Verrucomicrobial methanotrophs grow on diverse C3 compounds and use a homolog of particulate methane monoxygenase to oxidize acetone. <i>ISME Journal</i> , 2021, 15, 3636-3647.	4.4	29
4837	Response of Soil Fungal Diversity and Community Composition to Varying Levels of Bamboo Biochar in Red Soils. <i>Microorganisms</i> , 2021, 9, 1385.	1.6	29
4838	Effect of co-application of <i>Trichoderma</i> spp. with organic composts on plant growth enhancement, soil enzymes and fungal community in soil. <i>Archives of Microbiology</i> , 2021, 203, 4281-4291.	1.0	21
4839	The hepatotoxicity of altrazine exposure in mice involves the intestinal microbiota. <i>Chemosphere</i> , 2021, 272, 129572.	4.2	30
4840	Effects of dietary lipid levels on growth performance, hepatic health, lipid metabolism and intestinal microbiota on <i>Trachinotus ovatus</i> . <i>Aquaculture Nutrition</i> , 2021, 27, 1554-1568.	1.1	16
4841	A KMT2A-AFF1 gene regulatory network highlights the role of core transcription factors and reveals the regulatory logic of key downstream target genes. <i>Genome Research</i> , 2021, 31, 1159-1173.	2.4	16
4842	Bacterial community and composition of different traditional fermented dairy products in China, South Africa, and Sri Lanka by high-throughput sequencing of 16S rRNA genes. <i>LWT - Food Science and Technology</i> , 2021, 144, 111209.	2.5	12
4843	Fecal microbial composition and functional diversity of Wuzhishan pigs at different growth stages. <i>AMB Express</i> , 2021, 11, 88.	1.4	10
4844	The daily effect is more important than the diurnal effect when shaping photosynthetic picoeukaryotes (PPEs) communities in Lake Taihu at a small temporal scale. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	2
4846	Antidiabetic Function of <i>Lactobacillus fermentum</i> MF423-Fermented Rice Bran and Its Effect on Gut Microbiota Structure in Type 2 Diabetic Mice. <i>Frontiers in Microbiology</i> , 2021, 12, 682290.	1.5	28
4848	APB ϵ 13 improves the adverse outcomes caused by TGEV infection by correcting the intestinal microbial disorders in piglets. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2022, 106, 69-77.	1.0	3
4849	A diverse collection of B cells responded to HIV infection in infant BG505. <i>Cell Reports Medicine</i> , 2021, 2, 100314.	3.3	6
4850	Human transitional and IgM low mature na \bar{v} e B cells preserve permissive B ϵ cell receptors. <i>Immunology and Cell Biology</i> , 2021, 99, 865-878.	1.0	4
4851	Bacitracin Methylene Disalicylate Improves Intestinal Health by Modulating Its Development and Microbiota in Weaned Rabbits. <i>Frontiers in Microbiology</i> , 2021, 12, 579006.	1.5	2
4852	Variation in Soil Microbial Communities Along an Elevational Gradient in Alpine Meadows of the Qilian Mountains, China. <i>Frontiers in Microbiology</i> , 2021, 12, 684386.	1.5	16

#	ARTICLE	IF	CITATIONS
4853	Temporal variation in community structure of zoosporic fungi in Lake Biwa, Japan. <i>Aquatic Microbial Ecology</i> , 2021, 87, 17-28.	0.9	2
4854	Thermal Performance Curves of Multiple Isolates of <i>Batrachochytrium dendrobatidis</i> , a Lethal Pathogen of Amphibians. <i>Frontiers in Veterinary Science</i> , 2021, 8, 687084.	0.9	9
4855	The role of CTCF in the organization of the centromeric 11p15 imprinted domain interactome. <i>Nucleic Acids Research</i> , 2021, 49, 6315-6330.	6.5	11
4856	Shared and distinctive features of the gut microbiome of C57BL/6 mice from different vendors and production sites, and in response to a new vivarium. <i>Lab Animal</i> , 2021, 50, 185-195.	0.2	17
4857	<i>Lactobacillus acidophilus</i> LA14 Alleviates Liver Injury. <i>MSystems</i> , 2021, 6, e0038421.	1.7	30
4858	Antibiotic resistome mostly relates to bacterial taxonomy along a suburban transmission chain. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 1.	3.3	5
4859	High throughput analysis of <i>MHC</i> and <i>MHC</i> diversity of Brazilian cattle populations. <i>Hla</i> , 2021, 98, 93-113.	0.4	8
4860	Comparison of Diazotrophic Composition and Distribution in the South China Sea and the Western Pacific Ocean. <i>Biology</i> , 2021, 10, 555.	1.3	4
4861	Effect of Aeration on Yeast Community Structure and Volatile Composition in Uninoculated Chardonnay Wines. <i>Fermentation</i> , 2021, 7, 97.	1.4	6
4863	Palmitic acid mediated change of rhizosphere and alleviation of <i>Fusarium</i> wilt disease in watermelon. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 3616-3623.	1.8	17
4864	Whole-Genome Duplication Facilitated the Evolution of C4 Photosynthesis in <i>Gynandropsis gynandra</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 4715-4731.	3.5	13
4865	Benchmarking bioinformatic tools for fast and accurate eDNA metabarcoding species identification. <i>Molecular Ecology Resources</i> , 2021, 21, 2565-2579.	2.2	35
4866	Early Alpine occupation backdates westward human migration in Late Glacial Europe. <i>Current Biology</i> , 2021, 31, 2484-2493.e7.	1.8	17
4867	Cross-taxon congruence of aquatic microbial communities across geological ages in Iceland: Stochastic and deterministic processes. <i>Science of the Total Environment</i> , 2021, 774, 145103.	3.9	2
4868	Structural and Functional Impacts of Microbiota on <i>Pyropia yezoensis</i> and Surrounding Seawater in Cultivation Farms along Coastal Areas of the Yellow Sea. <i>Microorganisms</i> , 2021, 9, 1291.	1.6	9
4869	Impact of sample collection on prokaryotic and eukaryotic diversity of niche environments of the oil-sand mining impacted Athabasca River.. <i>Canadian Journal of Microbiology</i> , 2021, 67, 813-826.	0.8	1
4870	The <i>Atg16l1</i> gene: characterization of wild type, knock-in, and knock-out phenotypes in rats. <i>Physiological Genomics</i> , 2021, 53, 269-281.	1.0	6
4871	Influence of Taxonomic and Functional Content of Microbial Communities on the Quality of Fermented Cocoa Pulp-Bean Mass. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0042521.	1.4	9

#	ARTICLE	IF	CITATIONS
4872	The surface bacterial community of an Australian kelp shows cross-continental variation and relative stability within regions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	13
4873	Dissolved organic matter (DOM) quality drives biogeographic patterns of soil bacterial communities and their association networks in semi-arid regions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
4874	Biomethanation of Napier Grass Mono-digestion in Single-Stage Anaerobic Completely Stirred Tank Reactors Seeded with Cow Manure and Anaerobic Sludge. <i>Bioenergy Research</i> , 2022, 15, 559-572.	2.2	4
4875	Fecal microbiota profile in patients with inflammatory bowel disease in Taiwan. <i>Journal of the Chinese Medical Association</i> , 2021, 84, 580-587.	0.6	6
4876	Gut Bacteria Associated With <i>Monochamus saltuarius</i> (Coleoptera: Cerambycidae) and Their Possible Roles in Host Plant Adaptations. <i>Frontiers in Microbiology</i> , 2021, 12, 687211.	1.5	25
4878	Patterns of yeast diversity distribution and its drivers in rhizosphere soil of Hami melon orchards in different regions of Xinjiang. <i>BMC Microbiology</i> , 2021, 21, 170.	1.3	8
4879	Southern introgression increases adaptive immune gene variability in northern range margin populations of Fire-bellied toad. <i>Ecology and Evolution</i> , 2021, 11, 9776-9790.	0.8	2
4880	Impacts of Seagrass on Benthic Microalgae and Phytoplankton Communities in an Experimentally Warmed Coral Reef Mesocosm. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
4881	Correlation of Key Physiological Properties of <i>Methanosarcina</i> Isolates with Environment of Origin. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0073121.	1.4	26
4882	Stochastic processes shape the bacterial community assembly in shrimp cultural pond sediments. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5013-5022.	1.7	20
4883	Supersaturated-oxygen aeration effects on a high-loaded membrane bioreactor (HL-MBR): Biological performance and microbial population dynamics. <i>Science of the Total Environment</i> , 2021, 771, 144847.	3.9	7
4884	Rice domestication influences the composition and function of the rhizosphere bacterial chemotaxis systems. <i>Plant and Soil</i> , 2021, 466, 81-99.	1.8	16
4885	Microbial community responses to land-use types and its ecological roles in mining area. <i>Science of the Total Environment</i> , 2021, 775, 145753.	3.9	20
4886	Aboveground and Belowground Plant Traits Explain Latitudinal Patterns in Topsoil Fungal Communities From Tropical to Cold Temperate Forests. <i>Frontiers in Microbiology</i> , 2021, 12, 633751.	1.5	5
4887	Humus microhabitat affects distributions of soil fungi and bacteria in a temperate mountain forest. <i>Ecology and Evolution</i> , 2021, 11, 9148-9158.	0.8	5
4888	Long-term phytoremediation using the symbiotic <i>Pongamia pinnata</i> reshaped soil micro-ecological environment. <i>Science of the Total Environment</i> , 2021, 774, 145112.	3.9	9
4889	<i>Holdemanella biformis</i> improves glucose tolerance and regulates GLP-1 signaling in obese mice. <i>FASEB Journal</i> , 2021, 35, e21734.	0.2	18
4890	Intestinal Microbiota Mediates High-Fructose and High-Fat Diets to Induce Chronic Intestinal Inflammation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 654074.	1.8	39

#	ARTICLE	IF	CITATIONS
4891	High-Quality Genome Reconstruction of <i>Candida albicans</i> CHN1 Using Nanopore and Illumina Sequencing and Hybrid Assembly. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029921.	0.3	3
4892	Optimized bacterial DNA isolation method for microbiome analysis of human tissues. <i>MicrobiologyOpen</i> , 2021, 10, e1191.	1.2	21
4893	Application of Polyaluminium Chloride Coagulant in Urban River Water Treatment Influenced the Microbial Community in River Sediment. <i>Water (Switzerland)</i> , 2021, 13, 1791.	1.2	4
4894	Development of β -globin gene correction in human hematopoietic stem cells as a potential durable treatment for sickle cell disease. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	82
4895	<i>Bacillus subtilis</i> BSH has a protective effect on <i>Salmonella</i> infection by regulating the intestinal flora structure in chickens. <i>Microbial Pathogenesis</i> , 2021, 155, 104898.	1.3	5
4896	<i>Burkholderia</i> from Fungus Gardens of Fungus-Growing Ants Produces Antifungals That Inhibit the Specialized Parasite <i>Escovopsis</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0017821.	1.4	8
4897	A synbiotic intervention modulates meta-omics signatures of gut redox potential and acidity in elective caesarean born infants. <i>BMC Microbiology</i> , 2021, 21, 191.	1.3	13
4898	Particle size rather than concentration of silver nanoparticles mainly affects soil N ₂ -fixing bacterial communities. <i>International Journal of Environmental Science and Technology</i> , 2022, 19, 5611-5622.	1.8	3
4899	Seasonal Variation Characteristics of Bacteria and Fungi in PM _{2.5} in Typical Basin Cities of Xi'an and Linfen, China. <i>Atmosphere</i> , 2021, 12, 809.	1.0	7
4900	Tissue Type: A Crucial Factor Influencing the Fungal Diversity and Communities in Sichuan Pork Bacon. <i>Frontiers in Microbiology</i> , 2021, 12, 655500.	1.5	5
4901	The gut microbiome of the Sunda pangolin (<i>Manis javanica</i>) reveals its adaptation to specialized myrmecophagy. <i>PeerJ</i> , 2021, 9, e11490.	0.9	7
4902	Effects of soil water regime and nitrogen addition on ectomycorrhizal community structure of <i>Picea asperata</i> seedlings. <i>Journal of Plant Nutrition and Soil Science</i> , 2021, 184, 415-429.	1.1	3
4903	Geographic Distance and Habitat Type Influence Fungal Communities in the Arctic and Antarctic Sites. <i>Microbial Ecology</i> , 2021, 82, 224-232.	1.4	5
4904	Gut microbiota mediates cognitive impairment in young mice after multiple neonatal exposures to sevoflurane. <i>Aging</i> , 2021, 13, 16733-16748.	1.4	8
4905	Use of High-Throughput Sequencing to Identify Fungal Communities on the Surface of <i>Citri Reticulatae</i> Pericarpium During the 3-Year Aging Process. <i>Current Microbiology</i> , 2021, 78, 3142-3151.	1.0	12
4906	Intercropping of Tea (<i>Camellia sinensis</i> L.) and Chinese Chestnut: Variation in the Structure of Rhizosphere Bacterial Communities. <i>Journal of Soil Science and Plant Nutrition</i> , 2021, 21, 2178-2190.	1.7	30
4907	Quantitative evaluation of chromosomal rearrangements in gene-edited human stem cells by CAST-Seq. <i>Cell Stem Cell</i> , 2021, 28, 1136-1147.e5.	5.2	95
4908	Distinct bacterial communities in the environmental water, sediment and intestine between two crayfish-plant coculture ecosystems. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5087-5101.	1.7	17

#	ARTICLE	IF	CITATIONS
4909	Characterization of CH ₄ -oxidizing and N ₂ O-reducing Bacterial Consortia Enriched from the Rhizospheres of Maize and Tall Fescue. <i>Microbiology and Biotechnology Letters</i> , 2021, 49, 225-238.	0.2	3
4910	Î±-Terpineol fumigation alleviates negative plant-soil feedbacks of <i>Panax notoginseng</i> via suppressing Ascomycota and enriching antagonistic bacteria. <i>Phytopathology Research</i> , 2021, 3, .	0.9	13
4911	Comparative Analyses of the Gut Microbiome of Two Fox Species, the Red Fox (<i>Vulpes Vulpes</i>) and Corsac Fox (<i>Vulpes Corsac</i>), that Occupy Different Ecological Niches. <i>Microbial Ecology</i> , 2022, 83, 753-765.	1.4	15
4912	Procoagulant and Antimicrobial Effects of Chitosan in Wound Healing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7067.	1.8	27
4913	Decrease in abundance of bacteria of the genus <i>Bifidobacterium</i> in gut microbiota may be related to pre-eclampsia progression in women from East China. <i>Food and Nutrition Research</i> , 2021, 65, .	1.2	17
4914	Dietary Moutan Cortex Radicis Improves Serum Antioxidant Capacity and Intestinal Immunity and Alters Colonic Microbiota in Weaned Piglets. <i>Frontiers in Nutrition</i> , 2021, 8, 679129.	1.6	10
4915	Distinct tumor bacterial microbiome in lung adenocarcinomas manifested as radiological subsolid nodules. <i>Translational Oncology</i> , 2021, 14, 101050.	1.7	11
4916	Changes in Digestive Microbiota, Rumen Fermentations and Oxidative Stress around Parturition Are Alleviated by Live Yeast Feed Supplementation to Gestating Ewes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 447.	1.5	8
4917	Evaluation of Indigenous Olive Biocontrol Rhizobacteria as Protectants against Drought and Salt Stress. <i>Microorganisms</i> , 2021, 9, 1209.	1.6	8
4918	Population structure, activity potential and ecotype partitioning of <i>Pseudoalteromonas</i> along the vertical water column of the New Britain Trench. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	1
4919	Microbial Composition of Fermented Korean Soy Paste (Doenjang) Prepared by Adding Different Herbs during Fermentation. <i>Fermentation</i> , 2021, 7, 93.	1.4	3
4920	Effects of <i>Rhizophagus intraradices</i> on Plant Growth and the Composition of Microbial Communities in the Roots of Continuous Cropping Soybean at Maturity. <i>Sustainability</i> , 2021, 13, 6623.	1.6	9
4921	Effect of capsaicinoids in hot pepper powder on microbial community and free sugar during kimchi fermentation. <i>Journal of Food Science</i> , 2021, 86, 3195-3204.	1.5	7
4922	Synergistic Application of Molecular Markers and Community-Based Microbial Source Tracking Methods for Identification of Fecal Pollution in River Water During Dry and Wet Seasons. <i>Frontiers in Microbiology</i> , 2021, 12, 660368.	1.5	9
4923	Characterization of growth phenotypes and gastrointestinal tract microbiota in sheep fed with caragana. <i>Journal of Applied Microbiology</i> , 2021, 131, 2763-2779.	1.4	6
4924	Comparison of fungal community composition within different intestinal segments of tilapia and bighead carp. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1961-1971.	0.6	7
4925	Probiotics Improve Eating Disorders in Mandarin Fish (<i>Siniperca chuatsi</i>) Induced by a Pellet Feed Diet via Stimulating Immunity and Regulating Gut Microbiota. <i>Microorganisms</i> , 2021, 9, 1288.	1.6	23
4927	Consuming Different Structural Parts of Bamboo Induce Gut Microbiome Changes in Captive Giant Pandas. <i>Current Microbiology</i> , 2021, 78, 2998-3009.	1.0	9

#	ARTICLE	IF	CITATIONS
4928	Molecular gut content analysis indicates the inter- and intra-guild predation patterns of spiders in conventionally managed vegetable fields. <i>Ecology and Evolution</i> , 2021, 11, 9543-9552.	0.8	17
4929	Joint contributions of the gut microbiota and host genetics to feed efficiency in chickens. <i>Microbiome</i> , 2021, 9, 126.	4.9	58
4930	Temperature and microbial interactions drive the deterministic assembly processes in sediments of hot springs. <i>Science of the Total Environment</i> , 2021, 772, 145465.	3.9	85
4931	Probiotic <i>Streptococcus salivarius</i> K12 Alleviates Radiation-Induced Oral Mucositis in Mice. <i>Frontiers in Immunology</i> , 2021, 12, 684824.	2.2	18
4932	Grazing intensity induced alternations of soil microbial community composition in aggregates drive soil organic carbon turnover in a desert steppe. <i>Agriculture, Ecosystems and Environment</i> , 2021, 313, 107387.	2.5	26
4933	CRISPAItRations: A validated cloud-based approach for interrogation of double-strand break repair mediated by CRISPR genome editing. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 21, 478-491.	1.8	18
4934	Characterization of chilled chicken spoilage using an integrated microbiome and metabolomics analysis. <i>Food Research International</i> , 2021, 144, 110328.	2.9	38
4935	Historical genomics reveals the evolutionary mechanisms behind multiple outbreaks of the host-specific coffee wilt pathogen <i>Fusarium xylarioides</i> . <i>BMC Genomics</i> , 2021, 22, 404.	1.2	9
4936	Characterization of the gut microbiota in Chinese children with overweight and obesity using 16S rRNA gene sequencing. <i>PeerJ</i> , 2021, 9, e11439.	0.9	16
4937	Proper environmental DNA metabarcoding data transformation reveals temporal stability of fish communities in a dendritic river system. <i>Environmental DNA</i> , 2021, 3, 1007-1022.	3.1	27
4938	Integrated metabolomics and 16S rDNA sequencing to investigate the mechanism of immune-enhancing effect of health Tonic oral liquid. <i>Food Research International</i> , 2021, 144, 110323.	2.9	9
4939	Soil Stoichiometry Mediates Links Between Tree Functional Diversity and Soil Microbial Diversity in a Temperate Forest. <i>Ecosystems</i> , 2022, 25, 291-307.	1.6	12
4940	Characterization of vaginal fungal communities in healthy women and women with bacterial vaginosis (BV); a pilot study. <i>Microbial Pathogenesis</i> , 2021, 161, 105055.	1.3	13
4941	Enhanced Ruminal Fermentation Parameters and Altered Rumen Bacterial Community Composition by Formulated Rumen Buffer Agents Fed to Dairy Cows with a High-Concentrate Diet. <i>Agriculture (Switzerland)</i> , 2021, 11, 554.	1.4	8
4942	Ecological strategies of biological and chemical control agents on wildfire disease of tobacco (<i>Nicotiana tabacum</i> L.). <i>BMC Microbiology</i> , 2021, 21, 184.	1.3	9
4943	Seasonal dynamics of mycoplankton in the Yellow Sea reflect the combined effect of riverine inputs and hydrographic conditions. <i>Molecular Ecology</i> , 2021, 30, 3624-3637.	2.0	11
4944	Immunocompetent birds choose larger breeding colonies. <i>Journal of Animal Ecology</i> , 2021, 90, 2325-2335.	1.3	6
4945	Untapped Potential of Moving Bed Biofilm Reactors with Different Biocarrier Types for Bilge Water Treatment: A Laboratory-Scale Study. <i>Water (Switzerland)</i> , 2021, 13, 1810.	1.2	11

#	ARTICLE	IF	CITATIONS
4946	Interkingdom Gut Microbiome and Resistome of the Cockroach <i>Blattella germanica</i> . <i>MSystems</i> , 2021, 6, .	1.7	13
4947	Linking enhanced soil nitrogen mineralization to increased fungal decomposition capacity with Moso bamboo invasion of broadleaf forests. <i>Science of the Total Environment</i> , 2021, 771, 144779.	3.9	33
4948	Keystone species determine the selection mechanism of multispecies biofilms for bacteria from soil aggregates. <i>Science of the Total Environment</i> , 2021, 773, 145069.	3.9	11
4949	Nanobodies from camelid mice and llamas neutralize SARS-CoV-2 variants. <i>Nature</i> , 2021, 595, 278-282.	13.7	154
4950	Anaerobic degradation of high-concentration polycyclic aromatic hydrocarbons (PAHs) in seawater sediments. <i>Marine Pollution Bulletin</i> , 2021, 167, 112294.	2.3	13
4951	Sinus Microbiota in Patients With Eosinophilic and Non-Eosinophilic Chronic Rhinosinusitis With Nasal Polyps. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 672355.	1.8	7
4952	Phagotrophic Protists and Their Associates: Evidence for Preferential Grazing in an Abiotically Driven Soil Ecosystem. <i>Microorganisms</i> , 2021, 9, 1555.	1.6	6
4953	Two <i>Apriona</i> Species Sharing a Host Niche Have Different Gut Microbiome Diversity. <i>Microbial Ecology</i> , 2022, 83, 1059-1072.	1.4	10
4954	Rhizobacterial communities and crop development in response to long-term tillage practices in maize and soybean fields on the Loess Plateau of China. <i>Catena</i> , 2021, 202, 105319.	2.2	13
4955	Functional development of a V3/glycan-specific broadly neutralizing antibody isolated from a case of HIV superinfection. <i>ELife</i> , 2021, 10, .	2.8	6
4957	Microbiota continuum along the chicken oviduct and its association with host genetics and egg formation. <i>Poultry Science</i> , 2021, 100, 101104.	1.5	20
4959	Indicative Marker Microbiome Structures Deduced from the Taxonomic Inventory of 67 Full-Scale Anaerobic Digesters of 49 Agricultural Biogas Plants. <i>Microorganisms</i> , 2021, 9, 1457.	1.6	8
4960	A metabolic CRISPR-Cas9 screen in Chinese hamster ovary cells identifies glutamine-sensitive genes. <i>Metabolic Engineering</i> , 2021, 66, 114-122.	3.6	17
4961	Dietary supplementation of N-carbamylglutamate promotes growth performance by modulating the homeostasis of gut microbiota in tilapia (<i>Oreochromis niloticus</i>). <i>Aquaculture Reports</i> , 2021, 20, 100750.	0.7	5
4962	The growth of plants and indigenous bacterial community were significantly affected by cadmium contamination in soil-plant system. <i>AMB Express</i> , 2021, 11, 103.	1.4	7
4963	Community structure and activity potentials of archaeal communities in hadal sediments of the Mariana and Mussau trenches. <i>Marine Life Science and Technology</i> , 2022, 4, 150-161.	1.8	6
4964	Depth-dependent influence of biochar application on the abundance and community structure of diazotrophic under sugarcane growth. <i>PLoS ONE</i> , 2021, 16, e0253970.	1.1	16
4966	Effects of fermented mulberry leaves on growth, serum antioxidant capacity, digestive enzyme activities and microbial compositions of the intestine in crucian (<i>Carassius carassius</i>). <i>Aquaculture Research</i> , 2021, 52, 6356-6366.	0.9	6

#	ARTICLE	IF	CITATIONS
4967	Effects of rearing system (floor vs. cage) and sex on performance, meat quality and enteric microorganism of yellow feather broilers. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1907-1920.	1.7	16
4968	Temporal Comparison of Microbial Community Structure in an Australian Winery. <i>Fermentation</i> , 2021, 7, 134.	1.4	2
4969	Habitats Are More Important Than Seasons in Shaping Soil Bacterial Communities on the Qinghai-Tibetan Plateau. <i>Microorganisms</i> , 2021, 9, 1595.	1.6	9
4970	The Development of the Gut Microbiota and Short-Chain Fatty Acids of Layer Chickens in Different Growth Periods. <i>Frontiers in Veterinary Science</i> , 2021, 8, 666535.	0.9	28
4971	Analysis of gut microbiota in three species belonging to different genera (<i>Hemitragus</i> , <i>Pseudois</i> , and) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i> 2021, 11, 12129-12140.	0.8	3
4972	Phylogeographic analysis delimits three evolutionary significant units of least chipmunks in North America and identifies unique genetic diversity within the imperiled <i>Peñasco</i> population. <i>Ecology and Evolution</i> , 2021, 11, 12114-12128.	0.8	3
4973	Comparative analysis of the rectal and caecal microbial community composition and function in adult Erhualian and Sushan pigs. <i>Journal of Animal and Feed Sciences</i> , 2021, 30, 248-259.	0.4	0
4974	Effects of dietary lipid levels on growth performance, plasma biochemistry, lipid metabolism and intestinal microbiota of juvenile golden pompano (<i>Trachinotus ovatus</i>). <i>Aquaculture Nutrition</i> , 2021, 27, 1683-1698.	1.1	13
4975	Dynamic changes in microbial community structure in farming pond water and their effect on the intestinal microbial community profile in juvenile common carp (<i>Cyprinus carpio</i> L.). <i>Genomics</i> , 2021, 113, 2547-2560.	1.3	9
4976	Culture-Based and Culture-Independent Assessments of Endophytic Fungal Diversity in Aquatic Plants in Southwest China. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	11
4977	Impact of microecological agents on water environment restoration and microbial community structures of trench system in a Baiyangdian wetland ecosystem. <i>Journal of Applied Microbiology</i> , 2022, 132, 2450-2463.	1.4	7
4978	<i>Ganoderma lucidum</i> promotes sleep through a gut microbiota-dependent and serotonin-involved pathway in mice. <i>Scientific Reports</i> , 2021, 11, 13660.	1.6	19
4980	Non-Lactobacillus-Dominated Vaginal Microbiota Is Associated With a Tubal Pregnancy in Symptomatic Chinese Women in the Early Stage of Pregnancy: A Nested Caseâ€“Control Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 659505.	1.8	4
4981	The Enhancement of Intestinal Immunity in Offspring Piglets by Maternal Probiotic or Synbiotic Supplementation Is Associated With the Alteration of Gut Microbiota. <i>Frontiers in Nutrition</i> , 2021, 8, 686053.	1.6	21
4983	Roux-en-Y Gastric Bypass Improved Insulin Resistance via Alteration of the Human Gut Microbiome and Alleviation of Endotoxemia. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	5
4984	Caecal microbiota could effectively increase chicken growth performance by regulating fat metabolism. <i>Microbial Biotechnology</i> , 2022, 15, 844-861.	2.0	23
4985	New genetic markers for Sapotaceae phylogenomics: More than 600 nuclear genes applicable from family to population levels. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107123.	1.2	17
4986	Unveiling the Patterns of Reticulated Evolutionary Processes with Phylogenomics: Hybridization and Polyploidy in the Genus <i>Rosa</i> . <i>Systematic Biology</i> , 2022, 71, 547-569.	2.7	18

#	ARTICLE	IF	CITATIONS
4987	Extended Ecological Restoration of Bacterial Communities in the Godavari River During the COVID-19 Lockdown Period: a Spatiotemporal Meta-analysis. <i>Microbial Ecology</i> , 2021, 82, 365-376.	1.4	11
4988	Cropland to Miscanthus conversion alters soil bacterial and archaeal communities influencing N cycle in Northern China. <i>GCB Bioenergy</i> , 2021, 13, 1528-1544.	2.5	3
4989	Environmental DNA metabarcoding uncovers environmental correlates of fish communities in spatially heterogeneous freshwater habitats. <i>Ecological Indicators</i> , 2021, 126, 107698.	2.6	22
4990	Distribution of Hydrogen-Producing Bacteria in Tibetan Hot Springs, China. <i>Frontiers in Microbiology</i> , 2021, 12, 569020.	1.5	4
4991	Molecular diet studies of water mites reveal prey biodiversity. <i>PLoS ONE</i> , 2021, 16, e0254598.	1.1	10
4992	High-throughput detection of eukaryotic parasites and arboviruses in mosquitoes. <i>Biology Open</i> , 2021, 10, .	0.6	2
4993	Assessment of total bacterial diversity in whiteleg shrimps and its aquaculture environment in Pangkajene and Banyuwangi, Indonesia. <i>Asia-Pacific Journal of Molecular Biology and Biotechnology</i> , 2021, 10, 26-37.	0.2	0
4994	Characteristic dysbiosis in gout and the impact of a uric acid-lowering treatment, febuxostat on the gut microbiota. <i>Journal of Genetics and Genomics</i> , 2021, 48, 781-791.	1.7	23
4995	Absence of Significant Off-Target Splicing Variation with a U7snRNA Vector Targeting <i>DMD</i> Exon 2 Duplications. <i>Human Gene Therapy</i> , 2021, 32, 1346-1359.	1.4	8
4996	Succession of the microbial communities and function prediction during short-term peach sawdust-based composting. <i>Bioresource Technology</i> , 2021, 332, 125079.	4.8	62
4997	Fermentation characteristics and bacterial dynamics during Chinese sauerkraut fermentation by <i>Lactobacillus curvatus</i> LC-20 under varied salt concentrations reveal its potential in low-salt suan cai production. <i>Journal of Bioscience and Bioengineering</i> , 2021, 132, 33-40.	1.1	8
4998	Response of Root-Associated Bacterial Communities to Different Degrees of Soft Rot Damage in <i>Amorphophallus konjac</i> Under a <i>Robinia pseudoacacia</i> Plantation. <i>Frontiers in Microbiology</i> , 2021, 12, 652758.	1.5	4
4999	Seasonal Variation of Microbial Diversity of Coastal Sediment in Tongyeong, South Korea, Using 16S rRNA Gene Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0044621.	0.3	2
5000	Strong Replication Interference Between Hepatitis Delta Viruses in Human Liver Chimeric Mice. <i>Frontiers in Microbiology</i> , 2021, 12, 671466.	1.5	5
5001	The Microbial Community of Poultry Farm Waste and Its Role in Hydrogen Sulfide Production. <i>Microbiology</i> , 2021, 90, 507-511.	0.5	2
5002	Temporal differences in microbial composition of Poisses cheese rinds during ripening and storage. <i>Journal of Dairy Science</i> , 2021, 104, 7500-7508.	1.4	11
5003	Biparatopic single-domain antibodies against Axl achieve ultra-high affinity through intramolecular engagement. <i>Biochemical and Biophysical Research Communications</i> , 2021, 562, 154-161.	1.0	4
5004	Microbial profile of placentas from Tanzanian mothers with adverse pregnancy outcomes and periodontitis. <i>Oral Diseases</i> , 2023, 29, 772-785.	1.5	6

#	ARTICLE	IF	CITATIONS
5005	Effect of the herbal <i>Houttuynia cordata</i> floating bed on the Nile tilapia pond culturing system. <i>Aquaculture Reports</i> , 2021, 20, 100680.	0.7	1
5006	Effects of Continuous Cropping of <i>Codonopsis tangshen</i> on Rhizospheric Soil Bacterial Community as Determined by Pyrosequencing. <i>Diversity</i> , 2021, 13, 317.	0.7	5
5007	A sliver of the past: The decimation of the genetic diversity of the Mexican wolf. <i>Molecular Ecology</i> , 2021, 30, 6340-6354.	2.0	6
5008	Dynamics in Bacterial Community Affected by Mesoscale Eddies in the Northern Slope of the South China Sea. <i>Microbial Ecology</i> , 2022, 83, 823-836.	1.4	6
5009	Phylogenomic systematics of the spotted skunks (Carnivora, Mephitidae, Spilogale): Additional species diversity and Pleistocene climate change as a major driver of diversification. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107266.	1.2	9
5010	Investigations of soil autotrophic ammonia oxidizers in farmlands through genetics and big data analysis. <i>Science of the Total Environment</i> , 2021, 777, 146091.	3.9	12
5011	Minimal-moderate variation of human oral virome and microbiome in IgA deficiency. <i>Scientific Reports</i> , 2021, 11, 14913.	1.6	5
5012	<i>Bacteroides uniformis</i> CECT 7771 Modulates the Brain Reward Response to Reduce Binge Eating and Anxiety-Like Behavior in Rat. <i>Molecular Neurobiology</i> , 2021, 58, 4959-4979.	1.9	20
5013	Translocation of vaginal microbiota is involved in impairment and protection of uterine health. <i>Nature Communications</i> , 2021, 12, 4191.	5.8	70
5014	Modulation of the Intestinal Microbiota by the Early Intervention with <i>Clostridium Butyricum</i> in Muscovy Ducks. <i>Antibiotics</i> , 2021, 10, 826.	1.5	5
5015	Dietary Supplementation of Shredded, Steam-Exploded Pine Particles Decreases Pathogenic Microbes in the Cecum of Acute Heat-Stressed Broilers. <i>Animals</i> , 2021, 11, 2252.	1.0	12
5016	Designing specific bacterial 16S primers to sequence and quantitate plant endo-bacteriome. <i>Science China Life Sciences</i> , 2022, 65, 1000-1013.	2.3	11
5017	Warming intensifies soil pathogen negative feedback on a temperate tree. <i>New Phytologist</i> , 2021, 231, 2297-2307.	3.5	13
5018	Negative impacts of excessive nitrogen fertilization on the abundance and diversity of diazotrophs in black soil under maize monocropping. <i>Geoderma</i> , 2021, 393, 114999.	2.3	28
5019	Structure and driving factors of the soil microbial community associated with <i>Alhagi sparsifolia</i> in an arid desert. <i>PLoS ONE</i> , 2021, 16, e0254065.	1.1	14
5020	Characterization of Early Life Stress-Affected Gut Microbiota. <i>Brain Sciences</i> , 2021, 11, 913.	1.1	14
5021	Study on Microbial Community Succession and Protein Hydrolysis of Donkey Meat during Refrigerated Storage Based on Illumina NOVA Sequencing Technology. <i>Food Science of Animal Resources</i> , 2021, 41, 701-714.	1.7	4
5022	Alterations of Gut Microbiota in Patients With Intestinal Tuberculosis That Different From Crohn's Disease. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 673691.	2.0	9

#	ARTICLE	IF	CITATIONS
5023	Description of Microbial Communities of Phosphate Mine Wastes in Morocco, a Semi-Arid Climate, Using High-Throughput Sequencing and Functional Prediction. <i>Frontiers in Microbiology</i> , 2021, 12, 666936.	1.5	7
5024	Administration of All-Trans Retinoic Acid to Pregnant Sows Alters Gut Bacterial Community of Neonatal Piglets With Different <i>Hoxa1</i> Genotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 712212.	1.5	1
5025	Major histocompatibility complex class II genetic diversity and the genetic influence on gut microbiota in Guizhou minipigs. <i>Folia Microbiologica</i> , 2021, 66, 997-1008.	1.1	0
5026	Impact of anthropogenic activities on changes of ichthyofauna in the middle and lower Xiang River. <i>Aquaculture and Fisheries</i> , 2022, 7, 693-702.	1.2	10
5027	Coupling Between the Responses of Plants, Soil, and Microorganisms Following Grazing Exclusion in an Overgrazed Grassland. <i>Frontiers in Plant Science</i> , 2021, 12, 640789.	1.7	16
5028	Alterations to arbuscular mycorrhizal fungal community composition is driven by warming at specific elevations. <i>PeerJ</i> , 2021, 9, e11792.	0.9	4
5029	Response of soil bacterial communities to organic carbon input under soil freeze-thaw in forest ecosystems. <i>European Journal of Soil Biology</i> , 2021, 105, 103333.	1.4	7
5030	Grazing accelerates labile and recalcitrant soil carbon loss driving by rare microbial taxa in a desert steppe. <i>Land Degradation and Development</i> , 2021, 32, 4241-4253.	1.8	13
5031	Short-term response of pelagic planktonic communities after inoculation with the mass cultured dinoflagellate <i>Alexandrium</i> affine in a large-scale mesocosm experiment. <i>Journal of Applied Phycology</i> , 2021, 33, 3123-3137.	1.5	3
5033	Peptide-tiling screens of cancer drivers reveal oncogenic protein domains and associated peptide inhibitors. <i>Cell Systems</i> , 2021, 12, 716-732.e7.	2.9	9
5034	The Nexus between Fire and Soil Bacterial Diversity in the African Miombo Woodlands of Niassa Special Reserve, Mozambique. <i>Microorganisms</i> , 2021, 9, 1562.	1.6	6
5035	Impact of supplementary <i>Lactobacillus casei</i> K17 on growth and gut health of largemouth bass <i>Micropterus salmoides</i> . <i>Aquaculture Reports</i> , 2021, 20, 100734.	0.7	3
5036	Soil pH and Organic Carbon Properties Drive Soil Bacterial Communities in Surface and Deep Layers Along an Elevational Gradient. <i>Frontiers in Microbiology</i> , 2021, 12, 646124.	1.5	36
5037	Effects of dietary supplementation with a laminarin-rich extract on the growth performance and gastrointestinal health in broilers. <i>Poultry Science</i> , 2021, 100, 101179.	1.5	14
5038	Consistent Application of Inorganic N-Fertilizer Caused Retrogressive Succession of Cyanobacteria in an Upland Agricultural Soil of China. <i>Microbiology</i> , 2021, 90, 538-541.	0.5	0
5039	Microbial Composition in the Duodenum and Ileum of Yellow Broilers With High and Low Feed Efficiency. <i>Frontiers in Microbiology</i> , 2021, 12, 689653.	1.5	11
5040	Antibiotic-Induced Dysbiosis of Microbiota Promotes Chicken Lipogenesis by Altering Metabolomics in the Cecum. <i>Metabolites</i> , 2021, 11, 487.	1.3	18
5042	Bacterial Community Spacing Is Mainly Shaped by Unique Species in the Subalpine Natural Lakes of China. <i>Frontiers in Microbiology</i> , 2021, 12, 669131.	1.5	3

#	ARTICLE	IF	CITATIONS
5043	Distinct Functions and Assembly Mechanisms of Soil Abundant and Rare Bacterial Taxa Under Increasing Pyrene Stresses. <i>Frontiers in Microbiology</i> , 2021, 12, 689762.	1.5	26
5044	Carbon sources of benthic fauna in temperate lakes across multiple trophic states. <i>Biogeosciences</i> , 2021, 18, 4369-4388.	1.3	7
5045	Effect of straw application time on soil properties and microbial community in the Northeast China Plain. <i>Journal of Soils and Sediments</i> , 2021, 21, 3137-3149.	1.5	20
5046	Effect of a Multispecies Probiotic Mixture on the Growth and Incidence of Diarrhea, Immune Function, and Fecal Microbiota of Pre-weaning Dairy Calves. <i>Frontiers in Microbiology</i> , 2021, 12, 681014.	1.5	25
5047	AMF colonization and community of a temperate invader and co-occurring natives grown under different CO ₂ concentrations for 3 years. <i>Journal of Plant Ecology</i> , 2022, 15, 437-449.	1.2	5
5048	Effect of glucose on the soil bacterial diversity and function in the rhizosphere of <i>Cerasus sachalinensis</i> . <i>Horticultural Plant Journal</i> , 2021, 7, 307-317.	2.3	12
5049	A robust sequencing assay of a thousand amplicons for the high-throughput population monitoring of Alpine ibex immunogenetics. <i>Molecular Ecology Resources</i> , 2022, 22, 66-85.	2.2	7
5050	Oceanographic structure and seasonal variation contribute to high heterogeneity in mesozooplankton over small spatial scales. <i>ICES Journal of Marine Science</i> , 2021, 78, 3288-3302.	1.2	5
5051	Improved immobilization of soil cadmium by regulating soil characteristics and microbial community through reductive soil disinfestation. <i>Science of the Total Environment</i> , 2021, 778, 146222.	3.9	20
5052	Gut bacteria communities differ between <i>Gynaephora</i> species endemic to different altitudes of the Tibetan Plateau. <i>Science of the Total Environment</i> , 2021, 777, 146115.	3.9	11
5053	HLA class-I-peptide stability mediates CD8 ⁺ T cell immunodominance hierarchies and facilitates HLA-associated immune control of HIV. <i>Cell Reports</i> , 2021, 36, 109378.	2.9	17
5056	Effects of Dietary Supplementation with Protected Sodium Butyrate on Gut Microbiota in Growing-Finishing Pigs. <i>Animals</i> , 2021, 11, 2137.	1.0	15
5057	Endophytic Fungal Community of Tobacco Leaves and Their Potential Role in the Formation of 'Cherry-Red' Tobacco. <i>Frontiers in Microbiology</i> , 2021, 12, 658116.	1.5	4
5058	Intraspecific differences in the diet of Kuril harbor seals (<i>Phoca vitulina stejnegeri</i>) in Erimo, Hokkaido, using DNA barcoding diet analysis. <i>Mammal Research</i> , 2021, 66, 553-563.	0.6	0
5059	Dynamic Alterations of the Distal Intestinal Microbiota, Transcriptome, and Metabolome of Hybrid Grouper by Î ² -Conglycinin With Reconciliations by Sodium Butyrate in Feed. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
5060	Fermented and Germinated Processing Improved the Protective Effects of Foxtail Millet Whole Grain Against Dextran Sulfate Sodium-Induced Acute Ulcerative Colitis and Gut Microbiota Dysbiosis in C57BL/6 Mice. <i>Frontiers in Nutrition</i> , 2021, 8, 694936.	1.6	13
5061	Skin Microbiota of the Captive Giant Panda (<i>Ailuropoda Melanoleuca</i>) and the Distribution of Opportunistic Skin Disease-Associated Bacteria in Different Seasons. <i>Frontiers in Veterinary Science</i> , 2021, 8, 666486.	0.9	3
5062	Sensitive detection of tumor mutations from blood and its application to immunotherapy prognosis. <i>Nature Communications</i> , 2021, 12, 4172.	5.8	16

#	ARTICLE	IF	CITATIONS
5063	Variations of root-associated bacterial cooccurrence relationships in paddy soils under chlorantranilprole (CAP) stress. <i>Science of the Total Environment</i> , 2021, 779, 146247.	3.9	6
5064	An Exploratory Study for the Association of Gut Microbiome with Efficacy of Immune Checkpoint Inhibitor in Patients with Hepatocellular Carcinoma. <i>Journal of Hepatocellular Carcinoma</i> , 2021, Volume 8, 809-822.	1.8	17
5065	16S rRNA gene amplicon sequencing of gut microbiota in gestational diabetes mellitus and their correlation with disease risk factors. <i>Journal of Endocrinological Investigation</i> , 2022, 45, 279-289.	1.8	17
5066	How Does Pikeperch Sander <i>Lucioperca</i> Respond to Dietary Insect Meal <i>Hermetia illucens</i> ? Investigation on Gut Microbiota, Histomorphology, and Antioxidant Biomarkers. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	10
5067	The Genome Analysis of the Human Lung-Associated <i>Streptomyces</i> sp. TR1341 Revealed the Presence of Beneficial Genes for Opportunistic Colonization of Human Tissues. <i>Microorganisms</i> , 2021, 9, 1547.	1.6	3
5068	Shift in archaeal community along a soil profile in coastal wheat-maize rotation fields of different reclamation ages. <i>Land Degradation and Development</i> , 2021, 32, 4162-4173.	1.8	6
5069	Consecutive soybean (<i>Glycine max</i>) planting and covering improve acidified tea garden soil. <i>PLoS ONE</i> , 2021, 16, e0254502.	1.1	2
5070	Genomic Analysis and Stability Evaluation of the Phenol-Degrading Bacterium <i>Acinetobacter</i> sp. DW-1 During Water Treatment. <i>Frontiers in Microbiology</i> , 2021, 12, 687511.	1.5	6
5071	Fungal Community Analyses of Endophytic Fungi from Two Oak Species, <i>Quercus mongolica</i> and <i>Quercus serrata</i> , in Korea. <i>Mycobiology</i> , 2021, 49, 385-395.	0.6	8
5072	Arbuscular mycorrhizal fungal community structure following different grazing intensities in an alpine grassland. <i>Soil Science Society of America Journal</i> , 2021, 85, 1620-1633.	1.2	9
5073	The inhibition effect of tea polyphenols on soil nitrification is greater than denitrification in tea garden soil. <i>Science of the Total Environment</i> , 2021, 778, 146328.	3.9	25
5074	Arbuscular mycorrhizal fungal communities of topsoil and subsoil of an annual maize-wheat rotation after 15-years of differential mineral and organic fertilization. <i>Agriculture, Ecosystems and Environment</i> , 2021, 315, 107442.	2.5	9
5075	The metabolic process of aerobic granular sludge treating piggery wastewater: Microbial community, denitrification genes and mathematical model calculation. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 105392.	3.3	18
5076	Effects of Human, Caprine, and Bovine Milk Fat Globules on Microbiota Adhesion and Gut Microecology. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 9778-9787.	2.4	4
5077	Electrocatalytic deep dehalogenation of florfenicol using Fe-doped CoP nanotubes array for blocking resistance gene expression and microbial inhibition during biochemical treatment. <i>Water Research</i> , 2021, 201, 117361.	5.3	19
5078	Decisive Effects of Life Stage on the Gut Microbiota Discrepancy Between Two Wild Populations of Hibernating Asiatic Toads (<i>Bufo gargarizans</i>). <i>Frontiers in Microbiology</i> , 2021, 12, 665849.	1.5	6
5080	Tuber pseudohimalayense ascomata-compartments strongly select their associated bacterial microbiome from nearby pine forest soils independently of their maturation stage. <i>Pedobiologia</i> , 2021, 87-88, 150743.	0.5	9
5081	Effects of nitrogen addition on rhizospheric soil microbial communities of poplar plantations at different ages. <i>Forest Ecology and Management</i> , 2021, 494, 119328.	1.4	28

#	ARTICLE	IF	CITATIONS
5083	The Novel Interplay between Commensal Gut Bacteria and Metabolites in Diet-Induced Hyperlipidemic Rats Treated with Simvastatin. <i>Journal of Proteome Research</i> , 2021, , .	1.8	5
5084	The microbial population structure and function of peanut peanut and their effects on aflatoxin contamination. <i>LWT - Food Science and Technology</i> , 2021, 148, 111285.	2.5	4
5085	Local community assembly processes shape ð-diversity of soil <i>phoD</i>-harbouring communities in the Northern Hemisphere steppes. <i>Global Ecology and Biogeography</i> , 2021, 30, 2273-2285.	2.7	19
5086	Quantitative characterization of the B cell receptor repertoires of human immunized with commercial rabies virus vaccine. <i>Human Vaccines and Immunotherapeutics</i> , 2021, 17, 2538-2546.	1.4	2
5087	Crude oil biodegradation in upper and supratidal seashores. <i>Journal of Hazardous Materials</i> , 2021, 416, 125919.	6.5	16
5088	Washed Microbiota Transplantation Lowers Blood Pressure in Patients With Hypertension. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 679624.	1.8	34
5090	Modulation of gut microbiota by chondroitin sulfate calcium complex during alleviation of osteoporosis in ovariectomized rats. <i>Carbohydrate Polymers</i> , 2021, 266, 118099.	5.1	16
5091	Inoculating with the microbial agents to start up the aerobic composting of mushroom residue and wood chips at low temperature. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 105294.	3.3	40
5092	FROGS: a powerful tool to analyse the diversity of fungi with special management of internal transcribed spacers. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	19
5093	Comparison of Gut Microbiota of 96 Healthy Dogs by Individual Traits: Breed, Age, and Body Condition Score. <i>Animals</i> , 2021, 11, 2432.	1.0	37
5094	The Influence of Cesarean Section on the Composition and Development of Gut Microbiota During the First 3 Months of Life. <i>Frontiers in Microbiology</i> , 2021, 12, 691312.	1.5	8
5095	High-Throughput Single-Cell Technology Reveals the Contribution of Horizontal Gene Transfer to Typical Antibiotic Resistance Gene Dissemination in Wastewater Treatment Plants. <i>Environmental Science & Technology</i> , 2021, 55, 11824-11834.	4.6	33
5096	Diversity and functions of bacterial communities in water and sediment from the watershed of the Tama River flowing a highly urbanized area. <i>Fisheries Science</i> , 2021, 87, 697-715.	0.7	5
5097	The diarrhetic shellfish-poisoning toxin, okadaic acid, provokes gastropathy, dysbiosis and susceptibility to bacterial infection in a non-rodent bioassay, <i>Galleria mellonella</i> . <i>Archives of Toxicology</i> , 2021, 95, 3361-3376.	1.9	14
5098	Microbial Communities and Physicochemical Characteristics of Traditional Dajiang and Sufu in North China Revealed by High-Throughput Sequencing of 16S rRNA. <i>Frontiers in Microbiology</i> , 2021, 12, 665243.	1.5	6
5099	Succession of Fungal Communities at Different Developmental Stages of Cabernet Sauvignon Grapes From an Organic Vineyard in Xinjiang. <i>Frontiers in Microbiology</i> , 2021, 12, 718261.	1.5	18
5100	The apicoplast of <i>Haemoproteus columbae</i> : A comparative study of this organelle genome in Haemosporida. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107185.	1.2	8
5101	Metagenomic Analysis of Bacterial Diversity in Traditional Fermented Foods Reveals Food-Specific Dominance of Specific Bacterial Taxa. <i>Fermentation</i> , 2021, 7, 167.	1.4	13

#	ARTICLE	IF	CITATIONS
5102	Detection of archived lamivudine-associated resistance mutations in virologically suppressed, lamivudine-experienced HIV-infected adults by different genotyping techniques (GEN-PRO study). <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 3263-3271.	1.3	5
5103	Microbial composition differs between production systems and is associated with growth performance and carcass quality in pigs. <i>Animal Microbiome</i> , 2021, 3, 57.	1.5	7
5104	Rumen Fermentation, Digestive Enzyme Activity, and Bacteria Composition between Pre-Weaning and Post-Weaning Dairy Calves. <i>Animals</i> , 2021, 11, 2527.	1.0	14
5105	Impact of biocontrol microbes on soil microbial diversity in ginger (<i>Zingiber</i>) Tj ETQq1 1 0.784314 rgBT /Overlock_10 Tf 50_622 Td (b	1.7	14
5106	Metabolic Differentiation of Co-occurring <i>Accumulibacter</i> Clades Revealed through Genome-Resolved Metatranscriptomics. <i>MSystems</i> , 2021, 6, e0047421.	1.7	15
5107	<i>Prevotella copri</i> increases fat accumulation in pigs fed with formula diets. <i>Microbiome</i> , 2021, 9, 175.	4.9	100
5108	Quantitative Analysis of Bacterial Genes Expression as Prognostic Markers of Metabolic Disorders with the Aim of the Dairy Cattle's Health Monitoring. <i>Smart Innovation, Systems and Technologies</i> , 2022, , 29-39.	0.5	0
5109	Gut and Vagina Microbiota Associated With Estrus Return of Weaning Sows and Its Correlation With the Changes in Serum Metabolites. <i>Frontiers in Microbiology</i> , 2021, 12, 690091.	1.5	8
5110	Analytical Performance of NGS-Based Molecular Genetic Tests Used in the Diagnostic Workflow of Pheochromocytoma/Paraganglioma. <i>Cancers</i> , 2021, 13, 4219.	1.7	3
5111	Folic Acid Absorption Characteristics and Effect on Cecal Microbiota of Laying Hens. <i>Frontiers in Veterinary Science</i> , 2021, 8, 720851.	0.9	7
5112	Rapid target validation in a Cas9-inducible hiPSC derived kidney model. <i>Scientific Reports</i> , 2021, 11, 16532.	1.6	7
5113	Combining Multiple Markers in Environmental DNA Metabarcoding to Assess Deep-Sea Benthic Biodiversity. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	20
5114	Soil biota shift with land use change from pristine rainforest and Savannah (Cerrado) to agriculture in southern Amazonia. <i>Molecular Ecology</i> , 2021, 30, 4899-4912.	2.0	10
5115	Lower relative abundance of ectomycorrhizal fungi under a warmer and drier climate is linked to enhanced soil organic matter decomposition. <i>New Phytologist</i> , 2021, 232, 1399-1413.	3.5	27
5116	Variations in bacterial and archaeal community structure and diversity along the soil profiles of a peatland in Southwest China. <i>Environmental Science and Pollution Research</i> , 2022, 29, 2276-2286.	2.7	5
5118	Assessment of microbial α -diversity in one meter squared topsoil. <i>Soil Ecology Letters</i> , 2022, 4, 224-236.	2.4	10
5119	The Spatial and Temporal Characterization of Gut Microbiota in Broilers. <i>Frontiers in Veterinary Science</i> , 2021, 8, 712226.	0.9	26
5120	The Transcriptional Response of Soil Bacteria to Long-Term Warming and Short-Term Seasonal Fluctuations in a Terrestrial Forest. <i>Frontiers in Microbiology</i> , 2021, 12, 666558.	1.5	8

#	ARTICLE	IF	CITATIONS
5121	Method for quick DNA barcode reference library construction. <i>Ecology and Evolution</i> , 2021, 11, 11627-11638.	0.8	14
5122	Microbial Reconstitution Improves Aging-Driven Lacrimal Gland Circadian Dysfunction. <i>American Journal of Pathology</i> , 2021, 191, 2091-2116.	1.9	11
5123	Gut Microbial Diversity in Female Patients With Invasive Mole and Choriocarcinoma and Its Differences Versus Healthy Controls. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 704100.	1.8	4
5124	Two community types occur in gut microbiota of large-sample wild plateau pikas (<i>Ochotona</i>) Tj ETQq1 1 0.784314 rgBT/Overlook	1.3	14
5126	Diversity and Paleodemography of the Addax (<i>Addax nasomaculatus</i>), a Saharan Antelope on the Verge of Extinction. <i>Genes</i> , 2021, 12, 1236.	1.0	8
5127	Comparative analysis of rumen fermentation parameters and bacterial profiles during adaption to different fattening stages in beef cattle fed TMR with various forage silage. <i>Animal Feed Science and Technology</i> , 2021, 278, 115006.	1.1	8
5128	Exploring prevalence of potential pathogens and fecal indicators in geographically distinct river systems through comparative metagenomics. <i>Environmental Pollution</i> , 2021, 282, 117003.	3.7	7
5129	Seasonal Dietary Shifts Alter the Gut Microbiota of Avivorous Bats: Implication for Adaptation to Energy Harvest and Nutritional Utilization. <i>MSphere</i> , 2021, 6, e0046721.	1.3	16
5130	Truffle Microbiome Is Driven by Fruit Body Compartmentalization Rather than Soils Conditioned by Different Host Trees. <i>MSphere</i> , 2021, 6, e0003921.	1.3	10
5131	Using Fecal DNA Metabarcoding to Investigate Foraging Reveals the Effects of Specific Herbage on the Improved n-3 Fatty Acid (PUFA) Composition in the Longissimus Dorsi Muscle of Grazing Tan Sheep. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 9725-9734.	2.4	1
5132	An example of DNA methylation as a means to quantify stress in wildlife using killer whales. <i>Scientific Reports</i> , 2021, 11, 16822.	1.6	5
5133	Diversity and abundance of antibiotic resistance genes in rhizosphere soil and endophytes of leafy vegetables: Focusing on the effect of the vegetable species. <i>Journal of Hazardous Materials</i> , 2021, 415, 125595.	6.5	44
5134	LYmphoid NeXt-Generation Sequencing (LYNX) Panel. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 959-974.	1.2	11
5135	Development of a tRNA-Derived Small RNA Prognostic Panel and Their Potential Functions in Osteosarcoma. <i>Frontiers in Oncology</i> , 2021, 11, 652040.	1.3	2
5136	Temporal Changes in the Function of Bacterial Assemblages Associated With Decomposing Earthworms. <i>Frontiers in Microbiology</i> , 2021, 12, 682224.	1.5	5
5137	Infection Heterogeneity and Microbiota Differences in Chicks Infected by <i>Salmonella enteritidis</i> . <i>Microorganisms</i> , 2021, 9, 1705.	1.6	8
5138	Biosorption of Copper in Swine Manure Using <i>Aspergillus</i> and Yeast: Characterization and Its Microbial Diversity Study. <i>Frontiers in Microbiology</i> , 2021, 12, 687533.	1.5	2
5139	Effects of Age, Diet CP, NDF, EE, and Starch on the Rumen Bacteria Community and Function in Dairy Cattle. <i>Microorganisms</i> , 2021, 9, 1788.	1.6	9

#	ARTICLE	IF	CITATIONS
5140	The Effect of Ryegrass Silage Feeding on Equine Fecal Microbiota and Blood Metabolite Profile. <i>Frontiers in Microbiology</i> , 2021, 12, 715709.	1.5	0
5141	Deciphering the Shifts in Microbial Community Diversity From Material Pretreatment to Saccharification Process of Fuyu-Flavor Bajjiu. <i>Frontiers in Microbiology</i> , 2021, 12, 705967.	1.5	16
5142	Microbial dysbiosis together with nutrient imbalance cause the replant problem of upper six flue-cured tobacco in Central Henan. <i>Journal of Plant Diseases and Protection</i> , 0, , 1.	1.6	4
5143	Linking soil bacterial diversity to satellite-derived vegetation productivity: a case study in arid and semi-arid desert areas. <i>Environmental Microbiology</i> , 2021, 23, 6137-6147.	1.8	1
5145	Bacterial Consumption of T4 Phages. <i>Microorganisms</i> , 2021, 9, 1852.	1.6	0
5146	Development of the first microsatellite markers using high-throughput sequencing for a hexaploid coastal species, <i>Tournefortia argentea</i> L. f. (Boraginaceae). <i>Molecular Biology Reports</i> , 2021, 48, 7049-7055.	1.0	1
5147	Phosphorus availability increases pathobiome abundance and invasion of rhizosphere microbial networks by <i>Ralstonia</i> . <i>Environmental Microbiology</i> , 2021, 23, 5992-6003.	1.8	28
5148	Degradation Characteristics and Microbial Community of Phosphine Biopurification Systems. <i>Environmental Engineering Science</i> , 2021, 38, 802-810.	0.8	0
5149	Exploration of the Characteristics of Intestinal Microbiota and Metabolomics in Different Rat Models of Mongolian Medicine. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	0.5	2
5150	Construction and evaluation of a bioluminescent <i>Pseudomonas aeruginosa</i> reporter for use in preservative efficacy testing. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	0
5151	Influence of different phytoremediation on soil microbial diversity and community composition in saline-alkaline land. <i>International Journal of Phytoremediation</i> , 2022, 24, 507-517.	1.7	9
5152	Impact of nisin on <i>Clostridioides difficile</i> and microbiota composition in a faecal fermentation model of the human colon. <i>Journal of Applied Microbiology</i> , 2022, 132, 1397-1408.	1.4	7
5153	Genomic insights into the diversity, virulence and resistance of <i>Klebsiella pneumoniae</i> extensively drug resistant clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
5154	Nasopharyngeal microbiome reveals the prevalence of opportunistic pathogens in SARS-CoV-2 infected individuals and their association with host types. <i>Microbes and Infection</i> , 2022, 24, 104880.	1.0	31
5155	Connection between the Gut Microbiota of Largemouth Bass (<i>Micropterus salmoides</i>) and Microbiota of the Pond Culture Environment. <i>Microorganisms</i> , 2021, 9, 1770.	1.6	18
5157	Probiotic supplements alleviate gestational diabetes mellitus by restoring the diversity of gut microbiota: a study based on 16S rRNA sequencing. <i>Journal of Microbiology</i> , 2021, 59, 827-839.	1.3	13
5158	Mucosal Microbiota and Metabolome in the Ileum of Hu Sheep Offered a Low-Grain, Pelleted or Non-pelleted High-Grain Diet. <i>Frontiers in Microbiology</i> , 2021, 12, 718884.	1.5	4
5159	Assembly Processes and Co-occurrence Patterns of Abundant and Rare Bacterial Community in the Eastern Indian Ocean. <i>Frontiers in Microbiology</i> , 2021, 12, 616956.	1.5	9

#	ARTICLE	IF	CITATIONS
5160	Assessing the Influence of Environmental Sources on the Gut Mycobiome of Tibetan Macaques. <i>Frontiers in Microbiology</i> , 2021, 12, 730477.	1.5	3
5161	Seasonal Sampling of a Microbial Community in the Sediment of Geoje-Hansan Bay, Republic of Korea. <i>Microbiology Resource Announcements</i> , 2021, 10, e0056621.	0.3	1
5162	Pearl Oyster Bacterial Community Structure Is Governed by Location and Tissue-Type, but <i>Vibrio</i> Species Are Shared Among Oyster Tissues. <i>Frontiers in Microbiology</i> , 2021, 12, 723649.	1.5	6
5163	Deciphering the Endophytic and Rhizospheric Microbial Communities of a Metallophyte <i>Commelina communis</i> in Different Cu-Polluted Soils. <i>Microorganisms</i> , 2021, 9, 1689.	1.6	4
5164	Functional analysis of pristine estuarine marine sediments. <i>Science of the Total Environment</i> , 2021, 781, 146526.	3.9	16
5165	Changes of the intestinal microbiota along the gut of Japanese Eel (<i>Anguilla japonica</i>). <i>Letters in Applied Microbiology</i> , 2021, 73, 529-541.	1.0	3
5166	Change the original microbial community structure in the hydrolysis acidification tank to enhance the COD removal performance of oily wastewater. <i>Water Science and Technology</i> , 2021, 84, 1477-1486.	1.2	0
5167	Mining the Factors Driving the Evolution of the Pit Mud Microbiome under the Impact of Long-Term Production of Strong-Flavor Baijiu. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0088521.	1.4	36
5168	Impact of operational conditions on methane yield and microbial community composition during biological methanation in in situ and hybrid reactor systems. <i>Biotechnology for Biofuels</i> , 2021, 14, 170.	6.2	10
5169	Gut Microbiota Composition is Associated with Responses to Peanut Intervention in Multiple Parameters Among Adults with Metabolic Syndrome Risk. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2001051.	1.5	6
5170	Soil microbial community and network changes after long-term use of plastic mulch and nitrogen fertilization on semiarid farmland. <i>Geoderma</i> , 2021, 396, 115086.	2.3	65
5171	Mitogenome Phylogeny Including Data from Additional Subspecies Provides New Insights into the Historical Biogeography of the Eurasian lynx <i>Lynx lynx</i> . <i>Genes</i> , 2021, 12, 1216.	1.0	12
5172	Evaluation of the Dietary Black Soldier Fly Larvae Meal (<i>Hermetia illucens</i>) on Growth Performance, Intestinal Health, and Disease Resistance to <i>Vibrio parahaemolyticus</i> of the Pacific White Shrimp (<i>Litopenaeus vannamei</i>). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11
5173	Phylosymbiotic Structures of the Microbiota in <i>Mollitrichosiphum tenuicorpus</i> (Hemiptera: Aphididae: Tj ETQq1 1 Q.784314 rgBT /Overl	1.4	5
5174	Parasitism to mutualism continuum for Joshua trees inoculated with different communities of arbuscular mycorrhizal fungi from a desert elevation gradient. <i>PLoS ONE</i> , 2021, 16, e0256068.	1.1	7
5175	Diversity and geographic variation of endosymbiotic bacteria in natural populations of the pea aphid (<i>Acyrtosiphon pisum</i>) in China. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 788-797.	0.4	5
5176	Increasing relative abundance of non-cyanobacterial photosynthetic organisms drives ecosystem multifunctionality during the succession of biological soil crusts. <i>Geoderma</i> , 2021, 395, 115052.	2.3	12
5177	Legacy effects of temporary grassland in annual crop rotation on soil ecosystem services. <i>Science of the Total Environment</i> , 2021, 780, 146140.	3.9	16

#	ARTICLE	IF	CITATIONS
5178	Seasonal Variation in the Faecal Microbiota of Mature Adult Horses Maintained on Pasture in New Zealand. <i>Animals</i> , 2021, 11, 2300.	1.0	5
5179	Effective control of large deletions after double-strand breaks by homology-directed repair and dsODN insertion. <i>Genome Biology</i> , 2021, 22, 236.	3.8	36
5180	The comparison of ZFNs, TALENs, and SpCas9 by GUIDE-seq in HPV-targeted gene therapy. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 1466-1478.	2.3	18
5181	Alteration of Gut Microbiota Relates to Metabolic Disorders in Primary Aldosteronism Patients. <i>Frontiers in Endocrinology</i> , 2021, 12, 667951.	1.5	21
5184	Effects of dietary forage to concentrate ratio on nutrient digestibility, ruminal fermentation and rumen bacterial composition in Angus cows. <i>Scientific Reports</i> , 2021, 11, 17023.	1.6	43
5185	Methylation of the RIN3 Promoter is Associated with Transient Ischemic Stroke/Mild Ischemic Stroke with Early Cognitive Impairment. <i>Neuropsychiatric Disease and Treatment</i> , 2021, Volume 17, 2587-2598.	1.0	5
5186	Increase in carbohydrate content and variation in microbiome are related to the drought tolerance of <i>Codonopsis pilosula</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 165, 19-35.	2.8	12
5187	An emerging chemical fumigant: two-sided effects of dazomet on soil microbial environment and plant response. <i>Environmental Science and Pollution Research</i> , 2022, 29, 3022-3036.	2.7	8
5189	Amelioration of Hepatic Steatosis in Mice through <i>Bacteroides uniformis</i> CBA7346-Mediated Regulation of High-Fat Diet-Induced Insulin Resistance and Lipogenesis. <i>Nutrients</i> , 2021, 13, 2989.	1.7	15
5190	Seasonal and annual changes in the microbial communities of Ofunato Bay, Japan, based on metagenomics. <i>Scientific Reports</i> , 2021, 11, 17277.	1.6	4
5191	Sulfidogenic Microbial Communities of the Uzen High-Temperature Oil Field in Kazakhstan. <i>Microorganisms</i> , 2021, 9, 1818.	1.6	13
5192	Replacement of fish meal with Methanotroph (<i>Methylococcus capsulatus</i> , Bath) bacteria meal in the diets of Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2021, 541, 736801.	1.7	45
5193	The fungal community outperforms the bacterial community in predicting plant health status. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 6499-6513.	1.7	18
5194	Two-stage anoxic-oxic (A/O) system for the treatment of coking wastewater: Full-scale performance and microbial community analysis. <i>Chemical Engineering Journal</i> , 2021, 417, 129204.	6.6	39
5195	Effects of sulfamethoxazole on nitrogen removal and molecular ecological network in integrated vertical-flow constructed wetland. <i>Ecotoxicology and Environmental Safety</i> , 2021, 219, 112292.	2.9	16
5196	Dynamics of the Sydney rock oyster microbiota before and during a QX disease event. <i>Aquaculture</i> , 2021, 541, 736821.	1.7	2
5197	Exploring changes in bacterioplankton community structure in response to tannic acid, a major component of mangrove litterfall of Sundarbans mangrove ecosystem: a laboratory mesocosm approach. <i>Environmental Science and Pollution Research</i> , 2022, 29, 2107-2121.	2.7	5
5198	Within-host evolutionary dynamics of seasonal and pandemic human influenza A viruses in young children. <i>ELife</i> , 2021, 10, .	2.8	8

#	ARTICLE	IF	CITATIONS
5199	Effects of different antibiotic operation modes on anaerobic digestion of dairy manure: Focus on microbial population dynamics. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 105521.	3.3	7
5200	A Study on Burrows-Wheeler Aligner's Performance Optimization for Ancient DNA Mapping. <i>Lecture Notes in Networks and Systems</i> , 2022, , 105-114.	0.5	1
5201	High salinity gradients and intermediate spatial scales shaped similar biogeographical and co-occurrence patterns of microeukaryotes in a tropical freshwater-saltwater ecosystem. <i>Environmental Microbiology</i> , 2021, 23, 4778-4796.	1.8	13
5202	Aged Ripe Pu-erh Tea Reduced Oxidative Stress-Mediated Inflammation in Dextran Sulfate Sodium-Induced Colitis Mice by Regulating Intestinal Microbes. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 10592-10605.	2.4	51
5203	Specific inhibition of <i>Streptococcus bovis</i> by endolysin LyJH307 supplementation shifts the rumen microbiota and metabolic pathways related to carbohydrate metabolism. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 93.	2.1	10
5204	Effect of intestinal microecology on postnatal weight gain in very preterm infants in intensive care units. <i>Gut Pathogens</i> , 2021, 13, 49.	1.6	2
5205	Pain after upper limb surgery under peripheral nerve block is associated with gut microbiome composition and diversity. <i>Neurobiology of Pain (Cambridge, Mass)</i> , 2021, 10, 100072.	1.0	5
5206	Effect of High Sulfur Diet on Rumen Fermentation, Microflora, and Epithelial Barrier Function in Steers. <i>Animals</i> , 2021, 11, 2545.	1.0	7
5207	Distinct bacterial community of a solid-state fermented Chinese traditional food huase sufu revealed by high-throughput sequencing. <i>Food Science and Biotechnology</i> , 2021, 30, 1233-1241.	1.2	4
5208	Application of DNA metabarcoding to characterize the diet of the moon jellyfish <i>Aurelia coerulea</i> polyps and ephyrae. <i>Acta Oceanologica Sinica</i> , 2021, 40, 160-167.	0.4	2
5209	Blended controlled-release nitrogen fertilizer with straw returning improved soil nitrogen availability, soil microbial community, and root morphology of wheat. <i>Soil and Tillage Research</i> , 2021, 212, 105045.	2.6	48
5210	Diversity, Composition, Taxa Biomarkers, and Functional Genes of Fish Gut Microbes in Peat Swamp Forests and its Converted Areas in North Selangor, Malaysia. <i>Pertanika Journal of Science and Technology</i> , 2021, 44, .	0.1	0
5211	Effect of East Asian atmospheric particulate matter deposition on bacterial activity and community structure in the oligotrophic Northwest Pacific. <i>Environmental Pollution</i> , 2021, 283, 117088.	3.7	4
5212	Plant beneficial rhizobacteria community structure changes through developmental stages of peanut and maize. <i>Rhizosphere</i> , 2021, 19, 100407.	1.4	15
5213	Comparative analysis of chicken cecal microbial diversity and taxonomic composition in response to dietary variation using 16S rRNA amplicon sequencing. <i>Molecular Biology Reports</i> , 2021, 48, 7203-7214.	1.0	3
5214	Unveiling the Gut Microbiota and Resistome of Wild Cotton Mice, <i>Peromyscus gossypinus</i> , from Heavy Metal- and Radionuclide-Contaminated Sites in the Southeastern United States. <i>Microbiology Spectrum</i> , 2021, 9, e0009721.	1.2	4
5215	Long-term organic fertilization regulates the abundance of major nitrogen-cycling-related genes in aggregates from an acidic Ultisol. <i>Applied Soil Ecology</i> , 2021, 165, 104014.	2.1	17
5216	Lactic Acid Bacteria Strains Differently Modulate Gut Microbiota and Metabolic and Immunological Parameters in High-Fat Diet-Fed Mice. <i>Frontiers in Nutrition</i> , 2021, 8, 718564.	1.6	14

#	ARTICLE	IF	CITATIONS
5217	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
5218	No tillage and residue mulching method on bacterial community diversity regulation in a black soil region of Northeastern China. PLoS ONE, 2021, 16, e0256970.	1.1	17
5219	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
5220	Planifilum fulgidum Is the Dominant Functional Microorganism in Compost Containing Spent Mushroom Substrate. Sustainability, 2021, 13, 10002.	1.6	9
5221	Abundance and diversity of carbon-fixing bacterial communities in karst wetland soil ecosystems. Catena, 2021, 204, 105418.	2.2	40
5222	Metagenomic Analysis of Suansun, a Traditional Chinese Unsalted Fermented Food. Processes, 2021, 9, 1669.	1.3	5
5223	Draft Genome Sequence of the Anoxygenic Phototrophic Bacterium <i>Rhodospirillum rubrum</i> sp. Strain Az07, Isolated from a Brackish Canal. Microbiology Resource Announcements, 2021, 10, e0058521.	0.3	0
5224	Unraveling the bacterial diversity of Cangar Hot Spring, Indonesia by Next Generation Sequencing of 16S rRNA gene. Biodiversitas, 2021, 22, .	0.2	0
5225	Acute oral colchicine caused gastric mucosal injury and disturbance of associated microbiota in mice. Toxicology, 2021, 461, 152908.	2.0	11
5226	Genomic Epidemiology and Strain Taxonomy of <i>Corynebacterium diphtheriae</i> . Journal of Clinical Microbiology, 2021, 59, e0158121.	1.8	12
5227	Deep Investigating the Changes of Gut Microbiome and Its Correlation With the Shifts of Host Serum Metabolome Around Parturition in Sows. Frontiers in Microbiology, 2021, 12, 729039.	1.5	7
5228	Liquid Organic Fertilizer Amendment Alters Rhizosphere Microbial Community Structure and Co-occurrence Patterns and Improves Sunflower Yield Under Salinity-Alkalinity Stress. Microbial Ecology, 2022, 84, 423-438.	1.4	19
5229	Roots of the xerophyte Panicum turgidum host a cohort of ionizing-radiation-resistant biotechnologically-valuable bacteria. Saudi Journal of Biological Sciences, 2022, 29, 1260-1268.	1.8	4
5230	Variations in the Community Structure of Fungal Microbiota Associated with Apple Fruit Shaped by Fruit Bagging-Based Practice. Journal of Fungi (Basel, Switzerland), 2021, 7, 764.	1.5	4
5231	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
5232	Improved library preparation protocols for amplicon sequencing-based noninvasive fetal genotyping for RHD-positive D antigen-negative alleles. BMC Research Notes, 2021, 14, 380.	0.6	0
5233	Geography-dependent symbiont communities in two oligophagous aphid species. FEMS Microbiology Ecology, 2021, 97, .	1.3	6
5234	Accumulation of beneficial bacteria in the rhizosphere of maize (Zea mays L.) grown in a saline soil in responding to a consortium of plant growth promoting rhizobacteria. Annals of Microbiology, 2021, 71, .	1.1	20

#	ARTICLE	IF	CITATIONS
5235	Effects of <i>Bacillus subtilis</i> on jejunal integrity, redox status, and microbial composition of intrauterine growth restriction suckling piglets. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	12
5236	Rumen bacteria influence milk protein yield of yak grazing on the Qinghai-Tibet plateau. <i>Animal Bioscience</i> , 2021, 34, 1466-1478.	0.8	8
5237	Assessing the potential use of a feed additive based on biochar on broilers feeding upon productive performance, pH of digestive organs, cecum fermentation and bacterial community. <i>Animal Feed Science and Technology</i> , 2021, 279, 115039.	1.1	14
5238	Bacterial and fungal communities in the sandstone biofilms of two famous Buddhist grottoes in China. <i>International Biodeterioration and Biodegradation</i> , 2021, 163, 105267.	1.9	17
5239	Characterization of Shiga Toxin 2a Encoding Bacteriophages Isolated From High-Virulent O145:H25 Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 728116.	1.5	1
5240	A role for arthropods as vectors of multidrug-resistant Enterobacterales in surgical site infections from South Asia. <i>Nature Microbiology</i> , 2021, 6, 1259-1270.	5.9	16
5241	Effects of chilling rate on the freshness and microbial community composition of lamb carcasses. <i>LWT - Food Science and Technology</i> , 2022, 153, 112559.	2.5	14
5242	Different Responses of Soil Bacterial Communities to Nitrogen Addition in Moss Crust. <i>Frontiers in Microbiology</i> , 2021, 12, 665975.	1.5	6
5243	The unusual microbiota of the traditional Bulgarian dairy product Krokmach – A pilot metagenomics study. <i>International Journal of Dairy Technology</i> , 2022, 75, 139-149.	1.3	8
5244	Community Structure and Function of Epiphytic Bacteria Associated With <i>Myriophyllum spicatum</i> in Baiyangdian Lake, China. <i>Frontiers in Microbiology</i> , 2021, 12, 705509.	1.5	14
5245	Effects of steam-flaked grains on foals' growth and faecal microbiota. <i>BMC Veterinary Research</i> , 2021, 17, 293.	0.7	1
5246	Genome Analysis of <i>Acinetobacter lwoffii</i> Strains Isolated from Permafrost Soils Aged from 15 Thousand to 1.8 Million Years Revealed Their Close Relationships with Present-Day Environmental and Clinical Isolates. <i>Biology</i> , 2021, 10, 871.	1.3	5
5247	Effects of <i>Helicobacter pylori</i> Infection on the Oral Microbiota of Reflux Esophagitis Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 732613.	1.8	8
5248	Altered fecal microbiota composition in individuals who abuse methamphetamine. <i>Scientific Reports</i> , 2021, 11, 18178.	1.6	23
5249	Methane emissions and methanogenic community investigation from constructed wetlands in Chengdu City. <i>Urban Climate</i> , 2021, 39, 100956.	2.4	9
5250	Fish environmental DNA in Tokyo Bay: A feasibility study on the availability of environmental DNA for fisheries. <i>Regional Studies in Marine Science</i> , 2021, 47, 101950.	0.4	6
5251	Deciphering microbial mechanisms underlying soil organic carbon storage in a wheat-maize rotation system. <i>Science of the Total Environment</i> , 2021, 788, 147798.	3.9	23
5252	Sugarcane-Legume Intercropping Can Enrich the Soil Microbiome and Plant Growth. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	1.8	12

#	ARTICLE	IF	CITATIONS
5253	Dietary Energy Levels Affect Carbohydrate Metabolism-Related Bacteria and Improve Meat Quality in the Longissimus Thoracis Muscle of Yak (<i>Bos grunniens</i>). <i>Frontiers in Veterinary Science</i> , 2021, 8, 718036.	0.9	17
5254	Age-Related Changes in the Ruminal Microbiota and Their Relationship With Rumen Fermentation in Lambs. <i>Frontiers in Microbiology</i> , 2021, 12, 679135.	1.5	19
5255	Gut Microbial Divergence Between Three Hadal Amphipod Species from the Isolated Hadal Trenches. <i>Microbial Ecology</i> , 2021, , 1.	1.4	5
5256	Chemistry-specific responses due to rice-microbe interactions in the rhizosphere to counteract mefenacet stress. <i>Pesticide Biochemistry and Physiology</i> , 2021, 179, 104970.	1.6	1
5257	Insights into the bacterial and fungal communities and microbiome that causes a microbe outbreak on ancient wall paintings in the Majijshan Grottoes. <i>International Biodeterioration and Biodegradation</i> , 2021, 163, 105250.	1.9	38
5258	Comparison of the Bulk and Rhizosphere Soil Prokaryotic Communities Between Wild and Reintroduced <i>Manglietiastrum sinicum</i> Plants, a Threatened Species with Extremely Small Populations. <i>Current Microbiology</i> , 2021, 78, 3877-3890.	1.0	1
5259	Elucidating gene expression adaptation of phylogenetically divergent coral holobionts under heat stress. <i>Nature Communications</i> , 2021, 12, 5731.	5.8	29
5260	Chloropicrin alternated with dazomet improved the soil's physicochemical properties, changed microbial communities and increased strawberry yield. <i>Ecotoxicology and Environmental Safety</i> , 2021, 220, 112362.	2.9	12
5261	Influences of non-IgE-mediated cow's milk protein allergy-associated gut microbial dysbiosis on regulatory T cell-mediated intestinal immune tolerance and homeostasis. <i>Microbial Pathogenesis</i> , 2021, 158, 105020.	1.3	13
5262	New Estimation of Antibiotic Resistance Genes in Sediment Along the Haihe River and Bohai Bay in China: A Comparison Between Single and Successive DNA Extraction Methods. <i>Frontiers in Microbiology</i> , 2021, 12, 705724.	1.5	1
5263	Soil potentials to resist continuous cropping obstacle: Three field cases. <i>Environmental Research</i> , 2021, 200, 111319.	3.7	71
5264	Effects of fish meal replacement with low-gossypol cottonseed meal on the intestinal barrier of juvenile golden pompano (<i>Trachinotus ovatus</i>). <i>Aquaculture Research</i> , 2022, 53, 285-299.	0.9	5
5265	Distinct Assembly Processes and Determinants of Soil Microbial Communities between Farmland and Grassland in Arid and Semiarid Areas. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0101021.	1.4	7
5266	Spatial distribution of sediment archaeal and bacterial communities relates to the source of organic matter and hypoxia – a biogeographical study on Lake Remoray (France). <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	2
5267	Growth inhibition of methanogens for the enhancement of TCE dechlorination. <i>Science of the Total Environment</i> , 2021, 787, 147648.	3.9	11
5268	Full-Scale Clinical Data and Reshaped Intestinal Microbiome on a Short-Term Low-Phosphorus Diet among Healthy Adults. , 2021, 31, 448-458.		2
5269	Response of soil bacterial communities, antibiotic residuals, and crop yields to organic fertilizer substitution in North China under wheat-maize rotation. <i>Science of the Total Environment</i> , 2021, 785, 147248.	3.9	31
5270	Aquatic microbial community is partially functionally redundant: Insights from an in situ reciprocal transplant experiment. <i>Science of the Total Environment</i> , 2021, 786, 147433.	3.9	3

#	ARTICLE	IF	CITATIONS
5272	Anaerobic co-digestion of raw glycerol and swine manure: microbial communities. <i>Biomass Conversion and Biorefinery</i> , 2023, 13, 7127-7138.	2.9	5
5273	Agricultural management and cultivation period alter soil enzymatic activity and bacterial diversity in litchi (<i>Litchi chinensis</i> Sonn.) orchards. , 2021, 62, 13.		2
5274	Viral Characteristics of the Warm Atlantic and Cold Arctic Water Masses in the Nordic Seas. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0116021.	1.4	12
5275	Dietary bile acid supplementation reveals beneficial effects on intestinal healthy status of tongue sole (<i>Cynoglossus semilaevis</i>). <i>Fish and Shellfish Immunology</i> , 2021, 116, 52-60.	1.6	18
5276	Distribution of the potential pathogenic <i>Alternaria</i> on plant leaves determines foliar fungal communities around the disease spot. <i>Environmental Research</i> , 2021, 200, 111715.	3.7	10
5277	Characterization of the chicken T cell receptor $\hat{1}^3$ repertoire by high-throughput sequencing. <i>BMC Genomics</i> , 2021, 22, 683.	1.2	4
5278	Bacteriophage: A Useful Tool for Studying Gut Bacteria Function of Housefly Larvae, <i>Musca domestica</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0059921.	1.2	10
5279	Fate of glacier surface snowâ€œoriginating bacteria in the glacierâ€œfed hydrologic continuums. <i>Environmental Microbiology</i> , 2021, 23, 6450-6462.	1.8	12
5280	Pressure ulcers microbiota dynamics and wound evolution. <i>Scientific Reports</i> , 2021, 11, 18506.	1.6	15
5281	<i>Bacillus subtilis</i> DSM29784 Alleviates Negative Effects on Growth Performance in Broilers by Improving the Intestinal Health Under Necrotic Enteritis Challenge. <i>Frontiers in Microbiology</i> , 2021, 12, 723187.	1.5	9
5282	Genome-wide functional screen of 3â€œUTR variants uncovers causal variants for human disease and evolution. <i>Cell</i> , 2021, 184, 5247-5260.e19.	13.5	62
5283	Rhizosphere Microbial Communities Are Significantly Affected by Optimized Phosphorus Management in a Slope Farming System. <i>Frontiers in Microbiology</i> , 2021, 12, 739844.	1.5	13
5284	The more straw we deep-bury, the more soil TOC will be accumulated: when soil bacteria abundance keeps growing. <i>Journal of Soils and Sediments</i> , 2022, 22, 162-171.	1.5	3
5285	Plant-mediated effects of long-term warming on soil microorganisms on the Qinghai-Tibet Plateau. <i>Catena</i> , 2021, 204, 105391.	2.2	32
5286	Recognize and assessment of key host humic-reducing microorganisms of antibiotic resistance genes in different biowastes composts. <i>Science of the Total Environment</i> , 2022, 806, 150736.	3.9	2
5287	Marked Seasonal Variation in Structure and Function of Gut Microbiota in Forest and Alpine Musk Deer. <i>Frontiers in Microbiology</i> , 2021, 12, 699797.	1.5	44
5288	Variations in dissolved O ₂ in a Chinese lake drive changes in microbial communities and impact sedimentary GDGT distributions. <i>Chemical Geology</i> , 2021, 579, 120348.	1.4	40
5289	Structural, functional, resistome and pathogenicity profiling of the Cooum river. <i>Microbial Pathogenesis</i> , 2021, 158, 105048.	1.3	8

#	ARTICLE	IF	CITATIONS
5290	Characterization of the nasopharynx microbiota in patients with nasopharyngeal carcinoma vs. healthy controls. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 1873-1880.	0.8	4
5291	Aridity-driven shift in biodiversityâ€“soil multifunctionality relationships. <i>Nature Communications</i> , 2021, 12, 5350.	5.8	164
5292	Promotion of pellet-feed feeding in mandarin fish (<i>Siniperca chuatsi</i>) by <i>Bdellovibrio bacteriovorus</i> is influenced by immune and intestinal flora. <i>Aquaculture</i> , 2021, 542, 736864.	1.7	15
5293	Evaluation of applying an alkaline green tea/ferrous iron system to lindane remediation impacts to soil and plant growth-promoting microbial community. <i>Science of the Total Environment</i> , 2021, 786, 147511.	3.9	8
5295	Structural changes in the gut microbiota community of the black-necked crane (<i>Grus nigricollis</i>) in the wintering period. <i>Archives of Microbiology</i> , 2021, 203, 6203-6214.	1.0	7
5296	<i>Lactobacillus plantarum</i> HY7715 Ameliorates Sarcopenia by Improving Skeletal Muscle Mass and Function in Aged Balb/c Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10023.	1.8	22
5297	Bacterial Community Analysis and Potential Functions of Core Taxa in Different Parts of the Fungus <i>Cantharellus cibarius</i> . <i>Polish Journal of Microbiology</i> , 2021, 70, 373-385.	0.6	3
5298	<i>Candida albicans</i> triggers qualitative and temporal responses in gut bacteria. <i>Journal De Mycologie Medicale</i> , 2021, 31, 101164.	0.7	4
5299	MULTIPLEXED SIV-SPECIFIC PAIRED RNA-GUIDED CAS9 NICKASES INACTIVATE PROVIRAL DNA. <i>Journal of Virology</i> , 2021, 95, e0088221.	1.5	2
5300	Impact of wastewater on the microbial diversity of periphyton and its tolerance to micropollutants in an engineered flow-through channel system. <i>Water Research</i> , 2021, 203, 117486.	5.3	31
5301	Thymic T-Cell Production Is Associated With Changes in the Gut Microbiota in Young Chicks. <i>Frontiers in Immunology</i> , 2021, 12, 700603.	2.2	4
5302	Appendectomy Is Associated With Alteration of Human Gut Bacterial and Fungal Communities. <i>Frontiers in Microbiology</i> , 2021, 12, 724980.	1.5	20
5303	Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. <i>Epigenetics and Chromatin</i> , 2021, 14, 44.	1.8	3
5304	Diversity of Mycobiota in Spanish Grape Berries and Selection of <i>Hanseniaspora uvarum</i> U1 to Prevent Mycotoxin Contamination. <i>Toxins</i> , 2021, 13, 649.	1.5	12
5305	Impact of Inosine on Chronic Unpredictable Mild Stress-Induced Depressive and Anxiety-Like Behaviors With the Alteration of Gut Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 697640.	1.8	23
5306	Resistance and Resilience of Fish Gut Microbiota to Silver Nanoparticles. <i>MSystems</i> , 2021, 6, e0063021.	1.7	17
5307	An investigation into the anaerobic spoilage microbiota of beef carcass and rump steak cuts using high-throughput sequencing. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	3
5309	Salt tolerance of halotolerant bacteria from coastal soils and sediments near saltern field of Hainan Island, China. <i>Archives of Microbiology</i> , 2021, 203, 5921-5930.	1.0	2

#	ARTICLE	IF	CITATIONS
5310	DNA hypomethylation leads to cGAS-induced autoinflammation in the epidermis. <i>EMBO Journal</i> , 2021, 40, e108234.	3.5	17
5311	Black Soldier Fly (<i>Hermetia illucens</i>) Larvae Meal Modulates Intestinal Morphology and Microbiota in Xuefeng Black-Bone Chickens. <i>Frontiers in Microbiology</i> , 2021, 12, 706424.	1.5	7
5312	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021, 12, 5483.	5.8	29
5313	The potential correlation between microbial communities and flavors in traditional fermented sour meat. <i>LWT - Food Science and Technology</i> , 2021, 149, 111873.	2.5	43
5314	Changes in soil physicochemical properties and bacterial communities at different soil depths after long-term straw mulching under a no-till system. <i>Soil</i> , 2021, 7, 595-609.	2.2	11
5315	Rhizosphere bacterial community dynamics of the cadmium hyperaccumulator <i>Sedum plumbizincicola</i> under a cadmium concentration gradient during phytoextraction. <i>Plant and Soil</i> , 2021, 468, 375-388.	1.8	3
5316	A new landscape of rabbit gut microbiota shaped by the infection of precocious parasites of <i>Eimeria intestinalis</i> . <i>Veterinary Parasitology</i> , 2021, 300, 109579.	0.7	4
5317	Efficient anaerobic bioremediation of high-concentration benzo[a]pyrene in marine environments. <i>Environmental Pollution</i> , 2021, 284, 117210.	3.7	13
5318	Similarities and differences of oligo/poly-saccharides™ impact on human fecal microbiota identified by in vitro fermentation. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7475-7486.	1.7	8
5319	Bacterial Composition Associated With Giant Colonies of the Harmful Algal Species <i>Phaeocystis globosa</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 737484.	1.5	8
5320	Determinants of brain swelling in pediatric and adult cerebral malaria. <i>JCI Insight</i> , 2021, 6, .	2.3	25
5321	Dinotefuran alters Collembola-fungi-bacteria interactions that control mineralization of maize and soil organic carbon. <i>Journal of Hazardous Materials</i> , 2021, 418, 126391.	6.5	11
5322	Distinct factors drive the diversity and composition of protistan consumers and phototrophs in natural soil ecosystems. <i>Soil Biology and Biochemistry</i> , 2021, 160, 108317.	4.2	34
5323	Sinomenine hydrochloride ameliorates dextran sulfate sodium-induced colitis in mice by modulating the gut microbiota composition whilst suppressing the activation of the NLRP3 inflammasome. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 1287.	0.8	14
5324	Effects of Adding Eubiotic Lignocellulose on the Growth Performance, Laying Performance, Gut Microbiota, and Short-Chain Fatty Acids of Two Breeds of Hens. <i>Frontiers in Veterinary Science</i> , 2021, 8, 668003.	0.9	10
5325	High royal jelly production does not impact the gut microbiome of honey bees. <i>Animal Microbiome</i> , 2021, 3, 60.	1.5	2
5326	A Molecular Survey of Bacterial Species in the Guts of Black Soldier Fly Larvae (<i>Hermetia illucens</i>) Reared on Two Urban Organic Waste Streams in Kenya. <i>Frontiers in Microbiology</i> , 2021, 12, 687103.	1.5	4
5327	Transition and regulation mechanism of bacterial biota in Kishu saba-narezushi (mackerel narezushi) during its fermentation step. <i>Journal of Bioscience and Bioengineering</i> , 2021, 132, 606-612.	1.1	8

#	ARTICLE	IF	CITATIONS
5330	Assembly of a Benthic Microbial Community in a Eutrophic Bay with a Long History of Oyster Culturing. <i>Microorganisms</i> , 2021, 9, 2019.	1.6	1
5331	Effect of Insect Live Larvae as Environmental Enrichment on Poultry Gut Health: Gut Mucin Composition, Microbiota and Local Immune Response Evaluation. <i>Animals</i> , 2021, 11, 2819.	1.0	16
5332	Diversity and community structure of endophytic <i>Bacillus</i> with antagonistic and antioxidant activity in the fruits of Xisha Wild Noni (<i>Morinda citrifolia</i> L.). <i>Microbial Pathogenesis</i> , 2021, 158, 105065.	1.3	3
5333	Insight into microbial community diversity and composition of two-stage anaerobic digestion: Focusing methanogenic stage. <i>Bioresource Technology Reports</i> , 2021, 15, 100764.	1.5	10
5334	Species pool and local ecological assembly processes shape the β -diversity of diazotrophs in grassland soils. <i>Soil Biology and Biochemistry</i> , 2021, 160, 108338.	4.2	24
5335	Identification of Cd-resistant microorganisms from heavy metal-contaminated soil and its potential in promoting the growth and Cd accumulation of bermudagrass. <i>Environmental Research</i> , 2021, 200, 111730.	3.7	50
5336	Biochar application enhances microbial interactions in mega-aggregates of farmland black soil. <i>Soil and Tillage Research</i> , 2021, 213, 105145.	2.6	29
5337	Evaluating the effect of microalga <i>Haematococcus pluvialis</i> bioaugmentation on aerobic membrane bioreactor in terms of performance, membrane fouling and microbial community structure. <i>Science of the Total Environment</i> , 2022, 807, 149908.	3.9	22
5338	Microbial community structure and metabolome profiling characteristics of soil contaminated by TNT, RDX, and HMX. <i>Environmental Pollution</i> , 2021, 285, 117478.	3.7	38
5339	Changes in soil bacterial communities with increasing distance from maize roots affected by ammonium and nitrate additions. <i>Geoderma</i> , 2021, 398, 115102.	2.3	20
5340	Complete genome sequencing and molecular characterization of SARS-COV-2 from COVID-19 cases in Alborz province in Iran. <i>Heliyon</i> , 2021, 7, e08027.	1.4	2
5341	Multiple Sources of Introduction of North American <i>Arabidopsis thaliana</i> from across Eurasia. <i>Molecular Biology and Evolution</i> , 2021, 38, 5328-5344.	3.5	6
5342	Tumor-Associated Microbiota in Proximal and Distal Colorectal Cancer and Their Relationships With Clinical Outcomes. <i>Frontiers in Microbiology</i> , 2021, 12, 727937.	1.5	18
5343	Dominant hyphae-associated bacteria of <i>Fusarium oxysporum</i> f. sp. <i>cucumerinum</i> in different cropping systems and insight into their functions. <i>Applied Soil Ecology</i> , 2021, 165, 103977.	2.1	7
5344	Effects of Total Dietary Fiber on Cecal Microbial Community and Intestinal Morphology of Growing White Pekin Duck. <i>Frontiers in Microbiology</i> , 2021, 12, 727200.	1.5	12
5345	Carcass decay deteriorates water quality and modifies the <i>nirS</i> denitrifying communities in different degradation stages. <i>Science of the Total Environment</i> , 2021, 785, 147185.	3.9	16
5346	Targeted gene disruption in a marsupial, <i>Monodelphis domestica</i> , by CRISPR/Cas9 genome editing. <i>Current Biology</i> , 2021, 31, 3956-3963.e4.	1.8	14
5347	Diversity and Co-Occurrence Patterns of Fungal and Bacterial Communities from Alkaline Sediments and Water of Julong High-Altitude Hot Springs at Tianchi Volcano, Northeast China. <i>Biology</i> , 2021, 10, 894.	1.3	7

#	ARTICLE	IF	CITATIONS
5348	Methanotroph community structure and processes in an inland river affected by natural gas macro-seeps. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
5349	Molecular studies of Iranian populations support the morphology-based taxonomic separation of <i>Medicago rigidula</i> and <i>M. rigiduloides</i> . <i>Phytotaxa</i> , 2021, 518, 281-299.	0.1	2
5350	Temporal Variations Rather than Long-Term Warming Control Extracellular Enzyme Activities and Microbial Community Structures in the High Arctic Soil. <i>Microbial Ecology</i> , 2022, 84, 168-181.	1.4	3
5351	Parasitoid Causes Cascading Effects on Plant-Induced Defenses Mediated Through the Gut Bacteria of Host Caterpillars. <i>Frontiers in Microbiology</i> , 2021, 12, 708990.	1.5	6
5352	Contrasting Vaginal Bacterial Communities Between Estrus and Non-estrus of Giant Pandas (<i>Ailuropoda melanoleuca</i>). <i>Frontiers in Microbiology</i> , 2021, 12, 707548.	1.5	2
5353	Effects of IQW and IRW on Inflammation and Gut Microbiota in ETEC-Induced Diarrhea. <i>Mediators of Inflammation</i> , 2021, 2021, 1-12.	1.4	9
5355	Diversity of arbuscular mycorrhizal fungi and its chemical drivers across dryland habitats. <i>Mycorrhiza</i> , 2021, 31, 685-697.	1.3	11
5356	Optimized design parameters for CRISPR Cas9 and Cas12a homology-directed repair. <i>Scientific Reports</i> , 2021, 11, 19482.	1.6	43
5357	Corpse decomposition increases the diversity and abundance of antibiotic resistance genes in different soil types in a fish model. <i>Environmental Pollution</i> , 2021, 286, 117560.	3.7	19
5358	Fresh chicken manure fumigation reduces the inhibition time of chloropicrin on soil bacteria and fungi and increases beneficial microorganisms. <i>Environmental Pollution</i> , 2021, 286, 117460.	3.7	9
5359	The diversity of soil mesofauna declines after bamboo invasion in subtropical China. <i>Science of the Total Environment</i> , 2021, 789, 147982.	3.9	14
5360	Effect of rice (<i>Oryza sativa</i> L.) genotype on yield: Evidence from recruiting spatially consistent rhizosphere microbiome. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108395.	4.2	27
5361	Changes of soil bacterial and fungal community structure along a natural aridity gradient in desert grassland ecosystems, Inner Mongolia. <i>Catena</i> , 2021, 205, 105470.	2.2	25
5362	Impacts of PBDE-47 exposure before, during and after pregnancy on the maternal gut microbiome and its association with host metabolism. <i>Ecotoxicology and Environmental Safety</i> , 2021, 222, 112530.	2.9	10
5363	Co-symbiosis of arbuscular mycorrhizal fungi (AMF) and diazotrophs promote biological nitrogen fixation in mangrove ecosystems. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108382.	4.2	34
5364	Microbial interkingdom associations across soil depths reveal network connectivity and keystone taxa linked to soil fine-fraction carbon content. <i>Agriculture, Ecosystems and Environment</i> , 2021, 320, 107559.	2.5	21
5365	Succession of diversity, functions, and interactions of the fungal community in activated sludge under aromatic hydrocarbon stress. <i>Environmental Research</i> , 2022, 204, 112143.	3.7	26
5366	Rhizosphere bacterial community composition affects cadmium and arsenic accumulation in rice (<i>Oryza sativa</i> L.). <i>Ecotoxicology and Environmental Safety</i> , 2021, 222, 112474.	2.9	18

#	ARTICLE	IF	CITATIONS
5367	Co-occurrence patterns and assembly processes of microeukaryotic communities in a semi-enclosed aquaculture bay. <i>Continental Shelf Research</i> , 2021, 228, 104550.	0.9	6
5368	Transcriptomic response of the intertidal limpet <i>Patella vulgata</i> to temperature extremes. <i>Journal of Thermal Biology</i> , 2021, 101, 103096.	1.1	4
5369	Organic manure induced soil food web of microbes and nematodes drive soil organic matter under jackfruit planting. <i>Applied Soil Ecology</i> , 2021, 166, 103994.	2.1	19
5370	Restriction of soil bacteria promoting high yield of super hybrid rice in the Huaihe Valley in central China by conventional ploughing intensity. <i>Soil and Tillage Research</i> , 2021, 214, 105169.	2.6	3
5371	The diversity and co-occurrence network of soil bacterial and fungal communities and their implications for a new indicator of grassland degradation. <i>Ecological Indicators</i> , 2021, 129, 107989.	2.6	66
5372	<i>Firmicutes</i> and <i>Blautia</i> in gut microbiota lessened in chronic liver diseases and hepatocellular carcinoma patients: a pilot study. <i>Bioengineered</i> , 2021, 12, 8233-8246.	1.4	21
5373	Stachyose inhibits vancomycin-resistant <i>Enterococcus</i> colonization and affects gut microbiota in mice. <i>Microbial Pathogenesis</i> , 2021, 159, 105094.	1.3	5
5374	Soil microbial and chemical responses to foliar <i>Epichloa</i> fungal infection in <i>Lolium perenne</i> , <i>Hordeum brevisubulatum</i> and <i>Achnatherum inebrians</i> . <i>Fungal Ecology</i> , 2021, 53, 101091.	0.7	3
5375	Microbial Diversity and Abundance of <i>Parabacteroides</i> Mediate the Associations Between Higher Intake of Flavonoid-Rich Foods and Lower Blood Pressure. <i>Hypertension</i> , 2021, 78, 1016-1026.	1.3	14
5376	Preferences for core microbiome composition and function by different definition methods: Evidence for the core microbiome of <i>Eucommia ulmoides</i> bark. <i>Science of the Total Environment</i> , 2021, 790, 148091.	3.9	19
5377	Crop rotation history constrains soil biodiversity and multifunctionality relationships. <i>Agriculture, Ecosystems and Environment</i> , 2021, 319, 107550.	2.5	48
5378	Effect of dietary histamine on intestinal morphology, inflammatory status, and gut microbiota in yellow catfish (<i>Pelteobagrus fulvidraco</i>). <i>Fish and Shellfish Immunology</i> , 2021, 117, 95-103.	1.6	17
5379	Effect of heavy metals pollution on the composition and diversity of the intestinal microbial community of a pygmy grasshopper (<i>Eucrotettix oculatus</i>). <i>Ecotoxicology and Environmental Safety</i> , 2021, 223, 112582.	2.9	22
5380	Water volume influences antibiotic resistomes and microbiomes during fish corpse decomposition. <i>Science of the Total Environment</i> , 2021, 789, 147977.	3.9	13
5381	Understanding variations in soil properties and microbial communities in bamboo plantation soils along a chromium pollution gradient. <i>Ecotoxicology and Environmental Safety</i> , 2021, 222, 112507.	2.9	28
5382	Maternal and environmental microbes dominate offspring microbial colonization in the giant freshwater prawn <i>Macrobrachium rosenbergii</i> . <i>Science of the Total Environment</i> , 2021, 790, 148062.	3.9	14
5383	Effects of heavy metals and organic matter fractions on the fungal communities in mangrove sediments from Techeng Isle, South China. <i>Ecotoxicology and Environmental Safety</i> , 2021, 222, 112545.	2.9	12
5384	Dominant plants affect litter decomposition mainly through modifications of the soil microbial community. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108399.	4.2	37

#	ARTICLE	IF	CITATIONS
5385	Mycobiota of <i>Eucommia ulmoides</i> bark: Diversity, rare biosphere and core taxa. <i>Fungal Ecology</i> , 2021, 53, 101090.	0.7	7
5386	Sodium butyrate alleviates cholesterol gallstones by regulating bile acid metabolism. <i>European Journal of Pharmacology</i> , 2021, 908, 174341.	1.7	17
5387	Integrated analysis reveals an association between the rhizosphere microbiome and root rot of arecanut palm. <i>Pedosphere</i> , 2021, 31, 725-735.	2.1	7
5388	Colonization by dark septate endophytes improves the growth and rhizosphere soil microbiome of licorice plants under different water treatments. <i>Applied Soil Ecology</i> , 2021, 166, 103993.	2.1	16
5389	Stigmasterol root exudation arising from <i>Pseudomonas</i> inoculation of the duckweed rhizosphere enhances nitrogen removal from polluted waters. <i>Environmental Pollution</i> , 2021, 287, 117587.	3.7	17
5390	Seasonal biofilm formation on floating microplastics in coastal waters of intensified mariculture area. <i>Marine Pollution Bulletin</i> , 2021, 171, 112914.	2.3	20
5391	Quantitative ecology associations between heterotrophic nitrification-aerobic denitrification, nitrogen-metabolism genes, and key bacteria in a tidal flow constructed wetland. <i>Bioresource Technology</i> , 2021, 337, 125449.	4.8	32
5392	Isolation of lindane- and endosulfan-degrading bacteria and dominance analysis in the microbial communities by culture-dependent and independent methods. <i>Microbiological Research</i> , 2021, 251, 126817.	2.5	7
5393	Community structures of bacteria and archaea associated with the biodeterioration of sandstone sculptures at the Beishiku Temple. <i>International Biodeterioration and Biodegradation</i> , 2021, 164, 105290.	1.9	34
5394	Changes in rumen fermentation and bacterial community in lactating dairy cows with subacute rumen acidosis following rumen content transplantation. <i>Journal of Dairy Science</i> , 2021, 104, 10780-10795.	1.4	20
5395	Microbial diversity of marine shrimp pond sediment and its variability due to the effect of immobilized media in biohydrogen and biohythane production. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 106166.	3.3	7
5396	A water-soluble β -glucan improves growth performance by altering gut microbiome and health in weaned pigs. <i>Animal Nutrition</i> , 2021, 7, 1345-1351.	2.1	9
5397	Microbial Community and Fermentation Characteristics of Native Grass Prepared Without or With Isolated Lactic Acid Bacteria on the Mongolian Plateau. <i>Frontiers in Microbiology</i> , 2021, 12, 731770.	1.5	18
5398	A new phenothiazine derivate is active against <i>Clostridioides difficile</i> and shows low cytotoxicity. <i>PLoS ONE</i> , 2021, 16, e0258207.	1.1	3
5399	Substrate type and plant phenolics influence epiphytic bacterial assembly during short-term succession. <i>Science of the Total Environment</i> , 2021, 792, 148410.	3.9	12
5400	Rapid pathogen discovery in diseased turbot (<i>Scophthalmus maximus</i>) using 16S rRNA high throughput sequencing. <i>Aquaculture Reports</i> , 2021, 21, 100835.	0.7	3
5401	Authentication of sea cucumber products using NGS-based DNA mini-barcoding. <i>Food Control</i> , 2021, 129, 108199.	2.8	13
5402	Variations of tongue coating microbiota in children with Henoch-SchÅ¶nlein purpura nephritis. <i>Microbial Pathogenesis</i> , 2021, 160, 105192.	1.3	0

#	ARTICLE	IF	CITATIONS
5403	Polystyrene microplastics induce microbial dysbiosis and dysfunction in surrounding seawater. <i>Environment International</i> , 2021, 156, 106724.	4.8	47
5404	Magnesium and nitrogen drive soil bacterial community structure under long-term apple orchard cultivation systems. <i>Applied Soil Ecology</i> , 2021, 167, 104103.	2.1	8
5405	Composition change and decreased diversity of microbial eukaryotes in the coastal upwelling waters of South China Sea. <i>Science of the Total Environment</i> , 2021, 795, 148892.	3.9	13
5406	Revealing the distribution characteristics of antibiotic resistance genes and bacterial communities in animal-aerosol-human in a chicken farm: From One-Health perspective. <i>Ecotoxicology and Environmental Safety</i> , 2021, 224, 112687.	2.9	24
5407	Temporal triggers of N ₂ O emissions during cyclical and seasonal variations of a full-scale sequencing batch reactor treating municipal wastewater. <i>Science of the Total Environment</i> , 2021, 797, 149093.	3.9	6
5408	Bacterial community structure and putative nitrogen-cycling functional traits along a charosphere gradient under waterlogged conditions. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108420.	4.2	21
5409	Linking changes in the soil microbial community to C and N dynamics during crop residue decomposition. <i>Journal of Integrative Agriculture</i> , 2021, 20, 3039-3059.	1.7	12
5410	Fertile islands lead to more conspicuous spatial heterogeneity of bacteria than soil physicochemical properties in a desert ecosystem. <i>Catena</i> , 2021, 206, 105526.	2.2	12
5411	Nitrogen fertilization has a stronger influence than cropping pattern on AMF community in maize/soybean strip intercropping systems. <i>Applied Soil Ecology</i> , 2021, 167, 104034.	2.1	14
5412	Efficiency and mechanism of reducing ammonia volatilization in alkaline farmland soil using <i>Bacillus amyloliquefaciens</i> biofertilizer. <i>Environmental Research</i> , 2021, 202, 111672.	3.7	21
5413	Multi-omics revealed the effects of rumen-protected methionine on the nutrient profile of milk in dairy cows. <i>Food Research International</i> , 2021, 149, 110682.	2.9	16
5414	Pathogenic hitchhiker diversity on international ships' ballast water at West Malaysia port. <i>Marine Pollution Bulletin</i> , 2021, 172, 112850.	2.3	13
5415	Seasonal variations in soil physicochemical properties and microbial community structure influenced by <i>Spartina alterniflora</i> invasion and <i>Kandelia obovata</i> restoration. <i>Science of the Total Environment</i> , 2021, 797, 149213.	3.9	25
5416	Dynamics of soil bacterial community diversity and composition at aggregate scales in a chronosequence of tea gardens. <i>Catena</i> , 2021, 206, 105486.	2.2	3
5417	Characterization of tissue-associated bacterial community of two <i>Bathymodiolus</i> species from the adjacent cold seep and hydrothermal vent environments. <i>Science of the Total Environment</i> , 2021, 796, 149046.	3.9	7
5418	Preferential temperature and ammonia concentration for in-situ growth of <i>Candidatus Nitrospira</i> ammonia oxidising archaea. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108405.	4.2	9
5419	Salinity gradients shape the nitrifier community composition in Nanliu River Estuary sediments and the ecophysiology of comammox <i>Nitrospira inopinata</i> . <i>Science of the Total Environment</i> , 2021, 795, 148768.	3.9	22
5420	<i>Vibrio parahaemolyticus</i> alters the community composition and function of intestinal microbiota in Pacific white shrimp, <i>Penaeus vannamei</i> . <i>Aquaculture</i> , 2021, 544, 737061.	1.7	23

#	ARTICLE	IF	CITATIONS
5421	Biological treatment of volatile organic compounds (VOCs)-containing wastewaters from wet scrubbers in semiconductor industry. <i>Chemosphere</i> , 2021, 282, 131137.	4.2	17
5422	Chiral enantiomers of the plant growth regulator paclobutrazol selectively affect community structure and diversity of soil microorganisms. <i>Science of the Total Environment</i> , 2021, 797, 148942.	3.9	12
5423	Novel Î ² -mannanase/GLP-1 fusion peptide high effectively ameliorates obesity in a mouse model by modifying balance of gut microbiota. <i>International Journal of Biological Macromolecules</i> , 2021, 191, 753-763.	3.6	25
5424	Soil microbial community composition but not diversity is affected by land-use types in the agro-pastoral ecotone undergoing frequent conversions between cropland and grassland. <i>Geoderma</i> , 2021, 401, 115165.	2.3	14
5425	Artificial light reduces foraging opportunities in wild least horseshoe bats. <i>Environmental Pollution</i> , 2021, 288, 117765.	3.7	16
5426	Effects of design parameters, microbial community and nitrogen removal on the field-scale multi-pond constructed wetlands. <i>Science of the Total Environment</i> , 2021, 797, 148989.	3.9	14
5427	Intrauterine antibiotic exposure affected neonatal gut bacteria and infant growth speed. <i>Environmental Pollution</i> , 2021, 289, 117901.	3.7	12
5428	Evolution of innate and adaptive immune genes in a non-model waterbird, the common tern. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105069.	1.0	6
5429	UV assisted backwashing for fouling control in membrane bioreactor operation. <i>Journal of Membrane Science</i> , 2021, 639, 119751.	4.1	16
5430	Effects of anode/cathode electroactive microorganisms on arsenic removal with organic/inorganic carbon supplied. <i>Science of the Total Environment</i> , 2021, 798, 149356.	3.9	7
5431	Meadow degradation increases spatial turnover rates of the fungal community through both niche selection and dispersal limitation. <i>Science of the Total Environment</i> , 2021, 798, 149362.	3.9	24
5432	Nitrifiers drive successions of particulate organic matter and microbial community composition in a starved macrocosm. <i>Environment International</i> , 2021, 157, 106776.	4.8	8
5433	Effect of biochar applied with plant growth-promoting rhizobacteria (PGPR) on soil microbial community composition and nitrogen utilization in tomato. <i>Pedosphere</i> , 2021, 31, 872-881.	2.1	21
5434	Homogenization of reservoir eukaryotic algal and cyanobacterial communities is accelerated by dam construction and eutrophication. <i>Journal of Hydrology</i> , 2021, 603, 126842.	2.3	8
5435	Productivity and quality of banana in response to chemical fertilizer reduction with bio-organic fertilizer: Insight into soil properties and microbial ecology. <i>Agriculture, Ecosystems and Environment</i> , 2021, 322, 107659.	2.5	35
5436	The interaction of acidophiles driving community functional responses to the re-inoculated chalcopyrite bioleaching process. <i>Science of the Total Environment</i> , 2021, 798, 149186.	3.9	12
5437	Fungal community composition and diversity in the rhizosphere soils of Argentina (syn. <i>Potentilla anserina</i>), on the Qinghai Plateau. <i>Fungal Ecology</i> , 2021, 54, 101107.	0.7	5
5438	Honey bee <i>Apis mellifera</i> larvae gut microbial and immune, detoxication responses towards flumethrin stress. <i>Environmental Pollution</i> , 2021, 290, 118107.	3.7	22

#	ARTICLE	IF	CITATIONS
5439	Alkaline phosphatase activity mediates soil organic phosphorus mineralization in a subalpine forest ecosystem. <i>Geoderma</i> , 2021, 404, 115376.	2.3	60
5440	Bioplastic accumulates antibiotic and metal resistance genes in coastal marine sediments. <i>Environmental Pollution</i> , 2021, 291, 118161.	3.7	20
5441	Dissolved organic carbon drives nutrient cycling via microbial community in paddy soil. <i>Chemosphere</i> , 2021, 285, 131472.	4.2	13
5442	Pollution alters methanogenic and methanotrophic communities and increases dissolved methane in small ponds. <i>Science of the Total Environment</i> , 2021, 801, 149723.	3.9	8
5443	NGS-Based Metagenomic Study of Four Traditional Bulgarian Green Cheeses from Tcherni Vit. <i>LWT - Food Science and Technology</i> , 2021, 152, 112278.	2.5	9
5444	Valorization of carbon dioxide and waste (Derived from the site of Eutrophication) into syngas using a catalytic thermo-chemical platform. <i>Bioresource Technology</i> , 2021, 341, 125858.	4.8	1
5445	Evolution of PM2.5 bacterial community structure in Beijing's suburban atmosphere. <i>Science of the Total Environment</i> , 2021, 799, 149387.	3.9	10
5446	The quality of compost was improved by low concentrations of fulvic acid owing to its optimization of the exceptional microbial structure. <i>Bioresource Technology</i> , 2021, 342, 125843.	4.8	17
5447	<i>Paracoccus</i> and <i>Achromobacter</i> bacteria contribute to rapid biodegradation of imidacloprid in soils. <i>Ecotoxicology and Environmental Safety</i> , 2021, 225, 112785.	2.9	18
5448	Propamocarb exposure has the potential to accelerate the formation of atherosclerosis in both WT and ApoE ^{-/-} mice accompanied by gut microbiota dysbiosis. <i>Science of the Total Environment</i> , 2021, 800, 149602.	3.9	7
5449	Improvement of nitrogen and phosphorus availability by <i>Pseudoalteromonas</i> sp. during salt-washing in saline-alkali soil. <i>Applied Soil Ecology</i> , 2021, 168, 104117.	2.1	25
5450	<i>Lycium barbarum</i> L. (goji berry) monocropping causes microbial diversity loss and induces <i>Fusarium</i> spp. enrichment at distinct soil layers. <i>Applied Soil Ecology</i> , 2021, 168, 104107.	2.1	17
5451	Key indicators for renewal and reconstruction of perennial trees soil: Microorganisms and phloridzin. <i>Ecotoxicology and Environmental Safety</i> , 2021, 225, 112723.	2.9	22
5452	The structure and assembly mechanisms of plastisphere microbial community in natural marine environment. <i>Journal of Hazardous Materials</i> , 2022, 421, 126780.	6.5	93
5453	Gut microbiota may contribute to the postnatal male reproductive abnormalities induced by prenatal dibutyl phthalate exposure. <i>Chemosphere</i> , 2022, 287, 132046.	4.2	25
5454	Soil carbon supplementation: Improvement of root-surrounding soil bacterial communities, sugar and starch content in tobacco (<i>N. tabacum</i>). <i>Science of the Total Environment</i> , 2022, 802, 149835.	3.9	15
5455	Subsoiling and conversion to conservation tillage enriched nitrogen cycling bacterial communities in sandy soils under long-term maize monoculture. <i>Soil and Tillage Research</i> , 2022, 215, 105197.	2.6	29
5456	Restoration of organic-matter-impooverished arable soils through the application of soil conditioner prepared via short-time hydrothermal fermentation. <i>Environmental Research</i> , 2022, 204, 112088.	3.7	4

#	ARTICLE	IF	CITATIONS
5457	Cut interkingdom predator-prey interactions are key determinants of shrimp health. <i>Aquaculture</i> , 2022, 546, 737304.	1.7	15
5458	Analysis of bacterial community functional diversity in late-stage shrimp (<i>Litopenaeus vannamei</i>) ponds using Biolog EcoPlates and PICRUSt2. <i>Aquaculture</i> , 2022, 546, 737288.	1.7	14
5459	Plant and soil elemental C:N:P ratios are linked to soil microbial diversity during grassland restoration on the Loess Plateau, China. <i>Science of the Total Environment</i> , 2022, 806, 150557.	3.9	22
5460	Adaption to hydrogen sulfide-rich environments: Strategies for active detoxification in deep-sea symbiotic mussels, <i>Gigantidas platifrons</i> . <i>Science of the Total Environment</i> , 2022, 804, 150054.	3.9	19
5461	Comparative study of the anti-obesity and gut microbiota modulation effects of green tea phenolics and their oxidation products in high-fat-induced obese mice. <i>Food Chemistry</i> , 2022, 367, 130735.	4.2	24
5462	Impacts of municipal wastewater treatment plant discharge on microbial community structure and function of the receiving river in Northwest Tibetan Plateau. <i>Journal of Hazardous Materials</i> , 2022, 423, 127170.	6.5	38
5463	Remediation of soils co-contaminated with cadmium and dichlorodiphenyltrichloroethanes by king grass associated with <i>Piriformospora indica</i> : Insights into the regulation of root excretion and reshaping of rhizosphere microbial community structure. <i>Journal of Hazardous Materials</i> , 2022, 422, 126936.	6.5	20
5464	Cd and Pb immobilisation with iron oxide/lignin composite and the bacterial community response in soil. <i>Science of the Total Environment</i> , 2022, 802, 149922.	3.9	18
5465	Metal(loid)s diffusion pathway triggers distinct microbiota responses in key regions of typical karst non-ferrous smelting assembly. <i>Journal of Hazardous Materials</i> , 2022, 423, 127164.	6.5	12
5466	Little environmental adaptation and high stability of bacterial communities in rhizosphere rather than bulk soils in rice fields. <i>Applied Soil Ecology</i> , 2022, 169, 104183.	2.1	22
5467	Plastic film mulching reduces microbial interactions in black soil of northeastern China. <i>Applied Soil Ecology</i> , 2022, 169, 104187.	2.1	18
5468	Recovery patterns of soil bacterial and fungal communities in Chinese boreal forests along a fire chronosequence. <i>Science of the Total Environment</i> , 2022, 805, 150372.	3.9	15
5469	From surviving to thriving, the assembly processes of microbial communities in stone biodeterioration: A case study of the West Lake UNESCO World Heritage area in China. <i>Science of the Total Environment</i> , 2022, 805, 150395.	3.9	25
5470	The potential role of fertilizer-derived exogenous bacteria on soil bacterial community assemblage and network formation. <i>Chemosphere</i> , 2022, 287, 132338.	4.2	23
5471	Drivers of microbial beta-diversity in wastewater treatment plants in China. <i>Journal of Environmental Sciences</i> , 2022, 115, 341-349.	3.2	5
5472	Microbiota associated with the rhizosphere of <i>Paeonia lactiflora</i> Pall. (ornamental cultivar). <i>Applied Soil Ecology</i> , 2022, 169, 104214.	2.1	9
5473	Response of soil bacterial community to agricultural reclamation in the Tengger desert, northwestern China. <i>Applied Soil Ecology</i> , 2022, 169, 104189.	2.1	6
5474	Insight to bacteria community response of organic management in apple orchard-bagasse fertilizer combined with biochar. <i>Chemosphere</i> , 2022, 286, 131693.	4.2	20

#	ARTICLE	IF	CITATIONS
5475	DNA metabarcoding using nrITS2 provides highly qualitative and quantitative results for airborne pollen monitoring. <i>Science of the Total Environment</i> , 2022, 806, 150468.	3.9	19
5476	Comprehensive Analysis of the Effect of Probiotic Intake by the Mother on Human Breast Milk and Infant Fecal Microbiota. <i>Journal of Korean Medical Science</i> , 2021, 36, e58.	1.1	6
5477	Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. <i>Annals of Translational Medicine</i> , 2021, 9, 32-32.	0.7	16
5478	Reclassification of <i>Sphaerotilus natans</i> subsp. <i>sulfidivorans</i> Gridneva et al. 2011 as <i>Sphaerotilus sulfidivorans</i> sp. nov. and comparative genome analysis of the genus <i>Sphaerotilus</i> . <i>Archives of Microbiology</i> , 2021, 203, 1595-1599.	1.0	8
5480	Assessing the efficacy of eDNA metabarcoding for measuring microbial biodiversity within forest ecosystems. <i>Scientific Reports</i> , 2021, 11, 1629.	1.6	16
5481	Arbuscular mycorrhizal fungal colonization and soil pH induced by nitrogen and phosphorus additions affects leaf C:N:P stoichiometry in Chinese fir (<i>Cunninghamia lanceolata</i>) forests. <i>Plant and Soil</i> , 2021, 461, 421-440.	1.8	28
5482	<i>Amyntas corticis</i> genome reveals molecular mechanisms behind global distribution. <i>Communications Biology</i> , 2021, 4, 135.	2.0	6
5483	Effects of three different mannans on obesity and gut microbiota in high-fat diet-fed C57BL/6J mice. <i>Food and Function</i> , 2021, 12, 4606-4620.	2.1	37
5485	CTCF-binding element regulates ESC differentiation via orchestrating long-range chromatin interaction between enhancers and HoxA. <i>Journal of Biological Chemistry</i> , 2021, 296, 100413.	1.6	9
5486	Effect of host breeds on gut microbiome and serum metabolome in meat rabbits. <i>BMC Veterinary Research</i> , 2021, 17, 24.	0.7	20
5487	Effects of Different Land Use Patterns on Soil Microbial Diversity of Stone Mountain Slope. <i>Sustainable Development</i> , 2021, 11, 672-687.	0.0	1
5488	Arbuscular Mycorrhizal Fungal Communities in the Soils of Desert Habitats. <i>Microorganisms</i> , 2021, 9, 229.	1.6	19
5489	The Therapeutic Efficacy of Curcumin vs. Metformin in Modulating the Gut Microbiota in NAFLD Rats: A Comparative Study. <i>Frontiers in Microbiology</i> , 2020, 11, 555293.	1.5	27
5490	Fecal microbiota composition associates with the capacity of human peripheral blood monocytes to differentiate into immunogenic dendritic cells <i>in vitro</i> . <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	9
5491	Efficient genotyping with backwards compatibility: converting a legacy microsatellite panel for muskellunge (<i>Esox masquinongy</i>) to genotyping-by-sequencing chemistry. <i>Conservation Genetics Resources</i> , 2021, 13, 151-159.	0.4	2
5492	Effects of Long-Term Bare Fallow During the Winter-Wheat Growth Season on the Soil Chemical Properties, Fungal Community Composition, and the Occurrence of Maize Fungal Diseases in North China. <i>Plant Disease</i> , 2021, 105, 2575-2584.	0.7	7
5493	Comparison and interpretation of characteristics of Rhizosphere microbiomes of three blueberry varieties. <i>BMC Microbiology</i> , 2021, 21, 30.	1.3	12
5494	Plant and Animal-Type Feedstuff Shape the Gut Microbiota and Metabolic Processes of the Chinese Mitten Crab <i>Eriocheir sinensis</i> . <i>Frontiers in Veterinary Science</i> , 2021, 8, 589624.	0.9	10

#	ARTICLE	IF	CITATIONS
5495	Repeated Application of Rice Straw Stabilizes Soil Bacterial Community Composition and Inhibits Clubroot Disease. <i>Agriculture (Switzerland)</i> , 2021, 11, 108.	1.4	4
5496	Alteration of the fecal microbiota in Chinese patients with <i>Schistosoma japonicum</i> infection. <i>Parasite</i> , 2021, 28, 1.	0.8	16
5498	Tropical and temperate wastewater treatment plants assemble different and diverse microbiomes. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 853-867.	1.7	5
5499	Plant Compartments and Developmental Stages Modulate the Balance between Niche-Based and Neutral Processes in Soybean Microbiome. <i>Microbial Ecology</i> , 2021, 82, 416-428.	1.4	27
5500	Ancient DNA from the Asiatic Wild Dog (<i>Cuon alpinus</i>) from Europe. <i>Genes</i> , 2021, 12, 144.	1.0	5
5501	Complete Genome Sequence of <i>Mycobacterium bovis</i> BCG SL222 Sofia, the First WHO Reference Reagent for the <i>M. bovis</i> BCG Vaccine of the Russian BCG-I Substrain. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
5502	Draft Genome Sequences of <i>Idiomarina abyssalis</i> Strain KJE, <i>Marinobacter salarius</i> Strain NP2017, and <i>Marinobacter salarius</i> Strain AT3901, Isolated from Deep-Sea Sediment near the Western Flank of the Mid-Atlantic Ridge. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
5503	Bacterial diversity and lipid biomarkers in sea ice and sinking particulate organic material during the melt season in the Canadian Arctic. <i>Elementa</i> , 2021, 9, .	1.1	3
5504	<i>Limosilactobacillus fermentum</i> JL-3 isolated from Jiangshui ameliorates hyperuricemia by degrading uric acid. <i>Gut Microbes</i> , 2021, 13, 1-18.	4.3	68
5505	<i>Wolbachia</i> and <i>Spiroplasma</i> could influence bacterial communities of the spider mite <i>Tetranychus truncatus</i> . <i>Experimental and Applied Acarology</i> , 2021, 83, 197-210.	0.7	6
5506	Taxonomic Composition and Diversity of the Gut Microbiota in Relation to Habitual Dietary Intake in Korean Adults. <i>Nutrients</i> , 2021, 13, 366.	1.7	19
5507	Intestinal α -1-2-Fucosylation Contributes to Obesity and Steatohepatitis in Mice. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 293-320.	2.3	14
5508	Parkinson's Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5509	Unraveling Mechanisms and Impact of Microbial Recruitment on Oilseed Rape (<i>Brassica napus</i> L.) and the Rhizosphere Mediated by Plant Growth-Promoting Rhizobacteria. <i>Microorganisms</i> , 2021, 9, 161.	1.6	28
5510	Effects of cranberry beverages on oxidative stress and gut microbiota in subjects with <i>Helicobacter pylori</i> infection: a randomized, double-blind, placebo-controlled trial. <i>Food and Function</i> , 2021, 12, 6878-6888.	2.1	7
5511	Contribution of sample processing to gut microbiome analysis in the model Lepidoptera, silkworm <i>Bombyx mori</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4658-4668.	1.9	16
5512	Community structure of fungal pathogens causing spikelet rot disease of naked oat from different ecological regions of China. <i>Scientific Reports</i> , 2021, 11, 1243.	1.6	5
5513	Dynamics and competition of CRISPR-Cas9 ribonucleoproteins and AAV donor-mediated NHEJ, MMEJ and HDR editing. <i>Nucleic Acids Research</i> , 2021, 49, 969-985.	6.5	90

#	ARTICLE	IF	CITATIONS
5514	Soil organic carbon and total nitrogen predict large-scale distribution of soil fungal communities in temperate and alpine shrub ecosystems. <i>European Journal of Soil Biology</i> , 2021, 102, 103270.	1.4	10
5515	High throughput sequencing of the bacterial composition and dynamic succession in Daqu for Chinese sesame flavour liquor. <i>Journal of the Institute of Brewing</i> , 2020, 126, 98-104.	0.8	32
5516	Effect of storage, temperature, and extraction kit on the phylogenetic composition detected in the human milk microbiota. <i>MicrobiologyOpen</i> , 2021, 10, e1127.	1.2	14
5517	Microbiota succession during aerobic stability of maize silage inoculated with <i>Lentilactobacillus buchneri</i> NCIMB 40788 and <i>Lentilactobacillus hilgardii</i> CNCM 4785. <i>MicrobiologyOpen</i> , 2021, 10, e1153.	1.2	31
5518	Revisiting the phosphotyrosine binding pocket of Fyn SH2 domain led to the identification of novel SH2 superbinders.. <i>Protein Science</i> , 2021, 30, 558-570.	3.1	9
5519	Analysis of microbial utilization of rice straw in paddy soil using a DNA-SIP approach. <i>Soil Science Society of America Journal</i> , 2020, 84, 99-114.	1.2	16
5520	De Novo Transcriptome Assembly in Polyploid Species. <i>Methods in Molecular Biology</i> , 2017, 1536, 209-221.	0.4	13
5521	Transcriptomics and Proteomics of Foodborne Bacterial Pathogens. , 2017, , 167-200.		1
5522	Metagenomic Methods: From Seawater to the Database. , 2019, , 3-16.		1
5523	Analysis of the developing gut microbiota in young dairy calves—impact of colostrum microbiota and gut disturbances. <i>Tropical Animal Health and Production</i> , 2021, 53, 50.	0.5	20
5524	Comparison Between the Gut Microbiota in Different Gastrointestinal Segments of Large-Tailed Han and Small-Tailed Han Sheep Breeds with High-Throughput Sequencing. <i>Indian Journal of Microbiology</i> , 2020, 60, 436-450.	1.5	4
5525	Diversity and composition of microbiota during fermentation of traditional Nuodeng ham. <i>Journal of Microbiology</i> , 2021, 59, 20-28.	1.3	9
5526	The microbiome and metabolome of Napier grass silages prepared with screened lactic acid bacteria during ensiling and aerobic exposure. <i>Animal Feed Science and Technology</i> , 2020, 269, 114673.	1.1	34
5527	The Sydney rock oyster microbiota is influenced by location, season and genetics. <i>Aquaculture</i> , 2020, 527, 735472.	1.7	17
5528	Anaerobic digestion of aqueous phase from hydrothermal liquefaction of <i>Spirulina</i> using biostimulated sludge. <i>Bioresource Technology</i> , 2020, 312, 123552.	4.8	12
5529	Changes in rhizobacterial community mediating atrazine dissipation by arbuscular mycorrhiza. <i>Chemosphere</i> , 2020, 256, 127046.	4.2	27
5530	Aerobic degradation of high tetramethylammonium hydroxide (TMAH) and its impacts on nitrification and microbial community. <i>Chemosphere</i> , 2020, 258, 127146.	4.2	17
5531	Zokor disturbances indicated positive soil microbial responses with carbon cycle and mineral encrustation in alpine grassland. <i>Ecological Engineering</i> , 2020, 144, 105702.	1.6	15

#	ARTICLE	IF	CITATIONS
5532	Labile fractions of soil nutrients shape the distribution of bacterial communities towards phosphorus recycling systems over elevation gradients in Gongga Mountain, SW China. <i>European Journal of Soil Biology</i> , 2020, 98, 103185.	1.4	19
5533	Fetal and early postnatal lead exposure measured in teeth associates with infant gut microbiota. <i>Environment International</i> , 2020, 144, 106062.	4.8	21
5534	Growth inhibition of sulfate-reducing bacteria for trichloroethylene dechlorination enhancement. <i>Environmental Research</i> , 2020, 187, 109629.	3.7	17
5535	Keystone taxa of water microbiome respond to environmental quality and predict water contamination. <i>Environmental Research</i> , 2020, 187, 109666.	3.7	33
5536	Contributions of ammonia-oxidising bacteria and archaea to nitrification under long-term application of green manure in alkaline paddy soil. <i>Geoderma</i> , 2020, 374, 114419.	2.3	19
5537	Antidiabetic Effects of Gegen Qinlian Decoction via the Gut Microbiota Are Attributable to Its Key Ingredient Berberine. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 721-736.	3.0	70
5538	Integral approach using bacterial microbiome to stabilize municipal solid waste. <i>Journal of Environmental Management</i> , 2020, 265, 110528.	3.8	14
5539	Homogeneous selection drives antibiotic resistome in two adjacent sub-watersheds, China. <i>Journal of Hazardous Materials</i> , 2020, 398, 122820.	6.5	46
5540	Biofilm as a live and in-situ formed membrane for solids separation in bioreactors: Biofilm succession governs resistance variation demonstrated during the start-up period. <i>Journal of Membrane Science</i> , 2020, 608, 118197.	4.1	9
5541	Effects of laying breeder hens dietary β -carotene, curcumin, allicin, and sodium butyrate supplementation on the jejunal microbiota and immune response of their offspring chicks. <i>Poultry Science</i> , 2020, 99, 3807-3816.	1.5	13
5542	Meteorological factors had more impact on airborne bacterial communities than air pollutants. <i>Science of the Total Environment</i> , 2017, 601-602, 703-712.	3.9	138
5543	Effects of pyrolysis temperature on soil-plant-microbe responses to <i>Solidago canadensis</i> L.-derived biochar in coastal saline-alkali soil. <i>Science of the Total Environment</i> , 2020, 731, 138938.	3.9	61
5544	Anaerobic oxidation of methane and associated microbiome in anoxic water of Northwestern Siberian lakes. <i>Science of the Total Environment</i> , 2020, 736, 139588.	3.9	67
5545	Hospital discharges in urban sanitation systems: Long-term monitoring of wastewater resistome and microbiota in relationship to their eco-exposome. <i>Water Research X</i> , 2020, 7, 100045.	2.8	49
5546	Effects of different molecular weights of chitosan on methane production and bacterial community structure in vitro. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1644-1655.	1.7	15
5547	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	13.7	130
5548	Generating quantitative binding landscapes through fractional binding selections combined with deep sequencing and data normalization. <i>Nature Communications</i> , 2020, 11, 297.	5.8	10
5549	Base editors for simultaneous introduction of C-to-T and A-to-G mutations. <i>Nature Biotechnology</i> , 2020, 38, 865-869.	9.4	137

#	ARTICLE	IF	CITATIONS
5550	Investigating seafood substitution problems and consequences in Taiwan using molecular barcoding and deep microbiome profiling. <i>Scientific Reports</i> , 2020, 10, 21997.	1.6	8
5551	Soil fungal and bacterial communities in southern boreal forests of the Greater Khingan Mountains and their relationship with soil properties. <i>Scientific Reports</i> , 2020, 10, 22025.	1.6	15
5552	Systematic, continental scale temporal monitoring of marine pelagic microbiota by the Australian Marine Microbial Biodiversity Initiative. <i>Scientific Data</i> , 2018, 5, 180130.	2.4	41
5553	Gut dysbiosis is associated with primary hypothyroidism with interaction on gut-thyroid axis. <i>Clinical Science</i> , 2020, 134, 1521-1535.	1.8	52
5554	Early Gut Microbiota Changes in Preterm Infants with Bronchopulmonary Dysplasia: A Pilot Caseâ€“Control Study. <i>American Journal of Perinatology</i> , 2021, 38, 1142-1149.	0.6	9
5555	What Else Is in <i>Salviae officinalis folium</i> ? Comprehensive Species Identification of Plant Raw Material by DNA Metabarcoding. <i>Planta Medica</i> , 2018, 84, 428-433.	0.7	2
5556	Functional plasticity and evolutionary adaptation of allosteric regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25445-25454.	3.3	65
5557	Seasonal variation of epiphytic bacteria in the phyllosphere of <i>Gingko biloba</i> , <i>Pinus bungeana</i> and <i>Sabina chinensis</i> . <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	30
5558	Temporal and spatial interactions modulate the soybean microbiome. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	17
5559	Vertical stratification patterns of methanotrophs and their genetic controllers in water columns of oxygen-stratified boreal lakes. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	29
5560	<i>Legionella</i> antimicrobial sensitivity testing: comparison of microbroth dilution with BCYE and LASARUS solid media. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1197-1204.	1.3	7
5561	HAPHIPE: Haplotype Reconstruction and Phylodynamics for Deep Sequencing of Intrahost Viral Populations. <i>Molecular Biology and Evolution</i> , 2021, 38, 1677-1690.	3.5	9
5562	Experimental manipulation of selfish genetic elements links genes to microbial community function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190681.	1.8	18
5563	<i>Corynebacterium lowii</i> sp. nov. and <i>Corynebacterium oculi</i> sp. nov., derived from human clinical disease and an emended description of <i>Corynebacterium mastitidis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2803-2812.	0.8	40
5564	<i>Psychrobacter pasteurii</i> and <i>Psychrobacter piechaudii</i> sp. nov., two novel species within the genus <i>Psychrobacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3192-3197.	0.8	13
5565	Changes in bacterial diversity and composition in the faeces and colon of weaned piglets after feeding fermented soybean meal. <i>Journal of Medical Microbiology</i> , 2018, 67, 1181-1190.	0.7	21
5566	Characterization of pelvic and cervical microbiotas from patients with pelvic inflammatory disease. <i>Journal of Medical Microbiology</i> , 2018, 67, 1519-1526.	0.7	22
5567	Effects of <i>Eclipta prostrata</i> on gut microbiota of SAMP6 mice with osteoporosis. <i>Journal of Medical Microbiology</i> , 2019, 68, 402-416.	0.7	17

#	ARTICLE	IF	CITATIONS
5568	Encapsulated cyclosporine does not change the composition of the human microbiota when assessed ex vivo and in vivo. <i>Journal of Medical Microbiology</i> , 2020, 69, 854-863.	0.7	12
5569	Assessing the genomic relatedness and evolutionary rates of persistent verotoxigenic <i>Escherichia coli</i> serotypes within a closed beef herd in Canada. <i>Microbial Genomics</i> , 2020, 6, .	1.0	4
5709	Core microbial communities of lacustrine microbialites sampled along an alkalinity gradient. <i>Environmental Microbiology</i> , 2021, 23, 51-68.	1.8	26
5710	Effect on the ensilage performance and microbial community of adding <i>Neolamarckia cadamba</i> leaves to corn stalks. <i>Microbial Biotechnology</i> , 2020, 13, 1502-1514.	2.0	10
5711	Comparative analysis of DNA extraction methods to study the body surface microbiota of insects: A case study with ant cuticular bacteria. <i>Molecular Ecology Resources</i> , 2017, 17, e34-e45.	2.2	20
5712	Self-reported bowel symptoms are associated with differences in overall gut microbiota composition and enrichment of <i>Blautia</i> in a population-based cohort. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2021, 36, 174-180.	1.4	25
5713	Highlighting patterns of fungal diversity and composition shaped by ocean currents using the East China Sea as a model. <i>Molecular Ecology</i> , 2018, 27, 564-576.	2.0	37
5714	Synergistic Lethal Mutagenesis of Hepatitis C Virus. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	10
5715	Improved Reference Genome Sequence of <i>Coccidioides immitis</i> Strain WA_211, Isolated in Washington State. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	9
5716	Eleven High-Quality Reference Genome Sequences and 360 Draft Assemblies of Shiga Toxin-Producing <i>Escherichia coli</i> Isolates from Human, Food, Animal, and Environmental Sources in Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
5717	Amylases in the Human Vagina. <i>MSphere</i> , 2020, 5, .	1.3	30
5718	Heritable Gut Microbiome Associated with <i>Salmonella enterica</i> Serovar Pullorum Infection in Chickens. <i>MSystems</i> , 2021, 6, .	1.7	15
5719	Different Effects of Wild and Cultivated Soybean on Rhizosphere Bacteria. <i>Microbiology</i> , 2019, 88, 720-728.	0.5	5
5720	Analyzing Vomit of <i>Platalea minor</i> (Black-faced Spoonbill) to Identify Food Components using Next-Generation Sequencing and Microscopy. <i>Hangug Hwangyeong Saengmul Haghoeji</i> , 2018, 36, 165-173.	0.1	1
5721	Dual epithelial and immune cell function of Dvl1 regulates gut microbiota composition and intestinal homeostasis. <i>JCI Insight</i> , 2016, 1, .	2.3	11
5722	Mucosal-associated invariant T cell-rich congenic mouse strain allows functional evaluation. <i>Journal of Clinical Investigation</i> , 2015, 125, 4171-4185.	3.9	143
5723	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	78
5724	The impact of the anti-diabetic drug metformin on the intestinal microbiome of larval brown trout (<i>Salmo trutta f. fario</i>). <i>Environmental Sciences Europe</i> , 2020, 32, .	2.6	13

#	ARTICLE	IF	CITATIONS
5725	Transcriptome analysis of <i>Anastrepha fraterculus</i> sp. 1 males, females, and embryos: insights into development, courtship, and reproduction. <i>BMC Genetics</i> , 2020, 21, 136.	2.7	3
5726	Marine bacterial communities in the upper gulf of Thailand assessed by Illumina next-generation sequencing platform. <i>BMC Microbiology</i> , 2020, 20, 19.	1.3	28
5727	Dissection of the cecal microbial community in chickens after <i>Eimeria tenella</i> infection. <i>Parasites and Vectors</i> , 2020, 13, 56.	1.0	56
5728	The effects of <i>Rhodopseudomonas palustris</i> PSB06 and CGA009 with different agricultural applications on rice growth and rhizosphere bacterial communities. <i>AMB Express</i> , 2019, 9, 173.	1.4	17
5729	Specific enrichment of microbes and increased ruminal propionate production: the potential mechanism underlying the high energy efficiency of Holstein heifers fed steam-flaked corn. <i>AMB Express</i> , 2019, 9, 209.	1.4	27
5730	Dissimilarity of microbial diversity of pond water, shrimp intestine and sediment in Aquamimicry system. <i>AMB Express</i> , 2020, 10, 180.	1.4	23
5731	Variations of rhizospheric soil microbial communities in response to continuous <i>Andrographis paniculata</i> cropping practices. , 2020, 61, 18.		19
5732	Soil microbiota manipulation and its role in suppressing soil-borne plant pathogens in organic farming systems under the light of microbiome-assisted strategies. <i>Chemical and Biological Technologies in Agriculture</i> , 2020, 7, .	1.9	66
5733	A Preliminary Study of Microbiota Diversity in Saliva and Bronchoalveolar Lavage Fluid from Patients with Primary Bronchogenic Carcinoma. <i>Medical Science Monitor</i> , 2019, 25, 2819-2834.	0.5	40
5734	Proteobacteria Acts as a Pathogenic Risk-Factor for Chronic Abdominal Pain and Diarrhea in Post-Cholecystectomy Syndrome Patients: A Gut Microbiome Metabolomics Study. <i>Medical Science Monitor</i> , 2019, 25, 7312-7320.	0.5	26
5735	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. <i>F1000Research</i> , 2017, 6, 618.	0.8	7
5736	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. <i>F1000Research</i> , 2017, 6, 618.	0.8	5
5737	Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers. <i>F1000Research</i> , 2015, 4, 1422.	0.8	33
5738	Polysaccharide from wild morels alters the spatial structure of gut microbiota and the production of short-chain fatty acids in mice. <i>Bioscience of Microbiota, Food and Health</i> , 2020, 39, 219-226.	0.8	10
5739	Characterization of microbiota in systemic-onset juvenile idiopathic arthritis with different disease severities. <i>World Journal of Clinical Cases</i> , 2019, 7, 2734-2745.	0.3	16
5740	Metagenomic analysis of microbial community in over-fermented tempeh. <i>Biodiversitas</i> , 2019, 20, 1106-1114.	0.2	15
5741	SARNAclust: Semi-automatic detection of RNA protein binding motifs from immunoprecipitation data. <i>PLoS Computational Biology</i> , 2018, 14, e1006078.	1.5	6
5742	Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by <i>Entamoeba</i> and Subsistence. <i>PLoS Genetics</i> , 2015, 11, e1005658.	1.5	171

#	ARTICLE	IF	CITATIONS
5743	<i>Yersinia enterocolitica</i> , a Neglected Cause of Human Enteric Infections in CÔte d'Ivoire. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005216.	1.3	30
5744	Automated Universal BRAF State Detection within the Activation Segment in Skin Metastases by Pyrosequencing-Based Assay U-BRAFV600. <i>PLoS ONE</i> , 2013, 8, e59221.	1.1	13
5745	Optimizing Information in Next-Generation-Sequencing (NGS) Reads for Improving De Novo Genome Assembly. <i>PLoS ONE</i> , 2013, 8, e69503.	1.1	8
5746	Extensive Recombination Due to Heteroduplexes Generates Large Amounts of Artificial Gene Fragments during PCR. <i>PLoS ONE</i> , 2014, 9, e106658.	1.1	23
5747	Effects of Vendor and Genetic Background on the Composition of the Fecal Microbiota of Inbred Mice. <i>PLoS ONE</i> , 2015, 10, e0116704.	1.1	268
5748	Biochar in Co-Contaminated Soil Manipulates Arsenic Solubility and Microbiological Community Structure, and Promotes Organochlorine Degradation. <i>PLoS ONE</i> , 2015, 10, e0125393.	1.1	45
5749	HPV Infection and Cervical Screening in Socially Isolated Indigenous Women Inhabitants of the Amazonian Rainforest. <i>PLoS ONE</i> , 2015, 10, e0133635.	1.1	48
5750	Microbial Community Dynamics and Activity Link to Indigo Production from Indole in Bioaugmented Activated Sludge Systems. <i>PLoS ONE</i> , 2015, 10, e0138455.	1.1	7
5751	A Novel Human scFv Library with Non-Combinatorial Synthetic CDR Diversity. <i>PLoS ONE</i> , 2015, 10, e0141045.	1.1	18
5752	Exploring the Gastrointestinal 'Nemabiome' Deep Amplicon Sequencing to Quantify the Species Composition of Parasitic Nematode Communities. <i>PLoS ONE</i> , 2015, 10, e0143559.	1.1	181
5753	Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0145031.	1.1	28
5754	Microbial Community Structure and Arsenic Biogeochemistry in an Acid Vapor-Formed Spring in Tengchong Geothermal Area, China. <i>PLoS ONE</i> , 2016, 11, e0146331.	1.1	36
5755	Haplotype-Phased Synthetic Long Reads from Short-Read Sequencing. <i>PLoS ONE</i> , 2016, 11, e0147229.	1.1	29
5756	Comparison of Sample Preparation Methods Used for the Next-Generation Sequencing of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2016, 11, e0148676.	1.1	54
5757	Next-Generation Sequencing of a Single Domain Antibody Repertoire Reveals Quality of Phage Display Selected Candidates. <i>PLoS ONE</i> , 2016, 11, e0149393.	1.1	30
5758	Influence of the Biliary System on Biliary Bacteria Revealed by Bacterial Communities of the Human Biliary and Upper Digestive Tracts. <i>PLoS ONE</i> , 2016, 11, e0150519.	1.1	70
5759	Comparison of Boiling and Robotics Automation Method in DNA Extraction for Metagenomic Sequencing of Human Oral Microbes. <i>PLoS ONE</i> , 2016, 11, e0154389.	1.1	32
5760	Composition and Predicted Metabolic Capacity of Upper and Lower Airway Microbiota of Healthy Dogs in Relation to the Fecal Microbiota. <i>PLoS ONE</i> , 2016, 11, e0154646.	1.1	58

#	ARTICLE	IF	CITATIONS
5761	Complexity and Dynamics of the Winemaking Bacterial Communities in Berries, Musts, and Wines from Apulian Grape Cultivars through Time and Space. PLoS ONE, 2016, 11, e0157383.	1.1	60
5762	Early Gut Microbiota Perturbations Following Intrapartum Antibiotic Prophylaxis to Prevent Group B Streptococcal Disease. PLoS ONE, 2016, 11, e0157527.	1.1	81
5763	Distribution and Diversity of Bacteria and Fungi Colonization in Stone Monuments Analyzed by High-Throughput Sequencing. PLoS ONE, 2016, 11, e0163287.	1.1	51
5764	Bacterial Communities in the Rhizospheres of Three Mangrove Tree Species from Beilun Estuary, China. PLoS ONE, 2016, 11, e0164082.	1.1	51
5765	A Microbiological Map of the Healthy Equine Gastrointestinal Tract. PLoS ONE, 2016, 11, e0166523.	1.1	118
5766	Bacterial Communities Associated with Houseflies (<i>Musca domestica</i> L.) Sampled within and between Farms. PLoS ONE, 2017, 12, e0169753.	1.1	69
5767	Bacterial diversity of bacteriomes and organs of reproductive, digestive and excretory systems in two cicada species (Hemiptera: Cicadidae). PLoS ONE, 2017, 12, e0175903.	1.1	23
5768	Protective effect of aplysin on liver tissue and the gut microbiota in alcohol-fed rats. PLoS ONE, 2017, 12, e0178684.	1.1	19
5769	A comparative study revealed first insights into the diversity and metabolisms of the microbial communities in the sediments of Pacmanus and Desmos hydrothermal fields. PLoS ONE, 2017, 12, e0181048.	1.1	7
5770	Inferring microbial interactions in thermophilic and mesophilic anaerobic digestion of hog waste. PLoS ONE, 2017, 12, e0181395.	1.1	36
5771	DUDE-Seq: Fast, flexible, and robust denoising for targeted amplicon sequencing. PLoS ONE, 2017, 12, e0181463.	1.1	47
5772	Effects of <i>Eimeria tenella</i> infection on chicken caecal microbiome diversity, exploring variation associated with severity of pathology. PLoS ONE, 2017, 12, e0184890.	1.1	109
5773	Modulation of the gut microbiota by the mixture of fish oil and krill oil in high-fat diet-induced obesity mice. PLoS ONE, 2017, 12, e0186216.	1.1	55
5774	Rhizospheric microbial communities associated with wild and cultivated frankincense producing <i>Boswellia sacra</i> tree. PLoS ONE, 2017, 12, e0186939.	1.1	13
5775	Composition and diversity of rhizosphere fungal community in <i>Coptis chinensis</i> Franch. continuous cropping fields. PLoS ONE, 2018, 13, e0193811.	1.1	44
5776	Biological invasions alter environmental microbiomes: A meta-analysis. PLoS ONE, 2020, 15, e0240996.	1.1	13
5777	Broiler chickens and early life programming: Microbiome transplant-induced cecal community dynamics and phenotypic effects. PLoS ONE, 2020, 15, e0242108.	1.1	16
5778	Illumina-based analysis yields new insights into the diversity and composition of endophytic fungi in cultivated <i>Huperzia serrata</i> . PLoS ONE, 2020, 15, e0242258.	1.1	14

#	ARTICLE	IF	CITATIONS
5779	Gut mycobiomes are altered in people with type 2 Diabetes Mellitus and Diabetic Retinopathy. PLoS ONE, 2020, 15, e0243077.	1.1	60
5780	Response of oat morphologies, root exudates, and rhizosphere fungal communities to amendments in a saline-alkaline environment. PLoS ONE, 2020, 15, e0243301.	1.1	5
5781	Estimating virus effective population size and selection without neutral markers. PLoS Pathogens, 2017, 13, e1006702.	2.1	18
5782	Early genistein exposure of California mice and effects on the gut microbiota-brain axis. Journal of Endocrinology, 2019, 242, 139-157.	1.2	21
5783	Intercropping of wheat changed cucumber rhizosphere bacterial community composition and inhibited cucumber Fusarium wilt disease. Scientia Agricola, 2020, 77, .	0.6	10
5784	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
5785	Gut microbial profile analysis by MiSeq sequencing of pancreatic carcinoma patients in China. Oncotarget, 2017, 8, 95176-95191.	0.8	160
5786	Breast tissue, oral and urinary microbiomes in breast cancer. Oncotarget, 2017, 8, 88122-88138.	0.8	134
5787	Specific alterations in gut microbiota are associated with prognosis of Budd-Chiari syndrome. Oncotarget, 2018, 9, 3303-3320.	0.8	7
5788	Massive parallel<i>IGHV</i> gene sequencing reveals a germinal center pathway in origins of human multiple myeloma. Oncotarget, 2015, 6, 13229-13240.	0.8	21
5789	Liquid biopsy monitoring uncovers acquired RAS-mediated resistance to cetuximab in a substantial proportion of patients with head and neck squamous cell carcinoma. Oncotarget, 2016, 7, 42988-42995.	0.8	64
5790	Microbiomes of Inflammatory Thoracic Aortic Aneurysms Due to Giant Cell Arteritis and Clinically Isolated Aortitis Differ From Those of Non-Inflammatory Aneurysms. Pathogens and Immunity, 2019, 4, 105.	1.4	22
5791	Two different Oenococcus oeni lineages are associated to either red or white wines in Burgundy: genomics and metabolomics insights. Oeno One, 2017, 51, 309.	0.7	34
5793	The alterations of gut microbiota in mice with chronic pancreatitis. Annals of Translational Medicine, 2019, 7, 464-464.	0.7	26
5794	Variations in gut microbial profiles in ankylosing spondylitis: disease phenotype-related dysbiosis. Annals of Translational Medicine, 2019, 7, 571-571.	0.7	29
5795	Environmental DNA Collected from Snow Tracks is Useful for Identification of Mammalian Species. Zoological Science, 2019, 36, 198.	0.3	32
5797	The Rice Leaf Microbiome Has a Conserved Community Structure Controlled by Complex Host-Microbe Interactions. SSRN Electronic Journal, 0, , .	0.4	14
5798	MagnEdit-interacting factors that recruit DNA-editing enzymes to single base targets. Life Science Alliance, 2020, 3, e201900606.	1.3	7

#	ARTICLE	IF	CITATIONS
5799	Multilevel genome typing: genomics-guided scalable resolution typing of microbial pathogens. <i>Eurosurveillance</i> , 2020, 25, .	3.9	12
5800	Short communication: High-throughput sequencing approach to investigate Italian artisanal cheese production. <i>Journal of Dairy Science</i> , 2020, 103, 10015-10021.	1.4	12
5801	Cutting wedge: bacterial community diversity and structure associated with the cheese rind and curd of seven natural rind cheeses. <i>Fine Focus</i> , 2017, 3, 09-31.	0.2	1
5802	The Diversity of the Endobiotic Bacterial Communities in the Four Jellyfish Species. <i>Polish Journal of Microbiology</i> , 2019, 68, 465-476.	0.6	1
5803	Uncovering cryptochrome/photolyase gene diversity in aquatic microbiomes exposed to diverse UV-B regimes. <i>Aquatic Microbial Ecology</i> , 2020, 85, 141-154.	0.9	10
5804	Ecology, histopathology, and microbial ecology of a white-band disease outbreak in the threatened staghorn coral <i>Acropora cervicornis</i> . <i>Diseases of Aquatic Organisms</i> , 2020, 137, 217-237.	0.5	37
5805	Use of DNA metabarcoding for stomach content analysis in the invasive lionfish <i>Pterois volitans</i> in Puerto Rico. <i>Marine Ecology - Progress Series</i> , 2016, 558, 181-191.	0.9	75
5806	Intestinal Barrier Breakdown and Mucosal Microbiota Disturbance in Neuromyelitis Optic Spectrum Disorders. <i>Frontiers in Immunology</i> , 2020, 11, 2101.	2.2	16
5807	Differences in Gut Microbial and Serum Biochemical Indices Between Sows With Different Productive Capacities During Perinatal Period. <i>Frontiers in Microbiology</i> , 2019, 10, 3047.	1.5	22
5808	Schistosomiasis Vector Snails and Their Microbiota Display a Phyllosymbiosis Pattern. <i>Frontiers in Microbiology</i> , 2019, 10, 3092.	1.5	28
5809	Metatranscriptomics From a Small Aquatic System: Microeukaryotic Community Functions Through the Diurnal Cycle. <i>Frontiers in Microbiology</i> , 2020, 11, 1006.	1.5	8
5810	Pathogen Infection and Host-Resistance Interactively Affect Root-Associated Fungal Communities in Watermelon. <i>Frontiers in Microbiology</i> , 2020, 11, 605622.	1.5	12
5811	Regular Biochar and Bacteria-Inoculated Biochar Alter the Composition of the Microbial Community in the Soil of a Chinese Fir Plantation. <i>Forests</i> , 2020, 11, 951.	0.9	13
5812	Ethnic Differences Shape the Alpha but Not Beta Diversity of Gut Microbiota from School Children in the Absence of Environmental Differences. <i>Microorganisms</i> , 2020, 8, 254.	1.6	17
5813	Targeted Mutagenesis of the Female-Suppressor SyG1 Gene in Tetraploid Kiwifruit by CRISPR/CAS9. <i>Plants</i> , 2021, 10, 62.	1.6	8
5814	Characterization of hepatitis B virus X gene quasispecies complexity in mono-infection and hepatitis delta virus superinfection. <i>World Journal of Gastroenterology</i> , 2019, 25, 1566-1579.	1.4	7
5815	Human milk mycobiota composition: relationship with gestational age, delivery mode, and birth weight. <i>Beneficial Microbes</i> , 2020, 11, 151-162.	1.0	18
5816	Effects of Mycorrhiza and Drought Stress on the Diversity of Fungal Community in Soils and Roots of Trifoliate Orange. <i>Biotechnology</i> , 2018, 18, 32-41.	0.5	11

#	ARTICLE	IF	CITATIONS
5817	Human Milk Microbial Community Structure Is Relatively Stable and Related to Variations in Macronutrient and Micronutrient Intakes in Healthy Lactating Women. <i>Journal of Nutrition</i> , 2017, 147, 1739-1748.	1.3	120
5818	Prevalence of Opportunistic Pathogens and Diversity of Microbial Communities in the Water System of a Pulmonary Hospital. <i>Biomedical and Environmental Sciences</i> , 2020, 33, 248-259.	0.2	7
5819	Decapod crustacean larval community structure of the submarine canyon off Blanes (NW) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 Td	0.3	5
5820	Bioinformatic Suggestions on MiSeq-Based Microbial Community Analysis. <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 765-770.	0.9	47
5821	Fecal Microbiota Transplantation (FMT) Alleviates Experimental Colitis in Mice by Gut Microbiota Regulation. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 1132-1141.	0.9	89
5822	Temporal Dynamics of Air Bacterial Communities in a University Health Centre Using Illumina MiSeq Sequencing. <i>Aerosol and Air Quality Research</i> , 2020, 20, 966-980.	0.9	7
5823	16S Metagenomic Comparison of Plasmodium falciparumâ€“Infected and Noninfected Anopheles gambiae and Anopheles funestus Microbiota from Senegal. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 1489-1498.	0.6	9
5824	The impact of short-term acute heat stress on the rumen microbiome of Hanwoo steers. <i>Journal of Animal Science and Technology</i> , 2020, 62, 208-217.	0.8	22
5826	High-Throughput Sequencing Analysis of Endophytic Bacteria Diversity in Fruits of White and Red Pitayas from Three Different Origins. <i>Polish Journal of Microbiology</i> , 2018, 67, 27-35.	0.6	12
5827	Microbiological Characteristics of Gouda Cheese Manufactured with Pasteurized and Raw Milk during Ripening Using Next Generation Sequencing. <i>Food Science of Animal Resources</i> , 2019, 39, 585-600.	1.7	16
5828	Description of microbial diversity associated with ticks Hyalomma dromedarii (Acari: Ixodidae) isolated from camels in Hail region (Saudi Arabia) using massive sequencing of 16S rDNA. <i>Bioinformation</i> , 2020, 16, 602-610.	0.2	6
5829	Targeted, homology-driven gene insertion in stem cells by ZFN-loaded â€“all-in-oneâ€™ lentiviral vectors. <i>ELife</i> , 2016, 5, .	2.8	15
5830	Resolving the prevalence of somatic transposition in Drosophila. <i>ELife</i> , 2017, 6, .	2.8	57
5831	Embryo polarity in moth flies and mosquitoes relies on distinct old genes with localized transcript isoforms. <i>ELife</i> , 2019, 8, .	2.8	25
5832	Nanopore direct RNA sequencing maps the complexity of Arabidopsis mRNA processing and m6A modification. <i>ELife</i> , 2020, 9, .	2.8	312
5833	Altered expression of a quality control protease in E. coli reshapes the in vivo mutational landscape of a model enzyme. <i>ELife</i> , 2020, 9, .	2.8	37
5834	A small protein encoded by a putative lncRNA regulates apoptosis and tumorigenicity in human colorectal cancer cells. <i>ELife</i> , 2020, 9, .	2.8	43
5835	Hfq CLASH uncovers sRNA-target interaction networks linked to nutrient availability adaptation. <i>ELife</i> , 2020, 9, .	2.8	68

#	ARTICLE	IF	CITATIONS
5836	Deciphering the regulatory genome of <i>Escherichia coli</i> , one hundred promoters at a time. <i>ELife</i> , 2020, 9, .	2.8	31
5837	Phylogenomics of white-eyes, a "great speciator"™, reveals Indonesian archipelago as the center of lineage diversity. <i>ELife</i> , 2020, 9, .	2.8	17
5838	Comparison of the diversity of cultured and total bacterial communities in marine sediment using culture-dependent and sequencing methods. <i>PeerJ</i> , 2020, 8, e10060.	0.9	7
5839	H ₂ -saturation of high affinity H ₂ -oxidizing bacteria alters the ecological niche of soil microorganisms unevenly among taxonomic groups. <i>PeerJ</i> , 2016, 4, e1782.	0.9	26
5840	Comprehensive profiling of retroviral integration sites using target enrichment methods from historical koala samples without an assembled reference genome. <i>PeerJ</i> , 2016, 4, e1847.	0.9	16
5841	Rapid response of arbuscular mycorrhizal fungal communities to short-term fertilization in an alpine grassland on the Qinghai-Tibet Plateau. <i>PeerJ</i> , 2016, 4, e2226.	0.9	29
5842	Whole gut microbiome composition of damselfish and cardinalfish before and after reef settlement. <i>PeerJ</i> , 2016, 4, e2412.	0.9	52
5843	Characterization, development and multiplexing of microsatellite markers in three commercially exploited reef fish and their application for stock identification. <i>PeerJ</i> , 2016, 4, e2418.	0.9	4
5844	A method for high precision sequencing of near full-length 16S rRNA genes on an Illumina MiSeq. <i>PeerJ</i> , 2016, 4, e2492.	0.9	59
5845	Antibiotic resistance potential of the healthy preterm infant gut microbiome. <i>PeerJ</i> , 2017, 5, e2928.	0.9	34
5846	Putative archaeal viruses from the mesopelagic ocean. <i>PeerJ</i> , 2017, 5, e3428.	0.9	46
5847	A longitudinal study of the diabetic skin and wound microbiome. <i>PeerJ</i> , 2017, 5, e3543.	0.9	93
5848	Characterisation of microsatellite and SNP markers from Miseq and genotyping-by-sequencing data among parapatric <i>Urophora cardui</i> (Tephritidae) populations. <i>PeerJ</i> , 2017, 5, e3582.	0.9	3
5849	Composition, diversity and function of intestinal microbiota in pacific white shrimp (<i>Litopenaeus</i>) Tj ETQq1 1 0.784314 rgBT /Overbo	0.9	108
5850	A microbial survey of the International Space Station (ISS). <i>PeerJ</i> , 2017, 5, e4029.	0.9	52
5851	Impacts of diarrhea on the immune system, intestinal environment, and expression of PGRPs in New Zealand rabbits. <i>PeerJ</i> , 2017, 5, e4100.	0.9	12
5852	16S rRNA gene sequencing reveals effects of photoperiod on cecal microbiota of broiler roosters. <i>PeerJ</i> , 2018, 6, e4390.	0.9	22
5853	Inulin-type fructan improves diabetic phenotype and gut microbiota profiles in Rats. <i>PeerJ</i> , 2018, 6, e4446.	0.9	127

#	ARTICLE	IF	CITATIONS
5854	Assessing soil bacterial community and dynamics by integrated high-throughput absolute abundance quantification. PeerJ, 2018, 6, e4514.	0.9	60
5855	Pumpkin powdery mildew disease severity influences the fungal diversity of the phyllosphere. PeerJ, 2018, 6, e4559.	0.9	27
5856	Applying fecal microbiota transplantation (FMT) to treat recurrent <i>Clostridium difficile</i> infections (rCDI) in children. PeerJ, 2018, 6, e4663.	0.9	24
5857	Sexually dimorphic venom proteins in long-jawed orb-weaving spiders (<i>Tetragnatha</i>) comprise novel gene families. PeerJ, 2018, 6, e4691.	0.9	21
5858	The bacterial communities of <i>Drosophila suzukii</i> collected from undamaged cherries. PeerJ, 2014, 2, e474.	0.9	62
5859	Effects of preservation method on canine (<i>Canis lupus familiaris</i>) fecal microbiota. PeerJ, 2018, 6, e4827.	0.9	18
5860	Can non-destructive DNA extraction of bulk invertebrate samples be used for metabarcoding?. PeerJ, 2018, 6, e4980.	0.9	57
5861	Biases during DNA extraction affect characterization of the microbiota associated with larvae of the Pacific white shrimp, <i>Litopenaeus vannamei</i> . PeerJ, 2018, 6, e5257.	0.9	23
5862	Compositional and predicted functional analysis of the gut microbiota of <i>Radix auricularia</i> (Linnaeus) via high-throughput Illumina sequencing. PeerJ, 2018, 6, e5537.	0.9	44
5863	Assessment of the bacterial community structure in shallow and deep sediments of the Perdido Fold Belt region in the Gulf of Mexico. PeerJ, 2018, 6, e5583.	0.9	26
5864	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
5865	Shifts in community composition and co-occurrence patterns of phyllosphere fungi inhabiting <i>Mussaenda shikokiana</i> along an elevation gradient. PeerJ, 2018, 6, e5767.	0.9	20
5866	Pollen metabarcoding reveals broad and species-specific resource use by urban bees. PeerJ, 2019, 7, e5999.	0.9	27
5867	Mycorrhization of <i>Quercus acutissima</i> with Chinese black truffle significantly altered the host physiology and root-associated microbiomes. PeerJ, 2019, 7, e6421.	0.9	18
5868	The microbes we eat: abundance and taxonomy of microbes consumed in a day's worth of meals for three diet types. PeerJ, 2014, 2, e659.	0.9	85
5869	Epizootic ulcerative syndrome causes cutaneous dysbacteriosis in hybrid snakehead (<i>Channa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	0.9	6
5870	Captivity causes taxonomic and functional convergence of gut microbial communities in bats. PeerJ, 2019, 7, e6844.	0.9	21
5871	Patterned progression of gut microbiota associated with necrotizing enterocolitis and late onset sepsis in preterm infants: a prospective study in a Chinese neonatal intensive care unit. PeerJ, 2019, 7, e7310.	0.9	18

#	ARTICLE	IF	CITATIONS
5872	The effects of spatial and temporal replicate sampling on eDNA metabarcoding. PeerJ, 2019, 7, e7335.	0.9	48
5873	Effect of dietary concentrate to forage ratio on growth performance, rumen fermentation and bacterial diversity of Tibetan sheep under barn feeding on the Qinghai-Tibetan plateau. PeerJ, 2019, 7, e7462.	0.9	60
5874	Group B <i>Streptococcus</i> colonization induces <i>Prevotella</i> and <i>Megasphaera</i> abundance-featured vaginal microbiome compositional change in non-pregnant women. PeerJ, 2019, 7, e7474.	0.9	10
5875	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
5876	Biochar application significantly affects the N pool and microbial community structure in purple and paddy soils. PeerJ, 2019, 7, e7576.	0.9	11
5877	Yak rumen microbial diversity at different forage growth stages of an alpine meadow on the Qinghai-Tibet Plateau. PeerJ, 2019, 7, e7645.	0.9	37
5878	A draft genome and transcriptome of common milkweed (<i>Asclepias syriaca</i>) as resources for evolutionary, ecological, and molecular studies in milkweeds and Apocynaceae. PeerJ, 2019, 7, e7649.	0.9	19
5879	Adapterama II: universal amplicon sequencing on Illumina platforms (TaggiMatrix). PeerJ, 2019, 7, e7786.	0.9	47
5880	Microbial community structure analysis in <i>Acer palmatum</i> bark and isolation of novel bacteria IAD-21 of the candidate division FBP. PeerJ, 2019, 7, e7876.	0.9	10
5881	Effects of particle size of ground alfalfa hay on caecal bacteria and archaea populations of rabbits. PeerJ, 2019, 7, e7910.	0.9	2
5882	Systematic evaluation of the gut microbiome of swamp eel (<i>Monopterus albus</i>) by 16S rRNA gene sequencing. PeerJ, 2019, 7, e8176.	0.9	6
5883	Alteration of the gut microbiota associated with childhood obesity by 16S rRNA gene sequencing. PeerJ, 2020, 8, e8317.	0.9	74
5884	Airborne microbial biodiversity and seasonality in Northern and Southern Sweden. PeerJ, 2020, 8, e8424.	0.9	22
5885	Microbial communities on fish eggs from <i>Acanthopagrus schlegelii</i> and <i>Halichoeres nigrescens</i> at the XuWen coral reef in the Gulf of Tonkin. PeerJ, 2020, 8, e8517.	0.9	5
5886	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
5887	Responses of rhizosphere soil bacteria to 2-year tillage rotation treatments during fallow period in semiarid southeastern Loess Plateau. PeerJ, 2020, 8, e8853.	0.9	7
5888	Comparative study of gut microbiota in Tibetan wild asses (<i>Equus kiang</i>) and domestic donkeys (<i>Equus asinus</i>) on the Qinghai-Tibet plateau. PeerJ, 2020, 8, e9032.	0.9	20
5889	Analyzing bacterial community in pit mud of Yibin Baijiu in China using high throughput sequencing. PeerJ, 2020, 8, e9122.	0.9	17

#	ARTICLE	IF	CITATIONS
5890	Influence of hydropower stations on the water microbiota in the downstream of Jinsha River, China. PeerJ, 2020, 8, e9500.	0.9	8
5891	Gut microbiota of obese and diabetic Thai subjects and interplay with dietary habits and blood profiles. PeerJ, 2020, 8, e9622.	0.9	7
5892	Microbiome dynamics in the tissue and mucus of acroporid corals differ in relation to host and environmental parameters. PeerJ, 2020, 8, e9644.	0.9	30
5893	Multi-omics analysis to examine microbiota, host gene expression and metabolites in the intestine of black tiger shrimp (<i>Penaeus monodon</i>) with different growth performance. PeerJ, 2020, 8, e9646.	0.9	22
5894	Oral microbial diversity analysis among atrophic glossitis patients and healthy individuals. Journal of Oral Microbiology, 2021, 13, 1984063.	1.2	2
5895	Gut Ruminococcaceae Levels Correlate with Risk of Antibiotic-Associated Diarrhea. SSRN Electronic Journal, 0, , .	0.4	0
5896	A low abundance of genus Bacteroides in gut microbiota is negatively correlated with blood phenylalanine levels in Uyghur patients with phenylketonuria. Translational Pediatrics, 2021, 10, 2521-2532.	0.5	4
5897	Vaginal Microbiome Components as Correlates of Cervical Human Papillomavirus Infection. Journal of Infectious Diseases, 2022, 226, 1084-1097.	1.9	7
5898	Effects of Reducing Nitrogen Fertilizer and Improving Organic Fertilizer on Crop Yield, Soil Quality and Microbial Community in Five Years Wheat-Rice Rotation Field. Journal of Biobased Materials and Bioenergy, 2021, 15, 449-458.	0.1	2
5899	NGS-metabarcoding revealing novel foraminiferal diversity in the Western Pacific Magellan Seamount sediments. Journal of Oceanology and Limnology, 2021, 39, 1718-1729.	0.6	6
5900	Community Assembly and Co-occurrence Patterns Underlying the Core and Satellite Bacterial Sub-communities in the Tibetan Lakes. Frontiers in Microbiology, 2021, 12, 695465.	1.5	8
5901	Filtering Effect of Rhinogobio cylindricus Gut Microbiota Relieved Influence of the Three Gorges Dam on the Gut Microbiota Composition. Water (Switzerland), 2021, 13, 2697.	1.2	4
5902	Metagenomic Analysis of the Microbial Community in the Underground Coal Fire Area (Kemerovo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Aquificae, and Firmicutes. Microbiology, 2021, 90, 578-587.	0.5	5
5903	Short Chain Fatty Acids Prevent Glyoxylate-Induced Calcium Oxalate Stones by GPR43-Dependent Immunomodulatory Mechanism. Frontiers in Immunology, 2021, 12, 729382.	2.2	11
5904	Genomic and environmental influences on resilience in a cold-water fish near the edge of its range. Evolutionary Applications, 2021, 14, 2794-2814.	1.5	3
5905	Elevated CO_2 affects the rhizosphere microbial community and the growth of two invader plant species differently in semiarid Mediterranean soils. Land Degradation and Development, 2022, 33, 117-132.	1.8	6
5906	Deletion and replacement of long genomic sequences using prime editing. Nature Biotechnology, 2022, 40, 227-234.	9.4	90
5907	Profiling the T Cell Receptor Alpha/Delta Locus in Salmonids. Frontiers in Immunology, 2021, 12, 753960.	2.2	6

#	ARTICLE	IF	CITATIONS
5908	The Characteristics of Intestinal Bacterial Community in Three Omnivorous Fishes and Their Interaction with Microbiota from Habitats. <i>Microorganisms</i> , 2021, 9, 2125.	1.6	4
5909	Flaxseed Powder Attenuates Non-Alcoholic Steatohepatitis via Modulation of Gut Microbiota and Bile Acid Metabolism through Gutâ€“Liver Axis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10858.	1.8	15
5910	Bacterial Inhibition on <i>Beauveria bassiana</i> Contributes to Microbiota Stability in <i>Delia antiqua</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 710800.	1.5	4
5911	Dietary Filamentous Fungi and Duration of Feeding Modulates Gut Microbial Composition in Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
5912	Dynamic Microbial Shifts and Signatures of Long-Term Remission in Allergic Rhinitis After an Herbal Formula Treatment. <i>Frontiers in Immunology</i> , 2021, 12, 774966.	2.2	2
5913	A dual-reporter system for investigating and optimizing protein translation and folding in <i>E. coli</i> . <i>Nature Communications</i> , 2021, 12, 6093.	5.8	12
5914	Time-course alterations of gut microbiota and short-chain fatty acids after short-term lincomycin exposure in young swine. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8441-8456.	1.7	18
5915	Effect of straw biochar amendment on tobacco growth, soil properties, and rhizosphere bacterial communities. <i>Scientific Reports</i> , 2021, 11, 20727.	1.6	17
5916	Effect of blending encapsulated essential oils and organic acids as an antibiotic growth promoter alternative on growth performance and intestinal health in broilers with necrotic enteritis. <i>Poultry Science</i> , 2022, 101, 101563.	1.5	37
5917	Gut microbiota dysbiosis contributes to the development of chronic obstructive pulmonary disease. <i>Respiratory Research</i> , 2021, 22, 274.	1.4	56
5918	Distinct Responses of Rare and Abundant Microbial Taxa to <i>In Situ</i> Chemical Stabilization of Cadmium-Contaminated Soil. <i>MSystems</i> , 2021, 6, e0104021.	1.7	43
5921	Effects of applying cellulase and starch on the fermentation characteristics and microbial communities of Napier grass (<i>Pennisetum purpureum</i> Schum.) silage. <i>Journal of Animal Science and Technology</i> , 2021, 63, 1301-1313.	0.8	6
5922	A Snapshot Picture of the Fungal Composition of Bee Bread in Four Locations in Bulgaria, Differing in Anthropogenic Influence. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 845.	1.5	2
5923	Migration effects on the intestinal microbiota of Tibetans. <i>PeerJ</i> , 2021, 9, e12036.	0.9	4
5924	Environmental effects of nanoparticles on the ecological succession of gut microbiota across zebrafish development. <i>Science of the Total Environment</i> , 2022, 806, 150963.	3.9	22
5925	Physicochemical Factors Drive Bacterial Communities in an Aquaculture Environment. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	7
5926	The Native Dietary Habits of the Two Sympatric Bee Species and Their Effects on Shaping Midgut Microorganisms. <i>Frontiers in Microbiology</i> , 2021, 12, 738226.	1.5	3
5927	Truffle species strongly shape their surrounding soil mycobiota in a <i>Pinus armandii</i> forest. <i>Archives of Microbiology</i> , 2021, 203, 6303-6314.	1.0	1

#	ARTICLE	IF	CITATIONS
5928	Abnormalities in Gut Microbiota and Metabolism in Patients With Chronic Spontaneous Urticaria. <i>Frontiers in Immunology</i> , 2021, 12, 691304.	2.2	20
5929	Observed Antibody Space: A diverse database of cleaned, annotated, and translated unpaired and paired antibody sequences. <i>Protein Science</i> , 2022, 31, 141-146.	3.1	98
5930	Draft Genome Sequence of the Anoxygenic Phototrophic Bacterium <i>Rhodospirillum rubrum</i> sp. Strain U11-2br, Isolated from a Mountain Lake on the Ulagan Plateau. <i>Microbiology Resource Announcements</i> , 2021, 10, e0067521.	0.3	0
5931	Gut Microbial Alterations in Diarrheal Baer's Pochards (<i>Aythya baeri</i>). <i>Frontiers in Veterinary Science</i> , 2021, 8, 756486.	0.9	5
5932	Dynamic Evolution and Correlation between Metabolites and Microorganisms during Manufacturing Process and Storage of Fu Brick Tea. <i>Metabolites</i> , 2021, 11, 703.	1.3	18
5933	Enhanced Biodegradation of Dissolved Organic Carbon in the Western Boundary Kuroshio Current When Intruded to the Marginal South China Sea. <i>Journal of Geophysical Research: Oceans</i> , 2021, 126, e2021JC017585.	1.0	10
5934	Changes in the gut microbiota diversity of brown frogs (<i>Rana dybowskii</i>) after an antibiotic bath. <i>BMC Veterinary Research</i> , 2021, 17, 333.	0.7	6
5935	BMI, Alcohol Consumption and Gut Microbiome Species Richness Are Related to Structural and Functional Neurological Abnormalities. <i>Nutrients</i> , 2021, 13, 3743.	1.7	2
5936	Alleviation Effects of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> XLTG11 on Dextran Sulfate Sodium-Induced Colitis in Mice. <i>Microorganisms</i> , 2021, 9, 2093.	1.6	21
5937	Florfenicol Enhances Colonization of a <i>Salmonella enterica</i> Serovar <i>Enteritidis</i> <i>flor</i> Mutant with Major Alterations to the Intestinal Microbiota and Metabolome in Neonatal Chickens. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0168121.	1.4	12
5938	Alleviation Effects of GQD, a Traditional Chinese Medicine Formula, on Diabetes Rats Linked to Modulation of the Gut Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 740236.	1.8	14
5939	NO ₃ ⁻ is an important driver of nitrite-dependent anaerobic methane oxidation bacteria and CH ₄ fluxes in the reservoir riparian zone. <i>Environmental Science and Pollution Research</i> , 2022, 29, 16138-16151.	2.7	7
5940	<i>Lactobacillus reuteri</i> Alleviates Gastrointestinal Toxicity of Rituximab by Regulating the Proinflammatory T Cells in vivo. <i>Frontiers in Microbiology</i> , 2021, 12, 645500.	1.5	5
5941	Microbial Profiles of Patients With Antipsychotic-Related Constipation Treated With Electroacupuncture. <i>Frontiers in Medicine</i> , 2021, 8, 737713.	1.2	5
5942	Obesity Modulates the Gut Microbiome in Triple-Negative Breast Cancer. <i>Nutrients</i> , 2021, 13, 3656.	1.7	15
5943	Heavy metals and microbiome are negligible drivers than mobile genetic elements in determining particle-attached and free-living resistomes in the Yellow River. <i>Journal of Hazardous Materials</i> , 2022, 424, 127564.	6.5	15
5944	Labile organic carbon fractions drive soil microbial communities after long-term fertilization. <i>Global Ecology and Conservation</i> , 2021, 32, e01867.	1.0	20
5945	Gut Microbiota Composition and Fecal Metabolic Profiling in Patients With Diabetic Retinopathy. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 732204.	1.8	26

#	ARTICLE	IF	CITATIONS
5946	Intestinal mycobiota composition and changes in children with thalassemia who underwent allogeneic hematopoietic stem cell transplantation. <i>Pediatric Blood and Cancer</i> , 2022, 69, e29411.	0.8	5
5947	Development of a Panel of Genotyping-in-Thousands by Sequencing in Capsicum. <i>Frontiers in Plant Science</i> , 2021, 12, 769473.	1.7	5
5948	Effect of the Manufacturing Process on the Microbiota, Organoleptic Properties and Volatilome of Three Salmon-Based Products. <i>Foods</i> , 2021, 10, 2517.	1.9	8
5949	A Comparison of Production Performance, Egg Quality, and Cecal Microbiota in Laying Hens Receiving Graded Levels of Vitamin B12. <i>Frontiers in Veterinary Science</i> , 2021, 8, 712183.	0.9	4
5950	A metagenomic study of the gut microbiome in PTB disease. <i>Microbes and Infection</i> , 2022, 24, 104893.	1.0	6
5951	Identification of a thermophilic protease-producing strain and its application in solid-state fermentation of soybean meal. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 2359-2370.	1.7	12
5952	Omics-based ecosurveillance uncovers the influence of estuarine macrophytes on sediment microbial function and metabolic redundancy in a tropical ecosystem. <i>Science of the Total Environment</i> , 2022, 809, 151175.	3.9	8
5953	Differences in Diet and Gut Microbiota Between Lactating and Non-lactating Asian Particolored Bats (<i>Vespertilio sinensis</i>): Implication for a Connection Between Diet and Gut Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 735122.	1.5	3
5954	A next-generation probiotic: <i>Akkermansia muciniphila</i> ameliorates chronic stress-induced depressive-like behavior in mice by regulating gut microbiota and metabolites. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8411-8426.	1.7	67
5955	Genetic Elucidation of Quorum Sensing and Cobamide Biosynthesis in Divergent Bacterial-Fungal Associations Across the Soil-Mangrove Root Interface. <i>Frontiers in Microbiology</i> , 2021, 12, 698385.	1.5	0
5956	Climbing Up and Down Binding Landscapes through Deep Mutational Scanning of Three Homologous Protein-Protein Complexes. <i>Journal of the American Chemical Society</i> , 2021, 143, 17261-17275.	6.6	11
5957	Co-occurrence of planktonic bacteria and archaea affects their biogeographic patterns in China coastal wetlands. <i>Environmental Microbiomes</i> , 2021, 16, 19.	2.2	19
5958	Sugar and organic acid availability modulate soil diazotroph community assembly and species co-occurrence patterns on the Tibetan Plateau. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8545-8560.	1.7	2
5959	Nitrogen rather than phosphorus driving the biogeographic patterns of abundant bacterial taxa in a eutrophic plateau lake. <i>Science of the Total Environment</i> , 2022, 806, 150947.	3.9	24
5960	Protistan-Bacterial Microbiota Exhibit Stronger Species Sorting and Greater Network Connectivity Offshore than Nearshore across a Coast-to-Basin Continuum. <i>MSystems</i> , 2021, 6, e0010021.	1.7	5
5961	Mechanisms for Electron Uptake by <i>Methanosarcina acetivorans</i> during Direct Interspecies Electron Transfer. <i>MBio</i> , 2021, 12, e0234421.	1.8	41
5962	The gut microbiota and microbial metabolites are associated with tail biting in pigs. <i>Scientific Reports</i> , 2021, 11, 20547.	1.6	14
5963	Biogeographic distribution patterns and assembly processes of <i>nirS</i> -type and <i>nirK</i> -type denitrifiers across the black soil zone in Northeast China. <i>Soil Science Society of America Journal</i> , 2022, 86, 1383-1396.	1.2	6

#	ARTICLE	IF	CITATIONS
5964	Comparison of Gut Bacterial Communities of Fall Armyworm (<i>Spodoptera frugiperda</i>) Reared on Different Host Plants. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11266.	1.8	24
5965	Microbial Communities of the Hydrothermal Scaly-Foot Snails From Kairei and Longqi Vent Fields. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
5966	Prediction of bacterial functional diversity in clay microcosms. <i>Heliyon</i> , 2021, 7, e08131.	1.4	4
5967	Microbiota and transcriptome changes of <i>Culex pipiens pallens</i> larvae exposed to <i>Bacillus thuringiensis israelensis</i> . <i>Scientific Reports</i> , 2021, 11, 20241.	1.6	3
5968	Maternal and Infant Immune Repertoire Sequencing Analysis Identifies Distinct Ig and TCR Development in Term and Preterm Infants. <i>Journal of Immunology</i> , 2021, 207, ji2100566.	0.4	3
5969	Analysis of Cow-Calf Microbiome Transfer Routes and Microbiome Diversity in the Newborn Holstein Dairy Calf Hindgut. <i>Frontiers in Nutrition</i> , 2021, 8, 736270.	1.6	16
5970	Pilot Study on the Forehead Skin Microbiome and Short Chain Fatty Acids Depending on the SC Functional Index in Korean Cohorts. <i>Microorganisms</i> , 2021, 9, 2216.	1.6	3
5971	Large-Scale Characterization of the Soil Microbiome in Ancient Tea Plantations Using High-Throughput 16S rRNA and Internal Transcribed Spacer Amplicon Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 745225.	1.5	12
5972	Different Non-cage Housing Systems Alter Duodenal and Cecal Microbiota Composition in Shendan Chickens. <i>Frontiers in Veterinary Science</i> , 2021, 8, 728538.	0.9	4
5973	The Effect of Lignin Composition on Ruminal Fiber Fractions Degradation from Different Roughage Sources in Water Buffalo (<i>Bubalus bubalis</i>). <i>Agriculture (Switzerland)</i> , 2021, 11, 1015.	1.4	16
5974	Earthworm activity optimized the rhizosphere bacterial community structure and further alleviated the yield loss in continuous cropping lily (<i>Lilium lancifolium</i> Thunb.). <i>Scientific Reports</i> , 2021, 11, 20840.	1.6	9
5975	Predicting the Role of the Human Gut Microbiome in Constipation Using Machine-Learning Methods: A Meta-Analysis. <i>Microorganisms</i> , 2021, 9, 2149.	1.6	8
5976	Lung Tissue Microbiome Is Associated With Clinical Outcomes of Idiopathic Pulmonary Fibrosis. <i>Frontiers in Medicine</i> , 2021, 8, 744523.	1.2	7
5977	Mixture of Five Fermented Herbs (Zhihuasi Tk) Alters the Intestinal Microbiota and Promotes the Growth Performance in Piglets. <i>Frontiers in Microbiology</i> , 2021, 12, 725196.	1.5	10
5978	Disentangling the Effects of Physicochemical, Genetic, and Microbial Properties on Phase-Driven Resistome Dynamics during Multiple Manure Composting Processes. <i>Environmental Science & Technology</i> , 2021, 55, 14732-14745.	4.6	16
5979	Effects of aquaculture waste feeds and antibiotics on marine benthic ecosystems in the Mediterranean Sea. <i>Science of the Total Environment</i> , 2022, 806, 151190.	3.9	21
5980	Metagenomics analysis of the fecal microbiota in Ring-necked pheasants (<i>Phasianus colchicus</i>) and Green pheasants (<i>Phasianus versicolor</i>) using next generation sequencing. <i>Saudi Journal of Biological Sciences</i> , 2022, 29, 1781-1788.	1.8	5
5981	Prokaryotic responses to a warm temperature anomaly in northeast subarctic Pacific waters. <i>Communications Biology</i> , 2021, 4, 1217.	2.0	14

#	ARTICLE	IF	CITATIONS
5982	Metagenomic Analysis Reveals <i>Neisseria bacilliformis</i> Variation in the Early Childhood Caries Plaque Microbiome. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-7.	0.5	7
5983	Comparative Study of the Gut Microbiota Among Four Different Marine Mammals in an Aquarium. <i>Frontiers in Microbiology</i> , 2021, 12, 769012.	1.5	13
5984	Dietary inulin supplementation modulates the composition and activities of carbohydrate-metabolizing organisms in the cecal microbiota of broiler chickens. <i>PLoS ONE</i> , 2021, 16, e0258663.	1.1	5
5985	Integrating Stochastic and Deterministic Process in the Biogeography of N ₂ -Fixing Cyanobacterium <i>Candidatus Atelocyanobacterium Thalassa</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 654646.	1.5	5
5986	Urbanization processes drive divergence at the major histocompatibility complex in a common waterbird. <i>PeerJ</i> , 2021, 9, e12264.	0.9	3
5987	Low-protein diets supplemented with methionine and lysine alter the gut microbiota composition and improve the immune status of growing lambs. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8393-8410.	1.7	14
5988	New Arsenite Oxidase Gene (<i>aiOA</i>) PCR Primers for Assessing Arsenite-Oxidizer Diversity in the Environment Using High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 691913.	1.5	2
5990	The Influence of Above-Ground Herbivory on the Response of Arctic Soil Methanotrophs to Increasing CH ₄ Concentrations and Temperatures. <i>Microorganisms</i> , 2021, 9, 2080.	1.6	4
5991	Alleviative Effects of Exopolysaccharide Produced by <i>Lactobacillus helveticus</i> KLDS1.8701 on Dextran Sulfate Sodium-Induced Colitis in Mice. <i>Microorganisms</i> , 2021, 9, 2086.	1.6	18
5992	In-Vitro Characterization of Growth Inhibition against the Gut Pathogen of Potentially Probiotic Lactic Acid Bacteria Strains Isolated from Fermented Products. <i>Microorganisms</i> , 2021, 9, 2141.	1.6	11
5993	Characteristics and Driving Factors of Rhizosphere Bacterial Communities of Chinese Fir Provenances. <i>Forests</i> , 2021, 12, 1362.	0.9	11
5994	Insights into soil bacterial and physicochemical properties of annual ryegrass-maize rotation (ARMR) system in southern China. <i>Scientific Reports</i> , 2021, 11, 20125.	1.6	2
5995	Low neutral and immunogenetic diversity in northern fringe populations of the green toad <i>Bufo viridis</i> : implications for conservation. <i>Conservation Genetics</i> , 2022, 23, 139-149.	0.8	4
5996	Short-term grazing exclusions reduced soil organic carbon but not bacterial diversity in the sagebrush desert, Northwest China. <i>Global Ecology and Conservation</i> , 2021, 31, e01872.	1.0	9
5997	Compositional and structural changes in soil microbial communities in response to straw mulching and plant revegetation in an abandoned artificial pasture in Northeast China. <i>Global Ecology and Conservation</i> , 2021, 31, e01871.	1.0	10
5998	Temporal variability of microbial communities during the past 600 years in a Tibetan lake sediment core. <i>Palaeogeography, Palaeoclimatology, Palaeoecology</i> , 2021, 584, 110678.	1.0	8
5999	Ammonia stress disrupts intestinal microbial community and amino acid metabolism of juvenile yellow catfish (<i>Pelteobagrus fulvidraco</i>). <i>Ecotoxicology and Environmental Safety</i> , 2021, 227, 112932.	2.9	36
6000	Rumen-protected glucose supplementation in transition dairy cows shifts fermentation patterns and enhances mucosal immunity. <i>Animal Nutrition</i> , 2021, 7, 1182-1188.	2.1	2

#	ARTICLE	IF	CITATIONS
6001	Correlation between microbial communities and flavor compounds during the fifth and sixth rounds of sauce-flavor baijiu fermentation. <i>Food Research International</i> , 2021, 150, 110741.	2.9	25
6014	chapter 6 Ubiquitous Healthy Diatoms in the Deep Sea Confirm Deep Carbon Injection by the Biological Pump. , 2017, , 123-148.		0
6038	Development and validation of <i>Acacia koa</i> and <i>A. koaia</i> nuclear SSRs using Illumina sequencing. <i>Silvae Genetica</i> , 2018, 67, 20-25.	0.4	1
6043	New Procedure of Raw Illumina MiSeq Data Filtering For the Amplicon Metagenomic Libraries. <i>Mathematical Biology and Bioinformatics</i> , 2018, 13, 159-168.	0.1	0
6072	Palaeogenome Reveals Genetic Contribution of Extinct Giant Panda to Extant Populations. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6073	The Effect of Chitooligosaccharides on Gut Microbiota in Diabetic Mice. <i>Open Access Library Journal (oalib)</i> , 2019, 06, 1-5.	0.1	0
6075	Effects of <i>Streptococcus salivarius</i> K12 on Experimental Periodontitis and Oral Microbiota in Mice. <i>Journal of Biosciences and Medicines</i> , 2019, 07, 95-111.	0.1	1
6076	Aardwolf Population Diversity and Phylogenetic Positioning Inferred Using Complete Mitochondrial Genomes. <i>African Journal of Wildlife Research</i> , 2019, 49, .	0.2	0
6090	Metagenomic Analysis Reveals Correlation Between Microbiome Structure and Leonardite Characteristics from Kazakhstan Coal Deposits. <i>Eurasian Chemico-Technological Journal</i> , 2019, 21, 135.	0.3	5
6093	Effects of the algicidal bacterium CZBC1 on microalgal and bacterial communities in shrimp culture. <i>Aquaculture Environment Interactions</i> , 2019, 11, 279-290.	0.7	4
6097	Stochastic and deterministic drivers of seasonal variation of fungal community in tobacco field soil. <i>PeerJ</i> , 2019, 7, e6962.	0.9	1
6105	Improvement of subsoil physicochemical and microbial properties by short-term fallow practices. <i>PeerJ</i> , 2019, 7, e7501.	0.9	4
6107	Changes in planktonic bivalve larvae of <i>Tegillarca granosa</i> and <i>Anadara kagoshimensis</i> in the Boseong coastal waters of South Korea. <i>Hangug Hwangyeong Saengmul Haghojeji</i> , 2019, 37, 351-361.	0.1	2
6109	Genome Sequence of a <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Corvallis</i> Strain Isolated from Human Blood. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
6111	Exploring Toxin Evolution: Venom Protein Transcript Sequencing and Transcriptome-Guided High-Throughput Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2068, 97-127.	0.4	3
6119	Archaeal and methanogenic communities in the rice field under different fertilizer applications. <i>Biodiversitas</i> , 2019, 20, .	0.2	1
6123	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> . <i>PeerJ</i> , 2019, 7, e8051.	0.9	2
6125	Gut microbiota of the scimitar-horned oryx, <i>Oryx dammah</i> . <i>Folia Zoologica</i> , 2019, 68, 269.	0.9	1

#	ARTICLE	IF	CITATIONS
6129	Connection the Rhizomicrobiome and Plant MAPK Gene Expression Response to Pathogenic <i>Fusarium oxysporum</i> in Wild and Cultivated Soybean. <i>Plant Pathology Journal</i> , 2019, 35, 623-634.	0.7	1
6132	The effect of curative resection on fecal microbiota in patients with colorectal cancer: a prospective pilot study. <i>Annals of Surgical Treatment and Research</i> , 2020, 99, 44.	0.4	3
6134	Quantitative mapping of binding specificity landscapes for homologous targets by using a high-throughput method. <i>Biochemical Journal</i> , 2020, 477, 1701-1719.	1.7	3
6135	Characterization of the bacterial microbiota composition and evolution at different intestinal tract in wild pigs (<i>Sus scrofa ussuricus</i>). <i>PeerJ</i> , 2020, 8, e9124.	0.9	8
6138	VizSciFlow: A Visually Guided Scripting Framework for Supporting Complex Scientific Data Analysis. <i>Proceedings of the ACM on Human-Computer Interaction</i> , 2020, 4, 1-37.	2.5	6
6140	Can Ferret Badgers (<i>Melogale moschata</i>) Cross the Rabies Epidemic Boundary in Western Taiwan?. <i>Mammal Study</i> , 2020, 45, 189.	0.2	0
6142	Microbial Community Dynamics in the Gastrointestinal Tract of Indigenous Omani Chickens. <i>International Journal of Poultry Science</i> , 2020, 19, 309-320.	0.6	1
6143	Changes in the fecal microbiome of the Yangtze finless porpoise during a short-term therapeutic treatment. <i>Open Life Sciences</i> , 2020, 15, 296-310.	0.6	5
6144	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. <i>Medical Science Monitor</i> , 2020, 26, e921557.	0.5	8
6146	Metagenomic analysis and biodiversity of Lactic Acid Bacteria (LAB) on masin (fermented sauce) from Sumbawa, West Nusa Tenggara, Indonesia. <i>Biodiversitas</i> , 2020, 21, .	0.2	0
6161	Differential nasopharyngeal microbiota composition in children according to respiratory health status. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
6162	Higher ammonium-to-nitrate ratio shapes distinct soil nitrifying community and favors the growth of <i>Moso bamboo</i> in contrast to broadleaf tree species. <i>Biology and Fertility of Soils</i> , 2021, 57, 1171-1182.	2.3	17
6163	Fate of bacterial community, antibiotic resistance genes and gentamicin residues in soil after three-year amendment using gentamicin fermentation waste. <i>Chemosphere</i> , 2022, 291, 132734.	4.2	25
6164	Locus-Specific DNA Methylation Editing in Melanoma Cell Lines Using a CRISPR-Based System. <i>Cancers</i> , 2021, 13, 5433.	1.7	7
6165	Metabolomics Analyses Reveal Metabolites Affected by Plant Growth-Promoting Endophytic Bacteria in Roots of the Halophyte <i>Mesembryanthemum crystallinum</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 11813.	1.8	13
6166	Pedosedimentary and microbial investigation of a karst sequence record. <i>Science of the Total Environment</i> , 2021, , 151297.	3.9	1
6167	Depth-dependent variability of biological nitrogen fixation and diazotrophic communities in mangrove sediments. <i>Microbiome</i> , 2021, 9, 212.	4.9	24
6168	Arbuscular mycorrhizal fungi promote small-scale vegetation recovery in the forest understorey. <i>Oecologia</i> , 2021, 197, 685-697.	0.9	1

#	ARTICLE	IF	CITATIONS
6169	Salivary microbiome profiling reveals a dysbiotic schizophrenia-associated microbiota. NPJ Schizophrenia, 2021, 7, 51.	2.0	22
6170	Comparison of Auxin and Cytokinins Concentrations, and the Structure of Bacterial Community between Host Twigs and Lithosaphonecrus arcoverticus Galls. Insects, 2021, 12, 982.	1.0	2
6171	Patterns in the Microbial Community of Salt-Tolerant Plants and the Functional Genes Associated with Salt Stress Alleviation. Microbiology Spectrum, 2021, 9, e0076721.	1.2	27
6172	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
6173	Investigating the Reciprocal Interrelationships among the Ruminal Microbiota, Metabolome, and Mastitis in Early Lactating Holstein Dairy Cows. Animals, 2021, 11, 3108.	1.0	9
6175	Compositional changes in human gut microbiota reveal a putative role of intestinal mycobacteria in metabolic and biological decline during aging. Nutrition and Healthy Aging, 2021, , 1-15.	0.5	4
6176	Comparative Effects of Compound Enzyme and Antibiotics on Growth Performance, Nutrient Digestibility, Blood Biochemical Index, and Intestinal Health in Weaned Pigs. Frontiers in Microbiology, 2021, 12, 768767.	1.5	12
6178	Bacterial epiphyte and endophyte communities of seagrass Thalassia hemprichii : the impact of feed extract solution. Environmental Microbiology Reports, 2021, 13, 757-772.	1.0	2
6179	New Method for Genome-Scale Functional Genomic Study in Bacteria with Superior Performance: CRISPR Interference Screen. Methods in Molecular Biology, 2022, 2377, 123-141.	0.4	0
6180	Supplemental Bacillus subtilis PB6 Improves Growth Performance and Gut Health in Broilers Challenged with Clostridium perfringens. Journal of Immunology Research, 2021, 2021, 1-11.	0.9	12
6181	Microbial inoculations improved rice yields by altering the presence of soil rare bacteria. Microbiological Research, 2022, 254, 126910.	2.5	11
6182	Gut microbiota response to antibiotics is personalized and depends on baseline microbiota. Microbiome, 2021, 9, 211.	4.9	32
6183	Gut Microbiota in Canine Idiopathic Epilepsy: Effects of Disease and Treatment. Animals, 2021, 11, 3121.	1.0	11
6184	An Introductory Overview of Open-Source and Commercial Software Options for the Analysis of Forensic Sequencing Data. Genes, 2021, 12, 1739.	1.0	6
6185	Multimodal neuroimaging fusion biomarkers mediate the association between gut microbiota and cognition. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2022, 113, 110468.	2.5	18
6186	Biogeography of the large intestinal mucosal and luminal microbiome in cynomolgus macaques with depressive-like behavior. Molecular Psychiatry, 2022, 27, 1059-1067.	4.1	17
6187	Environmental Water and Sediment Microbial Communities Shape Intestine Microbiota for Host Health: The Central Dogma in an Anthropogenic Aquaculture Ecosystem. Frontiers in Microbiology, 2021, 12, 772149.	1.5	8
6188	Integrative Analysis of LGR5/6 Gene Variants, Gut Microbiota Composition and Osteoporosis Risk in Elderly Population. Frontiers in Microbiology, 2021, 12, 765008.	1.5	8

#	ARTICLE	IF	CITATIONS
6190	Systematic Survey of the Alteration of the Faecal Microbiota in Rats With Gastrointestinal Disorder and Modulation by Multicomponent Drugs. <i>Frontiers in Pharmacology</i> , 2021, 12, 670335.	1.6	4
6193	Oxygen concentration affects frequency and range of transconjugants for the incompatibility (Inc) P-1 and P-7 plasmids pBP136 and pCAR1. <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 1005-1015.	0.6	1
6194	Elucidation of genomic organizations of transgenic soybean plants through de novo genome assembly with short paired-end reads. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	6
6196	iPSC for modeling neurodegenerative disorders. <i>Regenerative Therapy</i> , 2020, 15, 332-339.	1.4	22
6197	Metagenomic Analysis of Rhizosphere Bacteria in Desert Plant <i>Calotropis procera</i> . <i>Geomicrobiology Journal</i> , 2021, 38, 375-383.	1.0	7
6198	Comparison of thrombus, gut, and oral microbiomes in Korean patients with ST-elevation myocardial infarction: a case-control study. <i>Experimental and Molecular Medicine</i> , 2020, 52, 2069-2079.	3.2	20
6199	Comparative genomic analysis of the principal <i>Cryptosporidium</i> species that infect humans. <i>PeerJ</i> , 2020, 8, e10478.	0.9	7
6202	Comparative Analysis of the Gut Microbiota of Adult Mosquitoes From Eight Locations in Hainan, China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 596750.	1.8	13
6203	Differences in Geological Conditions Have Reshaped the Structure and Diversity of Microbial Communities in Oily Soils. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
6204	Diverse crop rotations influence the bacterial and fungal communities in root, rhizosphere and soil and impact soil microbial processes. <i>Applied Soil Ecology</i> , 2022, 169, 104241.	2.1	17
6205	Soil properties and plant community-level traits mediate arbuscular mycorrhizal fungal response to nitrogen enrichment and altered precipitation. <i>Applied Soil Ecology</i> , 2022, 169, 104245.	2.1	4
6206	Assembly processes of abundant and rare microbial communities in orchard soil under a cover crop at different periods. <i>Geoderma</i> , 2022, 406, 115543.	2.3	51
6207	Leaf surface microtopography shaping the bacterial community in the phyllosphere: evidence from 11 tree species. <i>Microbiological Research</i> , 2022, 254, 126897.	2.5	11
6208	Abundance, diversity and diffusion of antibiotic resistance genes in cat feces and dog feces. <i>Environmental Pollution</i> , 2022, 292, 118364.	3.7	10
6209	Soil characteristics and microbial community structure on along elevation gradient in a <i>Pinus armandii</i> forest of the Qinling Mountains, China. <i>Forest Ecology and Management</i> , 2022, 503, 119793.	1.4	7
6210	Seasonal distribution of antibiotic resistance genes in the Yellow River water and tap water, and their potential transmission from water to human. <i>Environmental Pollution</i> , 2022, 292, 118304.	3.7	44
6211	Unraveling microbiomes and functions associated with strategic tillage, stubble, and fertilizer management. <i>Agriculture, Ecosystems and Environment</i> , 2022, 323, 107686.	2.5	8
6212	Succession, sources, and assembly of bacterial community in the developing crab larval microbiome. <i>Aquaculture</i> , 2022, 548, 737600.	1.7	5

#	ARTICLE	IF	CITATIONS
6213	Long-term P fertilization significantly altered the diversity, composition and mycorrhizal traits of arbuscular mycorrhizal fungal communities in a wheat-maize rotation. <i>Applied Soil Ecology</i> , 2022, 170, 104261.	2.1	16
6214	Short-term cellulose addition decreases microbial diversity and network complexity in an Ultisol following 32-year fertilization. <i>Agriculture, Ecosystems and Environment</i> , 2022, 325, 107744.	2.5	20
6215	Bioremediation of an oxyfluorfen-polluted soil using biostimulants obtained by fermentation processes: Effect on biological properties. <i>Applied Soil Ecology</i> , 2022, 170, 104270.	2.1	7
6216	Simulated root exudates stimulate the abundance of Saccharimonadales to improve the alkaline phosphatase activity in maize rhizosphere. <i>Applied Soil Ecology</i> , 2022, 170, 104274.	2.1	49
6217	Characteristics of the Tongue Coating Microbiome in Patients Infected With Adenovirus. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6218	Characterizing Relationship of Microbial Community in <i>Xiaoqu</i> and Volatiles of Light-aroma-type <i>Xiaoqu</i> Baijiu. <i>Food Science and Technology Research</i> , 2020, 26, 749-758.	0.3	7
6220	Comparison of the Gut Microbiota in the Tibetan Wild Ass (<i>Equus kiang</i>) Collected from High and Low Altitude. <i>Pakistan Journal of Zoology</i> , 2020, 52, .	0.1	1
6221	A Bioinformatics Primer for the Analysis of Illumina MiSeq Data of Litter-Associated Fungi and Bacteria. , 2020, , 573-582.		0
6231	Effect of Fucoïdan on Gut Microbiota and its Clinical Efficacy in <i>Helicobacter Pylori</i> Eradication: Randomised Controlled Trial. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6238	Dysbiosis of Gut Microbiota Promotes Hepatocellular Carcinoma Progression by Regulating the Immune Response. <i>Journal of Immunology Research</i> , 2021, 2021, 1-13.	0.9	12
6239	Correlation Between Microbial Diversity and Volatile Flavor Compounds of Suan zuo rou, a Fermented Meat Product From Guizhou, China. <i>Frontiers in Microbiology</i> , 2021, 12, 736525.	1.5	7
6240	Distinct Composition and Assembly Processes of Bacterial Communities in a River from the Arid Area: Ecotypes or Habitat Types?. <i>Microbial Ecology</i> , 2022, 84, 769-779.	1.4	2
6241	Effect of Chicken Manure-Based Fertiliser on Bacterial Communities and Diversity of Tomato Endosphere Microbiota. <i>Agriculture</i> , 2021, 67, 144-154.	0.2	3
6242	Community Profile and Drivers of Predatory Myxobacteria under Different Compost Manures. <i>Microorganisms</i> , 2021, 9, 2193.	1.6	11
6243	Pivotal Dominant Bacteria Ratio and Metabolites Related to Healthy Body Index Revealed by Intestinal Microbiome and Metabolomics. <i>Indian Journal of Microbiology</i> , 2022, 62, 130-141.	1.5	0
6244	Major population splits coincide with episodes of rapid climate change in a forest-dependent bird. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211066.	1.2	1
6245	Chemical fertilizer reduction combined with organic materials enhances nematode community structure stability. <i>Archives of Agronomy and Soil Science</i> , 2023, 69, 399-416.	1.3	0
6246	Unveiling the occurrence, hosts and mobility potential of antibiotic resistance genes in the deep ocean. <i>Science of the Total Environment</i> , 2022, 816, 151539.	3.9	14

#	ARTICLE	IF	CITATIONS
6247	Characteristics of the Gut Microbiome and IL-13/TGF- β 1 Mediated Fibrosis in Post-Kasai Cholangitis of Biliary Atresia. <i>Frontiers in Pediatrics</i> , 2021, 9, 751204.	0.9	4
6249	RNA-seq library preparation for comprehensive transcriptome analysis in cancer cells: The impact of insert size. <i>Genomics</i> , 2021, 113, 4149-4162.	1.3	6
6250	Healthier Communities of Phytoplankton and Bacteria Achieved via the Application of Modified Clay in Shrimp Aquaculture Ponds. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 11569.	1.2	6
6251	Metataxonomic investigation of the microbial community in the trachea and oropharynx of healthy controls and diabetic patients using endotracheal tubes. <i>PLoS ONE</i> , 2021, 16, e0259596.	1.1	2
6252	Features of Microbiocenoses of Various Biotopes in Women as Potential Miscarriage Risk Factor. <i>Epidemiologia I Vaksinoprofilaktika</i> , 2021, 20, 107-114.	0.2	0
6253	Contrasting Patterns and Drivers of Soil Fungal Communities between Two Ecosystems Divided by the Treeline. <i>Microorganisms</i> , 2021, 9, 2280.	1.6	1
6254	Properties of ammonia-oxidising bacteria and archaea in a hypereutrophic urban river network. <i>Freshwater Biology</i> , 0, , .	1.2	2
6255	Changes in microbial community and enzyme activity in soil under continuous pepper cropping in response to <i>Trichoderma hamatum</i> MHT1134 application. <i>Scientific Reports</i> , 2021, 11, 21585.	1.6	10
6256	Environmental Factors Influencing Phyllosphere Bacterial Communities in Giant Pandas'™ Staple Food Bamboos. <i>Frontiers in Microbiology</i> , 2021, 12, 748141.	1.5	2
6257	Effect of Long-Term and Short-Term Imbalanced Zn Manipulation on Gut Microbiota and Screening for Microbial Markers Sensitive to Zinc Status. <i>Microbiology Spectrum</i> , 2021, 9, e0048321.	1.2	17
6258	Microbial Surface Biofilm Responds to the Growth-Reproduction-Senescence Cycle of the Dominant Coral Reef Macroalgae <i>Sargassum</i> spp.. <i>Life</i> , 2021, 11, 1199.	1.1	0
6259	Ripened Pu-Erh Tea Improved the Enterohepatic Circulation in a Circadian Rhythm Disorder Mice Model. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 13533-13545.	2.4	20
6260	Soil bacterial and fungal communities are linked with plant functional types and soil properties under different grazing intensities. <i>European Journal of Soil Science</i> , 2022, 73, e13195.	1.8	12
6261	Biomarkers of Gut Microbiota in Chronic Spontaneous Urticaria and Symptomatic Dermographism. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 703126.	1.8	13
6262	Potential of Inulin-Fructooligosaccharides Extract Produced from Red Onion (<i>Allium cepa</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	1.6	5
6263	Skin Mycobiota of the Captive Giant Panda (<i>Ailuropoda melanoleuca</i>) and the Distribution of Opportunistic Dermatomycosis-Associated Fungi in Different Seasons. <i>Frontiers in Veterinary Science</i> , 2021, 8, 708077.	0.9	3
6264	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. <i>Nature Genetics</i> , 2021, 53, 1606-1615.	9.4	93
6265	Distinct co-occurrence patterns and driving forces of abundant and rare bacterial communities in the multispecies solid-state fermentation process of cereal vinegar. <i>Systems Microbiology and Biomanufacturing</i> , 2022, 2, 317-330.	1.5	2

#	ARTICLE	IF	CITATIONS
6266	Composition of Fecal Microbiota in Grazing and Feedlot Angus Beef Cattle. <i>Animals</i> , 2021, 11, 3167.	1.0	14
6267	The Dominating Role of Genetic Background in Shaping Gut Microbiota of Honeybee Queen Over Environmental Factors. <i>Frontiers in Microbiology</i> , 2021, 12, 722901.	1.5	3
6268	Faecal microbiota transplantation from patients with depression or healthy individuals into rats modulates mood-related behaviour. <i>Scientific Reports</i> , 2021, 11, 21869.	1.6	33
6269	Evaluation of the therapeutic effect and dose-effect of <i>Bifidobacterium breve</i> on the primary <i>Clostridioides difficile</i> infected mice. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 9243-9260.	1.7	7
6270	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	1.7	40
6271	Rhizosphere Microbiomes of Potato Cultivated under <i>Bacillus subtilis</i> Treatment Influence the Quality of Potato Tubers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12065.	1.8	10
6272	Effects of High-Forage Diets Containing Raw Flaxseeds or Soybean on In Vitro Ruminal Fermentation, Gas Emission, and Microbial Profile. <i>Microorganisms</i> , 2021, 9, 2304.	1.6	6
6273	Cryptic Molecular-Geographical Divergence within <i>Medicago minima</i> Revealed by SSR Markers. <i>Iranian Journal of Science and Technology, Transaction A: Science</i> , 2022, 46, 49-60.	0.7	1
6274	Dataset complexity impacts both MOTU delimitation and biodiversity estimates in eukaryotic 18S rRNA metabarcoding studies. <i>Environmental DNA</i> , 2022, 4, 363-384.	3.1	7
6275	The probiotic effects of AB23A on high-fat-diet-induced non-alcoholic fatty liver disease in mice may be associated with suppressing the serum levels of lipopolysaccharides and branched-chain amino acids. <i>Archives of Biochemistry and Biophysics</i> , 2021, 714, 109080.	1.4	30
6276	Changes of antibiotic resistance genes and bacterial communities in the advanced biological wastewater treatment system under low selective pressure of tetracycline. <i>Water Research</i> , 2021, 207, 117834.	5.3	41
6280	Vegetation drives the structure of active microbial communities on an acidogenic mine tailings deposit. <i>PeerJ</i> , 2020, 8, e10109.	0.9	16
6292	Composition and function of the microbiotas in the different parts of the midgut of <i>Pyrrhocoris sibiricus</i> (Hemiptera: Pyrrhocoridae) revealed using high-throughput sequencing of 16S rRNA. <i>European Journal of Entomology</i> , 0, 117, 352-371.	1.2	4
6296	DATMA: Distributed AuTomatic Metagenomic Assembly and annotation framework. <i>PeerJ</i> , 2020, 8, e9762.	0.9	2
6297	Fungal infection, decline and persistence in the only obligate troglodytic Neotropical salamander. <i>PeerJ</i> , 2020, 8, e9763.	0.9	5
6298	<i>Tuber melanosporum</i> shapes <i>nir</i> S-type denitrifying and ammonia-oxidizing bacterial communities in <i>Carya illinoensis</i> ectomycorrhizosphere soils. <i>PeerJ</i> , 2020, 8, e9457.	0.9	3
6299	Hydrological and soil physiochemical variables determine the rhizospheric microbiota in subtropical lakeshore areas. <i>PeerJ</i> , 2020, 8, e10078.	0.9	5
6310	Investigating Mitochondrial Transcriptomes and RNA Processing Using Circular RNA Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2192, 43-57.	0.4	1

#	ARTICLE	IF	CITATIONS
6311	RNase H-dependent PCR enables highly specific amplification of antibody variable domains from single B-cells. PLoS ONE, 2020, 15, e0241803.	1.1	4
6312	WHITE MULBERRY (MORUS ALBA L.) FRUIT-ASSOCIATED BACTERIAL AND FUNGAL MICROBIOTA. Journal of Environmental Engineering and Landscape Management, 2020, 28, 183-191.	0.4	1
6313	Evaluation of Fecal Microbiota Transfer as Treatment for Postweaning Diarrhea in Research-Colony Puppies. Journal of the American Association for Laboratory Animal Science, 2016, 55, 582-7.	0.6	15
6314	Modeling a Superorganism - Considerations Regarding the Use of "Dirty" Mice in Biomedical Research. Yale Journal of Biology and Medicine, 2017, 90, 361-371.	0.2	10
6315	Effects of Fenbendazole-impregnated Feed and Topical Moxidectin during Quarantine on the Gut Microbiota of C57BL/6 Mice. Journal of the American Association for Laboratory Animal Science, 2018, 57, 229-235.	0.6	8
6316	Alterations of fecal bacterial communities in patients with lung cancer. American Journal of Translational Research (discontinued), 2018, 10, 3171-3185.	0.0	38
6317	Changes and roles of intestinal fungal microbiota in coronary heart disease complicated with nonalcoholic fatty liver disease. American Journal of Translational Research (discontinued), 2020, 12, 3445-3460.	0.0	2
6318	Characteristics and Diversity of Endophytic Bacteria in Endangered Chinese Herb Based on Illumina Sequencing. Polish Journal of Microbiology, 2020, 69, 283-291.	0.6	0
6319	Dysbiosis of intestinal microbiota in critically ill patients and risk of in-hospital mortality. American Journal of Translational Research (discontinued), 2021, 13, 1548-1557.	0.0	4
6321	Tracking bacterial DNA patterns in septic progression using 16s rRNA gene amplicon sequencing analysis. International Journal of Clinical and Experimental Pathology, 2021, 14, 753-767.	0.5	0
6322	Screening of Key Fungal Strains in the Fermentation Process of the Chinese Medicinal Preparation "Lianzhifan Solution" Based on Metabolic Profiling and High-Throughput Sequencing Technology. Frontiers in Microbiology, 2021, 12, 727968.	1.5	0
6323	OUP accepted manuscript. Carcinogenesis, 2021, , .	1.3	3
6324	Changes in soil microbial communities from exposed rocks to arboreal rhizosphere during vegetation succession in a karst mountainous ecosystem. Journal of Plant Interactions, 2021, 16, 550-563.	1.0	7
6325	Heavy chain sequence-based classifier for the specificity of human antibodies. Briefings in Bioinformatics, 2022, 23, .	3.2	4
6326	Characterization of gut microbiota in captive Himalayan tahr (<i>Hemitragus jemlahicus</i>) and the limited effect of sex on intestinal microorganisms of tahr. , 2021, 88, 1177-1188.		0
6327	Dietary gamma-aminobutyric acid ameliorates growth impairment and intestinal dysfunction in turbot (<i>Scophthalmus maximus</i>) fed a high soybean meal diet. Food and Function, 2022, 13, 290-303.	2.1	8
6328	Disentangling the effects of nitrogen availability and soil acidification on microbial taxa and soil carbon dynamics in natural grasslands. Soil Biology and Biochemistry, 2022, 164, 108495.	4.2	26
6329	Co-occurrence of Bacillariophyceae-based- and Cryptophyceae-based planktonic food webs in a temperate estuarine ecosystem revealed via eDNA. Estuarine, Coastal and Shelf Science, 2022, 264, 107661.	0.9	2

#	ARTICLE	IF	CITATIONS
6330	Shift of soil fungal communities under afforestation in Nanliu River Basin, southwest China. <i>Journal of Environmental Management</i> , 2022, 302, 114130.	3.8	10
6331	Metagenomic approaches to study the culture-independent bacterial diversity of a polluted environment—a case study on north-eastern coast of Bay of Bengal, India. , 2022, , 81-107.		2
6332	Distribution of antibiotic resistance genes from human and animal origins to their receiving environments: A regional scale survey of urban settings. <i>Environmental Pollution</i> , 2022, 293, 118512.	3.7	13
6333	Food sources of common carp in a Hani Terrace integrated rice-fish system (Yunnan Province, China). <i>Aquaculture Reports</i> , 2022, 22, 100937.	0.7	1
6334	Consistent responses of soil bacterial communities to bioavailable silicon deficiency in croplands. <i>Geoderma</i> , 2022, 408, 115587.	2.3	5
6335	Community succession of the grape epidermis microbes of cabernet sauvignon (<i>Vitis vinifera</i> L.) from different regions in China during fruit development. <i>International Journal of Food Microbiology</i> , 2022, 362, 109475.	2.1	20
6336	The nitrification inhibitor nitrapyrin has non-target effects on the soil microbial community structure, composition, and functions. <i>Applied Soil Ecology</i> , 2022, 171, 104350.	2.1	9
6337	Glutamine alleviates I ² -conglycinin-induced enteritis in juvenile hybrid groupers <i>Epinephelus fuscoguttatus</i> ™— <i>Epinephelus lanceolatus</i> ™, by suppressing the MyD88/NF- κ B pathway. <i>Aquaculture</i> , 2022,7 549, 737735.		10
6338	Actinobacterial biofertilizer improves the yields of different plants and alters the assembly processes of rhizosphere microbial communities. <i>Applied Soil Ecology</i> , 2022, 171, 104345.	2.1	17
6339	Soil Ventilation Benefited Strawberry Growth via Microbial Communities and Nutrient Cycling Under High-Density Planting. <i>Frontiers in Microbiology</i> , 2021, 12, 666982.	1.5	1
6340	Diversity, Functions and Antibiotic Resistance of Sediment Microbial Communities From Lake Geneva Are Driven by the Spatial Distribution of Anthropogenic Contamination. <i>Frontiers in Microbiology</i> , 2021, 12, 738629.	1.5	8
6341	Fecal microbiota changes in NZB/W F1 mice after induction of lupus disease. <i>Scientific Reports</i> , 2021, 11, 22953.	1.6	7
6342	Predictive capabilities of in vitro colon bioaccessibility for estimating in vivo relative bioavailability of arsenic from contaminated soils: Arsenic speciation and gut microbiota considerations. <i>Science of the Total Environment</i> , 2022, 818, 151804.	3.9	9
6343	Sex Differences in Fecal Microbiota Correlation With Physiological and Biochemical Indices Associated With End-Stage Renal Disease Caused by Immunoglobulin a Nephropathy or Diabetes. <i>Frontiers in Microbiology</i> , 2021, 12, 752393.	1.5	3
6344	Changes in the growth, nutritional quality and gut microbiota of the adult Chinese mitten crab, <i>Eriocheir sinensis</i> , following overwinter rearing. <i>Aquaculture Research</i> , 2022, 53, 1348-1362.	0.9	4
6345	Geographic and position-based variations in phyllospheric bacterial communities present on flue-cured tobacco. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 9297-9308.	1.7	5
6346	Collection of Bacterial Community Associated with Size Fractionated Aerosols from Kuwait. <i>Data</i> , 2021, 6, 123.	1.2	6
6347	Analysis of changes in microbiome compositions related to the prognosis of colorectal cancer patients based on tissue-derived 16S rRNA sequences. <i>Journal of Translational Medicine</i> , 2021, 19, 485.	1.8	19

#	ARTICLE	IF	CITATIONS
6348	Soil bacterial community as impacted by addition of rice straw and biochar. <i>Scientific Reports</i> , 2021, 11, 22185.	1.6	28
6349	Metagenomics Analysis to Investigate the Microbial Communities and Their Functional Profile During Cyanobacterial Blooms in Lake Varese. <i>Microbial Ecology</i> , 2022, 83, 850-868.	1.4	15
6350	Technical solutions for minimizing wheat grain cadmium: A field study in North China. <i>Science of the Total Environment</i> , 2022, 818, 151791.	3.9	6
6351	Hyperoxia Provokes Time- and Dose-Dependent Gut Injury and Endotoxemia and Alters Gut Microbiome and Transcriptome in Mice. <i>Frontiers in Medicine</i> , 2021, 8, 732039.	1.2	10
6352	The potential effect of microbiota in predicting the freshness of chilled chicken. <i>British Poultry Science</i> , 2022, 63, 360-367.	0.8	1
6353	Exploring bacterial diversity via a curated and searchable snapshot of archived DNA sequences. <i>PLoS Biology</i> , 2021, 19, e3001421.	2.6	60
6354	Bacterial Abundance, Diversity and Activity During Long-Term Colonization of Non-biodegradable and Biodegradable Plastics in Seawater. <i>Frontiers in Microbiology</i> , 2021, 12, 734782.	1.5	35
6355	A Pilot Study: Composition and Diversity of 16S rRNA Based Skin Bacterial Microbiome in Indonesian Atopic Dermatitis Population. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 2021, Volume 14, 1737-1744.	0.8	5
6356	Glucose Addition Enhanced the Advanced Treatment of Coking Wastewater. <i>Water (Switzerland)</i> , 2021, 13, 3365.	1.2	9
6357	Comparison of Culturing and Metabarcoding Methods to Describe the Fungal Endophytic Assemblage of <i>Brachypodium rupestre</i> Growing in a Range of Anthropized Disturbance Regimes. <i>Biology</i> , 2021, 10, 1246.	1.3	5
6358	A comprehensive approach to stool donor screening for faecal microbiota transplantation in China. <i>Microbial Cell Factories</i> , 2021, 20, 216.	1.9	14
6359	Comparison of gastrointestinal microbiota in golden snub-nosed monkey (<i>Rhinopithecus roxellanae</i>), green monkey (<i>Chlorocebus aethiops sabaeus</i>), and ring-tailed lemur (<i>Lemur catta</i>) by high throughput sequencing. <i>Global Ecology and Conservation</i> , 2022, 33, e01946.	1.0	3
6360	Insignificant Response of Bacterioplankton Community to Elevated pCO ₂ During a Short-Term Microcosm Experiment in a Subtropical Eutrophic Coastal Ecosystem. <i>Frontiers in Microbiology</i> , 2021, 12, 730377.	1.5	1
6361	Effect of Chronic Exposure to Textile Wastewater Treatment Plant Effluents on Growth Performance, Oxidative Stress, and Intestinal Microbiota in Adult Zebrafish (<i>Danio rerio</i>). <i>Frontiers in Microbiology</i> , 2021, 12, 782611.	1.5	5
6362	Trophic niche overlap between round sardinella (<i>Sardinella aurita</i>) and sympatric pelagic fish species in the Western Mediterranean. <i>Ecology and Evolution</i> , 2021, 11, 16126-16142.	0.8	14
6363	Attributes of intestinal microbiota composition and their correlation with clinical primary nonresponse to anti-TNF- α agents in inflammatory bowel disease patients. <i>Bosnian Journal of Basic Medical Sciences</i> , 2021, , .	0.6	10
6364	Strong partitioning of soil bacterial community composition and co-occurrence networks along a small-scale elevational gradient on Zijin Mountain. <i>Soil Ecology Letters</i> , 2021, 3, 290-302.	2.4	13
6365	Uniqueness and Dependence of Bacterial Communities on Microplastics: Comparison with Water, Sediment, and Soil. <i>Microbial Ecology</i> , 2022, 84, 985-995.	1.4	11

#	ARTICLE	IF	CITATIONS
6366	The Effect of Antibiotic Treatment on the Bacterial Community of the Brown Planthopper and Its Correlation with Rice Virulence. <i>Agronomy</i> , 2021, 11, 2327.	1.3	0
6367	Regionally divergent patterns of grass carp relative abundance, feeding habits and trophic niches in the subtropical Pearl River basin. <i>Aquatic Ecology</i> , 2022, 56, 525-541.	0.7	3
6368	Combined Use of Vinasse and Nitrogen as Fertilizers Affects Nitrification, Ammonification, and Denitrification by Prokaryotes. <i>Frontiers in Soil Science</i> , 2021, 1, .	0.8	1
6369	Microbial Biogeography along the Gastrointestinal Tract Segments of Sympatric Subterranean Rodents (<i>Eospalax baileyi</i> and <i>Eospalax cansus</i>). <i>Animals</i> , 2021, 11, 3297.	1.0	2
6370	Fecal microbiota profiling in irritable bowel syndrome and inflammatory bowel disease patients with irritable bowel syndrome-type symptoms. <i>BMC Gastroenterology</i> , 2021, 21, 433.	0.8	2
6373	Bioarchaeological insights into the last plague of Imola (1630â€“1632). <i>Scientific Reports</i> , 2021, 11, 22253.	1.6	5
6374	Responses of Soil Bacterial Diversity to Fertilization are Driven by Local Environmental Context Across China. <i>Engineering</i> , 2022, 12, 164-170.	3.2	12
6375	Effects of symbiotic population impairment on microbiome composition and longevity of <i>Bactrocera dorsalis</i> . <i>Royal Society Open Science</i> , 2021, 8, 211104.	1.1	2
6376	Enrichment of <i>Burkholderia</i> in the Rhizosphere by Autotoxic Ginsenosides to Alleviate Negative Plant-Soil Feedback. <i>Microbiology Spectrum</i> , 2021, 9, e0140021.	1.2	24
6377	The Effect of Exogenous Bile Acids on Antioxidant Status and Gut Microbiota in Heat-Stressed Broiler Chickens. <i>Frontiers in Nutrition</i> , 2021, 8, 747136.	1.6	14
6378	Livestock manure spiked with the antibiotic tylosin significantly altered soil protist functional groups. <i>Journal of Hazardous Materials</i> , 2022, 427, 127867.	6.5	9
6379	Large-scale geography survey provides insights into the colonization history of a major aphid pest on its cultivated apple host in Europe, North America and North Africa. , 0, 1, .		0
6380	The Persistence of <i>Staphylococcus aureus</i> in Pressure Ulcers: A Colonising Role. <i>Genes</i> , 2021, 12, 1883.	1.0	4
6382	Distribution of Microbial Community Structure in Sediment from the Suyeong River and Bay of Busan, Republic of Korea, Determined by 16S rRNA Gene Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0077821.	0.3	2
6383	Antibiotics, antibiotic resistance genes and microbial community in grouper mariculture. <i>Science of the Total Environment</i> , 2022, 808, 152042.	3.9	26
6384	Time-controlled and muscle-specific CRISPR/Cas9-mediated deletion of CTG-repeat expansion in the DMPK gene. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 184-199.	2.3	4
6385	Microbial Communities Involved in Methane, Sulfur, and Nitrogen Cycling in the Sediments of the Barents Sea. <i>Microorganisms</i> , 2021, 9, 2362.	1.6	36
6386	Twenty-Four-Month Longitudinal Study Suggests Little to No Horizontal Gene Transfer In Situ between Third-Generation Cephalosporin-Resistant <i>Salmonella</i> and Third-Generation Cephalosporin-Resistant <i>Escherichia coli</i> in a Beef Cattle Feedyard. <i>Journal of Food Protection</i> , 2022, 85, 323-335.	0.8	2

#	ARTICLE	IF	CITATIONS
6388	Utilization of Shredded Steam-Exploded Pine Particles as a Dietary Ingredient to Modify Cecal Microbiota in Broilers. <i>Agriculture (Switzerland)</i> , 2021, 11, 1196.	1.4	5
6389	Gut microbiota reflect the crowding stress of space shortage, physical and non-physical contact in Brandt's voles (<i>Lasiopodomys brandtii</i>). <i>Microbiological Research</i> , 2022, 255, 126928.	2.5	5
6390	Differences Between Microbial Communities of Pinus Species Having Differing Level of Resistance to the Pine Wood Nematode. <i>Microbial Ecology</i> , 2022, 84, 1245-1255.	1.4	5
6391	Virulence Genotype and Phenotype of Multiple Antimicrobial-Resistant <i>Escherichia coli</i> Isolates from Broilers Assessed from a "One-Health" Perspective. <i>Journal of Food Protection</i> , 2022, 85, 336-354.	0.8	7
6392	Relevance of the microbial community to Sb and As biogeochemical cycling in natural wetlands. <i>Science of the Total Environment</i> , 2022, 818, 151826.	3.9	11
6393	Identification and Comparison of <i>Colletotrichum</i> Secreted Effector Candidates Reveal Two Independent Lineages Pathogenic to Soybean. <i>Pathogens</i> , 2021, 10, 1520.	1.2	7
6394	Metagenomic Analysis for Evaluating Change in Bacterial Diversity in TPH-Contaminated Soil after Soil Remediation. <i>Toxics</i> , 2021, 9, 319.	1.6	6
6395	Targeted delivery of Chinese herb pair-based berberine/tannin acid self-assemblies for the treatment of ulcerative colitis. <i>Journal of Advanced Research</i> , 2022, 40, 263-276.	4.4	24
6396	Dietary Amylose/Amylopectin Ratio Modulates Cecal Microbiota and Metabolites in Weaned Goats. <i>Frontiers in Nutrition</i> , 2021, 8, 774766.	1.6	7
6397	The Influence of Temperature and Host Gender on Bacterial Communities in the Asian Citrus Psyllid. <i>Insects</i> , 2021, 12, 1054.	1.0	4
6398	Contents of lobetyolin, syringin, and atractylolide III in <i>Codonopsis pilosula</i> are related to dynamic changes of endophytes under drought stress. <i>Chinese Medicine</i> , 2021, 16, 122.	1.6	8
6399	The Relationship between the Community Structure and Function of Bacterioplankton and the Environmental Response in Qingcaosha Reservoir. <i>Water (Switzerland)</i> , 2021, 13, 3155.	1.2	0
6400	<i>Clostridium butyricum</i> Alleviates Enterotoxigenic <i>Escherichia coli</i> K88-Induced Oxidative Damage Through Regulating the p62-Keap1-Nrf2 Signaling Pathway and Remodeling the Cecal Microbial Community. <i>Frontiers in Immunology</i> , 2021, 12, 771826.	2.2	23
6401	Early Gut Microbiota Colonisation of Premature Infants Fed with Breastmilk or Formula with or without Probiotics: A Cohort Study. <i>Nutrients</i> , 2021, 13, 4068.	1.7	11
6402	Microbiome differences in periodontal, peri-implant, and healthy sites: a cross-sectional pilot study. <i>Clinical Oral Investigations</i> , 2022, 26, 2771-2781.	1.4	15
6403	Unveiling Endophytic Bacterial Community Structures of Different Rice Cultivars Grown in a Cadmium-Contaminated Paddy Field. <i>Frontiers in Microbiology</i> , 2021, 12, 756327.	1.5	13
6404	Impact of Electrolyzed Water on the Microbial Spoilage Profile of Piedmontese Steak Tartare. <i>Microbiology Spectrum</i> , 2021, 9, e0175121.	1.2	4
6405	The Diversity Patterns of Rare to Abundant Microbial Eukaryotes Across a Broad Range of Salinities in a Solar Saltern. <i>Microbial Ecology</i> , 2022, 84, 1103-1121.	1.4	4

#	ARTICLE	IF	CITATIONS
6406	Effects of a traditional Chinese medicine formula containing the Coix seed and Lotus seed on the intestinal morphology and microbiota of local piglets. <i>AMB Express</i> , 2021, 11, 159.	1.4	4
6407	Prokaryotic community and diversity in coastal surface waters along the Western Antarctic Peninsula. <i>Polar Science</i> , 2022, 31, 100764.	0.5	6
6408	Effects of Dietary Mannan Oligosaccharides on Non-Specific Immunity, Intestinal Health, and Antibiotic Resistance Genes in Pacific White Shrimp <i>Litopenaeus vannamei</i> . <i>Frontiers in Immunology</i> , 2021, 12, 772570.	2.2	5
6409	Pre-flooding soil used in monocropping increased strawberry biomass and altered bacterial community composition. <i>Soil Science and Plant Nutrition</i> , 2021, 67, 643-652.	0.8	3
6410	Epiphytic Microbial Community and Post-Harvest Characteristics of Strawberry Fruits as Affected by Plant Nutritional Regime with Silicon. <i>Agronomy</i> , 2021, 11, 2407.	1.3	2
6411	The Role of Gut Microbiota and Microbiota-Related Serum Metabolites in the Progression of Diabetic Kidney Disease. <i>Frontiers in Pharmacology</i> , 2021, 12, 757508.	1.6	24
6412	A Comprehensive Annotation of the Channel Catfish (<i>Ictalurus punctatus</i>) T Cell Receptor Alpha/Delta, Beta, and Gamma Loci. <i>Frontiers in Immunology</i> , 2021, 12, 786402.	2.2	3
6413	Evaluations and comparisons of microbial diversities in four types of body fluids based on two 16S rRNA gene sequencing methods. <i>Forensic Science International</i> , 2022, 331, 111128.	1.3	5
6414	In-situ biogas upgrading in an anaerobic trickling filter bed reactor treating a thermal post-treated digestate. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 106780.	3.3	16
6415	Gastrointestinal tract microbial community of <i>Babylonia areolata</i> and its diversity are closely correlated with the outbreak of disease. <i>Aquaculture Research</i> , 2022, 53, 1636-1648.	0.9	1
6416	Lupus gut microbiota transplants cause autoimmunity and inflammation. <i>Clinical Immunology</i> , 2021, 233, 108892.	1.4	25
6417	Analysis of <i>Ficus hirta</i> Fig Endosymbionts Diversity and Species Composition. <i>Diversity</i> , 2021, 13, 636.	0.7	1
6418	Integrated metabolic and microbial analysis reveals host-microbial interactions in IgE-mediated childhood asthma. <i>Scientific Reports</i> , 2021, 11, 23407.	1.6	16
6419	Sodium butyrate inhibits colitis-associated colorectal cancer through preventing the gut microbiota dysbiosis and reducing the expression of NLRP3 and IL-1 β . <i>Journal of Functional Foods</i> , 2021, 87, 104862.	1.6	8
6420	N-Cycling Microbiome Recruitment Differences Between Modern and Wild <i>Zea mays</i> . <i>Phytobiomes Journal</i> , 2022, 6, 151-160.	1.4	5
6421	Dietary supplementation of montmorillonite promotes growth and intestinal health in turbot (<i>Scophthalmus maximus</i>). <i>Animal Feed Science and Technology</i> , 2022, 283, 115176.	1.1	7
6422	A holobiont view of island biogeography: Unravelling patterns driving the nascent diversification of a Hawaiian spider and its microbial associates. <i>Molecular Ecology</i> , 2022, 31, 1299-1316.	2.0	5
6423	Investigation of soil nutrients and associated rhizobacterial communities in different sugarcane genotypes in relation to sugar content. <i>Chemical and Biological Technologies in Agriculture</i> , 2021, 8, .	1.9	11

#	ARTICLE	IF	CITATIONS
6424	Biogeography, assembly processes and species coexistence patterns of microbial communities in metalloids-laden soils around mining and smelting sites. <i>Journal of Hazardous Materials</i> , 2022, 425, 127945.	6.5	29
6425	Host species identity shapes the diversity and structure of insect microbiota. <i>Molecular Ecology</i> , 2022, 31, 723-735.	2.0	21
6426	Bacterial, archaeal, and fungal community structure and interrelationships of deep-sea shrimp intestine and the surrounding sediment. <i>Environmental Research</i> , 2022, 205, 112461.	3.7	5
6427	Decoding gut microbiota by imaging analysis of fecal samples. <i>IScience</i> , 2021, 24, 103481.	1.9	2
6428	Effect of fecal microbiota transplantation in patients with slow transit constipation and the relative mechanisms based on the protein digestion and absorption pathway. <i>Journal of Translational Medicine</i> , 2021, 19, 490.	1.8	13
6429	Supplemental <i>Aspergillus</i> Lipase and Protease Preparations Display Powerful Bifidogenic Effects and Modulate the Gut Microbiota Community of Rats. <i>Fermentation</i> , 2021, 7, 294.	1.4	6
6430	Comparative Evaluation of the Ileum Microbiota Composition in Piglets at Different Growth Stages. <i>Frontiers in Microbiology</i> , 2021, 12, 765691.	1.5	7
6431	Revisiting proboscidean phylogeny and evolution through total evidence and palaeogenetic analyses including <i>Notiomastodon</i> ancient DNA. <i>IScience</i> , 2022, 25, 103559.	1.9	13
6432	Analysis of the relationship between bile duct and duodenal microbiota reveals that potential dysbacteriosis is the main cause of primary common bile duct stones. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 414-428.	1.8	6
6433	Effect of Nitrogen Addition on Soil Microbial Functional Gene Abundance and Community Diversity in Permafrost Peatland. <i>Microorganisms</i> , 2021, 9, 2498.	1.6	7
6434	Initial sample processing can influence the soil microbial metabarcoding surveys, revealed by <i>Leucocalocybe mongolica</i> fairy ring ecosystem. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 1427-1438.	0.5	6
6435	Mixed Planting Reduces the Effect of Cover Crop Variety on Soil Microbial Community Structure. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6436	Overactive STAT3 Drives Accumulation of Disease-Associated CD21 ^{low} B Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6438	Distribution of Microbial Communities of Sediment and Relationship with Surrounding Environmental Factors in a Typical Rural River, Southwest China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6439	Long-Term Metal Pollution Shifts Microbial Functional Profiles of Nitrification and Denitrification in Agricultural Soils. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6440	A More Diverse Cervical Microbiome Associates with Better Clinical Outcomes in Patients with Endometriosis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6441	Effects of temperature on composition and stability of bacterial community in colonial <i>Microcystis aeruginosa</i> culture systems. <i>Hupo Kexue/Journal of Lake Sciences</i> , 2021, 33, 1660-1674.	0.3	0
6442	Jianpi Huayu Decoction Enhances the Effect of Sorafenib and Alleviates Adverse Events in Hepatocellular Carcinoma by Remodeling the Gut Microbiota. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
6443	Rare soil species impact the rhizosphere bacterial communities and cadmium uptake by <i>Lolium multiflorum</i> Lam.. <i>Plant and Soil</i> , 2022, 473, 337-350.	1.8	3
6445	Duodenal microbiota makes an important impact in functional dyspepsia. <i>Microbial Pathogenesis</i> , 2022, 162, 105297.	1.3	5
6446	Intra- and inter-annual variability of nitrification in the rhizosphere of field-grown bioenergy sorghum. <i>GCB Bioenergy</i> , 2022, 14, 393-410.	2.5	6
6447	Identification of an Amylomaltase from the Halophilic Archaeon <i>Haloquadratum walsbyi</i> by Functional Metagenomics: Structural and Functional Insights. <i>Life</i> , 2022, 12, 85.	1.1	2
6448	Comparison and Analysis of Gut Microbiota in Children With IgA Vasculitis With Different Clinical Symptoms. <i>Frontiers in Pediatrics</i> , 2021, 9, 800677.	0.9	5
6449	Seasonal variation significantly affected bacterioplankton and eukaryoplankton community composition in Xijiang River, China. <i>Environmental Monitoring and Assessment</i> , 2022, 194, 55.	1.3	4
6450	Integrated microbiology and metabolomics analysis reveal responses of soil microorganisms and metabolic functions to phosphorus fertilizer on semiarid farm. <i>Science of the Total Environment</i> , 2022, 817, 152878.	3.9	40
6451	Gut Microbiome Distinguishes Patients With Epilepsy From Healthy Individuals. <i>Frontiers in Microbiology</i> , 2021, 12, 696632.	1.5	5
6452	Deciphering the bacterial microbiome in response to long-term mercury contaminated soil. <i>Ecotoxicology and Environmental Safety</i> , 2022, 229, 113062.	2.9	18
6453	Urogenital Microbiota: Potentially Important Determinant of PD-L1 Expression in Male Patients with Non-muscle Invasive Bladder Cancer. <i>BMC Microbiology</i> , 2022, 22, 7.	1.3	14
6454	ProSynAR: a reference aware read merger. <i>Bioinformatics</i> , 2022, 38, 2052-2053.	1.8	2
6455	Reduced calorie diet combined with NNMT inhibition establishes a distinct microbiome in DIO mice. <i>Scientific Reports</i> , 2022, 12, 484.	1.6	0
6456	Biodiversity of zooplankton in 0-3000 m waters from the eastern Indian Ocean in spring 2019 based on metabarcoding. , 2022, 1, 100005.		2
6457	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. <i>Cancer Cell</i> , 2022, 40, 70-87.e15.	7.7	120
6458	Environmental factors and interactions among microorganisms drive microbial community succession during fermentation of Nongxiangxing daqu. <i>Bioresource Technology</i> , 2022, 345, 126549.	4.8	60
6459	Organic fertilizer activates soil beneficial microorganisms to promote strawberry growth and soil health after fumigation. <i>Environmental Pollution</i> , 2022, 295, 118653.	3.7	44
6460	Shifts in chemical and microbiological properties belowground of invader <i>Ageratina adenophora</i> along an altitudinal gradient. <i>Journal of Plant Ecology</i> , 2022, 15, 561-570.	1.2	4
6461	Bacteria versus fungi for predicting anthropogenic pollution in subtropical coastal sediments: Assembly process and environmental response. <i>Ecological Indicators</i> , 2022, 134, 108484.	2.6	18

#	ARTICLE	IF	CITATIONS
6462	Resolvin D1 ameliorates hepatic steatosis by remodeling the gut microbiota and restoring the intestinal barrier integrity in DSS-induced chronic colitis. <i>International Immunopharmacology</i> , 2022, 103, 108500.	1.7	3
6463	From Alpha Diversity to Zzz: Interactions among sleep, the brain, and gut microbiota in the first year of life. <i>Progress in Neurobiology</i> , 2022, 209, 102208.	2.8	20
6464	Depth effects on bacterial community assembly processes in paddy soils. <i>Soil Biology and Biochemistry</i> , 2022, 165, 108517.	4.2	38
6465	Remediation of As and Cd contaminated sediment by biochars: Accompanied with the change of microbial community. <i>Journal of Environmental Chemical Engineering</i> , 2022, 10, 106912.	3.3	12
6466	Denitrifying halophilic archaea derived from salt dominate the degradation of nitrite in salted radish during pickling. <i>Food Research International</i> , 2022, 152, 110906.	2.9	14
6467	Insight into the root growth, soil quality, and assembly of the root-associated microbiome in the virus-free <i>Chrysanthemum morifolium</i> . <i>Industrial Crops and Products</i> , 2022, 176, 114362.	2.5	4
6468	Enhanced ex-situ biomethanation of hydrogen and carbon dioxide in a trickling filter bed reactor. <i>Biochemical Engineering Journal</i> , 2022, 179, 108311.	1.8	16
6469	<i>Pseudomonas</i> sp. TCd-1 significantly alters the rhizosphere bacterial community of rice in Cd contaminated paddy field. <i>Chemosphere</i> , 2022, 290, 133257.	4.2	15
6470	Effects of the lignite bioorganic fertilizer on greenhouse gas emissions and pathways of nitrogen and carbon cycling in saline-sodic farmlands at Northwest China. <i>Journal of Cleaner Production</i> , 2022, 334, 130080.	4.6	12
6471	A multi-dimensional evaluation of the NIST 1032 sample set across four forensic Y-STR multiplexes. <i>Forensic Science International: Genetics</i> , 2022, 57, 102655.	1.6	11
6472	Mangrove restoration promotes the anti-scourability of the sediments by modifying inherent microbial community and extracellular polymeric substance. <i>Science of the Total Environment</i> , 2022, 811, 152369.	3.9	12
6473	Metagenomic profiles of core and signature bacteria in the guts of white shrimp, <i>Litopenaeus vannamei</i> , with different growth rates. <i>Aquaculture</i> , 2022, 550, 737849.	1.7	13
6474	Microbial keystone taxa drive crop productivity through shifting aboveground-belowground mineral element flows. <i>Science of the Total Environment</i> , 2022, 811, 152342.	3.9	21
6475	Characterization of the gut microbiome in the beet armyworm <i>Spodoptera exigua</i> in response to the short-term thermal stress. <i>Journal of Asia-Pacific Entomology</i> , 2022, 25, 101863.	0.4	4
6476	Response mechanism of gut microbiome and metabolism of European seabass (<i>Dicentrarchus labrax</i>) to temperature stress. <i>Science of the Total Environment</i> , 2022, 813, 151786.	3.9	22
6477	Animal corpse degradation enriches antibiotic resistance genes but remains recalcitrant in drinking water microcosm. <i>International Biodeterioration and Biodegradation</i> , 2022, 168, 105372.	1.9	6
6478	Responsive changes of rumen microbiome and metabolome in dairy cows with different susceptibility to subacute ruminal acidosis. <i>Animal Nutrition</i> , 2022, 8, 331-340.	2.1	18
6479	Gut microbiome composition likely affects the growth of razor clam <i>Sinonovacula constricta</i> . <i>Aquaculture</i> , 2022, 550, 737847.	1.7	13

#	ARTICLE	IF	CITATIONS
6480	High N ₂ O reduction potential by denitrification in the nearshore site of a riparian zone. <i>Science of the Total Environment</i> , 2022, 813, 152458.	3.9	19
6481	Metagenomic profiles of the resistome in subtropical estuaries: Co-occurrence patterns, indicative genes, and driving factors. <i>Science of the Total Environment</i> , 2022, 810, 152263.	3.9	38
6482	Proteome and microbiota analyses characterizing dynamic coral-algae-microbe tripartite interactions under simulated rapid ocean acidification. <i>Science of the Total Environment</i> , 2022, 810, 152266.	3.9	6
6483	Short-term legacy effects of rice season irrigation and fertilization on the soil bacterial community of the subsequent wheat season in a rice-wheat rotation system. <i>Agricultural Water Management</i> , 2022, 263, 107446.	2.4	7
6484	Succession of soil bacterial community along a 46-year chronosequence artificial revegetation in an arid oasis-desert ecotone. <i>Science of the Total Environment</i> , 2022, 814, 152496.	3.9	15
6485	Alteration of bacterial communities and co-occurrence networks as a legacy effect upon exposure to polyethylene residues under field environment. <i>Journal of Hazardous Materials</i> , 2022, 426, 128126.	6.5	11
6486	Microbial diversity and ecology of geothermal springs in the high-grade metamorphic terrain of Sri Lanka. <i>Environmental Advances</i> , 2022, 7, 100166.	2.2	8
6487	The loss of above- and belowground biodiversity in degraded grasslands drives the decline of ecosystem multifunctionality. <i>Applied Soil Ecology</i> , 2022, 172, 104370.	2.1	28
6488	Occurrence and distribution of cyclic-alkane-consuming psychrophilic bacteria in the Yellow Sea and East China Sea. <i>Journal of Hazardous Materials</i> , 2022, 427, 128129.	6.5	7
6489	Methanogenesis pathways of methanogens and their responses to substrates and temperature in sediments from the South Yellow Sea. <i>Science of the Total Environment</i> , 2022, 815, 152645.	3.9	11
6491	Characteristics and Diversity of Endophytic Bacteria in Endangered Chinese Herb <i>Glehnia littoralis</i> Based on Illumina Sequencing. <i>Polish Journal of Microbiology</i> , 2020, 69, 283-291.	0.6	4
6492	Antibiotic-induced changes in <i>Tetranychus truncatus</i> bacterial community alter fecundity, longevity and sex-ratio. <i>Systematic and Applied Acarology</i> , 2020, 25, 1668-1682.	0.5	2
6494	Potential Solubility of Zinc, Nickel, and Copper from the Soil of a Contaminated Industrial Site Under Flooding and Drainage. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6495	Integrated omics analysis: the relationship between significantly increased <i>Klebsiella</i> post-hepatectomy and decreased hub-metabolite 3-methyl-2-oxobutanoic acid is associated with induced liver failure. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 326-343.	0.6	4
6496	Characterization and diversity of magnetotactic bacteria from sediments of Caroline Seamount in the Western Pacific Ocean. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 2027-2043.	0.6	6
6497	Metabolic and Neural Mechanisms Underlying the Associations Between Gut Bacteroides and Cognition: A Large-Scale Functional Network Connectivity Study. <i>Frontiers in Neuroscience</i> , 2021, 15, 750704.	1.4	6
6498	Microbial Communities and Functions in the Rhizosphere of Disease-Resistant and Susceptible <i>Camellia</i> spp.. <i>Frontiers in Microbiology</i> , 2021, 12, 732905.	1.5	6
6499	Apple microbial communities and differences between two main Chinese producing regions. <i>Food Quality and Safety</i> , 2022, 6, .	0.6	7

#	ARTICLE	IF	CITATIONS
6500	Dietary Effects on Biological Parameters and Gut Microbiota of <i>Harmonia axyridis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 818787.	1.5	6
6501	Changes in the taxonomic and functional structures of microbial communities during vegetable waste mixed silage fermentation. <i>Canadian Journal of Microbiology</i> , 2022, 68, 281-293.	0.8	4
6502	<i>Acremonium terricola</i> Culture's Dose-Response Effects on Lactational Performance, Antioxidant Capacity, and Ruminal Characteristics in Holstein Dairy Cows. <i>Antioxidants</i> , 2022, 11, 175.	2.2	10
6503	Multi-omics Analysis Revealed Coordinated Responses of Rumen Microbiome and Epithelium to High-Grain-Induced Subacute Rumen Acidosis in Lactating Dairy Cows. <i>MSystems</i> , 2022, 7, e0149021.	1.7	18
6505	Lactic Acid Bacteria Are Prevalent in the Infrabuccal Pockets and Crops of Ants That Prefer Aphid Honeydew. <i>Frontiers in Microbiology</i> , 2021, 12, 785016.	1.5	9
6506	Filtered mud improves sugarcane growth and modifies the functional abundance and structure of soil microbial populations. <i>PeerJ</i> , 2022, 10, e12753.	0.9	2
6507	Comparison of the Intestinal Structure and Intestinal Microbiome between Two Geographically Isolated Populations of <i>Culter alburnus</i> . <i>Animals</i> , 2022, 12, 342.	1.0	1
6508	Comparison of feeding diets including dried or ensiled peanut vines as forage sources on the growth performance, ruminal fermentation, and bacterial community in young Holstein bulls. <i>Animal Science Journal</i> , 2022, 93, e13675.	0.6	3
6509	If You Build It, Will They Come? An Environmental DNA Assessment of Fish Assemblages on Artificial Reefs in the Northern Gulf of Mexico. <i>Transactions of the American Fisheries Society</i> , 2022, 151, 297-321.	0.6	1
6510	Organic amendments combined with biochar for improving soil and plant quality in a <i>Torreya grandis</i> plantation. <i>Journal of Soils and Sediments</i> , 2022, 22, 1080-1094.	1.5	5
6511	Effects of Dietary Phospholipids on Growth Performance, Digestive Enzymes Activity and Intestinal Health of Largemouth Bass (<i>Micropterus salmoides</i>) Larvae. <i>Frontiers in Immunology</i> , 2021, 12, 827946.	2.2	12
6512	Gut dysbiosis is associated with acceleration of lupus nephritis. <i>Scientific Reports</i> , 2022, 12, 152.	1.6	17
6513	Nitrogen Advanced Treatment of Urban Sewage by Denitrification Deep-Bed Filter: Removal Performance and Metabolic Pathway. <i>Frontiers in Microbiology</i> , 2021, 12, 811697.	1.5	6
6514	Diversity and structure of the microbial community in rhizosphere soil of <i>Fritillaria ussuriensis</i> at different health levels. <i>PeerJ</i> , 2022, 10, e12778.	0.9	18
6515	Hybridization Affects the Structure and Function of Root Microbiome by Altering Gene Expression in Roots of Wheat Introgression Line Under Saline-Alkali Stress. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6516	Unlocking the Changes of Phyllosphere Fungal Communities of Fishscale Bamboo (<i>Phyllachora</i>) Tj ETQq1 1 0.784314,rgBT /Qverlock 10 0,9 1		
6517	Disturbance of Gut Bacteria and Metabolites Are Associated with Disease Severity and Predict Outcome of NMDAR Encephalitis: A Prospective Case-Control Study. <i>Frontiers in Immunology</i> , 2021, 12, 791780.	2.2	4
6518	Metabonomics Combined with 16S rRNA Gene Sequencing to Analyze the Changes of Gut Microbiota in Mice with Parkinson's Disease and the Intervention Effect of Cyanidin-3-O-Glucoside. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
6519	Host fruits shape the changes in the gut microbiota and development of <i>Bactrocera dorsalis</i> (Diptera: Tj ETQq0 0 0,rgBT /Overlock 10 T	0.4	6
6520	Effect of <i>Elymus nutan</i> on the assemblage of arbuscular mycorrhizal fungal communities enhanced by soil available nitrogen in the restoration succession of revegetated grassland on the Qinghai-Tibetan Plateau. <i>Land Degradation and Development</i> , 2022, 33, 931-944.	1.8	7
6521	Calebin-A prevents HFD-induced obesity in mice by promoting thermogenesis and modulating gut microbiota. <i>Journal of Traditional and Complementary Medicine</i> , 2023, 13, 119-127.	1.5	10
6522	The colonized microbiota composition in the peritoneal fluid in women with endometriosis. <i>Archives of Gynecology and Obstetrics</i> , 2022, 305, 1573-1580.	0.8	10
6523	Morphological, molecular, and biochemical study of cyanobacteria from a eutrophic Algerian reservoir (Cheffia). <i>Environmental Science and Pollution Research</i> , 2022, 29, 27624.	2.7	1
6524	Phyllosphere fungal communities of rubber trees exhibited biogeographical patterns, but not bacteria. <i>Environmental Microbiology</i> , 2022, 24, 3777-3790.	1.8	9
6525	Varying microbial utilization of straw-derived carbon with different long-term fertilization regimes explored by DNA stable-isotope probing. <i>European Journal of Soil Biology</i> , 2022, 108, 103379.	1.4	6
6526	The microbiome of wild and mass-reared new world screwworm, <i>Cochliomyia hominivorax</i> . <i>Scientific Reports</i> , 2022, 12, 1042.	1.6	2
6527	Spatio-Temporal Dynamics in Physico-Chemical Properties, Phytoplankton and Bacterial Diversity as an Indication of the Bovan Reservoir Water Quality. <i>Water (Switzerland)</i> , 2022, 14, 391.	1.2	7
6528	Diverse DNA modification in marine prokaryotic and viral communities. <i>Nucleic Acids Research</i> , 2022, 50, 1531-1550.	6.5	9
6529	Lentian Supplementation Protects the Gut-Liver Axis and Prevents Steatohepatitis: The Role of Gut Microbiota Involved. <i>Frontiers in Nutrition</i> , 2021, 8, 803691.	1.6	23
6530	BigFiRSt: A Software Program Using Big Data Technique for Mining Simple Sequence Repeats From Large-Scale Sequencing Data. <i>Frontiers in Big Data</i> , 2021, 4, 727216.	1.8	2
6531	Enhanced Biodegradation of High-Salinity and Low-Temperature Crude-Oil Wastewater by Immobilized Crude-Oil Biodegrading Microbiota. <i>Journal of Ocean University of China</i> , 2022, 21, 141-151.	0.6	3
6532	Effects of Emerging Pollutants and Heavy Metals on the Variation of Bacterial Communities in Estuarine Sediments. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6533	The gut microbiota of chickens in a commercial farm treated with a <i>Salmonella</i> phage cocktail. <i>Scientific Reports</i> , 2022, 12, 991.	1.6	15
6534	The Bacterial and Fungal Microbiota of <i>Robiola di Roccaverano</i> Protected Designation of Origin Raw Milk Cheese. <i>Frontiers in Microbiology</i> , 2021, 12, 776862.	1.5	9
6535	Improved and Flexible HDR Editing by Targeting Introns in iPSCs. <i>Stem Cell Reviews and Reports</i> , 2022, 18, 1822-1833.	1.7	6
6536	The Pass-on Effect of Tetracycline-Induced Honey Bee (<i>Apis mellifera</i>) Gut Community Dysbiosis. <i>Frontiers in Microbiology</i> , 2021, 12, 781746.	1.5	11

#	ARTICLE	IF	CITATIONS
6537	Dual inoculation of dark septate endophytes and <i>Trichoderma viride</i> drives plant performance and rhizosphere microbiome adaptations of <i>Astragalus mongholicus</i> to drought. <i>Environmental Microbiology</i> , 2022, 24, 324-340.	1.8	15
6539	Seaweed Fertilizer Prepared by EM-Fermentation Increases Abundance of Beneficial Soil Microbiome in Paddy (<i>Oryzasativa</i> L.) during Vegetative Stage. <i>Fermentation</i> , 2022, 8, 46.	1.4	7
6540	Encoding Genetic Circuits with DNA Barcodes Paves the Way for Machine Learning-Assisted Metabolite Biosensor Response Curve Profiling in Yeast. <i>ACS Synthetic Biology</i> , 2022, 11, 977-989.	1.9	13
6541	Comprehensive interrogation of the ADAR2 deaminase domain for engineering enhanced RNA editing activity and specificity. <i>ELife</i> , 2022, 11, .	2.8	19
6542	Maize/peanut intercropping improves nutrient uptake of side-row maize and system microbial community diversity. <i>BMC Microbiology</i> , 2022, 22, 14.	1.3	34
6543	Epidemiological and Microbiome Characterization of Black Tooth Stain in Preschool Children. <i>Frontiers in Pediatrics</i> , 2022, 10, 751361.	0.9	1
6544	Gut Ruminococcaceae levels at baseline correlate with risk of antibiotic-associated diarrhea. <i>IScience</i> , 2022, 25, 103644.	1.9	28
6545	Ancient Mitogenomes Suggest Stable Mitochondrial Clades of the Siberian Roe Deer. <i>Genes</i> , 2022, 13, 114.	1.0	3
6546	The influence of food processing methods on serum parameters, apparent total-tract macronutrient digestibility, fecal microbiota and SCFA content in adult beagles. <i>PLoS ONE</i> , 2022, 17, e0262284.	1.1	0
6547	Analysis of soil bacterial communities and physicochemical properties associated with <i>Fusarium</i> wilt disease of banana in Malaysia. <i>Scientific Reports</i> , 2022, 12, 999.	1.6	9
6548	High-sugar, high-fat, and high-protein diets promote antibiotic resistance gene spreading in the mouse intestinal microbiota. <i>Gut Microbes</i> , 2022, 14, 2022442.	4.3	23
6549	Highly Distinct Microbial Communities in Elevated Strings and Submerged Flarks in the Boreal Aapa-Type Mire. <i>Microorganisms</i> , 2022, 10, 170.	1.6	2
6550	A More Diverse Cervical Microbiome Associates with Better Clinical Outcomes in Patients with Endometriosis: A Pilot Study. <i>Biomedicines</i> , 2022, 10, 174.	1.4	15
6551	Linkages between soil respiration and soil eukaryotic microalgae following vegetation restoration in the Loess Plateau, China. <i>Land Degradation and Development</i> , 0, , .	1.8	2
6552	The changes of microbial diversity and flavor compounds during the fermentation of millet Huangjiu, a traditional Chinese beverage. <i>PLoS ONE</i> , 2022, 17, e0262353.	1.1	16
6553	A PARTHENOGENESIS allele from apomictic dandelion can induce egg cell division without fertilization in lettuce. <i>Nature Genetics</i> , 2022, 54, 84-93.	9.4	56
6554	Chestnut polysaccharides restore impaired spermatogenesis by adjusting gut microbiota and the intestinal structure. <i>Food and Function</i> , 2022, 13, 425-436.	2.1	3
6555	MDC, an <i>Ophiopogon japonicus</i> polysaccharide, inhibits non-alcoholic fatty liver disease by regulating the abundance of <i>Akkermansia muciniphila</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 196, 23-34.	3.6	24

#	ARTICLE	IF	CITATIONS
6556	Rhizosphere analysis of field-grown <i>Panax ginseng</i> with different degrees of red skin provides the basis for preventing red skin syndrome. <i>BMC Microbiology</i> , 2022, 22, 12.	1.3	6
6557	BRCA1 deficiency specific base substitution mutagenesis is dependent on translesion synthesis and regulated by 53BP1. <i>Nature Communications</i> , 2022, 13, 226.	5.8	11
6558	Mycotoxin Interactions along the Gastrointestinal Tract: In Vitro Semi-Dynamic Digestion and Static Colonic Fermentation of a Contaminated Meal. <i>Toxins</i> , 2022, 14, 28.	1.5	8
6559	First Report of Fecal Microflora of Wild Bar-Headed Goose in Tibet Plateau. <i>Frontiers in Veterinary Science</i> , 2021, 8, 791461.	0.9	6
6560	Differences in caecal microbiota composition and <i>Salmonella</i> carriage between experimentally infected inbred lines of chickens. <i>Genetics Selection Evolution</i> , 2022, 54, 7.	1.2	11
6561	Seasonal succession of bacterial communities in cultured <i>Caulerpa lentillifera</i> detected by high-throughput sequencing. <i>Open Life Sciences</i> , 2022, 17, 10-21.	0.6	4
6562	Compound Probiotics Improve the Diarrhea Rate and Intestinal Microbiota of Newborn Calves. <i>Animals</i> , 2022, 12, 322.	1.0	12
6563	Health improvements of type 2 diabetic patients through diet and diet plus fecal microbiota transplantation. <i>Scientific Reports</i> , 2022, 12, 1152.	1.6	41
6564	Soil Acidification Under Long-Term N Addition Decreases the Diversity of Soil Bacteria and Fungi and Changes Their Community Composition in a Semiarid Grassland. <i>Microbial Ecology</i> , 2023, 85, 221-231.	1.4	21
6565	Potato tillage method is associated with soil microbial communities, soil chemical properties, and potato yield. <i>Journal of Microbiology</i> , 2022, 60, 156-166.	1.3	7
6566	Supplementation of <i>Bacillus</i> sp. DU-106 Alleviates Antibiotic-Associated Diarrhea in Association with the Regulation of Intestinal Microbiota in Mice. <i>Probiotics and Antimicrobial Proteins</i> , 2022, 14, 372-383.	1.9	11
6567	Parkinson's Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. <i>MSystems</i> , 2022, 7, e0119121.	1.7	13
6569	Effects of sampling strategies and DNA extraction methods on eDNA metabarcoding: A case study of estuarine fish diversity monitoring. <i>Zoological Research</i> , 2022, 43, 192-204.	0.9	3
6570	Microbial composition in <i>Hyalomma anatolicum</i> collected from livestock in the United Arab Emirates using next-generation sequencing. <i>Parasites and Vectors</i> , 2022, 15, 30.	1.0	4
6571	Gut Microbiota Diversity and Overweight/Obesity in Infancy: Results from a Nested Case-control Study. <i>Current Medical Science</i> , 2022, 42, 210-216.	0.7	3
6572	Gallic Acid Alleviates Gut Dysfunction and Boosts Immune and Antioxidant Activities in Puppies Under Environmental Stress Based on Microbiome's Metabolomics Analysis. <i>Frontiers in Immunology</i> , 2021, 12, 813890.	2.2	27
6573	Does revegetation cause soil microbiota recovery? Evidence from revisiting a revegetation chronosequence 6 years after initial sampling. <i>Restoration Ecology</i> , 2022, 30, .	1.4	8
6574	Automating microsatellite screening and primer design from multi-individual libraries using Micro-Primers. <i>Scientific Reports</i> , 2022, 12, 295.	1.6	2

#	ARTICLE	IF	CITATIONS
6575	Immobilization of hexavalent chromium in contaminated soil by nano-sized layered double hydroxide intercalated with diethyldithiocarbamate: Fraction distribution, plant growth, and microbial evolution. <i>Journal of Hazardous Materials</i> , 2022, 430, 128382.	6.5	15
6576	Diversity and structure of the rhizosphere microbial communities of wild and cultivated ginseng. <i>BMC Microbiology</i> , 2022, 22, 2.	1.3	21
6577	Metagenomic Analysis of Bacterial Communities and Antibiotic Resistance Genes in <i>Penaeus monodon</i> Biofloc-Based Aquaculture Environments. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	6
6578	Regulatory Effects of Combined Dietary Supplementation With Essential Oils and Organic Acids on Microbial Communities of Cobb Broilers. <i>Frontiers in Microbiology</i> , 2021, 12, 814626.	1.5	6
6579	Exploring the role of gut microbiota in host feeding behavior among breeds in swine. <i>BMC Microbiology</i> , 2022, 22, 1.	1.3	34
6580	Epichloa Fungal Endophytes Influence Seed-Associated Bacterial Communities. <i>Frontiers in Microbiology</i> , 2021, 12, 795354.	1.5	10
6581	How habitat heterogeneity shapes bacterial and protistan communities in temperate coastal areas near estuaries. <i>Environmental Microbiology</i> , 2022, 24, 1775-1789.	1.8	13
6582	Pterostilbene exert an anti-inflammatory effect by attenuating inflammation, oxidative stress, and alteration of gut microbiota. <i>Journal of Food Biochemistry</i> , 2022, 46, e14011.	1.2	4
6583	Environmental selection overturns the decay relationship of soil prokaryotic community over geographic distance across grassland biotas. <i>ELife</i> , 2022, 11, .	2.8	5
6584	Microbiota of the Digestive Glands and Extrapallial Fluids of Clams Evolve Differently Over Time Depending on the Intertidal Position. <i>Microbial Ecology</i> , 2023, 85, 288-297.	1.4	4
6585	Gut microbiome alteration as a diagnostic tool and associated with inflammatory response marker in primary liver cancer. <i>Hepatology International</i> , 2022, 16, 99-111.	1.9	24
6586	<i>Bacillus velezensis</i> Strains for Protecting Cucumber Plants from Root-Knot Nematode <i>Meloidogyne incognita</i> in a Greenhouse. <i>Plants</i> , 2022, 11, 275.	1.6	14
6587	Do microbial planktonic communities reflect the ecological changes of Glorieuses coral reefs (Iles Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	2.3	2
6588	The Diversity of Bacteria Associated with the Invasive Gall Wasp <i>Dryocosmus kuriphilus</i> , Its Galls and a Specialist Parasitoid on Chestnuts. <i>Insects</i> , 2022, 13, 86.	1.0	1
6589	Metabarcoding reveals massive species diversity of Diptera in a subtropical ecosystem. <i>Ecology and Evolution</i> , 2022, 12, e8535.	0.8	12
6590	Scale-Dependent Effects of Growth Stage and Elevational Gradient on Rice Phyllosphere Bacterial and Fungal Microbial Patterns in the Terrace Field. <i>Frontiers in Plant Science</i> , 2021, 12, 766128.	1.7	1
6591	Contrasting Community Composition and Co-Occurrence Relationships of the Active Pico-Sized Haptophytes in the Surface and Subsurface Chlorophyll Maximum Layers of the Arctic Ocean in Summer. <i>Microorganisms</i> , 2022, 10, 248.	1.6	4
6592	Exploring an alternative source of DIETer to mitigate ammonia inhibition of swine manure by inoculum treating brewery wastewater. <i>Biomass Conversion and Biorefinery</i> , 0, , 1.	2.9	0

#	ARTICLE	IF	CITATIONS
6593	Hen raising helps chicks establish gut microbiota in their early life and improve microbiota stability after H9N2 challenge. <i>Microbiome</i> , 2022, 10, 14.	4.9	17
6594	A randomized double-blind cross-over trial to study the effects of resistant starch prebiotic in chronic kidney disease (ReSPECKD). <i>Trials</i> , 2022, 23, 72.	0.7	5
6595	Rhizosphere bacterial diversity and environmental function prediction of wild salt-tolerant plants in coastal silt soil. <i>Ecological Indicators</i> , 2022, 134, 108503.	2.6	17
6596	Single cell transcriptomic landscape of diabetic foot ulcers. <i>Nature Communications</i> , 2022, 13, 181.	5.8	111
6597	Individual copy number variation and extensive diversity between major MHC-DAB1 allelic lineages in the European bitterling. <i>Immunogenetics</i> , 2022, 74, 497-505.	1.2	2
6598	The response of bacterial communities to carbon dioxide in high-oxygen modified atmosphere packaged beef steaks during chilled storage. <i>Food Research International</i> , 2022, 151, 110872.	2.9	12
6599	Association Between Vaginal Gardnerella and Tubal Pregnancy in Women With Symptomatic Early Pregnancies in China: A Nested Case-Control Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 761153.	1.8	1
6600	Dynamic succession patterns and interactions of phyllospheric microorganisms during NOx exposure. <i>Journal of Hazardous Materials</i> , 2022, 430, 128371.	6.5	4
6601	Contrasting patterns of bacterial communities in the rearing water and gut of <i>Penaeus vannamei</i> in response to exogenous glucose addition. <i>Marine Life Science and Technology</i> , 2022, 4, 222-236.	1.8	13
6602	Peanut Rotation and Flooding Induce Rhizobacteriome Variation With Opposing Influences on the Growth and Medicinal Yield of <i>Corydalis yanhusuo</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 779302.	1.7	2
6603	Distinct soil bacterial patterns along narrow and broad elevational gradients in the grassland of Mt. Tianshan, China. <i>Scientific Reports</i> , 2022, 12, 136.	1.6	2
6604	Organic Fertilizers Shape Soil Microbial Communities and Increase Soil Amino Acid Metabolites Content in a Blueberry Orchard. <i>Microbial Ecology</i> , 2023, 85, 232-246.	1.4	17
6605	Environmental DNA metabarcoding reveals comparable responses to agricultural stressors on different trophic levels of a freshwater community. <i>Molecular Ecology</i> , 2022, 31, 1430-1443.	2.0	5
6606	Interaction of Gut Microbiota and Brain Function in Patients With Chronic Insomnia: A Regional Homogeneity Study. <i>Frontiers in Neuroscience</i> , 2021, 15, 804843.	1.4	13
6607	Comparative Study of <i>Bacillus amyloliquefaciens</i> X030 on the Intestinal Flora and Antibacterial Activity Against <i>Aeromonas</i> of Grass Carp. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 815436.	1.8	5
6608	Seasonal variations in the composition and functional profiles of gut microbiota reflect dietary changes in plateau pikas. <i>Integrative Zoology</i> , 2022, 17, 379-395.	1.3	30
6609	Berberine Relieves Metabolic Syndrome in Mice by Inhibiting Liver Inflammation Caused by a High-Fat Diet and Potential Association With Gut Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 752512.	1.5	16
6610	Metagenomic Comparisons between Soft and Hard Feces of Plateau Pikas (<i>Ochotona curzoniae</i>). <i>Animals</i> , 2022, 12, 149.	1.0	1

#	ARTICLE	IF	CITATIONS
6611	Synergistic effects of 3-nitrooxypropanol with fumarate in the regulation of propionate formation and methanogenesis in dairy cows in vitro. <i>Applied and Environmental Microbiology</i> , 2022, , AEM0190821.	1.4	5
6612	Evaluation of Bacterial Diversity and Evolutionary Dynamics of Gut <i>Bifidobacterium longum</i> Isolates Obtained from Older Individuals in Hubei Province, China. <i>Microbiology Spectrum</i> , 2022, , e0144221.	1.2	0
6613	Gastrointestinal Tract and Dietary Fiber Driven Alterations of Gut Microbiota and Metabolites in Durco × Bamei Crossbred Pigs. <i>Frontiers in Nutrition</i> , 2021, 8, 806646.	1.6	12
6614	Specific Rhizobacteria Responsible in the Rhizosphere System of <i>Kengyilia hirsuta</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 785971.	1.7	4
6615	Microbial mediators of plant community response to long-term N and P fertilization: Evidence of a role of plant responsiveness to mycorrhizal fungi. <i>Global Change Biology</i> , 2022, 28, 2721-2735.	4.2	12
6616	Cell-free DNA profiling informs all major complications of hematopoietic cell transplantation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	16
6617	Slope aspect determines the abundance and composition of nitrogen-cycling microbial communities in an alpine ecosystem. <i>Environmental Microbiology</i> , 2022, 24, 3598-3611.	1.8	6
6618	Plasma Lipid Profile and Intestinal Microflora in Pregnancy Women With Hypothyroidism and Their Correlation With Pregnancy Outcomes. <i>Frontiers in Endocrinology</i> , 2021, 12, 792536.	1.5	8
6619	Functional convergence of Yunnan snub-nosed monkey and bamboo-eating panda gut microbiomes revealing the driving by dietary flexibility on mammal gut microbiome. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 685-699.	1.9	13
6620	Comparative analysis of gut microbial composition and potential functions in captive forest and alpine musk deer. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 1325-1339.	1.7	15
6621	Organic matter and metal loadings influence the spatial gradient of the benthic bacterial community in a temperate estuary. <i>Marine and Freshwater Research</i> , 2022, 73, 428-440.	0.7	5
6622	Systematic decomposition of sequence determinants governing CRISPR/Cas9 specificity. <i>Nature Communications</i> , 2022, 13, 474.	5.8	23
6623	Genetic Influence on Frequencies of Myeloid-Derived Cell Subpopulations in Mouse. <i>Frontiers in Immunology</i> , 2021, 12, 760881.	2.2	3
6624	Growth performance, digestibility, blood metabolites, ruminal fermentation, and bacterial communities in response to the inclusion of gallic acid in the starter feed of preweaning dairy calves. <i>Journal of Dairy Science</i> , 2022, 105, 3078-3089.	1.4	11
6625	Long-term dechlorination of cis-DCE to ethene with co-immobilized <i>Dehalococcoides mccartyi</i> BAV1 and <i>Clostridium butyricum</i> in silica gel system. <i>Journal of Hazardous Materials</i> , 2022, 430, 128355.	6.5	6
6626	Variation of the Vaginal Microbiome During and After Pregnancy in Chinese Women. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 322-333.	3.0	15
6627	Exploring of seasonal dynamics of microbial community in multispecies fermentation of Shanxi mature vinegar. <i>Journal of Bioscience and Bioengineering</i> , 2022, 133, 375-381.	1.1	15
6628	Mitochondrial Cytochrome Oxidase Subunit 1: A Promising Molecular Marker for Species Identification in Foraminifera. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	9

#	ARTICLE	IF	CITATIONS
6629	Gene expression plasticity and frontloading promote thermotolerance in Pocillopora corals. , 0, 2, .		9
6630	An invasive Haemophilus influenzae serotype b infection in an Anglo-Saxon plague victim. Genome Biology, 2022, 23, 22.	3.8	13
6631	Phosphorus Limitation of Trees Influences Forest Soil Fungal Diversity in China. Forests, 2022, 13, 223.	0.9	11
6632	New Insight Into the Interspecies Shift of Anammox Bacteria Ca. "Brocadia" and Ca. "Jettenia" in Reactors Fed With Formate and Folate. Frontiers in Microbiology, 2021, 12, 802201.	1.5	13
6633	Stratification patterns of anammox granular sludge bed: Linking particle size distribution to microbial activity and community. Environmental Research, 2022, 210, 112763.	3.7	8
6634	Dietary rhamnogalacturonan-rich extracts of molokhia ameliorate high fat diet-induced obesity and gut dysbiosis. Journal of Nutritional Biochemistry, 2022, 103, 108954.	1.9	5
6635	Use of aqueous ozone rinsing to improve the disinfection efficacy and shorten the processing time of ultrasound-assisted washing of fresh produce. Ultrasonics Sonochemistry, 2022, 83, 105931.	3.8	14
6636	Spatio-temporal variation of bacterioplankton community structure in the Pearl River: impacts of artificial fishery habitat and physicochemical factors. BMC Ecology and Evolution, 2022, 22, 10.	0.7	0
6637	Characteristics of diurnal and seasonal changes in fish detection patterns using environmental DNA metabarcoding in a mountain stream. Limnologica, 2022, 93, 125955.	0.7	1
6638	Contrasting successional responses of soil bacteria and fungi to post-logging burn severity. Forest Ecology and Management, 2022, 508, 120059.	1.4	19
6639	Identification of core microbiota in the fermented grains of a Chinese strong-flavor liquor from Sichuan. LWT - Food Science and Technology, 2022, 158, 113140.	2.5	19
6640	When microclimates meet soil microbes: Temperature controls soil microbial diversity along an elevational gradient in subtropical forests. Soil Biology and Biochemistry, 2022, 166, 108566.	4.2	27
6641	Unraveling ecological risk of As/Sb and other metal(loid)s and fungal community responses in As/Sb smelting-intensive zone: A typical case study of Southwest China. Journal of Cleaner Production, 2022, 338, 130525.	4.6	5
6642	Cottonseed protein concentrate as fishmeal alternative for largemouth bass (Micropterus salmoides) supplemented a yeast-based paraprobiotic: Effects on growth performance, gut health and microbiome. Aquaculture, 2022, 551, 737898.	1.7	27
6643	Dynamic evolution and correlation between microorganisms and metabolites during manufacturing process and storage of Pu-erh tea. LWT - Food Science and Technology, 2022, 158, 113128.	2.5	18
6644	Jianpi Huayu Decoction enhances the effect of sorafenib and alleviates adverse events in hepatocellular carcinoma by remodeling the gut microbiota. Pharmacological Research Modern Chinese Medicine, 2022, 2, 100057.	0.5	0
6645	Unravelling biogeochemical drivers of methylmercury production in an Arctic fen soil and a bog soil. Environmental Pollution, 2022, 299, 118878.	3.7	8
6646	Reductive soil disinfestation with biochar amendment modified microbial community composition in soils under plastic greenhouse vegetable production. Soil and Tillage Research, 2022, 218, 105323.	2.6	16

#	ARTICLE	IF	CITATIONS
6647	Effects of replacing fish meal with corn gluten meal on growth performance, intestinal microbiota, mTOR pathway and immune response of abalone <i>Haliotis discus hannai</i> . <i>Aquaculture Reports</i> , 2022, 23, 101007.	0.7	10
6648	Hydrolysed fish protein powder is better at the growth performance, hepatopancreas and intestinal development of Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture Reports</i> , 2022, 23, 101025.	0.7	7
6649	Evaluating the flavor and divergent bacterial communities in corn-based zha-chili. <i>Food Bioscience</i> , 2022, 46, 101563.	2.0	8
6650	Biogeographic patterns of soil microbe communities in the deserts of the Hexi Corridor, northern China. <i>Catena</i> , 2022, 211, 106026.	2.2	14
6651	Influence of reductive soil disinfestation on the chemical and microbial characteristics of a greenhouse soil infested with <i>Fusarium oxysporum</i> . <i>Physiological and Molecular Plant Pathology</i> , 2022, 118, 101805.	1.3	9
6652	How do environmentally friendly antifouling alkaloids affect marine fouling microbial communities?. <i>Science of the Total Environment</i> , 2022, 820, 152910.	3.9	4
6653	Long-term fertilization lowers the alkaline phosphatase activity by impacting the phoD-harboring bacterial community in rice-winter wheat rotation system. <i>Science of the Total Environment</i> , 2022, 821, 153406.	3.9	15
6654	The effect of phosphate mining activities on rhizosphere bacterial communities of surrounding vegetables and crops. <i>Science of the Total Environment</i> , 2022, 821, 153479.	3.9	30
6655	Vegetation restoration facilitates belowground microbial network complexity and recalcitrant soil organic carbon storage in southwest China karst region. <i>Science of the Total Environment</i> , 2022, 820, 153137.	3.9	66
6656	Assessing synergistic effects of crop rotation pattern, tillage practice, and rhizosphere effect on soil bacterial community structure and assembly in China's Loess Plateau farmlands. <i>Applied Soil Ecology</i> , 2022, 174, 104411.	2.1	9
6657	Soil microorganisms facilitated the electrode-driven trichloroethene dechlorination to ethene by <i>Dehalococcoides</i> species in a bioelectrochemical system. <i>Environmental Research</i> , 2022, 209, 112801.	3.7	18
6658	DNA metabarcoding of fungal communities in Heshouwu (<i>Polygonum multiflorum</i> Thunb.). <i>Food Control</i> , 2022, 136, 108850.	2.8	5
6659	Determinants of heritable gene silencing for KRAB-dCas9- Δ DNMT3 and Ezh2-dCas9- Δ DNMT3 hit-and-run epigenome editing. <i>Nucleic Acids Research</i> , 2022, 50, 3239-3253.	6.5	17
6660	Single-cell genome-wide concurrent haplotyping and copy-number profiling through genotyping-by-sequencing. <i>Nucleic Acids Research</i> , 2022, 50, e63-e63.	6.5	17
6661	<i>Salsipaludibacter albus</i> gen. nov., sp. nov., a novel actinobacterial strain isolate from a Portuguese solar saltern and proposal of <i>Salsipaludibacteraceae</i> fam. nov. and <i>Salsipaludibacterales</i> ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
6662	Hydrology driven vertical distribution of prokaryotes and methane functional groups in a subtropical peatland. <i>Journal of Hydrology</i> , 2022, 608, 127592.	2.3	3
6664	A comparative study of bacterial diversity based on effects of three different shade shed types in the rhizosphere of <i>Panax quiquefolium</i> L.. <i>PeerJ</i> , 2022, 10, e12807.	0.9	2
6665	Habitats Show More Impacts Than Host Species in Shaping Gut Microbiota of Sympatric Rodent Species in a Fragmented Forest. <i>Frontiers in Microbiology</i> , 2022, 13, 811990.	1.5	4

#	ARTICLE	IF	CITATIONS
6666	The potential of soluble CD14 in discriminating nonalcoholic steatohepatitis from nonalcoholic fatty liver disease. <i>Hepatology Research</i> , 2022, 52, 508-521.	1.8	1
6667	Are microbes and metabolites influencing the parental consumption of nestlings's faeces in grey-backed shrikes?. <i>Environmental Epigenetics</i> , 0, , .	0.9	1
6668	Seasonal airway microbiome and transcriptome interactions promote childhood asthma exacerbations. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 204-213.	1.5	31
6669	Dynamics of Microbial Communities in Phototrophic Polyhydroxyalkanoate Accumulating Cultures. <i>Microorganisms</i> , 2022, 10, 351.	1.6	6
6670	Chemical fertilizer reduction with organic material amendments alters co-occurrence network patterns of bacterium-fungus-nematode communities under the wheat-maize rotation regime. <i>Plant and Soil</i> , 2022, 473, 605-623.	1.8	14
6671	Alteration of Porcine Intestinal Microbiota in Response to Dietary Manno-Oligosaccharide Supplementation. <i>Frontiers in Microbiology</i> , 2021, 12, 811272.	1.5	3
6672	Microbial diversity and community structure in deep-sea sediments of South Indian Ocean. <i>Environmental Science and Pollution Research</i> , 2022, 29, 45793-45807.	2.7	7
6673	Ileal Microbiota Alters the Immunity Statuses to Affect Body Weight in Muscovy Ducks. <i>Frontiers in Immunology</i> , 2022, 13, 844102.	2.2	3
6674	Effects of Cellulase and <i>Lactobacillus plantarum</i> on Fermentation Quality, Chemical Composition, and Microbial Community of Mixed Silage of Whole-Plant Corn and Peanut Vines. <i>Applied Biochemistry and Biotechnology</i> , 2022, 194, 2465-2480.	1.4	20
6675	Directed mutational scanning reveals a balance between acidic and hydrophobic residues in strong human activation domains. <i>Cell Systems</i> , 2022, 13, 334-345.e5.	2.9	58
6676	The landscape of promoter-centred RNA-DNA interactions in rice. <i>Nature Plants</i> , 2022, 8, 157-170.	4.7	15
6677	Acidic amelioration of soil amendments improves soil health by impacting rhizosphere microbial assemblies. <i>Soil Biology and Biochemistry</i> , 2022, 167, 108599.	4.2	26
6678	<i>Aspergillus</i> -Derived Cellulase Preparation Exhibits Prebiotic-like Effects on Gut Microbiota in Rats. <i>Fermentation</i> , 2022, 8, 71.	1.4	4
6679	Spatial and interspecific differences in coral-associated bacterial diversity in Hainan, China. <i>Marine Pollution Bulletin</i> , 2022, 175, 113321.	2.3	7
6680	Effects of dietary berberine hydrochloride inclusion on growth, antioxidant capacity, glucose metabolism and intestinal microbiome of largemouth bass (<i>Micropterus salmoides</i>). <i>Aquaculture</i> , 2022, 552, 738023.	1.7	21
6682	Soil properties across a hydrological gradient in saladas from northeast Spain: what are the implications for soil carbon stocks, CO ₂ efflux and microbial communities in a warming world?. <i>Wetlands Ecology and Management</i> , 0, , 1.	0.7	1
6683	Draft Genome Sequences of 77 Endemic Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Strains of SIT41 (TUR) Spoligotype from Bulgaria. <i>Microbiology Resource Announcements</i> , 2022, , e0111121.	0.3	0
6684	Alterations in the gut microbiome and metabolome profiles of septic rats treated with aminophylline. <i>Journal of Translational Medicine</i> , 2022, 20, 69.	1.8	5

#	ARTICLE	IF	CITATIONS
6685	Seaweeds influence oyster microbiota and disease susceptibility. <i>Journal of Animal Ecology</i> , 2022, 91, 805-818.	1.3	4
6686	Distinctive pattern and mechanism of precipitation changes affecting soil microbial assemblages in the Eurasian steppe. <i>IScience</i> , 2022, 25, 103893.	1.9	4
6687	The Epidermal Microbiome Within an Aggregation of Leopard Sharks (<i>Triakis semifasciata</i>) Has Taxonomic Flexibility with Gene Functional Stability Across Three Time-points. <i>Microbial Ecology</i> , 2023, 85, 747-764.	1.4	6
6688	Comparison of Rumen Fermentation Parameters and Microbiota of Yaks From Different Altitude Regions in Tibet, China. <i>Frontiers in Microbiology</i> , 2021, 12, 807512.	1.5	11
6689	Century-Long Homogenization of Algal Communities Is Accelerated by Nutrient Enrichment and Climate Warming in Lakes and Reservoirs of the North Temperate Zone. <i>Environmental Science & Technology</i> , 2022, 56, 3780-3790.	4.6	18
6690	Biochar Application Alleviated Rice Salt Stress via Modifying Soil Properties and Regulating Soil Bacterial Abundance and Community Structure. <i>Agronomy</i> , 2022, 12, 409.	1.3	25
6692	Inoculation of Barley (<i>Hordeum vulgare</i>) with the Endophyte <i>Epichloa bromicola</i> Affects Plant Growth, and the Microbial Community in Roots and Rhizosphere Soil. <i>Journal of Fungi (Basel)</i> , 2022, 8, 1061.	1.6	10
6693	<i>Lactiplantibacillus plantarum</i> Y15 alleviate type 2 diabetes in mice via modulating gut microbiota and regulating NF- κ B and insulin signaling pathway. <i>Brazilian Journal of Microbiology</i> , 2022, 53, 935-945.	0.8	10
6694	Profiling the Bladder Microbiota in Patients With Bladder Cancer. <i>Frontiers in Microbiology</i> , 2021, 12, 718776.	1.5	13
6695	Influence of Geographical Location on Maternal-Infant Microbiota: Study in Two Populations From Asia and Europe. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663513.	1.8	6
6696	Impacts of Continuous Cropping on Fungal Communities in the Rhizosphere Soil of Tibetan Barley. <i>Frontiers in Microbiology</i> , 2022, 13, 755720.	1.5	4
6698	Omics Analyses of Intestinal Microbiota and Hypothalamus Clock Genes in Circadian Disturbance Model Mice Fed with Green Tea Polyphenols. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 1890-1901.	2.4	6
6699	Post-termination Effects of Cover Crop Monocultures and Mixtures on Soil Inorganic Nitrogen and Microbial Communities on Two Organic Farms in Illinois. <i>Frontiers in Soil Science</i> , 2022, 2, .	0.8	3
6700	Response of microbial community diversity and subsoil properties to cow manure amendment in mollisols. <i>Archives of Agronomy and Soil Science</i> , 2023, 69, 785-802.	1.3	1
6701	Embryonic Exposure to Tryptophan Yields Bullying Victimization via Reprogramming the Microbiota-Gut-Brain Axis in a Chicken Model. <i>Nutrients</i> , 2022, 14, 661.	1.7	7
6704	Effects of Replacing Fish Meal with Distillers' Dried Grains with Solubles on the Growth Performance and Gut Microbiota in Juvenile Pacific Whiteleg Shrimp <i>Litopenaeus vannamei</i> . <i>North American Journal of Aquaculture</i> , 2022, 84, 191-205.	0.7	9
6705	Different spatiotemporal dynamics, ecological drivers and assembly processes of bacterial, archaeal and fungal communities in brackish-saline groundwater. <i>Water Research</i> , 2022, 214, 118193.	5.3	15
6706	Resistant starch type 2 and whole grain maize flours enrich different intestinal bacteria and metatranscriptomes. <i>Journal of Functional Foods</i> , 2022, 90, 104982.	1.6	4

#	ARTICLE	IF	CITATIONS
6707	Decreased levels and ecological risks of disinfection by-product chloroform in a field-scale artificial groundwater recharge project by colloid supplement. <i>Environment International</i> , 2022, 161, 107130.	4.8	2
6708	Inhibition of gut microbial β -glucuronidase effectively prevents carcinogen-induced microbial dysbiosis and intestinal tumorigenesis. <i>Pharmacological Research</i> , 2022, 177, 106115.	3.1	10
6709	The introduction of <i>Phoebe bournei</i> into <i>Cunninghamia lanceolata</i> monoculture plantations increased microbial network complexity and shifted keystone taxa. <i>Forest Ecology and Management</i> , 2022, 509, 120072.	1.4	17
6710	Polycyclic aromatic hydrocarbons at subcritical levels as novel indicators of microbial adaptation in a pre-industrial river delta. <i>Chemosphere</i> , 2022, 295, 133858.	4.2	7
6711	The Relationship Between Gut Microbiome Features and Chemotherapy Response in Gastrointestinal Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 781697.	1.3	13
6712	Green manure incorporation accelerates enzyme activity, plant growth, and changes in the fungal community of soil. <i>Archives of Microbiology</i> , 2022, 204, 7.	1.0	17
6713	Non-syntrophic methanogenic hydrocarbon degradation by an archaeal species. <i>Nature</i> , 2022, 601, 257-262.	13.7	83
6715	Identifying proximal RNA interactions from cDNA-encoded crosslinks with ShapeJumper. <i>PLoS Computational Biology</i> , 2021, 17, e1009632.	1.5	3
6716	Maize (<i>Zea mays</i> L.) Seedlings Rhizosphere Microbial Community as Responded to Acidic Biochar Amendment Under Saline Conditions. <i>Frontiers in Microbiology</i> , 2021, 12, 789235.	1.5	17
6717	Evaluation of Antibiotic Resistance of <i>Salmonella</i> Serotypes and Whole-Genome Sequencing of Multiresistant Strains Isolated from Food Products in Russia. <i>Antibiotics</i> , 2022, 11, 1.	1.5	17
6718	Alterations in gut bacterial and fungal microbiomes are associated with bacterial Keratitis, an inflammatory disease of the human eye. <i>Journal of Biosciences</i> , 2018, 43, 835-856.	0.5	17
6719	Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of prakriti. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	6
6720	Effect of Coexistent Endosulfan on the Biodegradation of Lindane by <i>Novosphingobium Barchaimii</i> and Microbial Enrichment Cultures. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6721	Crops Rotation Reduce the Abundance and Occurrence of Microbial Antibiotic Resistances in Wheat and Tomato Rhizosphere Soil Microbiome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6722	Infection with White Spot Syndrome Virus Affects the Microbiota in the Stomachs and Intestines of Kuruma Shrimp. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6723	Gut-Thyroid axis: How gut microbial dysbiosis associated with euthyroid thyroid cancer. <i>Journal of Cancer</i> , 2022, 13, 2014-2028.	1.2	13
6724	Facile Affinity Maturation of Single-Domain Antibodies Using Next-Generation DNA Sequencing. <i>Methods in Molecular Biology</i> , 2022, 2446, 245-268.	0.4	3
6726	Impact of Norway Spruce Pre-Degradation Stages Induced by <i>G. Trabeum</i> on Fungal and Bacterial Communities. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
6727	High Nitrite-Nitrogen Stress Intensity Drives Nitrite Anaerobic Oxidation to Nitrate and Inhibits Aceticlastic Methanogenesis. SSRN Electronic Journal, 0, , .	0.4	0
6728	Effects of the Microbial Action Network in the Humification of Industrial Composting of Chicken Manure. SSRN Electronic Journal, 0, , .	0.4	0
6729	Potassium-Rich Mining Waste Addition Can Shorten the Composting Period by Increasing the Abundance of Thermophilic Bacteria at High Temperature Period. SSRN Electronic Journal, 0, , .	0.4	0
6730	Nasopharyngeal microbial profiles associated with the risk of airway allergies in early childhood. Journal of Microbiology, Immunology and Infection, 2022, 55, 777-785.	1.5	5
6731	Amplicon sequencing reveals the arbuscular mycorrhizal fungal community composition in <i>Cryptomeria japonica</i> at one local site. Journal of Forest Research, 2022, 27, 399-407.	0.7	4
6732	Dynamic changes of rhizosphere soil bacterial community and nutrients in cadmium polluted soils with soybean-corn intercropping. BMC Microbiology, 2022, 22, 57.	1.3	16
6733	Different Assembly Patterns of Planktonic and Sedimentary Bacterial Community in a Few Connected Eutrophic Lakes. Water (Switzerland), 2022, 14, 723.	1.2	6
6734	The Role of Intestinal Microbiota in Regulating the Metabolism of Bile Acids Is Conserved Across Vertebrates. Frontiers in Microbiology, 2022, 13, 824611.	1.5	3
6735	Effects of Dietary Astragalus Polysaccharide Supplementation on the Th17/Treg Balance and the Gut Microbiota of Broiler Chickens Challenged With Necrotic Enteritis. Frontiers in Immunology, 2022, 13, 781934.	2.2	28
6736	Contrasting assembly mechanisms and drivers of soil rare and abundant bacterial communities in 22-year continuous and non-continuous cropping systems. Scientific Reports, 2022, 12, 3264.	1.6	10
6738	Soil fungal communities affect the chemical quality of flue-cured tobacco leaves in Bijie, Southwest China. Scientific Reports, 2022, 12, 2815.	1.6	12
6740	Differential Effect of Dietary Fibers in Intestinal Health of Growing Pigs: Outcomes in the Gut Microbiota and Immune-Related Indexes. Frontiers in Microbiology, 2022, 13, 843045.	1.5	5
6741	Receptiveness of soil bacterial diversity in relation to soil nutrient transformation and canopy growth in Chinese fir monoculture influenced by varying stand density. Trees - Structure and Function, 2022, 36, 1149-1160.	0.9	7
6742	Dominant tree mycorrhizal associations affect soil nitrogen transformation rates by mediating microbial abundances in a temperate forest. Biogeochemistry, 2022, 158, 405-421.	1.7	11
6743	The gut microbiota of bats confers tolerance to influenza virus (H1N1) infection in mice. Transboundary and Emerging Diseases, 2022, 69, .	1.3	7
6744	The Phylosymbiosis Pattern Between the Fig Wasps of the Same Genus and Their Associated Microbiota. Frontiers in Microbiology, 2021, 12, 800190.	1.5	1
6745	Captivity Shifts Gut Microbiota Communities in White-Lipped Deer (<i>Cervus albirostris</i>). Animals, 2022, 12, 431.	1.0	19
6746	Age-Associated Changes of Nasal Bacterial Microbiome in Patients With Chronic Rhinosinusitis. Frontiers in Cellular and Infection Microbiology, 2022, 12, 786481.	1.8	5

#	ARTICLE	IF	CITATIONS
6747	Airborne bacteria associated with particulate matter from a highly urbanised metropolis: A potential risk to the population's health. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 1.	3.3	1
6748	Amplicon sequencing of <i>Fusarium</i> translation elongation factor 1 \pm reveals that soil communities of <i>Fusarium</i> species are resilient to disturbances caused by crop and tillage practices. <i>Phytobiomes Journal</i> , 0, , .	1.4	1
6749	Combined Bioremediation of Bensulfuron-Methyl Contaminated Soils With Arbuscular Mycorrhizal Fungus and <i>Hansschlegelia zihuaiae</i> S113. <i>Frontiers in Microbiology</i> , 2022, 13, 843525.	1.5	10
6750	Effect and Mechanism of Titanium Nanomaterials on Microbial Community Structure and Function in Sequencing Batch Reactor. <i>ACS ES&T Water</i> , 2022, 2, 395-404.	2.3	2
6751	Sequence determinants of human gene regulatory elements. <i>Nature Genetics</i> , 2022, 54, 283-294.	9.4	87
6752	Comparative Analysis of Microbial Community Diversity and Dynamics on Diseased Tubers During Potato Storage in Different Regions of Qinghai China. <i>Frontiers in Genetics</i> , 2022, 13, 818940.	1.1	3
6753	Interactions Between Phenolic Acids and Microorganisms in Rhizospheric Soil From Continuous Cropping of <i>Panax notoginseng</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 791603.	1.5	30
6754	Genome Analysis of the Broad Host Range Necrotroph <i>Nalanthamala psidii</i> Highlights Genes Associated With Virulence. <i>Frontiers in Plant Science</i> , 2022, 13, 811152.	1.7	1
6756	Effects of Replacing Fishmeal by Raw or <i>Lactobacillus acidophilus</i> -Fermented Soybean Meal on Growth, Intestinal Digestive and Immune-Related Enzyme Activities, Morphology, and Microbiota in Turbot (<i>Scophthalmus maximus</i> L.). <i>Aquaculture Nutrition</i> , 2022, 2022, 1-13.	1.1	7
6757	Short-Term Snow Removal Alters Fungal but Not Bacterial Beta Diversity and Structure during the Spring Snowmelt Period in a Meadow Steppe of China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 234.	1.5	5
6758	Characterization of the fecal microbiota in gastrointestinal cancer patients and healthy people. <i>Clinical and Translational Oncology</i> , 2022, 24, 1134-1147.	1.2	9
6759	A Closer Examination of the "Abundant-Center" for Ectomycorrhizal Fungal Community Associated With <i>Picea crassifolia</i> in China. <i>Frontiers in Plant Science</i> , 2022, 13, 759801.	1.7	2
6760	Sugarcane-Peanut Intercropping System Enhances Bacteria Abundance, Diversity, and Sugarcane Parameters in Rhizospheric and Bulk Soils. <i>Frontiers in Microbiology</i> , 2021, 12, 815129.	1.5	20
6761	Microbiome Resilience and Health Implications for People in Half-Year Travel. <i>Frontiers in Immunology</i> , 2022, 13, 848994.	2.2	2
6762	Effect of g-C3N4 on biodiversity and structure of bacterial community in sediment of Xiangjiang River under tetracycline pressure. <i>Ecotoxicology</i> , 2022, 31, 503-515.	1.1	3
6763	Distinct gut microbiota profiles of Asian honey bee (<i>Apis cerana</i>) foragers. <i>Archives of Microbiology</i> , 2022, 204, 187.	1.0	2
6764	<i>Lycium barbarum</i> Polysaccharides as Antibiotic Substitutes Improve Growth Performance, Serum Immunity, Antioxidant Status, and Intestinal Health for Weaned Piglets. <i>Frontiers in Microbiology</i> , 2021, 12, 819993.	1.5	6
6766	Bacteria Associated With <i>Phaeocystis globosa</i> and Their Influence on Colony Formation. <i>Frontiers in Microbiology</i> , 2022, 13, 826602.	1.5	2

#	ARTICLE	IF	CITATIONS
6767	Multimiomics Reveals the Effect of Root Rot on Polygonati Rhizome and Identifies Pathogens and Biocontrol Strain. <i>Microbiology Spectrum</i> , 2022, 10, e0238521.	1.2	16
6768	Integrated analysis of microbe-host interactions in Crohn's disease reveals potential mechanisms of microbial proteins on host gene expression. <i>iScience</i> , 2022, 25, 103963.	1.9	7
6769	<i>Bacillus</i> symbiont drives alterations in intestinal microbiota and circulating metabolites of lepidopteran host. <i>Environmental Microbiology</i> , 2022, 24, 4049-4064.	1.8	13
6770	Impact of Biochar on Rhizosphere Bacterial Diversity Restoration Following Chloropicrin Fumigation of Planted Soil. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 2126.	1.2	12
6771	Murine Model for Measuring Effects of Humanized-Dosing of Antibiotics on the Gut Microbiome. <i>Frontiers in Microbiology</i> , 2022, 13, 813849.	1.5	1
6772	Change of soil microorganism communities under saline-sodic land degradation on the Songnen Plain in northeast China. <i>Journal of Plant Nutrition and Soil Science</i> , 2022, 185, 297-307.	1.1	6
6773	Data Filtering Algorithm for DNA Metabarcoding Studies of Ecological Communities. <i>Russian Journal of Genetics</i> , 2022, 58, 223-234.	0.2	0
6774	Treatment of gouty arthritis is associated with restoring the gut microbiota and promoting the production of short-chain fatty acids. <i>Arthritis Research and Therapy</i> , 2022, 24, 51.	1.6	11
6775	Genomic variations and epigenomic landscape of the Medaka Inbred Kiyosu-Karlsruhe (MIKK) panel. <i>Genome Biology</i> , 2022, 23, 58.	3.8	5
6776	The Crosstalk Between Saliva Bacteria and Fungi in Early Childhood Caries. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 845738.	1.8	6
6777	Nonsurgical Periodontal Treatment Options and Their Impact on Subgingival Microbiota. <i>Journal of Clinical Medicine</i> , 2022, 11, 1187.	1.0	10
6778	Biogeographical and seasonal dynamics of the marine Roseobacter community and ecological links to DMSP-producing phytoplankton. <i>ISME Communications</i> , 2022, 2, .	1.7	6
6779	Analysis of B Cell Receptor Repertoires Reveals Key Signatures of the Systemic B Cell Response after SARS-CoV-2 Infection. <i>Journal of Virology</i> , 2022, 96, JVI0160021.	1.5	24
6780	Anticyclonic Eddy Driving Significant Changes in Prokaryotic and Eukaryotic Communities in the South China Sea. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	6
6781	Changes of Intestinal Microflora in Colorectal Cancer Patients after Surgical Resection and Chemotherapy. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-16.	0.7	10
6782	Insights Into the Species-Specific Microbiota of Greenideinae (Hemiptera: Aphididae) With Evidence of Phyllosymbiosis. <i>Frontiers in Microbiology</i> , 2022, 13, 828170.	1.5	3
6783	Isolation of rhizosheath and analysis of microbial community structure around roots of <i>Stipa grandis</i> . <i>Scientific Reports</i> , 2022, 12, 2707.	1.6	1
6784	The planting of licorice increased soil microbial diversity and affected the growth and development of apple trees. <i>Communications in Soil Science and Plant Analysis</i> , 2022, 53, 1113-1125.	0.6	3

#	ARTICLE	IF	CITATIONS
6785	Impacts of continuous and rotational cropping practices on soil chemical properties and microbial communities during peanut cultivation. <i>Scientific Reports</i> , 2022, 12, 2758.	1.6	19
6786	Effects of Sodium Hyaluronate Eye Drops With or Without Preservatives on Ocular Surface Bacterial Microbiota. <i>Frontiers in Medicine</i> , 2022, 9, 793565.	1.2	4
6787	Comparison of genetically modified insect-resistant maize and non-transgenic maize revealed changes in soil metabolomes but not in rhizosphere bacterial community. <i>GM Crops and Food</i> , 2022, 13, 1-14.	2.0	13
6788	Microbiome structure and response to watering in rhizosphere of <i>Nitrosalsola vermiculata</i> and surrounding bulk soil. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2022, 50, 12567.	0.5	1
6789	The Impact of Instant Coffee and Decaffeinated Coffee on the Gut Microbiota and Depression-Like Behaviors of Sleep-Deprived Rats. <i>Frontiers in Microbiology</i> , 2022, 13, 778512.	1.5	10
6790	Changes in root microbiome during wheat evolution. <i>BMC Microbiology</i> , 2022, 22, 64.	1.3	12
6791	High-Throughput Sequencing-Based Analysis of Rhizosphere and Diazotrophic Bacterial Diversity Among Wild Progenitor and Closely Related Species of Sugarcane (<i>Saccharum</i> spp. Inter-Specific) Tj ETQq0 0 0 rgBT.7Overlook 10 Tf 50	1.7	10
6792	Effects of Ambient Microbiota on the Gut Microbiota of <i>Macrobrachium rosenbergii</i> . <i>Water (Switzerland)</i> , 2022, 14, 658.	1.2	1
6793	Long-term high-fructose high-fat diet feeding elicits insulin resistance, exacerbates dyslipidemia and induces gut microbiota dysbiosis in WHHL rabbits. <i>PLoS ONE</i> , 2022, 17, e0264215.	1.1	12
6794	Combined use of Oxford Nanopore and Illumina sequencing yields insights into soybean structural variation biology. <i>BMC Biology</i> , 2022, 20, 53.	1.7	10
6795	<i>Bacillus Calmette-Guérin</i> Treatment Changes the Tumor Microenvironment of Non-Muscle-Invasive Bladder Cancer. <i>Frontiers in Oncology</i> , 2022, 12, 842182.	1.3	2
6796	Grazing by Tibetan Sheep Enhances Soil Bacterial and Fungal Diversity in Cold Season Pastures of Alpine Meadows on the Northern Qinghai-Tibetan Plateau. <i>Journal of Soil Science and Plant Nutrition</i> , 2022, 22, 2434-2456.	1.7	9
6797	Correlation Analysis of Vaginal Microbiome Changes and Bacterial Vaginosis Plus Vulvovaginal Candidiasis Mixed Vaginitis Prognosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 860589.	1.8	8
6798	Comparison studies of epiphytic microbial communities on four macroalgae and their rocky substrates. <i>Marine Pollution Bulletin</i> , 2022, 176, 113435.	2.3	6
6799	Analysis of human clinical and environmental <i>Leptospira</i> to elucidate the eco-epidemiology of leptospirosis in Yaeyama, subtropical Japan. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010234.	1.3	3
6800	Salivary microbiota analysis of patients with membranous nephropathy. <i>Molecular Medicine Reports</i> , 2022, 25, .	1.1	4
6801	Co-evolution of interacting proteins through non-contacting and non-specific mutations. <i>Nature Ecology and Evolution</i> , 2022, 6, 590-603.	3.4	23
6802	Successions of rare and abundant microbial subcommunities during fish carcass decomposition in a microcosm under the influence of variable factors. <i>FEMS Microbiology Letters</i> , 2022, 369, .	0.7	1

#	ARTICLE	IF	CITATIONS
6803	Adapting to Novel Environments Together: Evolutionary and Ecological Correlates of the Bacterial Microbiome of the World's Largest Cavefish Diversification (Cyprinidae, <i>Sinocyclocheilus</i>). <i>Frontiers in Microbiology</i> , 2022, 13, 823254.	1.5	4
6804	A Comprehensive Network Integrating Signature Microbes and Crucial Soil Properties During Early Biological Soil Crust Formation on Tropical Reef Islands. <i>Frontiers in Microbiology</i> , 2022, 13, 831710.	1.5	3
6805	Metabolomics and microbiome reveal potential root microbiota affecting the alkaloidal metabolome in <i>Aconitum vilmorinianum</i> Kom.. <i>BMC Microbiology</i> , 2022, 22, 70.	1.3	8
6806	Stronger Geographic Limitations Shape a Rapid Turnover and Potentially Highly Connected Network of Core Bacteria on Microplastics. <i>Microbial Ecology</i> , 2023, 85, 1179-1189.	1.4	1
6807	Mitochondrion-encoded circular RNAs are widespread and translatable in plants. <i>Plant Physiology</i> , 2022, 189, 1482-1500.	2.3	9
6808	Bioaugmentation of Anammox Activated Sludge with a Nitrifying Bacterial Community as a Way to Increase the Nitrogen Removal Efficiency. <i>Microbiology</i> , 2022, 91, 133-142.	0.5	4
6809	Vaginal <i>Atopobium</i> is Associated with Spontaneous Abortion in the First Trimester: a Prospective Cohort Study in China. <i>Microbiology Spectrum</i> , 2022, 10, e0203921.	1.2	7
6810	Effects of Four Antibiotics on the Diversity of the Intestinal Microbiota. <i>Microbiology Spectrum</i> , 2022, 10, e0190421.	1.2	25
6811	Microbial Community Structure and Ecological Networks during Simulation of Diatom Sinking. <i>Microorganisms</i> , 2022, 10, 639.	1.6	4
6813	HAM-ART: An optimised culture-free Hi-C metagenomics pipeline for tracking antimicrobial resistance genes in complex microbial communities. <i>PLoS Genetics</i> , 2022, 18, e1009776.	1.5	14
6814	Multi-Omics Characterization of Type 2 Diabetes Mellitus-Induced Cognitive Impairment in the db/db Mouse Model. <i>Molecules</i> , 2022, 27, 1904.	1.7	6
6815	Microbial Diversity and Community Dynamics in the Intestines of Broiler Chicken Raised in an Open-Sided House. , 0, , .		1
6816	Effects of Long-Term Enclosed Environment on Human Health Based on the Analysis of Salivary Microbiota and Cytokines. <i>Microbiology Spectrum</i> , 2022, 10, e0025422.	1.2	3
6817	Study on the Bacterial Communities of the Biofilms on Titanium, Aluminum, and Copper Alloys at 5,772 m Undersea in Yap Trench. <i>Frontiers in Microbiology</i> , 2022, 13, 831984.	1.5	2
6818	In vitro and in silico parameters for precise cgMLST typing of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2022, 23, 235.	1.2	7
6819	<i>Lactobacillus plantarum</i> Lp3a improves functional constipation: evidence from a human randomized clinical trial and animal model. <i>Annals of Translational Medicine</i> , 2022, 10, 316-316.	0.7	7
6820	Distribution and Difference of Gastrointestinal Flora in Sheep with Different Body Mass Index. <i>Animals</i> , 2022, 12, 880.	1.0	6
6821	Differing Roles of Bacterial and Fungal Communities in Cotton Fields by Growth Stage. <i>Agronomy</i> , 2022, 12, 657.	1.3	2

#	ARTICLE	IF	CITATIONS
6822	Diversity and Potential Function of Prokaryotic and Eukaryotic Communities from Different Mangrove Sediments. <i>Sustainability</i> , 2022, 14, 3333.	1.6	8
6823	Intra- and interpopulation transposition of mobile genetic elements driven by antibiotic selection. <i>Nature Ecology and Evolution</i> , 2022, 6, 555-564.	3.4	37
6824	Diversity and Evolution of Pigment Types in Marine <i>Synechococcus</i> Cyanobacteria. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	15
6825	Peanut and cotton intercropping increases productivity and economic returns through regulating plant nutrient accumulation and soil microbial communities. <i>BMC Plant Biology</i> , 2022, 22, 121.	1.6	14
6826	Phosphorus Shapes Soil Microbial Community Composition and Network Properties During Grassland Expansion Into Shrubs in Tibetan Dry Valleys. <i>Frontiers in Plant Science</i> , 2022, 13, 848691.	1.7	6
6827	Disparity of Gut Microbiota Composition Among Elite Athletes and Young Adults With Different Physical Activity Independent of Dietary Status: A Matching Study. <i>Frontiers in Nutrition</i> , 2022, 9, 843076.	1.6	8
6828	Multi-Omics Analyses Characterize the Gut Microbiome and Metabolome Signatures of Soldiers Under Sustained Military Training. <i>Frontiers in Microbiology</i> , 2022, 13, 827071.	1.5	2
6829	Comparative study of gut microbiota from decomposer fauna in household composter using metataxonomic approach. <i>Archives of Microbiology</i> , 2022, 204, 210.	1.0	6
6830	Observation of the Gut Microbiota Profile in BALB/c Mice Induced by <i>Plasmodium yoelii</i> 17XL Infection. <i>Frontiers in Microbiology</i> , 2022, 13, 858897.	1.5	6
6831	Responses of Phyllosphere Microbiome to Ozone Stress: Abundance, Community Compositions and Functions. <i>Microorganisms</i> , 2022, 10, 680.	1.6	11
6832	Unique bacterial communities associated with components of an artificial aquarium ecosystem and their possible contributions to nutrient cycling in this microecosystem. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 72.	1.7	2
6833	Diversity Analysis of Bacterial and Function Prediction in Hurunge From Mongolia. <i>Frontiers in Nutrition</i> , 2022, 9, 835123.	1.6	7
6834	Characterization of the First Cultured Representative of <i>Candidatus</i> Thermofonsia Clade 2 within <i>Chloroflexi</i> Reveals Its Phototrophic Lifestyle. <i>MBio</i> , 2022, 13, e0028722.	1.8	8
6835	Biodiversity and Biogeography of Abundant and Rare Microbial Assemblages in the Western Subtropical Pacific Ocean. <i>Frontiers in Microbiology</i> , 2022, 13, 839562.	1.5	6
6836	Effect of rapeseed straw-derived biochar on soil bacterial community structure at tillering stage of <i>Oryza Sativa</i> . <i>Canadian Journal of Microbiology</i> , 2022, , .	0.8	1
6837	Postnatal intestinal mucosa and gut microbial composition develop hand in hand: A mouse study. <i>Biomedical Journal</i> , 2023, 46, 100519.	1.4	13
6838	Caudovirales bacteriophages are associated with improved executive function and memory in flies, mice, and humans. <i>Cell Host and Microbe</i> , 2022, 30, 340-356.e8.	5.1	50
6839	Insights into gut microbiota communities of <i>Poecilobdella manillensis</i> , a prevalent Asian medicinal leech. <i>Journal of Applied Microbiology</i> , 2022, 133, 1402-1413.	1.4	1

#	ARTICLE	IF	CITATIONS
6840	Effects of Growth Stage and Rearing Pattern on Pig Gut Microbiota. <i>Current Microbiology</i> , 2022, 79, 136.	1.0	8
6841	Comparative Analysis on Rhizosphere Soil and Endophytic Microbial Communities of Two Cultivars of <i>Cyperus esculentus</i> L. Var. <i>Sativus</i> . <i>Journal of Soil Science and Plant Nutrition</i> , 2022, 22, 2156-2168.	1.7	4
6842	Comparative microbiome analysis of <i>Diaphorina citri</i> and its associated parasitoids <i>Tamarixia radiata</i> and <i>Diaphorencyrtus aligarhensis</i> reveals <i>Wolbachia</i> as a dominant endosymbiont. <i>Environmental Microbiology</i> , 2022, 24, 1638-1652.	1.8	6
6843	High Abundance of Thaumarchaeota Found in Deep Metamorphic Subsurface in Eastern China. <i>Microorganisms</i> , 2022, 10, 542.	1.6	2
6844	Specific patterns and drivers of the bacterial communities in the sediment of two typical integrated multitrophic aquaculture systems. <i>Aquaculture International</i> , 0, , .	1.1	2
6845	Comparison of the composition and function of gut microbes between adult and juvenile <i>Cipangopaludina chinensis</i> in the rice snail system. <i>PeerJ</i> , 2022, 10, e13042.	0.9	6
6846	Stitchr: stitching coding TCR nucleotide sequences from V/J/CDR3 information. <i>Nucleic Acids Research</i> , 2022, 50, e68-e68.	6.5	8
6848	Comparison of Cecal Microbiota and Performance Indices Between Lean-Type and Fatty-Type Pekin Ducks. <i>Frontiers in Microbiology</i> , 2022, 13, 820569.	1.5	6
6849	Identifying large-scale recombination and capsular switching events in <i>Streptococcus agalactiae</i> strains causing disease in adults in the UK between 2014 and 2015. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
6850	Homogeneous selection is not always important in bacterial community in the eutrophic enclosed bay. <i>Ecological Processes</i> , 2022, 11, .	1.6	1
6851	Rumen Microbiome and Metabolome of High and Low Residual Feed Intake Angus Heifers. <i>Frontiers in Veterinary Science</i> , 2022, 9, 812861.	0.9	15
6852	Gut Microbial Characterization of Melon-Headed Whales (<i>Peponocephala electra</i>) Stranded in China. <i>Microorganisms</i> , 2022, 10, 572.	1.6	6
6853	Alleviating Soil Acidification Could Increase Disease Suppression of Bacterial Wilt by Recruiting Potentially Beneficial Rhizobacteria. <i>Microbiology Spectrum</i> , 2022, 10, e0233321.	1.2	15
6854	Normal Light-Dark and Short-Light Cycles Regulate Intestinal Inflammation, Circulating Short-chain Fatty Acids and Gut Microbiota in Period2 Gene Knockout Mice. <i>Frontiers in Immunology</i> , 2022, 13, 848248.	2.2	14
6855	Correlation analysis of the oral mucosal microbiome and diabetes mellitus using microbial DNA in elderly male subjects. <i>Oral Biology Research</i> , 2022, 46, 10-20.	0.0	1
6856	Positive Effects of Neutrophil Elastase Inhibitor (Sivelestat) on Gut Microbiome and Metabolite Profiles of Septic Rats. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 818391.	1.8	5
6857	Incomplete degradation products of galactomannan from <i>Sesbania canabina</i> modulated the caecal microbial community of laying hens. <i>Journal of Animal Science</i> , 2022, , .	0.2	4
6858	Stimulated Organic Carbon Cycling and Microbial Community Shift Driven by a Simulated Cold-Seep Eruption. <i>MBio</i> , 2022, 13, e0008722.	1.8	5

#	ARTICLE	IF	CITATIONS
6859	Therapeutic Effects of Bifidobacterium breve YH68 in Combination with Vancomycin and Metronidazole in a Primary Clostridioides difficile-Infected Mouse Model. Microbiology Spectrum, 2022, 10, e0067222.	1.2	5
6860	Loss of gut microbial diversity in the cultured, agastric fish, Mexican pike silverside (<i>Chirostoma) Tj ETQq1 1 0.784314 rgBT /Overlo	0.9	3
6861	Metabolic Alternations During Gestation in Dezhou Donkeys and the Link to the Gut Microbiota. Frontiers in Microbiology, 2022, 13, 801976.	1.5	2
6862	Similar Bacterial Communities among Different Populations of a Newly Emerging Invasive Species, Tuta absoluta (Meyrick). Insects, 2022, 13, 252.	1.0	8
6863	Structure and function of the soil microbiome underlying N2O emissions from global wetlands. Nature Communications, 2022, 13, 1430.	5.8	72
6864	Composition and short-term stability of gut microbiota in lean and spontaneously overweight healthy Labrador retriever dogs. Acta Veterinaria Scandinavica, 2022, 64, 8.	0.5	7
6865	The Extent and Pattern of Mariculture Impacts on Spatial and Seasonal Variations of Sediment Bacterial Communities Among Three Coastal Waters. Frontiers in Marine Science, 2022, 9, .	1.2	5
6866	Assessing Temporal Changes in Microbial Communities in Hyalomma dromedarii Collected From Camels in the UAE Using High-Throughput Sequencing. Frontiers in Veterinary Science, 2022, 9, 861233.	0.9	2
6867	Aqueous system-level processes and prokaryote assemblages in the ferruginous and sulfate-rich bottom waters of a post-mining lake. Biogeosciences, 2022, 19, 1723-1751.	1.3	5
6868	Synthetic introns enable splicing factor mutation-dependent targeting of cancer cells. Nature Biotechnology, 2022, 40, 1103-1113.	9.4	24
6869	Nasal Microbiome Change During and After Exacerbation in Asthmatic Children. Frontiers in Microbiology, 2021, 12, 833726.	1.5	8
6871	Spatio-temporal patterns of multi-trophic biodiversity and food-web characteristics uncovered across a river catchment using environmental DNA. Communications Biology, 2022, 5, 259.	2.0	23
6872	Effects of Pig Manure and Its Organic Fertilizer Application on Archaea and Methane Emission in Paddy Fields. Land, 2022, 11, 499.	1.2	3
6873	FrCas9 is a CRISPR/Cas9 system with high editing efficiency and fidelity. Nature Communications, 2022, 13, 1425.	5.8	17
6874	Gut Microbiota Modulation of Moderate Undernutrition in Infants through Gummy Lactobacillus plantarum Dad-13 Consumption: A Randomized Double-Blind Controlled Trial. Nutrients, 2022, 14, 1049.	1.7	10
6875	Effects of Exogenous Hydrogen Sulfide on Diabetic Metabolic Disorders in db/db Mice Are Associated With Gut Bacterial and Fungal Microbiota. Frontiers in Cellular and Infection Microbiology, 2022, 12, 801331.	1.8	1
6876	Exploiting the gut microbiota to predict the origins and quality traits of cultured sea cucumbers. Environmental Microbiology, 2022, 24, 3882-3897.	1.8	12
6877	Nitrogen driven niche differentiation in bacterioplankton communities of northeast coastal Bay of Bengal. Environmental Research Communications, 2022, 4, 035006.	0.9	5

#	ARTICLE	IF	CITATIONS
6878	Genetic assignment of fisheries bycatch reveals disproportionate mortality among Alaska Northern Fulmar breeding colonies. <i>Evolutionary Applications</i> , 2022, 15, 447-458.	1.5	4
6879	Sedimentary Nitrogen and Sulfur Reduction Functional-Couplings Interplay With the Microbial Community of Anthropogenic Shrimp Culture Pond Ecosystem. <i>Frontiers in Microbiology</i> , 2022, 13, 830777.	1.5	2
6880	The structure of microbial communities of activated sludge of large-scale wastewater treatment plants in the city of Moscow. <i>Scientific Reports</i> , 2022, 12, 3458.	1.6	38
6881	16S rRNA gene sequencing reveals altered composition of gut microbiota in postoperative individuals with renal stones. <i>Letters in Applied Microbiology</i> , 2022, 75, 271-280.	1.0	3
6882	<i>Syringa reticulata</i> subsp. <i>amurensis</i> growth influencing the microbial diversity and heavy metal contents in mixed substrate of municipal sludge and construction waste. <i>Environmental Pollutants and Bioavailability</i> , 2022, 34, 127-135.	1.3	1
6883	Complete mitogenome of <i>Antheraea formosana</i> Sonan, 1937 (Lepidoptera: Saturniidae): an endemic silkworm in Taiwan. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 446-447.	0.2	0
6884	Biochar Amendment and Nitrogen Fertilizer Contribute to the Changes in Soil Properties and Microbial Communities in a Paddy Field. <i>Frontiers in Microbiology</i> , 2022, 13, 834751.	1.5	30
6885	Comparative Respiratory Tract Microbiome Between Carbapenem-Resistant <i>Acinetobacter baumannii</i> Colonization and Ventilator Associated Pneumonia. <i>Frontiers in Microbiology</i> , 2022, 13, 782210.	1.5	5
6886	Global soil microbiomes: A new frontline of biome ecology research. <i>Global Ecology and Biogeography</i> , 2022, 31, 1120-1132.	2.7	19
6887	Bacterial microbiota of the contact lens surface and associated care behaviours. <i>Heliyon</i> , 2022, 8, e09038.	1.4	5
6888	Effects of Corn and Broken Rice Extrusion on the Feed Intake, Nutrient Digestibility, and Gut Microbiota of Weaned Piglets. <i>Animals</i> , 2022, 12, 818.	1.0	5
6889	Environmental Factors Drive Periphytic Algal Community Assembly in the Largest Long-Distance Water Diversion Channel. <i>Water (Switzerland)</i> , 2022, 14, 914.	1.2	9
6890	Multiple causal variants underlie genetic associations in humans. <i>Science</i> , 2022, 375, 1247-1254.	6.0	75
6891	Differences in microbiome composition and transcriptome profiles between male and female <i>Paederus fuscipes</i> harbouring pederin-producing bacteria. <i>Insect Molecular Biology</i> , 2022, 31, 457-470.	1.0	2
6892	Re-vegetation Improves Soil Quality by Decreasing Soil Conductivity and Altering Soil Microbial Communities: A Case Study of an Opencast Coal Mine in the Helan Mountains. <i>Frontiers in Microbiology</i> , 2022, 13, 833711.	1.5	2
6893	Experimental Warming Has Not Affected the Changes in Soil Organic Carbon During the Growing Season in an Alpine Meadow Ecosystem on the Qinghai-Tibet Plateau. <i>Frontiers in Plant Science</i> , 2022, 13, 847680.	1.7	3
6894	Bioremediation of decabromodiphenyl ether or benzo(a)pyrene-contaminated rice-paddy soil. <i>Journal of Soils and Sediments</i> , 2022, 22, 1397-1417.	1.5	3
6896	Er-Chen Decoction Alleviates High-Fat Diet-Induced Nonalcoholic Fatty Liver Disease in Rats through Remodeling Gut Microbiota and Regulating the Serum Metabolism. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	8

#	ARTICLE	IF	CITATIONS
6897	Composition and Functional Diversity of Epiphytic Bacterial and Fungal Communities on Marine Macrophytes in an Intertidal Zone. <i>Frontiers in Microbiology</i> , 2022, 13, 839465.	1.5	14
6898	Effects of dietary fibre on intestinal microbiota in geese evaluated by 16SrRNA gene sequencing. <i>Journal of Applied Microbiology</i> , 2022, , .	1.4	2
6899	Effects of cadmium contamination on bacterial and fungal communities in Panax ginseng-growing soil. <i>BMC Microbiology</i> , 2022, 22, 77.	1.3	8
6900	Spatial Pattern of Endophytic Fungi and the Symbiotic Germination of <i>Tulasnella</i> Fungi from Wild <i>Cymbidium goeringii</i> (Orchidaceae) in China. <i>Current Microbiology</i> , 2022, 79, 139.	1.0	0
6901	Illumina MiSeq Sequencing Reveals Correlations among Fruit Ingredients, Environmental Factors, and AMF Communities in Three <i>Lycium Barbarum</i> Producing Regions of China. <i>Microbiology Spectrum</i> , 2022, 10, e0229321.	1.2	11
6902	Leveraging eDNA metabarcoding to characterize nearshore fish communities in Southeast Alaska: Do habitat and tide matter?. <i>Environmental DNA</i> , 2022, 4, 868-880.	3.1	11
6903	Assessing the Effect of Smokeless Tobacco Consumption on Oral Microbiome in Healthy and Oral Cancer Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841465.	1.8	13
6904	Long Term Influence of Fertility and Rotation on Soil Nitrification Potential and Nitrifier Communities. <i>Frontiers in Soil Science</i> , 2022, 2, .	0.8	4
6905	Nasal Bacterial Microbiome Differs Between Healthy Controls and Those With Asthma and Allergic Rhinitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841995.	1.8	16
6906	Manure fertilization enhanced microbial immigration in the wheat rhizosphere. <i>Journal of Soils and Sediments</i> , 0, , 1.	1.5	0
6907	Characterization of Distinct Microbiota Associated with Scalp Dermatitis in Patients with Atopic Dermatitis. <i>Journal of Clinical Medicine</i> , 2022, 11, 1735.	1.0	8
6908	Successional Changes of Microbial Communities and Host-Microbiota Interactions Contribute to Dietary Adaptation in Allodiploid Hybrid Fish. <i>Microbial Ecology</i> , 2023, 85, 1190-1201.	1.4	10
6909	Comparison of changes in fecal microbiota of calves with and without dam. <i>PeerJ</i> , 2022, 10, e12826.	0.9	2
6910	Effects of Temperature and Nitrogen Application on Carbon and Nitrogen Accumulation and Bacterial Community Composition in Apple Rhizosphere Soil. <i>Frontiers in Plant Science</i> , 2022, 13, 859395.	1.7	9
6911	Small-sized salt-tolerant denitrifying and phosphorus removal aerobic granular sludge cultivated with mariculture waste solids to treat synthetic mariculture wastewater. <i>Biochemical Engineering Journal</i> , 2022, 181, 108396.	1.8	10
6912	The effect of inulin-type fructans on the intestinal immune function of antibiotic-treated mice. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 3265-3278.	1.7	2
6913	Infestation of Rice by Gall Midge Influences Density and Diversity of <i>Pseudomonas</i> and <i>Wolbachia</i> in the Host Plant Microbiome. <i>Current Genomics</i> , 2022, 23, 126-136.	0.7	1
6914	Gut Bacterial Flora of Open Nested Honeybee, <i>Apis florea</i> . <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	7

#	ARTICLE	IF	CITATIONS
6915	Abundant Species Diversity and Essential Functions of Bacterial Communities Associated with Dinoflagellates as Revealed from Metabarcoding Sequencing for Laboratory-Raised Clonal Cultures. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 4446.	1.2	7
6916	Comparison of feeding value, ruminal fermentation and bacterial community of a diet comprised of various corn silages or combination with wheat straw in finishing beef cattle. <i>Livestock Science</i> , 2022, 258, 104876.	0.6	2
6917	Swimming Exercise Modulates Gut Microbiota in CUMS-Induced Depressed Mice. <i>Neuropsychiatric Disease and Treatment</i> , 2022, Volume 18, 749-760.	1.0	14
6918	The Microbiome Structure of a Rice-Crayfish Integrated Breeding Model and Its Association with Crayfish Growth and Water Quality. <i>Microbiology Spectrum</i> , 2022, 10, e0220421.	1.2	10
6919	High nitrite nitrogen stress intensity drives nitrite anaerobic oxidation to nitrate and inhibits methanogenesis. <i>Science of the Total Environment</i> , 2022, 832, 155109.	3.9	8
6920	Dietary Nutrition and Gut Microbiota Composition in Patients With Hypertensive Disorders of Pregnancy. <i>Frontiers in Nutrition</i> , 2022, 9, 862892.	1.6	3
6921	Effect of novel <i>Lactobacillus paracaesi</i> microcapsule on growth performance, gut health and microbiome community of broiler chickens. <i>Poultry Science</i> , 2022, 101, 101912.	1.5	13
6922	Assessing rates of parasite coinfection and spatiotemporal strain variation via metabarcoding: Insights for the conservation of European turtle doves <i>Streptopelia turtur</i> . <i>Molecular Ecology</i> , 2022, 31, 2730-2751.	2.0	8
6923	Microbial soil legacies of crops under different water and nitrogen levels determine succeeding crop performance. <i>Plant and Soil</i> , 2023, 485, 167-180.	1.8	13
6924	Dysbiosis and intestinal inflammation caused by <i>Salmonella Typhimurium</i> in mice can be alleviated by preadministration of a lytic phage. <i>Microbiological Research</i> , 2022, 260, 127020.	2.5	9
6925	The human milk microbiome aligns with lactation stage and not birth mode. <i>Scientific Reports</i> , 2022, 12, 5598.	1.6	16
6926	A comparative analysis of carcass and meat traits, and rumen bacteria between Chinese Mongolian sheep and Dorper Chinese Mongolian crossbred sheep. <i>Animal</i> , 2022, 16, 100503.	1.3	8
6927	Observation of the cervical microbiome in the progression of cervical intraepithelial neoplasia. <i>BMC Cancer</i> , 2022, 22, 362.	1.1	6
6928	Soil metabolomics and bacterial functional traits revealed the responses of rhizosphere soil bacterial community to long-term continuous cropping of Tibetan barley. <i>PeerJ</i> , 2022, 10, e13254.	0.9	11
6929	Comparison of <i>Actinobacteria</i> communities from human-impacted and pristine karst caves. <i>MicrobiologyOpen</i> , 2022, 11, e1276.	1.2	6
6930	Linking transcriptional dynamics of CH ₄ -cycling grassland soil microbiomes to seasonal gas fluxes. <i>ISME Journal</i> , 2022, 16, 1788-1797.	4.4	12
6931	Shift in microbial communities mediated by vegetation-soil characteristics following subshrub encroachment in a semi-arid grassland. <i>Ecological Indicators</i> , 2022, 137, 108768.	2.6	7
6932	Gut Microbiome and Metabolomics Profiles of Allergic and Non-Allergic Childhood Asthma. <i>Journal of Asthma and Allergy</i> , 2022, Volume 15, 419-435.	1.5	11

#	ARTICLE	IF	CITATIONS
6933	Phosphate fertilizers facilitated the Cd contaminated soil remediation by sepiolite: Cd mobilization, plant toxicity, and soil microbial community. <i>Ecotoxicology and Environmental Safety</i> , 2022, 234, 113388.	2.9	21
6934	Dysbiosis in the Rhizosphere Microbiome of Standing Dead Korean Fir (<i>Abies koreana</i>). <i>Plants</i> , 2022, 11, 990.	1.6	6
6935	Analysis of endophyte diversity of two <i>Gentiana</i> plants species and the association with secondary metabolite. <i>BMC Microbiology</i> , 2022, 22, 90.	1.3	10
6936	Wastewater microorganisms impact the micropollutant biotransformation potential of natural stream biofilms. <i>Water Research</i> , 2022, 217, 118413.	5.3	17
6937	Speeding up the detection of invasive bivalve species using environmental DNA: A Nanopore and Illumina sequencing comparison. <i>Molecular Ecology Resources</i> , 2022, 22, 2232-2247.	2.2	16
6938	Effect of dietary honeysuckle (<i>Lonicera caerulea</i> L.) supplementation on lipid metabolism, immunity and intestinal microbiota in grass carp (<i>Ctenopharyngodon idellus</i>). <i>Aquaculture Reports</i> , 2022, 23, 101063.	0.7	8
6939	16S rRNA gene sequencing analysis reveals an imbalance in the intestinal flora of <i>Eriocheir sinensis</i> with hepatopancreatic necrosis disease. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100988.	0.4	3
6940	Spatiotemporal Variation of Microbial Communities in the Ultra-Oligotrophic Eastern Mediterranean Sea. <i>Frontiers in Microbiology</i> , 2022, 13, 867694.	1.5	7
6941	Bio-Matrix Pot Addition Enhanced the Vegetation Process of Iron Tailings by <i>Pennisetum giganteum</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 825660.	1.5	0
6942	The microbiota-gut-kidney axis mediates host osmoregulation in a small desert mammal. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 16.	2.9	9
6943	Heterogeneity of soil bacterial and bacteriophage communities in three rice agroecosystems and potential impacts of bacteriophage on nutrient cycling. <i>Environmental Microbiomes</i> , 2022, 17, 17.	2.2	11
6944	An insight into the changes in the microbial community of Kantuan sliced chicken during storage at different temperatures. <i>Journal of Food Processing and Preservation</i> , 2022, 46, .	0.9	2
6945	Colorectal microbiota after removal of colorectal cancer. <i>NAR Cancer</i> , 2022, 4, zcac011.	1.6	5
6946	A sustainable approach for removing nitrate: Studying the nitrate transformation and metabolic potential under different carbon source by microorganism. <i>Journal of Cleaner Production</i> , 2022, 346, 131169.	4.6	8
6947	Effects of emerging contaminants and heavy metals on variation in bacterial communities in estuarine sediments. <i>Science of the Total Environment</i> , 2022, 832, 155118.	3.9	20
6948	Microbial community changes in different underground compartments of potato affected yield and quality. <i>3 Biotech</i> , 2022, 12, 106.	1.1	10
6949	Correlations between oligosaccharides in breast milk and the composition of the gut microbiome in breastfed infants. <i>Journal of Dairy Science</i> , 2022, 105, 4818-4828.	1.4	0
6950	Impact of ozonated water disinfection on soil fungal community composition in continuous ginger field. <i>PLoS ONE</i> , 2022, 17, e0266619.	1.1	0

#	ARTICLE	IF	CITATIONS
6951	Exploring the response patterns of strong-flavor baijiu brewing microecosystem to fortified Daqu under different pit ages. <i>Food Research International</i> , 2022, 155, 111062.	2.9	23
6952	Food Neophobia and scarce olfactory performances are linked to oral microbiota. <i>Food Research International</i> , 2022, 155, 111092.	2.9	3
6953	Water masses and their associated temperature and cross-domain biotic factors co-shape upwelling microbial communities. <i>Water Research</i> , 2022, 215, 118274.	5.3	17
6954	Enhancing effect of <i>Platymonas</i> addition on water quality, microbial community diversity and shrimp performance in biofloc-based tanks for <i>Penaeus vannamei</i> nursery. <i>Aquaculture</i> , 2022, 554, 738057.	1.7	10
6955	Landscapes, management practices and their interactions shape soil fungal diversity in arable fields “Evidence from a nationwide farmers’ network. <i>Soil Biology and Biochemistry</i> , 2022, 168, 108652.	4.2	7
6956	DNA hydroxymethylation reprogramming of β -oxidation genes mediates early-life arsenic-evoked hepatic lipid accumulation in adult mice. <i>Journal of Hazardous Materials</i> , 2022, 430, 128511.	6.5	8
6957	Application of mixotrophic acidophiles for the bioremediation of cadmium-contaminated soils elevates cadmium removal, soil nutrient availability, and rice growth. <i>Ecotoxicology and Environmental Safety</i> , 2022, 236, 113499.	2.9	9
6958	Pathobiology of <i>Enterocytozoon hepatopenaei</i> (EHP) in shrimp: Diagnosis and interpretation from the gut bacterial community. <i>Aquaculture</i> , 2022, 554, 738169.	1.7	8
6959	Characterization and comparison of the bacterial community on environmental surfaces through a fresh-cut vegetables processing line in China. <i>Food Research International</i> , 2022, 155, 111075.	2.9	9
6960	Cleanup chlorinated ethene-polluted groundwater using an innovative immobilized <i>Clostridium butyricum</i> column scheme: A pilot-scale study. <i>Journal of Environmental Management</i> , 2022, 311, 114836.	3.8	10
6961	Flooding and drainage induced abiotic reactions control metal solubility in soil of a contaminated industrial site. <i>Chemosphere</i> , 2022, 297, 134032.	4.2	6
6962	Rare biosphere regulates the planktonic and sedimentary bacteria by disparate ecological processes in a large source water reservoir. <i>Water Research</i> , 2022, 216, 118296.	5.3	25
6963	Symbiotic bacteria on the cuticle protect the oriental fruit moth <i>Grapholita molesta</i> from fungal infection. <i>Biological Control</i> , 2022, 169, 104895.	1.4	6
6964	Effect of the coexistence of endosulfan on the lindane biodegradation by <i>Novosphingobium barchaimii</i> and microbial enrichment cultures. <i>Chemosphere</i> , 2022, 297, 134063.	4.2	9
6965	The host-specific resistome in environmental feces of Eurasian otters (<i>Lutra lutra</i>) and leopard cats (<i>Prionailurus bengalensis</i>) revealed by metagenomic sequencing. <i>One Health</i> , 2022, 14, 100385.	1.5	1
6966	Evaluation of rain-shelter cultivation mode effects on microbial diversity during Cabernet Sauvignon (<i>Vitis vinifera</i> L.) maturation in Jingyang, Shaanxi, China. <i>Food Research International</i> , 2022, 156, 111165.	2.9	8
6967	Combined effects of oxytetracycline and microplastic on wheat seedling growth and associated rhizosphere bacterial communities and soil metabolite profiles. <i>Environmental Pollution</i> , 2022, 302, 119046.	3.7	39
6968	Landscape context determines soil fungal diversity in a fragmented habitat. <i>Catena</i> , 2022, 213, 106163.	2.2	40

#	ARTICLE	IF	CITATIONS
6969	Shift and interaction of intestinal bacterial community in juvenile Chinese mitten crab <i>Eriocheir sinensis</i> upon astaxanthin feeding. <i>Aquaculture</i> , 2022, 555, 738203.	1.7	5
6970	Linking soil microbial community traits and organic carbon accumulation rate under long-term conservation tillage practices. <i>Soil and Tillage Research</i> , 2022, 220, 105360.	2.6	28
6971	Identification and action mechanism of lipid regulating components from <i>Rhei Radix et rhizoma</i> . <i>Journal of Ethnopharmacology</i> , 2022, 292, 115179.	2.0	9
6972	Effects of treatment processes on AOC removal and changes of bacterial diversity in a water treatment plant. <i>Journal of Environmental Management</i> , 2022, 311, 114853.	3.8	8
6973	Effects of choline chloride on intestinal microbiota and its association with liver fat accumulation in zebrafish. <i>Aquaculture Reports</i> , 2022, 24, 101096.	0.7	0
6974	Diversity and community composition of nirS-type denitrifying bacteria and ammonia-oxidizing archaea in biofilm samples attached to bio-substrate and abio-substrates in integrated ecological floating bed systems. <i>Ecological Engineering</i> , 2022, 180, 106641.	1.6	4
6975	Topographic attributes override impacts of agronomic practices on prokaryotic community structure. <i>Applied Soil Ecology</i> , 2022, 175, 104446.	2.1	2
6976	Temporal variation of management effects on soil microbial communities. <i>Geoderma</i> , 2022, 418, 115828.	2.3	6
6977	Positive effects of organic fertilizers and biofertilizers on soil microbial community composition and walnut yield. <i>Applied Soil Ecology</i> , 2022, 175, 104457.	2.1	32
6978	Temperature and precipitation dominates millennium changes of eukaryotic algal communities in Lake Yamzhog Yumco, Southern Tibetan Plateau. <i>Science of the Total Environment</i> , 2022, 829, 154636.	3.9	11
6979	Microbial habitat specificity largely affects microbial co-occurrence patterns and functional profiles in wetland soils. <i>Geoderma</i> , 2022, 418, 115866.	2.3	20
6980	The long-term decomposition of wild animal corpses leads to carbon and phosphorus accumulation and disturbs the ecological succession of the denitrification community encoded by narG. <i>Applied Soil Ecology</i> , 2022, 175, 104455.	2.1	8
6981	Combined toxic effects of thiamethoxam on intestinal flora, transcriptome and physiology of Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Science of the Total Environment</i> , 2022, 830, 154799.	3.9	20
6982	Long-term metal pollution shifts microbial functional profiles of nitrification and denitrification in agricultural soils. <i>Science of the Total Environment</i> , 2022, 830, 154732.	3.9	15
6983	Incubation habitats and aging treatments affect the formation of biofilms on polypropylene microplastics. <i>Science of the Total Environment</i> , 2022, 831, 154769.	3.9	22
6984	Taxonomic diversity and predictive metabolic functions of a heavy metal tolerant multiple azo dye degrading bacterial consortium from textile effluents. <i>International Biodeterioration and Biodegradation</i> , 2022, 171, 105421.	1.9	12
6985	Effects of Tartary buckwheat on physicochemical properties and microbial community of low salt natural fermented soybean paste. <i>Food Control</i> , 2022, 138, 108953.	2.8	9
6986	Spotted seals (<i>Phoca largha</i>) harbor unique gut microbiota shaped by their host habitat. <i>Science of the Total Environment</i> , 2022, 832, 155015.	3.9	7

#	ARTICLE	IF	CITATIONS
6987	Fungal key players of cellulose utilization: Microbial networks in aggregates of long-term fertilized soils disentangled using ¹³ C-DNA-stable isotope probing. <i>Science of the Total Environment</i> , 2022, 832, 155051.	3.9	10
6988	Microbial community structure and functions during chronosequence-based phytoremediation programme of Lignite tailing soil. <i>Environmental Technology and Innovation</i> , 2022, 27, 102447.	3.0	3
6989	Over two years study: Peanut biochar promoted potassium availability by mediating the relationship between bacterial community and soil properties. <i>Applied Soil Ecology</i> , 2022, 176, 104485.	2.1	22
6990	Altitudinal niches of symbiotic, associative and free-living diazotrophs driven by soil moisture and temperature in the alpine meadow on the Tibetan Plateau. <i>Environmental Research</i> , 2022, 211, 113033.	3.7	13
6991	Spatial dynamics of active microeukaryotes along a latitudinal gradient: Diversity, assembly process, and co-occurrence relationships. <i>Environmental Research</i> , 2022, 212, 113234.	3.7	5
6992	Biodiversity and Enzyme Activity of Marine Fungi with 28 New Records from the Tropical Coastal Ecosystems in Vietnam. <i>Mycobiology</i> , 2021, 49, 559-581.	0.6	10
6993	Distribution and Genetic Diversity of Hepatitis E Virus in Wild and Domestic Rabbits in Australia. <i>Pathogens</i> , 2021, 10, 1637.	1.2	6
6994	Integrative Analysis of the Gut Microbiota and Metabolome for <i>In Vitro</i> Human Gut Fermentation Modeling. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 15414-15424.	2.4	9
6995	Lignans dramatically enhance the resistance of <i>Fraxinus velutina</i> Torr. by adjusting the dominant bacterium group of <i>Agrilus planipennis</i> Fairmaire. <i>Pest Management Science</i> , 2022, 78, 1386-1397.	1.7	6
6996	Permafrost thaw with warming reduces microbial metabolic capacities in subsurface soils. <i>Molecular Ecology</i> , 2022, 31, 1403-1415.	2.0	12
6997	Development of SSR Databases Available for Both NGS and Capillary Electrophoresis in Apple, Pear and Tea. <i>Plants</i> , 2021, 10, 2796.	1.6	5
6998	Human Colonic Microbiota and Short-Term Postoperative Outcomes in Colorectal Cancer Patients: A Pilot Study. <i>Microorganisms</i> , 2022, 10, 41.	1.6	3
6999	Ciprofloxacin Causes the Greatest Bacterial Community Variation in Swine Manure Composting. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	7
7000	Analysis of rhizobacterial community associated with the occurrence of <i>Ganoderma</i> basal stem rot disease in oil palm by Illumina next-generation sequencing. <i>Archives of Microbiology</i> , 2022, 204, 31.	1.0	1
7001	Effects of Elevation and Distance from Highway on the Abundance and Community Structure of Bacteria in Soil along Qinghai-Tibet Highway. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 13137.	1.2	4
7002	<i>Cupriavidus</i> in the intestinal microbiota of Tibet endemic fish <i>Glyptosternum maculatum</i> can help it adapt to habitat of the Qinghai Tibet Plateau. <i>BMC Veterinary Research</i> , 2021, 17, 377.	0.7	5
7003	Ursodeoxycholic Acid Treatment Restores Gut Microbiota and Alleviates Liver Inflammation in Non-Alcoholic Steatohepatitic Mouse Model. <i>Frontiers in Pharmacology</i> , 2021, 12, 788558.	1.6	34
7004	Gastrodin attenuates perfluorooctanoic acid-induced liver injury by regulating gut microbiota composition in mice. <i>Bioengineered</i> , 2021, 12, 11546-11556.	1.4	14

#	ARTICLE	IF	CITATIONS
7005	Pi-Dan-Jian-Qing Decoction Ameliorates Type 2 Diabetes Mellitus Through Regulating the Gut Microbiota and Serum Metabolism. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 748872.	1.8	17
7006	Mulberry (<i>Morus alba</i> L.) leaf polysaccharide ameliorates insulin resistance and adipose deposition associated gut microbiota and lipid metabolites in high-fat diet-induced obese mice. <i>Food Science and Nutrition</i> , 2022, 10, 617-630.	1.5	14
7007	Governor Vessel Moxibustion Therapy Improves Microbiota Structure in Ankylosing Spondylitis Patients. <i>Disease Markers</i> , 2021, 2021, 1-8.	0.6	2
7008	The influence of rhizosphere soil fungal diversity and complex community structure on wheat root rot disease. <i>PeerJ</i> , 2021, 9, e12601.	0.9	4
7009	Soybean Î²-conglycinin and glycinin reduced growth performance and the intestinal immune defense and altered microbiome in juvenile pearl gentian groupers <i>Epinephelus fuscoguttatus</i> — <i>Epinephelus lanceolatus</i> . <i>Animal Nutrition</i> , 2022, 9, 193-203.	2.1	20
7010	Characteristics of root-associated bacterial community and nitrogen biochemical properties of two <i>Japonica</i> rice cultivars with different yields. <i>Food and Energy Security</i> , 2022, 11, .	2.0	0
7011	Multiple Data Demonstrate That Bacteria Regulating Reproduction Could Be Not the Cause for the Thelytoky of <i>Diglyphus Awani</i> (Hymenoptera: Eulophidae). <i>Insects</i> , 2022, 13, 9.	1.0	6
7012	Nicotine Oral Administration Attenuates DSS-Induced Colitis Through Upregulation of Indole in the Distal Colon and Rectum in Mice. <i>Frontiers in Medicine</i> , 2021, 8, 789037.	1.2	2
7013	Alterations of Suckling Piglet Jejunal Microbiota Due to Infection With Porcine Epidemic Diarrhea Virus and Protection Against Infection by <i>Lactobacillus salivarius</i> . <i>Frontiers in Veterinary Science</i> , 2021, 8, 771411.	0.9	4
7014	Effects of Dietary Supplementation with Mushroom or Vitamin D2-Enriched Mushroom Powders on Gastrointestinal Health Parameters in the Weaned Pig. <i>Animals</i> , 2021, 11, 3603.	1.0	9
7016	The Succession of Bacterial Community Attached on Biodegradable Plastic Mulches During the Degradation in Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 785737.	1.5	25
7017	Complete mitochondrial genome of <i>Manis pentadactyla pentadactyla</i> (Mammalia: Pholidota), an endemic subspecies of Chinese pangolin: mitogenome characterisation and phylogenetic implications. <i>Biodiversity Data Journal</i> , 2021, 9, e77961.	0.4	3
7018	Limited Introgression between Rock-Wallabies with Extensive Chromosomal Rearrangements. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	17
7019	Interaction between bacterial diversity and biogenic amines production in a salted mackerel stored at soft frozen (−7â„ƒ storage. <i>Food Science and Nutrition</i> , 2022, 10, 412-421.	1.5	0
7020	Dynamic and Assembly of Benthic Bacterial Community in an Industrial-Scale In-Pond Raceway Recirculating Culture System. <i>Frontiers in Microbiology</i> , 2021, 12, 797817.	1.5	9
7021	Biodegradation Kinetics of Fragrances, Plasticizers, UV Filters, and PAHs in a Mixture—Changing Test Concentrations over 5 Orders of Magnitude. <i>Environmental Science & Technology</i> , 2022, 56, 293-301.	4.6	10
7023	The Coexistence Relationship Between Plants and Soil Bacteria Based on Interdomain Ecological Network Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 745582.	1.5	6
7024	Shugan Hwei Decoction Alleviates Cecum Mucosal Injury and Improves Depressive- and Anxiety-Like Behaviors in Chronic Stress Model Rats by Regulating Cecal Microbiota and Inhibiting NLRP3 Inflammasome. <i>Frontiers in Pharmacology</i> , 2021, 12, 766474.	1.6	6

#	ARTICLE	IF	CITATIONS
7025	Size-Fractionated Filtration Combined with Molecular Methods Reveals the Size and Diversity of Picophytoplankton. <i>Biology</i> , 2021, 10, 1280.	1.3	0
7026	Effect of Housing Condition and Diet on the Gut Microbiota of Weanling Immunocompromised Mice. <i>Comparative Medicine</i> , 2021, 71, 485-491.	0.4	3
7027	Microbial Communities and Physiochemical Properties of Four Distinctive Traditionally Fermented Vegetables from North China and Their Influence on Quality and Safety. <i>Foods</i> , 2022, 11, 21.	1.9	8
7028	Soluble Polysaccharide Derived from <i>Laminaria japonica</i> Attenuates Obesity-Related Nonalcoholic Fatty Liver Disease Associated with Gut Microbiota Regulation. <i>Marine Drugs</i> , 2021, 19, 699.	2.2	19
7030	Anti-obesity and Gut Microbiota Modulation Effect of <i>Astragalus</i> Polysaccharides Combined with Berberine on High-Fat Diet-Fed Obese Mice. <i>Chinese Journal of Integrative Medicine</i> , 2023, 29, 617-625.	0.7	5
7031	Rokubacteria in Northern Peatlands: Habitat Preferences and Diversity Patterns. <i>Microorganisms</i> , 2022, 10, 11.	1.6	14
7032	Associations of physical activity with gut microbiota in pre-adolescent children. <i>Physical Activity and Nutrition</i> , 2021, 25, 24-37.	0.4	6
7033	Bacterial communities and their bioremediation capabilities in oil-contaminated agricultural soils. <i>Environmental Monitoring and Assessment</i> , 2022, 194, 9.	1.3	9
7034	Industrial Composting of Sewage Sludge: Study of the Bacteriome, Sanitation, and Antibiotic-Resistant Strains. <i>Frontiers in Microbiology</i> , 2021, 12, 784071.	1.5	7
7035	Humic substances composition and properties as an environmentally sustainable system: A review and way forward to soil conservation. <i>Journal of Plant Nutrition</i> , 2022, 45, 1072-1122.	0.9	16
7036	Grazing weakens competitive interactions between active methanotrophs and nitrifiers modulating greenhouse-gas emissions in grassland soils. <i>ISME Communications</i> , 2021, 1, .	1.7	5
7038	Bioaugmentation of Atrazine-Contaminated Soil With <i>Paenarthrobacter</i> sp. Strain AT-5 and Its Effect on the Soil Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 771463.	1.5	14
7039	Evaluation of Changes to the Oral Microbiome Based on 16S rRNA Sequencing among Children Treated for Cancer. <i>Cancers</i> , 2022, 14, 7.	1.7	3
7040	Soil Bacterial Community Shifts Are Driven by Soil Nutrient Availability along a Teak Plantation Chronosequence in Tropical Forests in China. <i>Biology</i> , 2021, 10, 1329.	1.3	16
7041	Organic Carbon Mineralization and Bacterial Community of Active Layer Soils Response to Short-Term Warming in the Great Hingâ€™an Mountains of Northeast China. <i>Frontiers in Microbiology</i> , 2021, 12, 802213.	1.5	18
7042	<i>Desulfovibrio desulfuricans</i> AY5 Isolated from a Patient with Autism Spectrum Disorder Binds Iron in Low-Soluble Greigite and Pyrite. <i>Microorganisms</i> , 2021, 9, 2558.	1.6	6
7043	The Impact of Extreme Weather Events on Bacterial Communities and Opportunistic Pathogens in a Drinking Water Treatment Plant. <i>Water (Switzerland)</i> , 2022, 14, 54.	1.2	2
7044	Impacts of Enriched Human Milk Cells on Fecal Metabolome and Gut Microbiome of Premature Infants with Stage I Necrotizing Enterocolitis: A Pilot Study. <i>Molecular Nutrition and Food Research</i> , 2022, 66, e2100342.	1.5	4

#	ARTICLE	IF	CITATIONS
7045	Multi-Omics Revealing the Response Patterns of Symbiotic Microorganisms and Host Metabolism in Scleractinian Coral <i>Pavona minuta</i> to Temperature Stresses. <i>Metabolites</i> , 2022, 12, 18.	1.3	7
7046	Modulation of intestinal morphology and microbiota by dietary <i>Macleaya cordata</i> extract supplementation in Xuefeng Black-boned Chicken. <i>Animal</i> , 2021, 15, 100399.	1.3	16
7049	Peat-Inhabiting Verrucomicrobia of the Order Methylophilales Do Not Possess Methanotrophic Capabilities. <i>Microorganisms</i> , 2021, 9, 2566.	1.6	9
7050	High-Throughput Sequencing Analysis of the Composition and Diversity of the Bacterial Community in <i>Cinnamomum camphora</i> Soil. <i>Microorganisms</i> , 2022, 10, 72.	1.6	6
7051	Developmental Change of Yolk Microbiota and Its Role on Early Colonization of Intestinal Microbiota in Chicken Embryo. <i>Animals</i> , 2022, 12, 16.	1.0	15
7052	Characteristics of fungal communities and the sources of mold contamination in mildewed tobacco leaves stored under different climatic conditions. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 131-144.	1.7	6
7053	Cadmium Speciation Distribution Responses to Soil Properties and Soil Microbes of Plow Layer and Plow Pan Soils in Cadmium-Contaminated Paddy Fields. <i>Frontiers in Microbiology</i> , 2021, 12, 774301.	1.5	7
7054	Composition and Function of Bacterial Communities of Bryophytes and Their Underlying Sediments in the Dajiuhe Peatland, Central China. <i>Journal of Earth Science (Wuhan, China)</i> , 2023, 34, 133-144.	1.1	3
7055	Plant and soil responses to grazing intensity drive changes in the soil microbiome in a desert steppe. <i>Plant and Soil</i> , 2023, 491, 219-237.	1.8	11
7056	Divergence in gut bacterial community between females and males in the wolf spider <i>Pardosa astrigera</i> . <i>Ecology and Evolution</i> , 2022, 12, e8823.	0.8	6
7057	Heat Stress Altered the Vaginal Microbiome and Metabolome in Rabbits. <i>Frontiers in Microbiology</i> , 2022, 13, 813622.	1.5	6
7058	Correlation between the salivary microbiology and H ₂ S concentration of the oral cavity. <i>Oral Diseases</i> , 2023, 29, 2283-2292.	1.5	2
7059	Neoadjuvant Intravenous Oncolytic Vaccinia Virus Therapy Promotes Anticancer Immunity in Patients. <i>Cancer Immunology Research</i> , 2022, 10, 745-756.	1.6	22
7060	Succession of the Gut Microbiome in the Tibetan Population of Minjiang River Basin. <i>Frontiers in Microbiology</i> , 2022, 13, 834335.	1.5	2
7061	The Coupling Response between Different Bacterial Metabolic Functions in Water and Sediment Improve the Ability to Mitigate Climate Change. <i>Water (Switzerland)</i> , 2022, 14, 1203.	1.2	6
7062	Shifts in the Bacterial Community Related to Quality Properties of Vacuum-Packaged Peeled Potatoes during Storage. <i>Foods</i> , 2022, 11, 1147.	1.9	7
7063	Amplicon-based sequencing and co-occurrence network analysis reveals notable differences of microbial community structure in healthy and dandruff scalps. <i>BMC Genomics</i> , 2022, 23, 312.	1.2	2
7065	Application of Manure Rather Than Plant-Origin Organic Fertilizers Alters the Fungal Community in Continuous Cropping Tobacco Soil. <i>Frontiers in Microbiology</i> , 2022, 13, 818956.	1.5	14

#	ARTICLE	IF	CITATIONS
7066	Aberrant promoter methylation contributes to LRIG1 silencing in basal/triple-negative breast cancer. <i>British Journal of Cancer</i> , 2022, 127, 436-448.	2.9	11
7067	Response of microbial community structure to chromium contamination in <i>Panax ginseng</i> -growing soil. <i>Environmental Science and Pollution Research</i> , 2022, , 1.	2.7	6
7068	Differences of Macroalgal Consumption by Eight Herbivorous Coral Reef Fishes From the Xisha Islands, China. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
7070	Sea Cucumber Body Vesicular Syndrome Is Driven by the Pond Water Microbiome via an Altered Gut Microbiota. <i>MSystems</i> , 2022, 7, e0135721.	1.7	6
7071	Development of Early-Life Gastrointestinal Microbiota in the Presence of Antibiotics Alters the Severity of Acute DSS-Induced Colitis in Mice. <i>Microbiology Spectrum</i> , 2022, , e0269221.	1.2	4
7072	<i>Bacillus subtilis</i> plays a role in the inhibition of transporter ABCB1 in Caco-2 cells. <i>Epilepsy Research</i> , 2022, 183, 106925.	0.8	2
7073	Integrated network analysis reveals that exogenous cadmium-tolerant endophytic bacteria inhibit cadmium uptake in rice. <i>Chemosphere</i> , 2022, 301, 134655.	4.2	7
7074	The responses of soil bacterial and archaeal communities to coastal embankments in three typical salt marshes of Eastern China. <i>Plant and Soil</i> , 0, , .	1.8	1
7075	Environmental factors affect the arbuscular mycorrhizal fungal community through the status of host plants in three patterns of Chinese fir in southern China. <i>Global Ecology and Conservation</i> , 2022, , e02121.	1.0	3
7076	Experimental colonization with <i>Blastocystis</i> ST4 is associated with protective immune responses and modulation of gut microbiome in a DSS-induced colitis mouse model. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 245.	2.4	25
7077	Macroaggregates Serve as Micro-Hotspots Enriched With Functional and Networked Microbial Communities and Enhanced Under Organic/Inorganic Fertilization in a Paddy Topsoil From Southeastern China. <i>Frontiers in Microbiology</i> , 2022, 13, 831746.	1.5	4
7078	Quorum Quenching Bacteria <i>Bacillus velezensis</i> DH82 on Biological Control of <i>Vibrio parahaemolyticus</i> for Sustainable Aquaculture of <i>Litopenaeus vannamei</i> . <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
7079	Salinity Is a Key Determinant for the Microeukaryotic Community in Lake Ecosystems of the Inner Mongolia Plateau, China. <i>Frontiers in Microbiology</i> , 2022, 13, 841686.	1.5	4
7080	Microbiome Analysis of Malacopathogenic Nematodes Suggests No Evidence of a Single Bacterial Symbiont Responsible for Gastropod Mortality. <i>Frontiers in Immunology</i> , 2022, 13, 878783.	2.2	9
7081	Analysis of sub-kilobase chromatin topology reveals nano-scale regulatory interactions with variable dependence on cohesin and CTCF. <i>Nature Communications</i> , 2022, 13, 2139.	5.8	48
7082	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation. <i>Nature Communications</i> , 2022, 13, 2042.	5.8	6
7084	Beneficial Alteration in Growth Performance, Immune Status, and Intestinal Microbiota by Supplementation of Activated Charcoal-Herb Extractum Complex in Broilers. <i>Frontiers in Microbiology</i> , 2022, 13, 856634.	1.5	3
7085	Xuanfei Baidu decoction attenuates intestinal disorders by modulating NF- κ B pathway, regulating T cell immunity and improving intestinal flora. <i>Phytotherapy Research</i> , 2022, 101, 154100.	2.3	16

#	ARTICLE	IF	CITATIONS
7086	Gut mycobiome dysbiosis in rats showing retinal changes indicative of diabetic retinopathy. PLoS ONE, 2022, 17, e0267080.	1.1	2
7087	Grape Cultivar Features Differentiate the Grape Rhizosphere Microbiota. Plants, 2022, 11, 1111.	1.6	10
7088	Heterophil/Lymphocyte Ratio Level Modulates Salmonella Resistance, Cecal Microbiota Composition and Functional Capacity in Infected Chicken. Frontiers in Immunology, 2022, 13, 816689.	2.2	13
7089	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
7090	Phosphonoacetate Modifications Enhance the Stability and Editing Yields of Guide RNAs for Cas9 Editors. Biochemistry, 2023, 62, 3512-3520.	1.2	2
7091	Influences of arsenate and/or phosphate adsorption to ferrihydrite on iron-reducing and arsenic-reducing microbial communities in paddy soil revealed by rRNA-13C-acetate probing. Soil Biology and Biochemistry, 2022, 169, 108679.	4.2	5
7092	Effects of Host Plants on Bacterial Community Structure in Larvae Midgut of Spodoptera frugiperda. Insects, 2022, 13, 373.	1.0	9
7093	Application of fast expectation-maximization microbial source tracking to discern fecal contamination in rivers exposed to low fecal inputs. Journal of Microbiology, 2022, , 1.	1.3	3
7094	Reduced Chemical Fertilizer Combined With Bio-Organic Fertilizer Affects the Soil Microbial Community and Yield and Quality of Lettuce. Frontiers in Microbiology, 2022, 13, 863325.	1.5	28
7095	Ecological circular agriculture: A case study evaluating biogas slurry applied to rice in two soils. Chemosphere, 2022, 301, 134628.	4.2	9
7096	Variation in gut microbial communities of <i>Chilo suppressalis</i> in the typical bivoltine areas of northern China. Journal of Applied Entomology, 2022, 146, 860-874.	0.8	3
7097	Effects of Bovine <i>Pichia kudriavzevii</i> T7, <i>Candida glabrata</i> B14, and <i>Lactobacillus plantarum</i> Y9 on Milk Production, Quality and Digestive Tract Microbiome in Dairy Cows. Microorganisms, 2022, 10, 842.	1.6	4
7098	Metal resistant gut microbiota facilitates snails feeding on metal hyperaccumulator plant <i>Sedum alfredii</i> in the phytoremediation field. Ecotoxicology and Environmental Safety, 2022, 236, 113514.	2.9	7
7099	Rhizobiales as the Key Member in the Synergistic Tris (2-chloroethyl) Phosphate (TCEP) Degradation by Two Bacterial Consortia. Water Research, 2022, 218, 118464.	5.3	10
7100	Characterising the tear bacterial microbiome in young adults. Experimental Eye Research, 2022, 219, 109080.	1.2	1
7101	Chronic nitrogen deposition drives microbial community change and disrupts bacterial-fungal interactions along a subtropical urbanization gradient. Soil Biology and Biochemistry, 2022, 169, 108676.	4.2	3
7102	Effect of dietary oxidized fish oil on growth performance, physiological homeostasis and intestinal microbiome in hybrid grouper (<i>Epi-nephelus fuscoguttatus</i> — <i>Epinephelus lanceolatus</i>). Aquaculture Reports, 2022, 24, 101130.	0.7	7
7103	Root microbiome changes associated with cadmium exposure and/or overexpression of a transgene that reduces Cd content in rice. Ecotoxicology and Environmental Safety, 2022, 237, 113530.	2.9	7

#	ARTICLE	IF	CITATIONS
7104	Thinned peach polyphenols alleviate obesity in high fat mice by affecting gut microbiota. <i>Food Research International</i> , 2022, 157, 111255.	2.9	18
8200	Differential responses of dominant and rare epiphytic bacteria from a submerged macrophyte to elevated CO ₂ . <i>Environmental Science and Pollution Research</i> , 2022, , 1.	2.7	0
8201	Lower abundance of <i>Bacteroides</i> and metabolic dysfunction are highly associated with the post-weaning diarrhea in piglets. <i>Science China Life Sciences</i> , 2022, 65, 2062-2075.	2.3	21
8202	Alterations of mucosa-attached microbiome and epithelial cell numbers in the cystic fibrosis small intestine with implications for intestinal disease. <i>Scientific Reports</i> , 2022, 12, 6593.	1.6	10
8203	Retrospective genomics highlights changes in genetic composition of tiger sharks (<i>Galeocerdo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	1.6	3
8204	A cross-sectional analysis about bacterial vaginosis, high-risk human papillomavirus infection, and cervical intraepithelial neoplasia in Chinese women. <i>Scientific Reports</i> , 2022, 12, 6609.	1.6	10
8205	Enhanced removal of antibiotics using <i>Eichhornia crassipes</i> root biomass in an aerobic hollow-fiber membrane bioreactor. <i>Biofouling</i> , 2022, 38, 223-234.	0.8	3
8206	Glycine betaine uptake and metabolism in marine microbial communities. <i>Environmental Microbiology</i> , 2022, 24, 2380-2403.	1.8	20
8207	Microbial activity and community structure in $PM_{2.5}$ at different heights in ground boundary layer of Beijing atmosphere under various air quality levels. <i>Environmental Microbiology</i> , 2022, 24, 4013-4029.	1.8	2
8208	Microbiability and microbiome-wide association analyses of feed efficiency and performance traits in pigs. <i>Genetics Selection Evolution</i> , 2022, 54, 29.	1.2	9
8211	Screening of Key Fungal Strains in the Fermentation Process of the Chinese Medicinal Preparation "Lianzhifan" Based on Metabolic Profiling and High-Throughput Sequencing Technology. <i>Frontiers in Microbiology</i> , 2021, 12, 727968.	1.5	1
8212	Environmental Difference and Spatial Distance Affect the Fidelity of Variation Source of Microbial Community Structure in Air-Dried Soils. <i>Microorganisms</i> , 2022, 10, 672.	1.6	1
8213	Distribution of Microbiota in Fine Particulate Matter Particles in Guangzhou, China. <i>Biomedical and Environmental Sciences</i> , 2020, 33, 306-314.	0.2	3
8214	Comparison of organic acids supplementation on the growth performance, intestinal characteristics and morphology, and cecal microflora in broilers fed corn-soybean meal diet. <i>Animal Bioscience</i> , 2022, 35, 1689-1697.	0.8	1
8215	Bacterial DNA Detection in the Blood of Healthy Subjects.. <i>Iranian Biomedical Journal</i> , 2022, , .	0.4	0
8216	Carbon Allocation Mediated by Arbuscular Mycorrhizal Fungi Alters the Soil Microbial Community Under Various Phosphorus Levels. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8217	Disentangling the Biogeographic Responses and Assembly Patterns of Fungal Communities in Metalliferous Mining and Smelting Ecospheres. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8218	Effects of the Microbial Action Network in the Humification of Industrial Composting of Chicken Manure. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
8219	Effects of Environmental Factors on Fungal Diversity and Composition in Coastal Sediments from Guangdong, China. SSRN Electronic Journal, 0, , .	0.4	0
8220	Predicted Functional Shifts Due to Type of Soil Microbiome and Watering of Two Wild Plants in Western Region of Saudi Arabia. <i>Phyton</i> , 2022, 91, 2249-2268.	0.4	1
8221	Yeast Display for the Identification of Peptide-MHC Ligands of Immune Receptors. <i>Methods in Molecular Biology</i> , 2022, 2491, 263-291.	0.4	3
8222	Sulfamox Forwarding Thiosulfate-Driven Denitrification and Anammox Process for Nitrogen Removal. SSRN Electronic Journal, 0, , .	0.4	1
8223	Effects of Altitude on the Digestion Performance, Serum Antioxidative Characteristics, Rumen Fermentation Parameters, and Rumen Bacteria of Sanhe Heifers. <i>Frontiers in Microbiology</i> , 2022, 13, 875323.	1.5	2
8224	Predictive Microbial Community and Functional Gene Expression Profiles in Pineapple Peel Fermentation Using 16S rRNA Gene Sequences. <i>Fermentation</i> , 2022, 8, 194.	1.4	5
8225	Dietary Supplementation of Ferrous Glycine Chelate Improves Growth Performance of Piglets by Enhancing Serum Immune Antioxidant Properties, Modulating Microbial Structure and Its Metabolic Function in the Early Stage. <i>Frontiers in Veterinary Science</i> , 2022, 9, 876965.	0.9	1
8226	Suppressive Effect of Soil Microbiomes Associated with Tropical Fruit Trees on <i>Meloidogyne enterobii</i> . <i>Microorganisms</i> , 2022, 10, 894.	1.6	2
8227	A starch and sucrose-reduced dietary intervention in irritable bowel syndrome patients produced a shift in gut microbiota composition along with changes in phylum, genus, and amplicon sequence variant abundances, without affecting the microRNA levels. <i>United European Gastroenterology Journal</i> , 2022, 10, 363-375.	1.6	11
8229	Fungal Microbiota Dysbiosis and Ecological Alterations in Gastric Cancer. <i>Frontiers in Microbiology</i> , 2022, 13, 889694.	1.5	10
8230	Using de novo genome assembly and high-throughput sequencing to characterize the MHC region in a non-model bird, the Eurasian coot. <i>Scientific Reports</i> , 2022, 12, 7031.	1.6	0
8231	Changes to the gut microbiota of a wild juvenile passerine in a multidimensional urban mosaic. <i>Scientific Reports</i> , 2022, 12, 6872.	1.6	9
8232	Recent Differentiation of Aquatic Bacterial Communities in a Hydrological System in the Cuatro Ciénegas Basin, After a Natural Perturbation. <i>Frontiers in Microbiology</i> , 2022, 13, 825167.	1.5	4
8233	ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. <i>Nature</i> , 2022, 606, 358-367.	13.7	67
8234	Insights into the Interactions Between Root Phenotypic Traits and the Rhizosphere Bacterial Community. <i>Current Microbiology</i> , 2022, 79, 176.	1.0	3
8235	Soil <sc>DNA</sc> chronosequence analysis shows bacterial community reásembly following postámining forest rehabilitation. <i>Restoration Ecology</i> , 2023, 31, .	1.4	3
8236	Effects of the Lipid Metabolites and the Gut Microbiota in ApoEá/á' Mice on Atherosclerosis Co-Depression From the Microbiota-Gut-Brain Axis. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 786492.	1.6	12
8237	Yiqi-Bushen-Tiaozhi Recipe Attenuated High-Fat and High-Fructose Diet Induced Nonalcoholic Steatohepatitis in Mice via Gut Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 824597.	1.8	5

#	ARTICLE	IF	CITATIONS
8238	Gallnut Tannic Acid Exerts Anti-stress Effects on Stress-Induced Inflammatory Response, Dysbiotic Gut Microbiota, and Alterations of Serum Metabolic Profile in Beagle Dogs. <i>Frontiers in Nutrition</i> , 2022, 9, 847966.	1.6	8
8239	Operable hepatitis B virus-related hepatocellular carcinoma: gut microbiota profile of patients at different ages. <i>Annals of Translational Medicine</i> , 2022, 10, 477-477.	0.7	3
8240	Factors driving the assembly of prokaryotic communities in bulk soil and rhizosphere of <i>Torreya grandis</i> along a 900-year age gradient. <i>Science of the Total Environment</i> , 2022, 837, 155573.	3.9	7
8241	The Probiotic Strain <i>Bifidobacterium animalis</i> ssp. <i>lactis</i> HY8002 Potentially Improves the Mucosal Integrity of an Altered Intestinal Microbial Environment. <i>Frontiers in Microbiology</i> , 2022, 13, 817591.	1.5	7
8242	Role of spt23 in <i>Saccharomyces cerevisiae</i> thermal tolerance. <i>Applied Microbiology and Biotechnology</i> , 2022, , 1.	1.7	2
8243	Microbiologically influenced corrosion of steel in coastal surface seawater contaminated by crude oil. <i>Npj Materials Degradation</i> , 2022, 6, .	2.6	21
8244	Products of gut microbial Toll/interleukin-1 receptor domain NADase activities in gnotobiotic mice and Bangladeshi children with malnutrition. <i>Cell Reports</i> , 2022, 39, 110738.	2.9	13
8245	Source Tracker Modeling Based on 16S rDNA Sequencing and Analysis of Microbial Contamination Sources for Pasteurized Milk. <i>Frontiers in Nutrition</i> , 2022, 9, 845150.	1.6	3
8246	Variation of Soil Microbial Community and Sterilization to <i>Fusarium oxysporum</i> f. sp. <i>niveum</i> Play Roles in Slightly Acidic Electrolyzed Water-Alleviated Watermelon Continuous Cropping Obstacle. <i>Frontiers in Microbiology</i> , 2022, 13, 837121.	1.5	3
8247	Global spatial dynamics and vaccine-induced fitness changes of <i>Bordetella pertussis</i> . <i>Science Translational Medicine</i> , 2022, 14, eabn3253.	5.8	22
8249	Multi-Omics Integration in Mice With Parkinson's Disease and the Intervention Effect of Cyanidin-3-O-Glucoside. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, 877078.	1.7	6
8250	Effects of cage versus floor rearing system on goose intestinal histomorphology and cecal microbial composition. <i>Poultry Science</i> , 2022, 101, 101931.	1.5	7
8251	Diversity Patterns of Protists Are Highly Affected by Methods Disentangling Biological Variants: A Case Study in <i>Oligotrich</i> (s.l.) Ciliates. <i>Microorganisms</i> , 2022, 10, 913.	1.6	2
8252	Analysis of Phyllosphere Microorganisms and Potential Pathogens of Tobacco Leaves. <i>Frontiers in Microbiology</i> , 2022, 13, 843389.	1.5	7
8253	Eutrophication in subtropical lakes reinforces the dominance of balanced-variation component in temporal bacterioplankton community heterogeneity by lessening stochastic processes. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
8254	Long-Term Compost Amendment Spurs Cellulose Decomposition by Driving Shifts in Fungal Community Composition and Promoting Fungal Diversity and Phylogenetic Relatedness. <i>MBio</i> , 2022, 13, e0032322.	1.8	5
8255	Green fluorescent protein gene as a tool to examine the efficacy of <i>Agrobacterium</i> -delivered CRISPR/Cas9 reagents to generate targeted mutations in the potato genome. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 150, 587-598.	1.2	1
8256	Interaction between MHC diversity and constitution, gut microbiota and Astrovirus infections in a neotropical bat. <i>Molecular Ecology</i> , 2022, 31, 3342-3359.	2.0	16

#	ARTICLE	IF	CITATIONS
8257	Analysis of bacterial and fungal communities in fermented fish (pla-ra) from Northeast Thailand. Archives of Microbiology, 2022, 204, 302.	1.0	2
8258	The Gut Microbiota of Healthy and Flavobacterium psychrophilum-Infected Rainbow Trout Fry Is Shaped by Antibiotics and Phage Therapies. Frontiers in Microbiology, 2022, 13, .	1.5	9
8259	Changes in the intestinal microbiota of Pacific white shrimp (Litopenaeus vannamei) with different severities of Enterocytozoon hepatopenaei infection. Journal of Invertebrate Pathology, 2022, 191, 107763.	1.5	11
8260	Abundance, Diversity and Functional Potentials of Planktonic Bacteria and Microeukaryotes in the Coral-Reef System of Xisha Islands, China. Journal of Ocean University of China, 2022, 21, 748-762.	0.6	2
8261	Agricultural Management Drive Bacterial Community Assembly in Different Compartments of Soybean Soil-Plant Continuum. Frontiers in Microbiology, 2022, 13, .	1.5	3
8262	Alterations of the Gut Microbiome and Fecal Metabolome in Colorectal Cancer: Implication of Intestinal Metabolism for Tumorigenesis. Frontiers in Physiology, 2022, 13, .	1.3	10
8264	Alterations of the gut microbiota in borderline personality disorder. Journal of Psychosomatic Research, 2022, , 110942.	1.2	3
8265	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
8266	Variation in Soil Denitrification among Fertilization Regimes and Its Microbial Mechanism. Geomicrobiology Journal, 2022, 39, 722-730.	1.0	1
8267	Microbial Diversity of the Chinese Tiger Frog (Hoplobatrachus rugulosus) on Healthy versus Ulcerated Skin. Animals, 2022, 12, 1241.	1.0	4
8268	Salinity Impact on Composition and Activity of Nitrate-Reducing Fe(II)-Oxidizing Microorganisms in Saline Lakes. Applied and Environmental Microbiology, 2022, , e0013222.	1.4	2
8269	Soil bacterial communities triggered by organic matter inputs associates with a high-yielding pear production. Soil, 2022, 8, 337-348.	2.2	7
8270	Gut Dysbiosis Is Associated With the Severity of Cryptogenic Stroke and Enhanced Systemic Inflammatory Response. Frontiers in Immunology, 2022, 13, .	2.2	8
8271	High-throughput sequencing reveals the main drivers of niche-differentiation of bacterial community in the surface sediments of the northern South China sea. Marine Environmental Research, 2022, 178, 105641.	1.1	6
8272	Characterization of Rhizosphere Microbial Communities for Disease Incidence and Optimized Concentration of Difenconazole Fungicide for Controlling of Wheat Dwarf Bunt. Frontiers in Microbiology, 2022, 13, .	1.5	3
8273	Abundant and Rare Microbial Communities Respectively Contribute to an Aquaculture Pond Ecosystem. Frontiers in Marine Science, 2022, 9, .	1.2	2
8274	Biofilm thickness restraint carriers enhance free nitrous acid inhibition for partial nitrification. Water Quality Research Journal of Canada, 0, , .	1.2	1
8275	The Improvement of Semen Quality by Dietary Fiber Intake Is Positively Related With Gut Microbiota and SCFA in a Boar Model. Frontiers in Microbiology, 2022, 13, .	1.5	6

#	ARTICLE	IF	CITATIONS
8276	Bacteria Community Inhabiting Heterobasidion Fruiting Body and Associated Wood of Different Decay Classes. <i>Frontiers in Microbiology</i> , 2022, 13, 864619.	1.5	2
8277	Comparison of Three Methods for Measuring Dietary Composition of Plains Hog-nosed Snakes. <i>Herpetologica</i> , 2022, 78, .	0.2	2
8278	The Application of Mixed Organic and Inorganic Fertilizers Drives Soil Nutrient and Bacterial Community Changes in Teak Plantations. <i>Microorganisms</i> , 2022, 10, 958.	1.6	8
8279	Modified Banxia Xiexin Decoction Ameliorates Polycystic Ovarian Syndrome With Insulin Resistance by Regulating Intestinal Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	11
8280	Association of Diet and Antimicrobial Resistance in Healthy U.S. Adults. <i>MBio</i> , 2022, 13, e0010122.	1.8	25
8281	Reshaping of the soil microbiome by the expansion of invasive plants: shifts in structure, diversity, co-occurrence, niche breadth, and assembly processes. <i>Plant and Soil</i> , 2022, 477, 629-646.	1.8	11
8282	Decreased Tissue Omega-6/Omega-3 Fatty Acid Ratio Prevents Chemotherapy-Induced Gastrointestinal Toxicity Associated with Alterations of Gut Microbiome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5332.	1.8	6
8283	Effects of fertilizer and waterlogging on the diversity and functioning of the microbial community in greenhouse cultivation soil. <i>Chemical and Biological Technologies in Agriculture</i> , 2022, 9, .	1.9	2
8284	Herbivory Protection via Volatile Organic Compounds Is Influenced by Maize Genotype, Not <i>Bacillus altitudinis</i> -Enriched Bacterial Communities. <i>Frontiers in Microbiology</i> , 2022, 13, 826635.	1.5	4
8285	Significant Differences in Gut Microbiota Between Irritable Bowel Syndrome with Diarrhea and Healthy Controls in Southwest China. <i>Digestive Diseases and Sciences</i> , 2023, 68, 106-127.	1.1	5
8286	The impacts of bovine milk, soy beverage, or almond beverage on the growing rat microbiome. <i>PeerJ</i> , 2022, 10, e13415.	0.9	1
8287	Regulating Root Fungal Community Using <i>Mortierella alpina</i> for <i>Fusarium oxysporum</i> Resistance in <i>Panax ginseng</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	12
8288	Bacterial and Archaeal Water and Sediment Communities of Two Hot Spring Streams in Tengchong, Yunnan Province, China. <i>Diversity</i> , 2022, 14, 381.	0.7	1
8289	Optimization of Preservation Methods Provides Insights into Photosynthetic Picoeukaryotes in Lakes. <i>Microbiology Spectrum</i> , 2022, , e0255721.	1.2	1
8290	Application of thifluzamide alters microbial network structure and affects methane cycle genes in rice-paddy soil. <i>Science of the Total Environment</i> , 2022, 838, 155769.	3.9	1
8291	Mycobiomes of the Ocular Surface in Bacterial Keratitis Patients. <i>Frontiers in Ophthalmology</i> , 2022, 2, .	0.2	1
8292	Periodontitis pathogen <i>Porphyromonas gingivalis</i> promotes pancreatic tumorigenesis via neutrophil elastase from tumor-associated neutrophils. <i>Gut Microbes</i> , 2022, 14, 2073785.	4.3	31
8293	Microbiota alterations in proline metabolism impact depression. <i>Cell Metabolism</i> , 2022, 34, 681-701.e10.	7.2	77

#	ARTICLE	IF	CITATIONS
8294	Long-term antibiotic exposure promotes mortality after systemic fungal infection by driving lymphocyte dysfunction and systemic escape of commensal bacteria. <i>Cell Host and Microbe</i> , 2022, 30, 1020-1033.e6.	5.1	37
8295	Microbial and Nonvolatile Chemical Diversities of Chinese Dark Teas Are Differed by Latitude and Pile Fermentation. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 5701-5714.	2.4	11
8296	The role of decaying logs in nursing soil fungal diversity varies with decay classes in the forest ecosystem. <i>European Journal of Soil Science</i> , 2022, 73, .	1.8	4
8297	Microbiota Comparison of Amur ide (<i>Leuciscus waleckii</i>) Intestine and Waters at Alkaline Water and Freshwater as the Living Environment. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
8298	Subchronic Toxicity of Microcystin-LR on Young Frogs (<i>Xenopus laevis</i>) and Their Gut Microbiota. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
8299	Probiotics mitigate <i>Helicobacter pylori</i> -induced gastric inflammation and premalignant lesions in INS ^{GAS} mice with the modulation of gastrointestinal microbiota. <i>Helicobacter</i> , 2022, 27, e12898.	1.6	16
8300	Adipose tissue-derived mesenchymal stem cells' acellular product extracellular vesicles as a potential therapy for Crohn's disease. <i>Journal of Cellular Physiology</i> , 2022, , .	2.0	6
8301	The impact of dromedary camel milk on mice gut microbiota. <i>Applied Biological Chemistry</i> , 2022, 65, .	0.7	3
8302	Integrating the salivary microbiome in the forensic toolkit by 16S rRNA gene: potential application in body fluid identification and biogeographic inference. <i>International Journal of Legal Medicine</i> , 2022, 136, 975-985.	1.2	12
8303	Gut Lignocellulose Activity and Microbiota in Asian Longhorned Beetle and Their Predicted Contribution to Larval Nutrition. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	10
8304	Rapid soil rewetting promotes limited N ₂ O emissions and suppresses NH ₃ volatilization under urea addition. <i>Environmental Research</i> , 2022, 212, 113402.	3.7	8
8305	Analysis of Intestinal Microbial Diversity of Four Species of Grasshoppers and Determination of Cellulose Digestibility. <i>Insects</i> , 2022, 13, 432.	1.0	3
8306	Short-Term Responses of Soil Microbial Communities to Changes in Air Temperature, Soil Moisture and UV Radiation. <i>Genes</i> , 2022, 13, 850.	1.0	5
8307	Changes in coral bacterial communities during a natural bleaching event linked to El Niño in the South China Sea. <i>Regional Studies in Marine Science</i> , 2022, 53, 102383.	0.4	2
8308	Successions and interactions of phyllospheric microbiome in response to NH ₃ exposure. <i>Science of the Total Environment</i> , 2022, 837, 155805.	3.9	6
8309	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. <i>Food Research International</i> , 2022, 156, 111347.	2.9	16
8310	Oral administration of <i>Euglena gracilis</i> paramylon ameliorates chemotherapy-induced leukocytopenia and gut dysbiosis in mice. <i>International Journal of Biological Macromolecules</i> , 2022, 211, 47-56.	3.6	1
8311	<i>Paenibacillus</i> 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. <i>Biology</i> , 2022, 11, 727.	1.3	5

#	ARTICLE	IF	CITATIONS
8312	Different dissolved organic matter composition between central and southern glaciers on the Tibetan Plateau. <i>Ecological Indicators</i> , 2022, 139, 108888.	2.6	4
8313	Bait input altered microbial community structure and increased greenhouse gases production in coastal wetland sediment. <i>Water Research</i> , 2022, 218, 118520.	5.3	58
8314	Tree species mixing enhances rhizosphere soil organic carbon mineralization of conifers in subtropical plantations. <i>Forest Ecology and Management</i> , 2022, 516, 120238.	1.4	9
8315	GPP (composition of <i>Ganoderma lucidum</i> polysaccharides and <i>Polyporus umbellatus</i> polysaccharides) protects against DSS-induced murine colitis by enhancing immune function and regulating intestinal flora. <i>Food Science and Human Wellness</i> , 2022, 11, 795-805.	2.2	10
8316	Transformation of sulfidized nanoscale zero-valent iron particles and its effects on microbial communities in soil ecosystems. <i>Environmental Pollution</i> , 2022, 306, 119363.	3.7	12
8317	Salinity affects microbial composition and function in artificially induced biocrusts: Implications for cyanobacterial inoculation in saline soils. <i>Soil Biology and Biochemistry</i> , 2022, 170, 108691.	4.2	3
8318	Differences in geological conditions have reshaped the structure and diversity of microbial communities in oily soils. <i>Environmental Pollution</i> , 2022, 306, 119404.	3.7	15
8319	Hybridization affects the structure and function of root microbiome by altering gene expression in roots of wheat introgression line under saline-alkali stress. <i>Science of the Total Environment</i> , 2022, 835, 155467.	3.9	10
8320	Environmental factors, bacterial interactions and plant traits jointly regulate epiphytic bacterial community composition of two alpine grassland species. <i>Science of the Total Environment</i> , 2022, 836, 155665.	3.9	11
8321	Heavy rainfall accelerates the temporal turnover but decreases the deterministic processes of buried gravesoil bacterial communities. <i>Science of the Total Environment</i> , 2022, 836, 155732.	3.9	11
8322	<i>Spartina alterniflora</i> invasion and mangrove restoration alter diversity and composition of sediment diazotrophic community. <i>Applied Soil Ecology</i> , 2022, 177, 104519.	2.1	12
8323	Two isolates of <i>Rhizophagus irregularis</i> select different strategies for improving plants phosphorus uptake at moderate soil P availability. <i>Geoderma</i> , 2022, 421, 115910.	2.3	14
8324	Nitrogen addition enhanced the polycyclic aromatic hydrocarbons dissipation through increasing the abundance of related degrading genes in the soils. <i>Journal of Hazardous Materials</i> , 2022, 435, 129034.	6.5	19
8325	Conversion of mangrove forests to shrimp ponds in southeastern China destabilizes sediment microbial networks. <i>Geoderma</i> , 2022, 421, 115907.	2.3	3
8326	Response of cotton root growth and rhizosphere soil bacterial communities to the application of acid compost tea in calcareous soil. <i>Applied Soil Ecology</i> , 2022, 177, 104523.	2.1	6
8327	Community assembly, potential functions and interactions between fungi and microalgae associated with biodeterioration of sandstone at the Beishiku Temple in Northwest China. <i>Science of the Total Environment</i> , 2022, 835, 155372.	3.9	19
8329	Black Truffles Affect <i>Quercus aliena</i> Physiology and Root-Associated nirK- and nirS-Type Denitrifying Bacterial Communities in the Initial Stage of Inoculation. <i>Frontiers in Microbiology</i> , 2022, 13, 792568.	1.5	2
8330	DNA metabarcoding uncovers the diet of subterranean rodents in China. <i>PLoS ONE</i> , 2022, 17, e0258078.	1.1	2

#	ARTICLE	IF	CITATIONS
8331	Influence of warm acupuncture on gut microbiota and metabolites in rats with insomnia induced by PCPA. PLoS ONE, 2022, 17, e0267843.	1.1	12
8332	Effect of Lactobacillus plantarum LMT1-48 on Body Fat in Overweight Subjects: A Randomized, Double-Blind, Placebo-Controlled Trial. Diabetes and Metabolism Journal, 2023, 47, 92-103.	1.8	11
8333	Maize (<i>Zea mays</i> L.) genotypes induce the changes of rhizosphere microbial communities. Archives of Microbiology, 2022, 204, 321.	1.0	1
8334	Inoculation with <i>Penicillium citrinum</i> aids ginseng in resisting <i>Fusarium oxysporum</i> by regulating the root and rhizosphere microbial communities. Rhizosphere, 2022, 22, 100535.	1.4	5
8335	Glucose Increases the Abundance of Phosphate Solubilizing Bacterial Community for Better Apple Seedling Growth and Phosphate Uptake. Agronomy, 2022, 12, 1181.	1.3	1
8336	Diversity of indigenous bacteria in fermented dough with <i>Saccharomyces cerevisiae</i> Y10 and <i>Torulaspota delbrueckii</i> Y22. Food Bioscience, 2022, 48, 101786.	2.0	2
8337	Effects of Forest Gaps on the Structure and Diversity of Soil Bacterial Communities in Weeping Cypress Forest Plantations. Frontiers in Microbiology, 2022, 13, .	1.5	6
8338	Comparative Analysis of the Microbial Community Structures Between Healthy and Anthracnose-Infected Strawberry Rhizosphere Soils Using Illumina Sequencing Technology in Yunnan Province, Southwest of China. Frontiers in Microbiology, 2022, 13, .	1.5	3
8339	Intestinal Immune Development Is Accompanied by Temporal Deviation in Microbiota Composition of Newly Hatched Pigeon Squabs. Microbiology Spectrum, 2022, 10, e0189221.	1.2	5
8340	Genetic relationships between efficiency traits and gut microbiota traits in growing pigs being fed with a conventional or a high-fiber diet. Journal of Animal Science, 2022, 100, .	0.2	7
8341	Compositional Shifts in Microbial Diversity under Traditional Banana Cropping Systems of Sub-Saharan Africa. Biology, 2022, 11, 756.	1.3	2
8342	Commensal bacteria-derived extracellular vesicles suppress ulcerative colitis through regulating the macrophages polarization and remodeling the gut microbiota. Microbial Cell Factories, 2022, 21, 88.	1.9	24
8343	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
8344	Aucubin Exerts Anticancer Activity in Breast Cancer and Regulates Intestinal Microbiota. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-10.	0.5	3
8345	Factors Impacting Microplastic Biofilm Community and Biological Risks Posed by Microplastics in Drinking Water Sources. Water, Air, and Soil Pollution, 2022, 233, .	1.1	9
8346	Engineered Cas9 extracellular vesicles as a novel gene editing tool. Journal of Extracellular Vesicles, 2022, 11, e12225.	5.5	47
8347	Availability of vitamin B12 and its lower ligand intermediate $\hat{1}\pm$ -ribazole impact prokaryotic and protist communities in oceanic systems. ISME Journal, 2022, 16, 2002-2014.	4.4	12
8348	Chromosome-level assembly, annotation and phylome of <i>Pelobates cultripes</i> , the western spadefoot toad. DNA Research, 2022, 29, .	1.5	1

#	ARTICLE	IF	CITATIONS
8349	Distinct strategies of the habitat generalists and specialists in sediment of Tibetan lakes. <i>Environmental Microbiology</i> , 2022, 24, 4153-4166.	1.8	12
8350	Small Intestine Microbiome and Metabolome of High and Low Residual Feed Intake Angus Heifers. <i>Frontiers in Microbiology</i> , 2022, 13, 862151.	1.5	7
8351	Effects of norfloxacin, copper, and their interactions on microbial communities in estuarine sediment. <i>Environmental Research</i> , 2022, 212, 113506.	3.7	8
8352	Comparative Analysis of the Gut Microbiota of Mandarin Fish (<i>Siniperca chuatsi</i>) Feeding on Compound Diets and Live Baits. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	4
8353	Survival status of <i>Penaeus vannamei</i> is associated with the homeostasis and assembly process of the intestinal bacterial community. <i>Aquaculture</i> , 2022, 558, 738398.	1.7	3
8355	Distribution of Vaginal and Gut Microbiome in Advanced Maternal Age. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	3
8356	Differences in Microbial Communities Stimulated by Malic Acid Have the Potential to Improve Nutrient Absorption and Fruit Quality of Grapes. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
8357	Multiple geochemical and microbial processes regulated by redox and organic matter control the vertical heterogeneity of As and Cd in paddy soil. <i>Science of the Total Environment</i> , 2022, 839, 156229.	3.9	2
8358	Bacterial Composition and Interactions in Raw Milk and Teat Skin of Dairy Cows. <i>Fermentation</i> , 2022, 8, 235.	1.4	3
8359	Monocot diet sources drive diversity of gut bacterial communities in <i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae) larvae. <i>Journal of Applied Entomology</i> , 2022, 146, 942-956.	0.8	6
8360	Plant roots send metabolic signals to microbes in response to long-term overgrazing. <i>Science of the Total Environment</i> , 2022, 842, 156241.	3.9	9
8361	Mechanism of Electron Acceptor Promoting Propionic Acid Transformation in Anaerobic Fermentation. <i>Energies</i> , 2022, 15, 3947.	1.6	1
8362	Soil community richness and composition jointly influence the multifunctionality of soil along the forest-steppe ecotone. <i>Ecological Indicators</i> , 2022, 139, 108900.	2.6	7
8363	Comparison of the performance of raw and <i>Lactobacillus paracasei</i> fermented soybean meal in diets for turbot (<i>Scophthalmus maximus</i> L.): Growth, intestinal morphology, apoptosis, tight junction, and microbiota. <i>Aquaculture Reports</i> , 2022, 24, 101184.	0.7	2
8364	Nitrite and nitrate reduction drive sediment microbial nitrogen cycling in a eutrophic lake. <i>Water Research</i> , 2022, 220, 118637.	5.3	28
8365	Fertilizers have a greater impact on the soil bacterial community than on the fungal community in a sandy farmland ecosystem, Inner Mongolia. <i>Ecological Indicators</i> , 2022, 140, 108972.	2.6	7
8366	Comparison of structure and diversity of benthic communities in the Okinawa Trough and Mariana Trench by environmental DNA metabarcoding. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 185, 103806.	0.6	2
8367	Use of sponge iron as an indirect electron donor to provide ferrous iron for nitrate-dependent ferrous oxidation processes: Denitrification performance and mechanism. <i>Bioresource Technology</i> , 2022, 357, 127318.	4.8	14

#	ARTICLE	IF	CITATIONS
8368	Multiple metal(loid) contamination reshaped the structure and function of soil archaeal community. <i>Journal of Hazardous Materials</i> , 2022, 436, 129186.	6.5	15
8369	Response relationship of environmental factors caused by toluene concentration during leaching of capillary zone. <i>Journal of Environmental Management</i> , 2022, 317, 115366.	3.8	3
8370	Temporal variation of the coupling relationship between methanogens and biogeochemical process in soil-microbes-rice system. <i>Chemosphere</i> , 2022, 303, 135099.	4.2	1
8371	Nutrient Enrichment Decreases Dissolved Organic Carbon Sequestration Potential of Tropical Seagrass Meadows by Mediating Bacterial Activity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8372	Magnesite Driven the Complementary Effects of Core Fungi by Optimizing the Physicochemical Parameters in Pig Manure Composting. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8374	Akkermansia Muciniphila Ameliorates Chronic Kidney Disease Interstitial Fibrosis Via the Gut-Renal Axis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8375	Soil Depth Exerts Stronger Impact on Bacterial Community than Elevation in Subtropical Forests of Huangshan Mountain. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8376	Influence of Dom and Microbes on Fe Biogeochemistry at a Riverbank Filtration Site. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8377	Structural and Functional Response of Soil Bacterial Community to Consecutive Spiking of Nzvi and Pahs Revealed by Universal and Sphingomonads-Specific 16s Rrna Primers. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8378	Changes in the rumen microbiota community in ketosis cows during propylene glycol treatment. <i>Food and Function</i> , 2022, 13, 7144-7156.	2.1	1
8379	The improvement of nonalcoholic steatohepatitis by Poria cocos polysaccharides associated with gut microbiota and NF- κ B/CCL3/CCR1 axis. <i>Phytomedicine</i> , 2022, 103, 154208.	2.3	15
8380	Phage Infection Benefits Marine Diatom Phaeodactylum tricornutum by Regulating the Associated Bacterial Community. <i>Microbial Ecology</i> , 2023, 86, 144-153.	1.4	2
8381	Lower Compositional Variation and Higher Network Complexity of Rhizosphere Bacterial Community in Constructed Wetland Compared to Natural Wetland. <i>Microbial Ecology</i> , 2023, 85, 965-979.	1.4	4
8382	Dietary Cysteamine Supplementation Remarkably Increased Feed Efficiency and Shifted Rumen Fermentation toward Glucogenic Propionate Production via Enrichment of Prevotella in Feedlot Lambs. <i>Microorganisms</i> , 2022, 10, 1105.	1.6	10
8383	CRISPR/Cas9 gRNA activity depends on free energy changes and on the target PAM context. <i>Nature Communications</i> , 2022, 13, .	5.8	31
8384	Intestinal Microflora Changes in Patients with Mild Alzheimer's Disease in a Chinese Cohort. <i>Journal of Alzheimer's Disease</i> , 2022, 88, 563-575.	1.2	11
8385	Assessing the Effect of Physicochemical Properties of Saline and Sodic Soil on Soil Microbial Communities. <i>Agriculture (Switzerland)</i> , 2022, 12, 782.	1.4	6
8386	A Case Study Demonstrates That the Litter of the Rare Species Cinnamomum migao Composed of Different Tissues Can Affect the Chemical Properties and Microbial Community Diversity in Topsoil. <i>Microorganisms</i> , 2022, 10, 1125.	1.6	2

#	ARTICLE	IF	CITATIONS
8387	Effects of Tea Treatments against High-Fat Diet-Induced Disorder by Regulating Lipid Metabolism and the Gut Microbiota. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-12.	0.7	9
8388	Distinct Elevational Patterns and Their Linkages of Soil Bacteria and Plant Community in An Alpine Meadow of the Qinghai-Tibetan Plateau. <i>Microorganisms</i> , 2022, 10, 1049.	1.6	1
8389	Nitrogen Cycling Microbial Diversity and Operational Taxonomic Unit Clustering: When to Prioritize Accuracy Over Speed. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	0
8390	Plant Interaction Patterns Shape the Soil Microbial Community and Nutrient Cycling in Different Intercropping Scenarios of Aromatic Plant Species. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	9
8391	Bacterioplankton community indicators for seasonal variation in a fragmented subtropical river. <i>Environmental Monitoring and Assessment</i> , 2022, 194, .	1.3	4
8392	Combined Organic and Inorganic Fertilization Can Enhance Dry Direct-Seeded Rice Yield by Improving Soil Fungal Community and Structure. <i>Agronomy</i> , 2022, 12, 1213.	1.3	8
8393	<sc>DNA</sc>-based networks reveal the ecological determinants of plant-herbivore interactions along environmental gradients. <i>Molecular Ecology</i> , 2023, 32, 6436-6448.	2.0	2
8395	Gut microbiome mediates the protective effects of exercise after myocardial infarction. <i>Microbiome</i> , 2022, 10, .	4.9	35
8396	Metabolite-based cell sorting workflow for identifying microbes producing carbonyls in tobacco leaves. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 4199-4209.	1.7	3
8397	Variations in the Gut Microbiota in Breast Cancer Occurrence and Bone Metastasis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	12
8398	Exploring the Dynamic of Bacterial Communities in Manila Clam (<i>Ruditapes philippinarum</i>) During Refrigerated Storage. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
8400	Prediction of protein-ligand binding affinity from sequencing data with interpretable machine learning. <i>Nature Biotechnology</i> , 2022, 40, 1520-1527.	9.4	38
8401	Comparison of gut microbiome and plasma metabolome profiles between domesticated and wild Eurasian perch (<i>Perca fluviatilis</i>). <i>Aquaculture Research</i> , 2022, 53, 4076-4086.	0.9	1
8403	Rhizosphere Soil Microbial Community Under Ice in a High-Latitude Wetland: Different Community Assembly Processes Shape Patterns of Rare and Abundant Microbes. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
8404	Effects of Lightning on Rhizosphere Soil Properties, Bacterial Communities, and Active Components of <i>Camellia sinensis</i> var. <i>assamica</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
8405	Effects of amino acid composition of yeast extract on the microbiota and aroma quality of fermented soy sauce. <i>Food Chemistry</i> , 2022, 393, 133289.	4.2	23
8406	High-throughput sequencing to evaluate the effects of methamphetamine on the succession of the bacterial community to estimate the postmortem interval. <i>Forensic Sciences Research</i> , 0, , 1-12.	0.9	3
8407	Changes to the microbiome of alfalfa during the growing season and after ensiling with <i>Lentilactobacillus buchneri</i> and <i>Lentilactobacillus hilgardii</i> inoculant. <i>Journal of Applied Microbiology</i> , 2022, 133, 2331-2347.	1.4	6

#	ARTICLE	IF	CITATIONS
8409	Mucosa-Colonizing Microbiota Correlate With Host Autophagy Signaling in Patients With Inflammatory Bowel Disease. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	5
8410	Gut Microbiota and Metabolite Changes in Patients With Ulcerative Colitis and <i>Clostridioides difficile</i> Infection. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	10
8411	Comparison of Dynamics of Udder Skin Microbiota From Grazing Yak and Cattle During the Perinatal Period on the Qinghai-Tibetan Plateau. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
8412	Soil microbe inoculation alters the bacterial communities and promotes root growth of <i>Atractylodes lancea</i> under heat stress. <i>Plant and Soil</i> , 2022, 478, 371-389.	1.8	9
8414	Soil Microbes Drive the Flourishing Growth of Plants From <i>Leucocalocybe mongolica</i> Fairy Ring. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
8415	Responses of Soil Microbiota to Different Control Methods of the <i>Spartina alterniflora</i> in the Yellow River Delta. <i>Microorganisms</i> , 2022, 10, 1122.	1.6	2
8416	Comparison of Microbial Populations in the Blood of Patients With Myocardial Infarction and Healthy Individuals. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	8
8418	Gut microbiome dysbiosis in patients with hepatitis B virus-related hepatocellular carcinoma after extended hepatectomy liver failure. <i>Annals of Translational Medicine</i> , 2022, 10, 549-549.	0.7	6
8419	Deep vertical rotary tillage increases the diversity of bacterial communities and alters the bacterial network structure in soil planted to corn. <i>Canadian Journal of Soil Science</i> , 0, , .	0.5	0
8420	Subsurface drainage influences the structure and assembly of soil bacterial and fungal communities in salinized cotton field. <i>Archives of Agronomy and Soil Science</i> , 0, , 1-17.	1.3	3
8421	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. <i>PeerJ</i> , 0, 10, e13552.	0.9	2
8423	Microbial diversity composition of apple tree roots and resistance of apple Valsa canker with different grafting rootstock types. <i>BMC Microbiology</i> , 2022, 22, .	1.3	6
8424	Antioxidant potential of <i>Pediococcus pentosaceus</i> strains from the sow milk bacterial collection in weaned piglets. <i>Microbiome</i> , 2022, 10, .	4.9	16
8425	Seasonal and spatial variability of zooplankton diversity in the Poyang Lake Basin using DNA metabarcoding. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
8426	Detecting Genetic Variation of Colonizing <i>Streptococcus agalactiae</i> Genomes in Humans: A Precision Protocol. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	0
8427	Gut Microbiota Signatures in Tumor, Para-Cancerous, Normal Mucosa, and Feces in Colorectal Cancer Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	9
8428	The occurrence and feeding of a critically endangered shark species, <i>Oxynotus centrina</i> in the Sea of Marmara. <i>Journal of Fish Biology</i> , 2022, 101, 728-735.	0.7	2
8429	Alterations of Gut Microbiome and Metabolite Profiles Associated With Anabolic Lipid Dysmetabolism in Thyroid Cancer. <i>Frontiers in Endocrinology</i> , 2022, 13, .	1.5	15

#	ARTICLE	IF	CITATIONS
8430	Metabarcoding analysis of different portions of the digestive tract of scorpions (Scorpiones,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Environmental DNA, 2022, 4, 1176-1186.	3.1	2
8431	Linkage of vegetation and abiotic attributes to grazing effects on biogeographical patterns of arbuscular mycorrhizal fungal communities in temperate grasslands. Plant and Soil, 0, , .	1.8	0
8432	Unraveling Nitrogen Fixing Potential of Endophytic Diazotrophs of Different Saccharum Species for Sustainable Sugarcane Growth. International Journal of Molecular Sciences, 2022, 23, 6242.	1.8	25
8433	A health survey of the reef forming scleractinian cold-water corals <i>Lophelia pertusa</i> and <i>Madrepora oculata</i> in a remote submarine canyon on the European continental margin, NE Atlantic. Journal of Invertebrate Pathology, 2022, 192, 107782.	1.5	1
8434	Application of Organic Fertilizer Changes the Rhizosphere Microbial Communities of a Gramineous Grass on Qinghaiâ€™Tibet Plateau. Microorganisms, 2022, 10, 1148.	1.6	11
8435	Root traits and soil nutrient and carbon availability drive soil microbial diversity and composition in a northern temperate forest. Plant and Soil, 2022, 479, 281-299.	1.8	7
8436	RNA-Seq and 16S rRNA Analysis Revealed the Effect of Deltamethrin on Channel Catfish in the Early Stage of Acute Exposure. Frontiers in Immunology, 2022, 13, .	2.2	4
8437	Resilience of the wheat root-associated microbiome to the disturbance of phenanthrene. Science of the Total Environment, 2022, 838, 156487.	3.9	7
8438	Comprehensive evaluation and efficient classification of BRCA1 RING domain missense substitutions. American Journal of Human Genetics, 2022, 109, 1153-1174.	2.6	6
8439	Composition and Diversity of Gut Bacterial Community in Different Life Stages of a Leaf Beetle <i>Gastrolina depressa</i> . Microbial Ecology, 2023, 86, 590-600.	1.4	10
8440	Environmental factors influence yak milk composition by modulating short-chain fatty acid metabolism in intestinal microorganisms. LWT - Food Science and Technology, 2022, 163, 113608.	2.5	3
8441	Abundant and rare bacteria possess different diversity and function in crop monoculture and rotation systems across regional farmland. Soil Biology and Biochemistry, 2022, 171, 108742.	4.2	19
8442	Phosphate mining activities affect crop rhizosphere fungal communities. Science of the Total Environment, 2022, 838, 156196.	3.9	9
8443	Infection with white spot syndrome virus affects the microbiota in the stomachs and intestines of kuruma shrimp. Science of the Total Environment, 2022, 839, 156233.	3.9	10
8444	In-depth insights into the disruption of the microbiota-gut-blood barrier of model organism (Bombyx) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747	3.9	7
8445	Bacterial diversity and community composition in the gut and rearing water of Pacific White shrimp <i>Penaeus vannamei</i> during an outbreak of white feces disease. Aquaculture, 2022, 559, 738431.	1.7	7
8446	Regulation of exogenous acyl homoserine lactones on sludge settling performance: Monitoring via ultrasonic time-domain reflectometry. Chemosphere, 2022, 303, 135019.	4.2	3
8450	Fermented noni (<i>Morinda citrifolia</i> L.) fruit juice improved oxidative stress and insulin resistance under the synergistic effect of Nrf2/ARE pathway and gut flora in db/db mice and HepG2 cells. Food and Function, 2022, 13, 8254-8273.	2.1	7

#	ARTICLE	IF	CITATIONS
8451	Somatic Hypermutation Spectra Are Independent of the Local Transcriptional and Epigenetic Landscape. SSRN Electronic Journal, 0, , .	0.4	0
8452	Linking Soil Microbial Community to the Molecular Composition of Dissolved Organic Matter in a Boreal Forest During Freeze-Thaw Cycles. SSRN Electronic Journal, 0, , .	0.4	0
8453	Oral Microbiota, a Potential Determinant for the Treatment Efficacy of Gastric <i>Helicobacter pylori</i> Eradication in Humans. Polish Journal of Microbiology, 2022, 71, 227-239.	0.6	2
8454	Computationally designed hyperactive Cas9 enzymes. Nature Communications, 2022, 13, .	5.8	8
8455	Bacterial DNA Detection in the Blood of Healthy Subjects. Iranian Biomedical Journal, 2022, 26, 230-239.	0.4	4
8456	An emerging unrated mobile reservoir for antibiotic resistant genes: Does transportation matter to the spread. Environmental Research, 2022, 213, 113634.	3.7	2
8457	Topical Fungal Infection Induces Shifts in the Gut Microbiota Structure of Brown Planthopper, <i>Nilaparvata lugens</i> (Homoptera: Delphacidae). Insects, 2022, 13, 528.	1.0	7
8458	Investigation on the Microbial Diversity of Fresh-Cut Lettuce during Processing and Storage Using High Throughput Sequencing and Their Relationship with Quality. Foods, 2022, 11, 1683.	1.9	5
8459	Selenium-Enriched Mushroom Powder Enhances Intestinal Health and Growth Performance in the Absence of Zinc Oxide in Post-Weaned Pig Diets. Animals, 2022, 12, 1503.	1.0	8
8460	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
8461	Phyllosphere bacterial and fungal communities vary with host species identity, plant traits and seasonality in a subtropical forest. Environmental Microbiomes, 2022, 17, .	2.2	12
8462	Partial organic fertilizer substitution promotes soil multifunctionality by increasing microbial community diversity and complexity. Pedosphere, 2023, 33, 407-420.	2.1	15
8463	Effects of Inoculation With <i>Acinetobacter</i> on Fermentation of Cigar Tobacco Leaves. Frontiers in Microbiology, 0, 13, .	1.5	18
8464	Changes in the Distribution Preference of Soil Microbial Communities During Secondary Succession in a Temperate Mountain Forest. Frontiers in Microbiology, 0, 13, .	1.5	2
8465	Landscape Composition and Soil Physical-Chemical Properties Drive the Assemblages of Bacteria and Fungi in Conventional Vegetable Fields. Microorganisms, 2022, 10, 1202.	1.6	14
8466	Proteomics Analysis of <i>Zygosaccharomyces mellis</i> in Response to Sugar Stress. Processes, 2022, 10, 1193.	1.3	1
8467	Structural and functional characteristics of microbiota in oropharynx of sub-healthy children with gastrointestinal heat retention syndrome differentiated by traditional Chinese medicine. Journal of Traditional Chinese Medical Sciences, 2022, , .	0.1	0
8468	Microbial Richness of Marine Biofilms Revealed by Sequencing Full-Length 16S rRNA Genes. Genes, 2022, 13, 1050.	1.0	6

#	ARTICLE	IF	CITATIONS
8469	Soil bacterial communities under slash and burn in Mozambique as revealed by a metataxonomic approach. <i>Pedosphere</i> , 2023, 33, 508-520.	2.1	0
8470	Dysbiosis of the Gut Microbiome Is Associated With Histopathology of Lung Cancer. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
8471	Effects of Dietary Antimicrobial Growth Promoters on Performance Parameters and Abundance and Diversity of Broiler Chicken Gut Microbiome and Selection of Antibiotic Resistance Genes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	10
8472	Combined transcriptome and metabolome analysis of <i>Nerium indicum</i> L. elaborates the key pathways that are activated in response to witches' broom disease. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
8474	A long noncoding RNA promotes parasite differentiation in African trypanosomes. <i>Science Advances</i> , 2022, 8, .	4.7	12
8476	Wild and Captive Environments Drive the Convergence of Gut Microbiota and Impact Health in Threatened Equids. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
8477	GREPore-seq: A robust workflow to detect changes after gene editing through long-range PCR and nanopore sequencing. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, , .	3.0	5
8478	Benzimidazole-Resistant Isolates with E198A/V/K Mutations in the β -Tubulin Gene Possess Different Fitness and Competitive Ability in <i>Botrytis cinerea</i> . <i>Phytopathology</i> , 2022, 112, 2321-2328.	1.1	3
8479	The Component and Functional Pathways of Gut Microbiota Are Altered in Populations with Poor Sleep Quality – A Preliminary Report. <i>Polish Journal of Microbiology</i> , 2022, 71, 241-250.	0.6	1
8480	Composition of bacterial community and isolation of bacteria responsible for diuron degradation in sediment and soil under anaerobic condition. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	1
8481	Changes of the Freshwater Microbial Community Structure and Assembly Processes during Different Sample Storage Conditions. <i>Microorganisms</i> , 2022, 10, 1176.	1.6	4
8482	Trypanosomatid Richness Among Rats, Opossums, and Dogs in the Caatinga Biome, Northeast Brazil, a Former Endemic Area of Chagas Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5
8483	Variations in Marine Bacterial and Archaeal Communities during an <i>Ulva prolifera</i> Green Tide in Coastal Qingdao Areas. <i>Microorganisms</i> , 2022, 10, 1204.	1.6	6
8485	Somatic retrotransposition in the developing rhesus macaque brain. <i>Genome Research</i> , 2022, 32, 1298-1314.	2.4	4
8486	Identification of Highly Cross-Reactive Mimotopes for a Public T Cell Response in Murine Melanoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
8487	Gut Microbiome Signatures in the Progression of Hepatitis B Virus-Induced Liver Disease. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	12
8488	Analysis of microbial diversity and succession during <i>Xiaoqu Baijiu</i> fermentation using high-throughput sequencing technology. <i>Engineering in Life Sciences</i> , 2022, 22, 495-504.	2.0	12
8489	Metagenomic profiles of the early life microbiome of Indonesian inpatient neonates and their influence on clinical characteristics. <i>Scientific Reports</i> , 2022, 12, .	1.6	3

#	ARTICLE	IF	CITATIONS
8490	Profiling <i>Fusobacterium</i> infection at high taxonomic resolution reveals lineage-specific correlations in colorectal cancer. <i>Nature Communications</i> , 2022, 13, .	5.8	10
8491	Leaf-Associated Epiphytic Fungi of <i>Ginkgo biloba</i> , <i>Pinus bungeana</i> and <i>Sabina chinensis</i> Exhibit Delicate Seasonal Variations. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 631.	1.5	4
8492	Fecal-associated microbiome differences between phlegm-dampness constitution and balanced constitution. <i>Journal of Traditional Chinese Medical Sciences</i> , 2022, , .	0.1	0
8493	Tetraploid Ancestry Provided Atlantic Salmon With Two Paralogous Functional T Cell Receptor Beta Regions Whereof One Is Completely Novel. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
8494	Analysis of Microbial Community, Volatile Flavor Compounds, and Flavor of Cigar Tobacco Leaves From Different Regions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	22
8495	A pan-genome data structure induced by pooled sequencing facilitates variant mining in heterogeneous germplasm. <i>Molecular Breeding</i> , 2022, 42, .	1.0	0
8496	Machine-learning-optimized Cas12a barcoding enables the recovery of single-cell lineages and transcriptional profiles. <i>Molecular Cell</i> , 2022, 82, 3103-3118.e8.	4.5	14
8498	<i>N</i> -Acetylglucosamine Promotes Tomato Plant Growth by Shaping the Community Structure and Metabolism of the Rhizosphere Microbiome. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
8499	Global warming responses of gut microbiota in moose (<i>Alces alces</i>) populations with different dispersal patterns. <i>Journal of Zoology</i> , 2022, 318, 63-73.	0.8	2
8500	Effect of live yeast supplementation in sow diet during gestation and lactation on sow and piglet fecal microbiota, health, and performance. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	4
8501	The Effects of DNA Extraction Kits and Primers on Prokaryotic and Eukaryotic Microbial Community in Freshwater Sediments. <i>Microorganisms</i> , 2022, 10, 1213.	1.6	4
8502	Biodegradation of arsenobetaine to inorganic arsenic regulated by specific microorganisms and metabolites in mice. <i>Toxicology</i> , 2022, 475, 153238.	2.0	3
8503	Microbiome-Metabolome Responses in Ruminal Content and Feces of Lactating Dairy Cows With N-Carbamylglutamate Supplementation Under Heat Stress. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	1
8504	Presence of <i>Blastocystis</i> in gut microbiota is associated with cognitive traits and decreased executive function. <i>ISME Journal</i> , 2022, 16, 2181-2197.	4.4	10
8505	Evaluation of different primers of the 18S rRNA gene to profile amoeba communities in environmental samples. , 2022, 1, 100057.		5
8506	Bacterial diversity in <i>Haemagogus leucocelaenus</i> (Diptera: Culicidae) from Vale do Ribeira, São Paulo, Brazil. <i>BMC Microbiology</i> , 2022, 22, .	1.3	4
8507	Effect of precision air supply cooling system with different cooling air speed on reproductive performance, stress status, immunoglobulin and fecal microbiota of lactating sows. <i>Journal of Thermal Biology</i> , 2022, 108, 103249.	1.1	4
8508	RNase III CLASH in MRSA uncovers sRNA regulatory networks coupling metabolism to toxin expression. <i>Nature Communications</i> , 2022, 13, .	5.8	14

#	ARTICLE	IF	CITATIONS
8509	Dynamic succession of microbial community in Nongxiangxing daqu and microbial roles involved in flavor formation. <i>Food Research International</i> , 2022, 159, 111559.	2.9	23
8510	Distribution of ammonia oxidizers and their role in N ₂ O emissions in the reservoir riparian zone. <i>Journal of Basic Microbiology</i> , 2022, 62, 1179-1192.	1.8	3
8512	Microbial succession and exploration of higher alcohols-producing core bacteria in northern Huangjiu fermentation. <i>AMB Express</i> , 2022, 12, .	1.4	9
8513	Characteristics of Wild Bird Resistomes and Dissemination of Antibiotic Resistance Genes in Interconnected Bird-Habitat Systems Revealed by Similarity of <i>bla</i> _{TEM} Polymorphic Sequences. <i>Environmental Science & Technology</i> , 2022, 56, 15084-15095.	4.6	18
8514	Dietary Tryptophan-Mediated Aryl Hydrocarbon Receptor Activation by the Gut Microbiota Alleviates <i>Escherichia coli</i> -Induced Endometritis in Mice. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	18
8515	Endophytic Fungal and Bacterial Microbiota Shift in Rice and Barnyardgrass Grown under Co-Culture Condition. <i>Plants</i> , 2022, 11, 1592.	1.6	2
8516	Proteome-Scale Screening to Identify High-Expression Signal Peptides with Minimal N-Terminus Biases via Yeast Display. <i>ACS Synthetic Biology</i> , 2022, 11, 2405-2416.	1.9	4
8517	Pathogen profiling of Australian rabbits by metatranscriptomic sequencing. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	3
8518	Posterior cingulate cortex reveals an expression profile of resilience in cognitively intact elders. <i>Brain Communications</i> , 2022, 4, .	1.5	10
8519	Draft Genome Sequences of <i>Erysipelothrix</i> sp. Strains Isolated from Stranded Septic Bottlenose Dolphins in Alabama, USA. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
8520	Altitude-adaption of gut microbiota in Tibetan chicken. <i>Poultry Science</i> , 2022, 101, 101998.	1.5	10
8521	Effects of urea supplementation on the nutritional quality and microbial community of alfalfa (<i>Medicago sativa</i> L.) silage. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	5
8522	Loss of MMR and TGFBR2 Increases the Susceptibility to Microbiota-Dependent Inflammation-Associated Colon Cancer. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 14, 693-717.	2.3	6
8523	<i>Saccharomyces Boulardii</i> Ameliorates Non-alcoholic Steatohepatitis in Mice Induced by a Methionine-Choline-Deficient Diet Through Gut-Liver Axis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8524	Gut microbiota in mucosa and feces of newly diagnosed, treatment-naïve adult inflammatory bowel disease and irritable bowel syndrome patients. <i>Gut Microbes</i> , 2022, 14, .	4.3	20
8525	Effect of Shrub Encroachment on Alpine Grass Soil Microbial Community Assembly. <i>Frontiers in Soil Science</i> , 0, 2, .	0.8	1
8526	Gut dysbiosis promotes prostate cancer progression and docetaxel resistance via activating NF- κ B-IL6-STAT3 axis. <i>Microbiome</i> , 2022, 10, .	4.9	48
8527	Comprehensive Analysis of Gut Microbiota and Fecal Bile Acid Profiles in Children With Biliary Atresia. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	6

#	ARTICLE	IF	CITATIONS
8528	HBV genome-enriched single cell sequencing revealed heterogeneity in HBV-driven hepatocellular carcinoma (HCC). BMC Medical Genomics, 2022, 15, .	0.7	6
8529	Changes in Soil Organic Carbon Fractions and Fungal Communities, Subsequent to Different Management Practices in Moso Bamboo Plantations. Journal of Fungi (Basel, Switzerland), 2022, 8, 640.	1.5	8
8530	Responses of Cyanobacterial Crusts and Microbial Communities to Extreme Environments of the Stratosphere. Microorganisms, 2022, 10, 1252.	1.6	2
8531	Partitioning of beta-diversity reveals distinct assembly mechanisms of plant and soil microbial communities in response to nitrogen enrichment. Ecology and Evolution, 2022, 12, .	0.8	4
8532	Nano- and micro-polystyrene plastics disturb gut microbiota and intestinal immune system in honeybee. Science of the Total Environment, 2022, 842, 156819.	3.9	22
8533	Reduction of microbial diversity in grassland soil is driven by long-term climate warming. Nature Microbiology, 2022, 7, 1054-1062.	5.9	86
8535	Changes in Gut Microbiota Composition Associated with the Presence of Enteric Protist <i>Blastocystis</i> in Captive Forest Musk Deer (<i>Moschus Berezovskii</i>). Microbiology Spectrum, 0, , .	1.2	1
8536	Effects of Habitat River Microbiome on the Symbiotic Microbiota and Multi-Organ Gene Expression of Captive-Bred Chinese Giant Salamander. Frontiers in Microbiology, 0, 13, .	1.5	5
8537	Response of Chinese mitten crab (<i>Eriocheir sinensis</i>) intestinal microbiota to commercial probiotic application. Aquaculture Research, 0, , .	0.9	2
8538	Gut Microbiota Characteristics Are Associated With Severity of Acute Radiation-Induced Esophagitis. Frontiers in Microbiology, 0, 13, .	1.5	3
8539	Ancient DNA from a 2700-year-old goitered gazelle (<i>Gazella subgutturosa</i>) supports gazelle hunting in Iron Age Central Asia. Royal Society Open Science, 2022, 9, .	1.1	1
8540	Dietary Mannan Oligosaccharides Enhance the Non-Specific Immunity, Intestinal Health, and Resistance Capacity of Juvenile Blunt Snout Bream (<i>Megalobrama amblycephala</i>) Against <i>Aeromonas hydrophila</i> . Frontiers in Immunology, 0, 13, .	2.2	15
8541	Effects of Diet on the Gut Microbial Communities of Nile Tilapia (<i>Oreochromis niloticus</i>) Across Their Different Life Stages. Frontiers in Marine Science, 0, 9, .	1.2	1
8542	Protocol for correlation analysis of the murine gut microbiome and meta-metabolome using 16S rDNA sequencing and UPLC-MS. STAR Protocols, 2022, 3, 101494.	0.5	0
8543	From the bacterial citrus microbiome to the selection of potentially host-beneficial microbes. New Biotechnology, 2022, 70, 116-128.	2.4	7
8544	Culture-dependent and culture-independent methods reveal microbe-clay mineral interactions by dissimilatory iron-reducing bacteria in an integral oilfield. Science of the Total Environment, 2022, 840, 156577.	3.9	13
8545	Negative effects of poly(butylene adipate-co-terephthalate) microplastics on Arabidopsis and its root-associated microbiome. Journal of Hazardous Materials, 2022, 437, 129294.	6.5	34
8546	Stronger effects of maize rhizosphere than phosphorus fertilization on phosphatase activity and phosphorus-mineralizing-related bacteria in acidic soils. Rhizosphere, 2022, 23, 100555.	1.4	13

#	ARTICLE	IF	CITATIONS
8547	Wheat cover crop alters soil microbial community and increases cucumber yield under different potassium regimes. <i>European Journal of Agronomy</i> , 2022, 139, 126567.	1.9	7
8548	Linkages between the temperature sensitivity of soil respiration and microbial life strategy are dependent on sampling season. <i>Soil Biology and Biochemistry</i> , 2022, 172, 108758.	4.2	30
8549	Temporal heterogeneity of bacterial communities and their responses to <i>Raphidiopsis raciborskii</i> blooms. <i>Microbiological Research</i> , 2022, 262, 127098.	2.5	1
8550	Cyanobacterial bloom intensities determine planktonic eukaryote community structure and stability. <i>Science of the Total Environment</i> , 2022, 838, 156637.	3.9	10
8551	Responses of edaphic factors and microbial community to terrestrial succession and experimental warming in coastal salt marshes. <i>Pedobiologia</i> , 2022, 93-94, 150821.	0.5	0
8552	Interlinkages between soil properties and keystone taxa under different tillage practices on the North China Plain. <i>Applied Soil Ecology</i> , 2022, 178, 104551.	2.1	15
8553	Soil texture and pH exhibit important effects on biological nitrogen fixation in paddy soil. <i>Applied Soil Ecology</i> , 2022, 178, 104571.	2.1	6
8554	In vivo engineered B cells secrete high titers of broadly neutralizing anti-HIV antibodies in mice. <i>Nature Biotechnology</i> , 2022, 40, 1241-1249.	9.4	29
8555	16S rRNA gene sequencing reveals an altered composition of gut microbiota in children with <i>Mycoplasma pneumoniae</i> pneumonia treated with azithromycin. <i>Journal of General and Applied Microbiology</i> , 2022, , .	0.4	1
8556	ç¥è¿žã±±ãšã¹ã†»ãœÿãĈãç”²çf·éĈšé†ã,žç”²çf·ã¼¼®ç”Ÿç%©ç¼4è¼/2ç»„,æ^çš„ã...³ç³». <i>Diqiu Kexue - Zhongguo Dizhi Daxue Xuebao/Earth Geosciences</i> , 2022, 47, 556.	0.1	1
8557	Response of Bacterial Diversity and Community Structure to Heavy Metals in Mangrove Sediments from South China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8558	Prior exposure to ciprofloxacin disrupts intestinal homeostasis and predisposes ayu (<i>Plecoglossus altivelis</i>) to subsequent <i>Pseudomonas plecoglossicida</i>-induced infection. <i>Zoological Research</i> , 2022, 43, 648-665.	0.9	3
8559	Eukaryotic Plankton Community Assembly and Influencing Factors between Continental Shelf and Slope Sites in the Northern South China Sea. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8560	Effects of Dietary Yeast Culture on Health Status in Digestive Tract of Juvenile Pacific White Shrimp <i>Litopenaeus Vannamei</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8561	Revealing the Impact of the Environment on the Ginsenosides in American Ginseng from Three Scales: Bioclimatic Factors, Soil Physicochemical Properties and Microbial Communities. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8562	Induced Bitter Gourd Yield Enhancement by Bio-Organic Fertilizer Application Associated with Rhizosphere Microflora Alteration. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8563	Impacts of groundwater level fluctuation on soil microbial community, alkane degradation efficiency and alkane-degrading gene diversity in the critical zone: Evidence from an accelerated water table fluctuation simulation. <i>Environmental Science and Pollution Research</i> , 2022, 29, 83060-83070.	2.7	2
8564	Integrated Analysis of the Alterations in Gut Microbiota and Metabolites of Mice Induced After Long-Term Intervention With Different Antibiotics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4

#	ARTICLE	IF	CITATIONS
8566	Gut microbiota differs in composition between adults with type 1 diabetes with or without depression and healthy control participants: a case-control study. <i>BMC Microbiology</i> , 2022, 22, .	1.3	7
8567	Comparison and Correlation Analysis of Immune Function and Gut Microbiota of Broiler Chickens Raised in Double-Layer Cages and Litter Floor Pens. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
8568	Soil-derived bacteria endow <i>Camellia</i> weevil with more ability to resist plant chemical defense. <i>Microbiome</i> , 2022, 10, .	4.9	12
8569	Regulatory Effect of <i>Lactiplantibacillus plantarum</i> 2-33 on Intestinal Microbiota of Mice With Antibiotic-Associated Diarrhea. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	11
8572	A Stronger Rhizosphere Impact on the Fungal Communities Compared to the Bacterial Communities in Pecan Plantations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
8573	Two New Species of Filamentous Sulfur Bacteria of the Genus <i>Thiothrix</i> , <i>Thiothrix winogradskyi</i> sp. nov. and <i>Candidatus Thiothrix sulfatifontis</i> sp. nov.. <i>Microorganisms</i> , 2022, 10, 1300.	1.6	6
8574	Reno-Protective Effect of Low Protein Diet Supplemented With \pm -Ketoacid Through Gut Microbiota and Fecal Metabolism in 5/6 Nephrectomized Mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	5
8575	Sparse logistic regression revealed the associations between HBV PreS quasispecies and hepatocellular carcinoma. <i>Virology Journal</i> , 2022, 19, .	1.4	1
8576	The Absence of STING Ameliorates Non-Alcoholic Fatty Liver Disease and Reforms Gut Bacterial Community. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
8577	Rhizosphere 16S-ITS Metabarcoding Profiles in Banana Crops Are Affected by Nematodes, Cultivation, and Local Climatic Variations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
8578	Ecological Responses of Core Phytoplankton by Latitudinal Differences in the Arctic Ocean in Late Summer Revealed by 18S rDNA Metabarcoding. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
8579	<i>Lactobacillus casei</i> SYF-08 Protects Against Pb-Induced Injury in Young Mice by Regulating Bile Acid Metabolism and Increasing Pb Excretion. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	1
8580	Differential Responses of Digesta- and Mucosa-Associated Jejunal Microbiota of Hu Sheep to Pelleted and Non-Pelleted High-Grain Diets. <i>Animals</i> , 2022, 12, 1695.	1.0	3
8581	Activation-Induced Cytidine Deaminase Impacts the Primary Antibody Repertoire in Naive Mice. <i>Journal of Immunology</i> , 2022, 208, 2632-2642.	0.4	0
8582	Effects on community composition and function <i>Pinus massoniana</i> infected by <i>Bursaphelenchus xylophilus</i> . <i>BMC Microbiology</i> , 2022, 22, .	1.3	4
8584	A Drying-Rewetting Cycle Imposes More Important Shifts on Soil Microbial Communities than Does Reduced Precipitation. <i>MSystems</i> , 2022, 7, .	1.7	12
8585	Environmental exposure to swine farms reshapes human gut microbiota. <i>Chemosphere</i> , 2022, 307, 135558.	4.2	5
8586	Insights on Gut and Skin Wound Microbiome in Stranded Indo-Pacific Finless Porpoise (<i>Neophocaena</i>) Tj ETQq1 1 0,784314 rgBT /Overl	1.6	3

#	ARTICLE	IF	CITATIONS
8587	Shen-Ling-Bai-Zhu-San (SL) and SL Derived-Polysaccharide (PL) Ameliorate the Severity of Diarrhea-Induced by High Lactose via Modification of Colonic Fermentation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
8588	Bacterial Metabolic Potential in Response to Climate Warming Alters the Decomposition Process of Aquatic Plant Litter in Shallow Lake Mesocosms. <i>Microorganisms</i> , 2022, 10, 1327.	1.6	0
8589	Altering Methane Emission, Fatty Acid Composition, and Microbial Profile during In Vitro Ruminant Fermentation by Manipulating Dietary Fatty Acid Ratios. <i>Fermentation</i> , 2022, 8, 310.	1.4	8
8591	Microhabitat Governs the Microbiota of the Pinewood Nematode and Its Vector Beetle: Implication for the Prevalence of Pine Wilt Disease. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
8592	Liver Transcriptome and Gut Microbiome Analysis Reveals the Effects of High Fructose Corn Syrup in Mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	3
8593	Identification and Characterization of a Novel Species of Genus <i>Akkermansia</i> with Metabolic Health Effects in a Diet-Induced Obesity Mouse Model. <i>Cells</i> , 2022, 11, 2084.	1.8	5
8594	Gut Bacterial Diversity and Community Structure of <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae) in the Welsh Onion-producing Areas of North China. <i>Journal of Economic Entomology</i> , 0, , .	0.8	0
8595	Octanoate Alleviates Dietary Soybean Oil-Induced Intestinal Physical Barrier Damage, Oxidative Stress, Inflammatory Response and Microbial Dysbiosis in Large Yellow Croaker (<i>Larimichthys Crocea</i>). <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
8596	Recombinant Muscovy Duck Parvovirus Led to Ileac Damage in Muscovy Ducklings. <i>Viruses</i> , 2022, 14, 1471.	1.5	1
8597	Analysis of bacterial diversity and genetic evolution of <i>Lactocaseibacillus paracasei</i> isolates in fermentation pit mud. <i>Journal of Applied Microbiology</i> , 2022, 133, 1821-1831.	1.4	1
8598	Comparison of the co-occurrence patterns of the gut microbial community between Bt-susceptible and Bt-resistant strains of the rice stem borer, <i>Chilo suppressalis</i> . <i>Journal of Pest Science</i> , 2023, 96, 299-315.	1.9	6
8599	Microbial Networks Reveal the Structure of Water Microbial Communities in Kalamaili Mountain Ungulate Nature Reserve. <i>Water (Switzerland)</i> , 2022, 14, 2188.	1.2	1
8600	Effect of the combination of superchilling and super-chilled storage on shelf-life and bacterial community dynamics of beef during long-term storage. <i>Meat Science</i> , 2022, 192, 108910.	2.7	4
8601	<i>Pseudomonas</i> spp. Enriched in Endophytic Community of Healthy Cotton Plants Inhibit Cotton Verticillium Wilt. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
8602	Effects of Land Use on the Soil Microbial Community in the Songnen Grassland of Northeast China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
8603	Diversity of <i>Fusarium</i> community assembly shapes mycotoxin accumulation of diseased wheat heads. <i>Molecular Ecology</i> , 2023, 32, 2504-2518.	2.0	7
8604	DNA Methylation and mRNA Expression of B7-H3 Gene in Ankylosing Spondylitis: A Case-Control Study. <i>Immunological Investigations</i> , 2022, 51, 2025-2034.	1.0	4
8605	Regulation of wheat bran feruloyl oligosaccharides in the intestinal antioxidative capacity of rats associated with the p38/JNK/Nrf2 signaling pathway and gut microbiota. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 6992-7002.	1.7	5

#	ARTICLE	IF	CITATIONS
8606	Microbes in a neutral-alkaline paddy soil react differentially to intact and acid washed biochar. <i>Journal of Soils and Sediments</i> , 2022, 22, 3137-3150.	1.5	1
8607	Major Histocompatibility Complex Variation and Haplotype Associated Survival in Response to Experimental Infection of Two Bd-GPL Strains Along a Latitudinal Gradient. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	6
8608	Riverine bacterioplankton and phytoplankton assembly along an environmental gradient induced by urbanization. <i>Limnology and Oceanography</i> , 2022, 67, 1943-1958.	1.6	21
8609	Comparative analysis of the intestinal tract microbiota and feeding habits of five sympatric flycatchers. <i>Avian Research</i> , 2022, , 100050.	0.5	1
8610	Nasal microbiota evolution within the congregate setting imposed by military training. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
8611	Characteristics of Gut Microbiota in Patients With Clear Cell Renal Cell Carcinoma. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
8612	Effects of Salinity on the Growth, Physiological Characteristics, and Intestinal Microbiota of the Echiura Worm (<i>Urechis uncinatus</i>). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
8613	Seasonal and Soil Microbiota Effects on the Adaptive Strategies of Wild Goitered Gazelles Based on the Gut Microbiota. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
8614	Benzoic Acid Metabolism and Lipopolysaccharide Synthesis of Intestinal Microbiome Affects the Health of Ruminants under Free-Range and Captive Mode. <i>Life</i> , 2022, 12, 1071.	1.1	2
8615	Assessing the Diet of a Predator Using a DNA Metabarcoding Approach. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
8616	Assessing Asiatic cheetahâ€™s individual diet using metabarcoding and its implication for conservation. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
8617	Comparative Genomics of Thaumarchaeota From Deep-Sea Sponges Reveal Their Niche Adaptation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8618	Native tree root exudates promote tolerance of simulated herbivory of an invasive tree via altered functional traits. <i>Plant and Soil</i> , 2022, 479, 389-404.	1.8	1
8619	Animal Activities of the Key Herbivore Plateau Pika (<i>Ochotona curzoniae</i>) on the Qinghai-Tibetan Plateau Affect Grassland Microbial Networks and Ecosystem Functions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
8620	Changes in the Species and Functional Composition of Activated Sludge Communities Revealed Mechanisms of Partial Nitrification Established by Ultrasonication. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8621	Orchid mycorrhizal fungi and ascomycetous fungi in epiphytic <i>Vanda falcata</i> roots occupy different niches during growth and development. <i>Mycorrhiza</i> , 2022, 32, 481-495.	1.3	2
8622	A comprehensive resource for <i>Bordetella</i> genomic epidemiology and biodiversity studies. <i>Nature Communications</i> , 2022, 13, .	5.8	11
8623	Microbial community changes during anaerobic nitrate reduction and Fe(II) oxidation of a coastal saline paddy soil under alkaline pH. <i>Journal of Soils and Sediments</i> , 0, , .	1.5	1

#	ARTICLE	IF	CITATIONS
8624	Effect of Doxycycline Use in the Early Broiler Production Cycle on the Microbiome. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8625	Coix Seed-Based Milk Fermented With <i>Limosilactobacillus reuteri</i> Improves Lipid Metabolism and Gut Microbiota in Mice Fed With a High-Fat Diet. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	4
8626	Bacteria related to tick-borne pathogen assemblages in <i>Ornithodoros cf. hasei</i> (Acari: Argasidae) and blood of the wild mammal hosts in the Orinoquia region, Colombia. <i>Experimental and Applied Acarology</i> , 2022, 87, 253-271.	0.7	4
8627	Dietary Concentrate-to-Forage Ratio Affects Rumen Bacterial Community Composition and Metabolome of Yaks. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	18
8628	Stochastic processes shape the aggregation of free-living and particle-attached bacterial communities in the Yangtze River Estuary, China. <i>Journal of Basic Microbiology</i> , 2022, 62, 1514-1525.	1.8	5
8629	Differences in the methanogen community between the nearshore and offshore sediments of the South Yellow Sea. <i>Journal of Microbiology</i> , 2022, 60, 814-822.	1.3	2
8630	Seasonal variations of soil fungal diversity and communities in subalpine coniferous and broadleaved forests. <i>Science of the Total Environment</i> , 2022, 846, 157409.	3.9	13
8632	Functional Properties of Protein Hydrolysates on Growth, Digestive Enzyme Activities, Protein Metabolism, and Intestinal Health of Larval Largemouth Bass (<i>Micropterus salmoides</i>). <i>Frontiers in Immunology</i> , 0, 13, .	2.2	13
8633	Diversity of endophytic bacteria of mulberry (<i>Morus L.</i>) under cold conditions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8634	Microbial and Transcriptomic Profiling Reveals Diet-Related Alterations of Metabolism in Metabolic Disordered Mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
8635	Construction and characterization of microsatellite markers for the Neptune whelk, <i>Neptunea cumingii</i> . <i>Molecular Biology Reports</i> , 2022, 49, 9065-9069.	1.0	2
8636	Association of serum 25-hydroxyvitamin D (25(OH)D) levels with the gut microbiota and metabolites in postmenopausal women in China. <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	4
8637	Depicting Fecal Microbiota Characteristic in Yak, Cattle, Yak-Cattle Hybrid and Tibetan Sheep in Different Eco-Regions of Qinghai-Tibetan Plateau. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
8638	SmcHD1 underlies the formation of H3K9me3 blocks on the inactive X chromosome in mice. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	9
8639	Root-Associated Microbiota Response to Ecological Factors: Role of Soil Acidity in Enhancing Citrus Tolerance to Huanglongbing. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
8640	Effect of <i>Saccharomyces cerevisiae</i> culture mitigates heat stress-related damage in dairy cows by multi-omics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8641	Maternal and/or direct supplementation with a combination of a casein hydrolysate and yeast β -glucan on post-weaning performance and intestinal health in the pig. <i>PLoS ONE</i> , 2022, 17, e0265051.	1.1	1
8642	Combining eDNA and morphological approaches to reveal the impacts of long-term discharges of shale gas wastewaters on receiving waters. <i>Water Research</i> , 2022, 222, 118869.	5.3	8

#	ARTICLE	IF	CITATIONS
8643	Salinity-Linked Denitrification Potential in Endorheic Lake Bosten (China) and Its Sensitivity to Climate Change. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8644	Metagenomic analysis of the dynamical conversion of photosynthetic bacterial communities in different crop fields over different growth periods. <i>PLoS ONE</i> , 2022, 17, e0262517.	1.1	2
8645	Climate drives rhizosphere microbiome variation and divergent selection between geographically distant <i>Arabidopsis</i> populations. <i>New Phytologist</i> , 2022, 236, 608-621.	3.5	9
8646	Comparative Analysis of the Gut Microbiota of Three Sympatric Terrestrial Wild Bird Species Overwintering in Farmland Habitats. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
8647	Distribution of sediment microbial communities and their relationship with surrounding environmental factors in a typical rural river, Southwest China. <i>Environmental Science and Pollution Research</i> , 2022, 29, 84206-84225.	2.7	15
8649	High-Altitude Drives the Convergent Evolution of Alpha Diversity and Indicator Microbiota in the Gut Microbiomes of Ungulates. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
8650	Bacterial community in <i>Sinonovacula constricta</i> intestine and its relationship with culture environment. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 5211-5220.	1.7	2
8651	Changes in Microbial Diversity and Nutritional Components of Mare Milk Before and After Traditional Fermentation. <i>Frontiers in Sustainable Food Systems</i> , 0, 6, .	1.8	1
8652	The Impact of Environmental Habitats and Diets on the Gut Microbiota Diversity of True Bugs (Hemiptera: Heteroptera). <i>Biology</i> , 2022, 11, 1039.	1.3	9
8653	Actinobacteria Community and Their Antibacterial and Cytotoxic Activity on the Weizhou and Xieyang Volcanic Islands in the Beibu Gulf of China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
8654	Oregano Essential Oils Mediated Intestinal Microbiota and Metabolites and Improved Growth Performance and Intestinal Barrier Function in Sheep. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
8655	iCodon customizes gene expression based on the codon composition. <i>Scientific Reports</i> , 2022, 12, .	1.6	11
8656	Effect of Bergamot and Laoxianghuang Polysaccharides on Gut Microbiota Derived from Patients with Hyperlipidemia: An Integrative Analysis of Microbiome and Metabolome during In Vitro Fermentation. <i>Foods</i> , 2022, 11, 2039.	1.9	3
8657	Effects of Different Native Plants on Soil Remediation and Microbial Diversity in Jiulong Iron Tailings Area, Jiangxi. <i>Forests</i> , 2022, 13, 1106.	0.9	3
8658	Salmonella Phages Affect the Intestinal Barrier in Chicks by Altering the Composition of Early Intestinal Flora: Association With Time of Phage Use. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
8659	Gut microbiota composition in colorectal cancer patients is genetically regulated. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
8660	Healthy Gut Microbiome Composition Enhances Disease Resistance and Fat Deposition in Tibetan Pigs. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
8661	Local domestication of soybean leads to strong root selection and diverse filtration of root-associated bacterial communities. <i>Plant and Soil</i> , 2022, 480, 439-455.	1.8	5

#	ARTICLE	IF	CITATIONS
8662	Main Factors Influencing the Gut Microbiota of Datong Yaks in Mixed Group. <i>Animals</i> , 2022, 12, 1777.	1.0	1
8663	Characterization of the oral microbiome of children with type 1 diabetes in the acute and chronic phases. <i>Journal of Oral Microbiology</i> , 2022, 14, .	1.2	5
8664	16S rRNA gene sequencing analysis on changes in the intestinal flora of <i>Procambarus clarkii</i> with "Black May" disease. <i>Journal of Oceanology and Limnology</i> , 0, , .	0.6	0
8665	Soil microbes-mediated enzymes promoted the secondary succession in post-mining plantations on the Loess Plateau, China. <i>Soil Ecology Letters</i> , 2023, 5, 79-93.	2.4	4
8666	Antibiotic resistance genes and their links with bacteria and environmental factors in three predominant freshwater aquaculture modes. <i>Ecotoxicology and Environmental Safety</i> , 2022, 241, 113832.	2.9	16
8667	Application of potential probiotic strain <i>Streptomyces</i> sp. SH5 on anti- <i>Aeromonas</i> infection in zebrafish larvae. <i>Fish and Shellfish Immunology</i> , 2022, 127, 375-385.	1.6	8
8668	Two <i>Laminaria japonica</i> polysaccharides with distinct structure characterization affect gut microbiota and metabolites in hyperlipidemic mice differently. <i>Food Research International</i> , 2022, 159, 111615.	2.9	16
8669	Pollution pressure and soil depth drive prokaryotic microbial assemblage and co-occurrence patterns in an organic polluted site. <i>Journal of Hazardous Materials</i> , 2022, 438, 129570.	6.5	8
8670	Differences in microbiome of healthy Sprague Dawley rats with <i>Paragonimus proliferus</i> infection and potential pathogenic role of microbes in paragonimiasis. <i>Acta Tropica</i> , 2022, 233, 106578.	0.9	1
8671	Fungal communities differ with microplastic types in deep sea sediment enrichments of the Eastern Pacific. <i>International Biodeterioration and Biodegradation</i> , 2022, 173, 105461.	1.9	5
8672	Unraveling the contribution of pre-salting duration to microbial succession and changes of volatile and non-volatile organic compounds in Suancai (a Chinese traditional fermented vegetable) during fermentation. <i>Food Research International</i> , 2022, 159, 111673.	2.9	10
8673	Oligosaccharide and short-chain fatty acid: A double-edged sword in obese mice by regulating food intake and fat synthesis. <i>Food Research International</i> , 2022, 159, 111619.	2.9	8
8674	Application of slow-releasing green denaturing colloidal substrates to contain and bioremediate hexavalent-chromium plume. <i>Journal of Cleaner Production</i> , 2022, 365, 132769.	4.6	3
8675	Effect of low temperature and municipal wastewater organic loading on anaerobic granule reactor performance. <i>Bioresource Technology</i> , 2022, 360, 127616.	4.8	4
8676	Stratification of microbial communities and their functions in mossy biofilms colonizing the giant monolithic statue of buddha. <i>International Biodeterioration and Biodegradation</i> , 2022, 173, 105456.	1.9	3
8677	Magnesite driven the complementary effects of core fungi by optimizing the physicochemical parameters in pig manure composting. <i>Bioresource Technology</i> , 2022, 360, 127541.	4.8	13
8678	Grass-legume mixtures enhance forage production via the bacterial community. <i>Agriculture, Ecosystems and Environment</i> , 2022, 338, 108087.	2.5	21
8679	Acetic acid alters rhizosphere microbes and metabolic composition to improve willows drought resistance. <i>Science of the Total Environment</i> , 2022, 844, 157132.	3.9	15

#	ARTICLE	IF	CITATIONS
8680	High salt stress increases archaeal abundance and network connectivity in saline agricultural soils. <i>Catena</i> , 2022, 217, 106520.	2.2	10
8681	Mixed planting reduces the shaping ability of legume cover crop on soil microbial community structure. <i>Applied Soil Ecology</i> , 2022, 178, 104581.	2.1	4
8682	Improving biomethane fermentation through trace elements-driven microbial changes: Different effects of FeO combined with Co/Ni. <i>Process Biochemistry</i> , 2022, 121, 197-206.	1.8	4
8683	Response of microbiota and immune function to different hypotonic stress levels in giant freshwater prawn <i>Macrobrachium rosenbergii</i> post-larvae. <i>Science of the Total Environment</i> , 2022, 844, 157258.	3.9	2
8684	Comparative analysis of gut microbiota and fecal metabolome features among multiple depressive animal models. <i>Journal of Affective Disorders</i> , 2022, 314, 103-111.	2.0	10
8685	A new insight into the influencing factors of natural attenuation of chlorinated hydrocarbons contaminated groundwater: A long-term field study of a retired pesticide site. <i>Journal of Hazardous Materials</i> , 2022, 439, 129595.	6.5	17
8686	Artificial humic acid improves maize growth and soil phosphorus utilization efficiency. <i>Applied Soil Ecology</i> , 2022, 179, 104587.	2.1	16
8687	Effects of remediation agents on microbial community structure and function in soil aggregates contaminated with heavy metals. <i>Geoderma</i> , 2022, 425, 116030.	2.3	9
8688	Partial nitrification in free nitrous acid-treated sediment planting <i>Myriophyllum aquaticum</i> constructed wetland strengthens the treatment of black-odor water. <i>Science of the Total Environment</i> , 2022, 845, 157287.	3.9	7
8689	Disentangling biogeographic and underlying assembly patterns of fungal communities in metalliferous mining and smelting soils. <i>Science of the Total Environment</i> , 2022, 845, 157151.	3.9	7
8690	Response of soil microbial communities to petroleum hydrocarbons at a multi-contaminated industrial site in Lanzhou, China. <i>Chemosphere</i> , 2022, 306, 135559.	4.2	6
8691	Rapid conversion of alkaline bauxite residue through co-pyrolysis with waste biomass and its revegetation potential. <i>Journal of Environmental Sciences</i> , 2023, 127, 102-113.	3.2	3
8692	Bacterial Succession in Microbial Biofilm as a Potential Indicator for Postmortem Submersion Interval Estimation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8693	Gut Microbiota Characteristics of People with Obesity by Meta-Analysis of Existing Datasets. <i>Nutrients</i> , 2022, 14, 2993.	1.7	22
8694	Qige Huxin Formula Attenuates Isoprenaline-Induced Cardiac Fibrosis in Mice via Modulating Gut Microbiota and Protecting Intestinal Integrity. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	6
8695	Synthetic periphyton as a model system to understand species dynamics in complex microbial freshwater communities. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	6
8696	The effect of environment on intestinal microbial diversity of Panthera animals may exceed genetic relationship. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8697	Variance of coral anti-pathogen defense in response to transplantation between coral- and macroalgal-dominated reefs. <i>Coral Reefs</i> , 2022, 41, 1417-1431.	0.9	2

#	ARTICLE	IF	CITATIONS
8698	Microbial community composition and soil metabolism in the coexisting <i>Cordyceps militaris</i> and <i>Ophiocordyceps highlandensis</i> . <i>Journal of Basic Microbiology</i> , 2022, 62, 1254-1273.	1.8	1
8699	The interplay of gut microbiota between donors and recipients determines the efficacy of fecal microbiota transplantation. <i>Gut Microbes</i> , 2022, 14, .	4.3	19
8700	Delineation of the bacterial composition in exogenous endophthalmitis using 16S rDNA sequencing. <i>International Ophthalmology</i> , 2023, 43, 293-304.	0.6	1
8701	Multiomic Analyses Reveal the Effects of Supplementing Phytosterols on the Metabolic Function of the Rumen Microbiota in Perinatal Cows. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	3
8702	Effects of Dietary Bopu Powder Supplementation on Serum Antioxidant Capacity, Egg Quality, and Intestinal Microbiota of Laying Hens. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	4
8703	Phylogeography and population genetics of a widespread cold-adapted ant, <i>Prenolepis imparis</i> . <i>Molecular Ecology</i> , 2022, 31, 4884-4899.	2.0	0
8704	Rhizosphere bacterial communities and soil nutrient conditions reveal sexual dimorphism of <i>Populus deltoides</i> . <i>Journal of Forestry Research</i> , 2023, 34, 761-771.	1.7	6
8705	Frontloading of stress response genes enhances robustness to environmental change in chimeric corals. <i>BMC Biology</i> , 2022, 20, .	1.7	4
8706	Impacts of Rotation-Fallow Practices on Bacterial Community Structure in Paddy Fields. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
8707	<i>Campylobacter</i> Species of the Oral Microbiota as Prognostic Factor for Cardiovascular Outcome after Coronary Artery Bypass Grafting Surgery. <i>Biomedicines</i> , 2022, 10, 1801.	1.4	0
8708	The impact of symbiotic population crash (or reduction) on microbiome structure and composition. <i>International Journal of Pest Management</i> , 0, , 1-12.	0.9	0
8709	Long-term nitrogen deposition enhances microbial capacities in soil carbon stabilization but reduces network complexity. <i>Microbiome</i> , 2022, 10, .	4.9	26
8710	An amateur gut microbial configuration formed in giant panda for striving to digest cellulose in bamboo: Systematic evidence from intestinal digestive enzymes, functional genes and microbial structures. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8711	Effect of breast milk with or without bacteria on infant gut microbiota. <i>BMC Pregnancy and Childbirth</i> , 2022, 22, .	0.9	3
8712	Comparison of fungal communities and nonvolatile flavor components in black Huangjiu formed using different inoculation fermentation methods. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
8713	Soil properties, rhizosphere bacterial community, and plant performance respond differently to fumigation and bioagent treatment in continuous cropping fields. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
8714	Predictable Changes in Eelgrass Microbiomes with Increasing Wasting Disease Prevalence across 23° Latitude in the Northeastern Pacific. <i>MSystems</i> , 2022, 7, .	1.7	5
8715	Organelle 16S rRNA amplicon sequencing enables profiling of active gut microbiota in murine model. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 5715-5728.	1.7	3

#	ARTICLE	IF	CITATIONS
8716	A phylogenomic approach to species delimitation in the mango fruit fly (<i>Bactrocera</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (fra (Diptera: Tephritidae). <i>Systematic Entomology</i> , 2023, 48, 10-22.	1.7	5
8717	Correlations between behavior and hormone concentrations or gut microbiome imply that domestic cats (<i>Felis silvestris catus</i>) living in a group are not like "groupmates"™. <i>PLoS ONE</i> , 2022, 17, e0269589.	1.1	4
8718	Bacterial and fungal communities in indoor aerosols from two Kuwaiti hospitals. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
8719	Amplicon Sequencing Reveals Novel Fungal Species Responsible for a Controversial Tea Disease. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 782.	1.5	4
8720	Spatio-temporal monitoring of lake fish spawning activity using environmental <sc>DNA</sc> metabarcoding. <i>Environmental DNA</i> , 2023, 5, 849-860.	3.1	4
8721	Conversion of natural grassland to cropland alters microbial community assembly across northern China. <i>Environmental Microbiology</i> , 2022, 24, 5630-5642.	1.8	5
8722	GigaAssay " An adaptable high-throughput saturation mutagenesis assay platform. <i>Genomics</i> , 2022, 114, 110439.	1.3	9
8723	Uncovering temporospatial sensitive TBI targeting strategies via in vivo phage display. <i>Science Advances</i> , 2022, 8, .	4.7	3
8724	Differences in structure, volatile metabolites, and functions of microbial communities in Nongxiangxing daqu from different production areas. <i>LWT - Food Science and Technology</i> , 2022, 166, 113784.	2.5	21
8725	Effect of nickel (II) on the performance of anodic electroactive biofilms in bioelectrochemical systems. <i>Water Research</i> , 2022, 222, 118889.	5.3	17
8726	Introduction of exotic species <i>Sonneratia apetala</i> alters diazotrophic community and stimulates nitrogen fixation in mangrove sediments. <i>Ecological Indicators</i> , 2022, 142, 109179.	2.6	4
8727	Soil Nutrients and Microbial Community Characteristics of <i>Rhododendron rex</i> in Central Yunnan Province of China. <i>Journal of Biobased Materials and Bioenergy</i> , 2022, 16, 431-441.	0.1	1
8728	A Natural Gas Fermentation Bacterial Meal (FeedKind®) as a Functional Alternative Ingredient for Fishmeal in Diet of Largemouth Bass, <i>Micropterus salmoides</i> . <i>Antioxidants</i> , 2022, 11, 1479.	2.2	8
8729	Altitudinal Variation Influences Soil Fungal Community Composition and Diversity in Alpine "Gorge Region on the Eastern Qinghai Tibetan Plateau. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 807.	1.5	9
8730	Evaluation of the Efficacy of <i>Enterococcus faecium</i> L3 as a Feed Probiotic Additive in Chicken. <i>Probiotics and Antimicrobial Proteins</i> , 0, , .	1.9	2
8731	The dynamic effects of maternal high-calorie diet on glycolipid metabolism and gut microbiota from weaning to adulthood in offspring mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	7
8732	The Assessment of Dietary Organic Zinc on Zinc Homeostasis, Antioxidant Capacity, Immune Response, Glycolysis and Intestinal Microbiota in White Shrimp (<i>Litopenaeus vannamei</i> Boone, 1931). <i>Antioxidants</i> , 2022, 11, 1492.	2.2	11
8733	Chicken Gut Microbiota Responses to Dietary <i>Bacillus subtilis</i> Probiotic in the Presence and Absence of <i>Eimeria</i> Infection. <i>Microorganisms</i> , 2022, 10, 1548.	1.6	13

#	ARTICLE	IF	CITATIONS
8734	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
8735	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
8736	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
8737	A Pilot Study: Favorable Effects of <i>Clostridium butyricum</i> on Intestinal Microbiota for Adjuvant Therapy of Lung Cancer. Cancers, 2022, 14, 3599.	1.7	1
8738	Regulation of Dietary Protein Solubility Improves Ruminal Nitrogen Metabolism In Vitro: Role of Bacteria-Protozoa Interactions. Nutrients, 2022, 14, 2972.	1.7	6
8739	First Draft Genome Assembly of Tropical Bed Bug, <i>Cimex hemipterus</i> (F.). Data, 2022, 7, 101.	1.2	0
8740	High-fat diet-induced intestinal dysbiosis is associated with the exacerbation of Sjogren's syndrome. Frontiers in Microbiology, 0, 13, .	1.5	5
8741	Environmental filtering drives the establishment of the distinctive rhizosphere, bulk, and root nodule bacterial communities of <i>Sophora davidii</i> in hilly and gully regions of the Loess Plateau of China. Frontiers in Microbiology, 0, 13, .	1.5	6
8742	Human T-bet governs the generation of a distinct subset of CD11c ^{high} CD21 ^{low} B cells. Science Immunology, 2022, 7, .	5.6	33
8743	Influence of planting methods and organic amendments on rice yield and bacterial communities in the rhizosphere soil. Frontiers in Microbiology, 0, 13, .	1.5	7
8744	Comparative analysis of bacterial communities in olive psyllids, <i>Euphyllura straminea</i> and <i>Euphyllura pakistanica</i> expose proteobacteria dominance. Journal of Applied Entomology, 0, , .	0.8	0
8745	Natural Environmental Variation Determines Microbial Diversity Patterns in Serofluid Dish, a Traditional Chinese Fermented Vegetable Food. Current Microbiology, 2022, 79, .	1.0	1
8746	A metagenomic DNA sequencing assay that is robust against environmental DNA contamination. Nature Communications, 2022, 13, .	5.8	6
8747	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
8748	Microbial and Planktonic Community Characteristics of <i>Eriocheir sinensis</i> Culture Ponds Experiencing Harmful Algal Blooms. Fishes, 2022, 7, 180.	0.7	4
8749	Characteristics of gut microbiota in patients with gastric cancer by surgery, chemotherapy and lymph node metastasis. Clinical and Translational Oncology, 2022, 24, 2181-2190.	1.2	8
8750	Effects of biodegradable and polyethylene film mulches and their residues on soil bacterial communities. Environmental Science and Pollution Research, 2022, 29, 89698-89711.	2.7	6
8751	Interkingdom Plant-Soil Microbial Ecological Network Analysis under Different Anthropogenic Impacts in a Tropical Rainforest. Forests, 2022, 13, 1167.	0.9	2

#	ARTICLE	IF	CITATIONS
8752	Microbial ecology of sand fly breeding sites: aging and larval conditioning alter the bacterial community composition of rearing substrates. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
8753	Rhizosphere Microbial Communities and Geochemical Constraining Mechanism of Antimony Mine Waste-Adapted Plants in Southwestern China. <i>Microorganisms</i> , 2022, 10, 1507.	1.6	4
8754	Soil inoculum identity and rate jointly steer microbiomes and plant communities in the field. <i>ISME Communications</i> , 2022, 2, .	1.7	2
8755	Applying the concept of liquid biopsy to monitor the microbial biodiversity of marine coastal ecosystems. <i>ISME Communications</i> , 2022, 2, .	1.7	4
8756	Inoculation effect of <i>Pseudomonas</i> sp. TF716 on N ₂ O emissions during rhizoremediation of diesel-contaminated soil. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
8757	Great gerbil burrowing-induced microbial diversity shapes the rhizosphere soil microenvironments of <i>Haloxyylon ammodendron</i> in temperate deserts. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8758	The effect of added organic matter on the soil formation of oil-based drill cutting pyrolysis residue. <i>Environmental Science and Pollution Research</i> , 0, , .	2.7	0
8759	Enhancing control of multidrug-resistant plasmid and its host community with a prolonged thermophilic phase during composting. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8760	Detection of fish species composition using environmental DNA in aquarium trials. <i>Journal of Applied Ichthyology</i> , 0, , .	0.3	0
8761	Effects of feeding on different parts of <i>Ailanthus altissima</i> on the intestinal microbiota of <i>Eucryptorrhynchus scrobiculatus</i> and <i>Eucryptorrhynchus brandti</i> (Coleoptera: Curculionidae). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
8762	Meta-analysis of the microbial biomarkers in the gut–lung crosstalk in COVID-19, community-acquired pneumonia and <i>Clostridium difficile</i> infections. <i>Letters in Applied Microbiology</i> , 2022, 75, 1293-1306.	1.0	3
8763	Distinct community assembly and coexistence of arbuscular mycorrhizal fungi and diazotrophs across large scale soil fertility to improve functions in alfalfa cultivation systems. <i>Environmental Microbiology</i> , 0, , .	1.8	2
8764	Identification and implications of a core bacterial microbiome in 19 clonal cultures laboratory-reared for months to years of the cosmopolitan dinoflagellate <i>Karlodinium veneficum</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
8765	Changes in the Host Gut Microbiota during Parasitization by Parasitic Wasp <i>Cotesia vestalis</i> . <i>Insects</i> , 2022, 13, 760.	1.0	2
8766	Biodegradation and hydrolysis of rice straw with corn steep liquor and urea-alkali pretreatment. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
8767	Impact of a probiotic diet on well-being of healthy senior: <sc>THE PROBIOSENIOR PROJECT</sc>. <i>Journal of Applied Microbiology</i> , 0, , .	1.4	3
8768	Early gut microbiota in very low and extremely low birth weight preterm infants with feeding intolerance: a prospective case-control study. <i>Journal of Microbiology</i> , 2022, 60, 1021-1031.	1.3	5
8769	Differences in intestinal microflora of birds among different ecological types. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2

#	ARTICLE	IF	CITATIONS
8770	Mixed Fermentation of <i>Lactiplantibacillus plantarum</i> and <i>Bacillus licheniformis</i> Changed the Chemical Composition, Bacterial Community, and Rumen Degradation Rate of Tea Residue. <i>Fermentation</i> , 2022, 8, 380.	1.4	4
8771	Prevalence of Hepatitis C Virus Infection, Genotypes and Subtypes in Migrants from Pakistan in Barcelona, Spain. <i>Infection and Drug Resistance</i> , 0, Volume 15, 4637-4644.	1.1	2
8772	Organohalide Respiration with Diclofenac by <i>Dehalogenimonas</i> . <i>Environmental Science & Technology</i> , 2022, 56, 11266-11276.	4.6	5
8773	Effects of <i>Bacillus subtilis</i> A-5 and its fermented γ -polyglutamic acid on the rhizosphere bacterial community of Chinese cabbage. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
8774	Comparative analysis of bacterial communities in the sediment and seawater environments from marine large yellow croaker cages (Zhejiang coast, China). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
8775	Effect of a diet rich in galactose or fructose, with or without fructooligosaccharides, on gut microbiota composition in rats. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	1
8776	Dynamics of the fermentation quality and microbiota in <i>Ephedra sinica</i> treated native grass silage. <i>Journal of Applied Microbiology</i> , 0, , .	1.4	6
8777	Standing Genetic Diversity and Transmission Bottleneck Size Drive Adaptation in Bacteriophage Q β . <i>International Journal of Molecular Sciences</i> , 2022, 23, 8876.	1.8	4
8778	Microbial diversity and adaptive strategies in the Marsâ€šlike Qaidam Basin, North Tibetan Plateau, China. <i>Environmental Microbiology Reports</i> , 2022, 14, 873-885.	1.0	11
8779	Microbiota differences of skin and pharyngeal microbiota between patients with plaque and guttate psoriasis in China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8780	Comparative analysis of the fecal bacterial communities of hawksbill sea turtles (<i>Eretmochelys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.7	1
8781	Relationship between rumen microbial differences and traits among Hu sheep, Tan sheep, and Dorper sheep. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	11
8782	Gut microbiota in women with gestational diabetes mellitus has potential impact on metabolism in pregnant mice and their offspring. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
8783	Effects of scale worm parasitism on interactions between the symbiotic gill microbiome and gene regulation in deep sea mussel hosts. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8784	Fall Armyworm Gut Bacterial Diversity Associated with Different Developmental Stages, Environmental Habitats, and Diets. <i>Insects</i> , 2022, 13, 762.	1.0	12
8785	Characterization of microbial communities in anaerobic acidification reactors fed with casein and/or lactose. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 6301-6316.	1.7	3
8786	Characterization of the bacterial community structure in traditional Gifu ayu-narezushi (fermented) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	4
8787	Modeling spatial interaction networks of the gut microbiota. <i>Gut Microbes</i> , 2022, 14, .	4.3	8

#	ARTICLE	IF	CITATIONS
8788	Ecological risk assessment and identification of the distinct microbial groups in heavy metal-polluted river sediments. <i>Environmental Geochemistry and Health</i> , 2023, 45, 1311-1329.	1.8	5
8791	Towards Valeric Acid Production from Riboflavin-Assisted Waste Sludge: pH-Dependent Fermentation and Microbial Community. <i>Waste and Biomass Valorization</i> , 0, , .	1.8	0
8792	Metabarcoding survey of meroplankton communities in the South China Sea and Philippine Sea: Shedding light on inter-basin biogeography in the West Pacific. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
8793	The Yucatan minipig model: A new preclinical model of malnutrition induced by a low-calorie/low-protein diet. <i>Clinical Nutrition</i> , 2022, 41, 2077-2086.	2.3	2
8794	Alginate oligosaccharides increase boar semen quality by affecting gut microbiota and metabolites in blood and sperm. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8795	Effects of biochar and organic-inorganic fertilizer on pomelo orchard soil properties, enzymes activities, and microbial community structure. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
8796	Ultra Deep Sequencing of Circulating Cell-Free DNA as a Potential Tool for Hepatocellular Carcinoma Management. <i>Cancers</i> , 2022, 14, 3875.	1.7	2
8797	In vitro and in vivo Studies of Soybean Peptides on Milk Production, Rumen Fermentation, Ruminal Bacterial Community, and Blood Parameters in Lactating Dairy Cows. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
8798	Characteristics of oral microbiota in plateau and plain youthâ€”positive correlations between blood lipid level, metabolism and specific microflora in the plateau group. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
8799	Development of the gut microbiota in healthy twins during the first 2 years of life and associations with body mass index z-score: Results from the Wuhan twin birth cohort study. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
8800	Oral microbiome and serological analyses on association of Alzheimer's disease and periodontitis. <i>Oral Diseases</i> , 2023, 29, 3677-3687.	1.5	7
8801	Sequencing introduced false positive rare taxa lead to biased microbial community diversity, assembly, and interaction interpretation in amplicon studies. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	17
8802	Study on microbial community of â€œgreen-coveringâ€”Tuqu and the effect of fortified autochthonous <i>Monascus purpureus</i> on the flavor components of light-aroma-type Baijiu. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8803	Stochastic processes dominate assembly of soil fungal community in grazing excluded grasslands in northwestern China. <i>Journal of Soils and Sediments</i> , 2023, 23, 156-171.	1.5	9
8804	Investigation of Gut Bacterial Communities of Asian Citrus Psyllid (<i>Diaphorina citri</i>) Reared on Different Host Plants. <i>Insects</i> , 2022, 13, 694.	1.0	6
8805	Rumen Fermentation and Microbiome Responses to Enzymatic Hydrolysate of Cottonseed Protein Supplementation in Continuous In Vitro Culture. <i>Animals</i> , 2022, 12, 2113.	1.0	3
8806	An Investigation of the Effect of Water Additives on Broiler Growth and the Caecal Microbiota at Harvest. <i>Pathogens</i> , 2022, 11, 932.	1.2	1
8807	Impact of Clarified Apple Juices with Different Processing Methods on Gut Microbiota and Metabolomics of Rats. <i>Nutrients</i> , 2022, 14, 3488.	1.7	3

#	ARTICLE	IF	CITATIONS
8808	Analysis of microbial diversity and community structure of rhizosphere soil of Cistanche salsa from different host plants. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
8809	A Comparison of Rhizospheric and Endophytic Bacteria in Early and Late-Maturing Pumpkin Varieties. <i>Microorganisms</i> , 2022, 10, 1667.	1.6	3
8810	Acetate reprograms gut microbiota during alcohol consumption. <i>Nature Communications</i> , 2022, 13, .	5.8	34
8811	Network and machine learning analyses of estuarine microbial communities along a freshwater-marine mixed gradient. <i>Estuarine, Coastal and Shelf Science</i> , 2022, 277, 108026.	0.9	1
8812	Bioremediation of a Polluted Groundwater: Microbial Community Comparison of Treated and Untreated Aquifer through Next Generation Sequencing. <i>Water (Switzerland)</i> , 2022, 14, 2456.	1.2	1
8813	Differential Susceptibility of the Gut Microbiota to DSS Treatment Interferes in the Conserved Microbiome Association in Mouse Models of Colitis and Is Related to the Initial Gut Microbiota Difference. , 2022, 2022, 1-20.		10
8814	<i>Dendrobium officinale</i> Endophytes May Colonize the Intestinal Tract and Regulate Gut Microbiota in Mice. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-10.	0.5	0
8815	A universal approach to gene expression engineering. <i>Synthetic Biology</i> , 2022, 7, .	1.2	3
8816	Evaluating the Rhizosphere and Endophytic Microbiomes of a Bamboo Plant in Response to the Long-Term Application of Heavy Organic Amendment. <i>Plants</i> , 2022, 11, 2129.	1.6	3
8817	Humic Acid Improves Greenhouse Tomato Quality and Bacterial Richness in Rhizosphere Soil. <i>ACS Omega</i> , 2022, 7, 29823-29831.	1.6	5
8818	Different genotypes regulate the microbial community structure in the soybean rhizosphere. <i>Journal of Integrative Agriculture</i> , 2023, 22, 585-597.	1.7	4
8819	Overfertilization reduces tomato yield under long-term continuous cropping system via regulation of soil microbial community composition. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
8820	Flavonoid extract of saffron byâ€product alleviates hyperuricemia via inhibiting xanthine oxidase and modulating gut microbiota. <i>Phytotherapy Research</i> , 2022, 36, 4604-4619.	2.8	4
8822	Insight into functional microorganisms in wetâ€dry conversion to alleviate the toxicity of chromium fractions in red soil. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
8823	Complete Reductive Dechlorination of 4-Hydroxy-chlorothalonil by <i>Dehalogenimonas</i> Populations. <i>Environmental Science & Technology</i> , 2022, 56, 12237-12246.	4.6	9
8824	Recombination of repeat elements generates somatic complexity in human genomes. <i>Cell</i> , 2022, 185, 3025-3040.e6.	13.5	31
8825	Pipeline for developing polymorphic microsatellites in species without reference genomes. <i>3 Biotech</i> , 2022, 12, .	1.1	1
8827	Representativeness of Fecal Microbiota Is Limited to Cecum and Colon in Domestic Yak. <i>Sustainability</i> , 2022, 14, 10263.	1.6	0

#	ARTICLE	IF	CITATIONS
8828	A new pathway for anaerobic biotransformation of marine toxin domoic acid. <i>Environmental Science and Pollution Research</i> , 2023, 30, 5150-5160.	2.7	2
8829	Electroacupuncture ameliorates peptic ulcer disease in association with gastroduodenal microbiota modulation in mice. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	8
8830	Effects of the Partial Substitution of Corn with Wheat or Barley on the Growth Performance, Blood Antioxidant Capacity, Intestinal Health and Fecal Microbial Composition of Growing Pigs. <i>Antioxidants</i> , 2022, 11, 1614.	2.2	1
8831	Fecal microbial signatures of healthy Han individuals from three bio-geographical zones in Guangdong. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
8832	Trans-Species Fecal Transplant Revealed the Role of the Gut Microbiome as a Contributor to Energy Metabolism and Development of Skeletal Muscle. <i>Metabolites</i> , 2022, 12, 769.	1.3	1
8833	<i>Trypoxylus dichotomus</i> Gut Bacteria Provides an Effective System for Bamboo Lignocellulose Degradation. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
8834	Heritable vaginal bacteria influence immune tolerance and relate to early-life markers of allergic sensitization in infancy. <i>Cell Reports Medicine</i> , 2022, 3, 100713.	3.3	11
8835	Fungi stabilize multi-kingdom community in a high elevation timberline ecosystem. , 2022, 1, .		19
8836	Deficiency of migration inhibitory factor influences the gut microbiota of C57BL/6 mice infected with <i>Plasmodium berghei</i> ANKA. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8837	Characterization of the Intestinal Fungal Microbiome in HIV and HCV Mono-Infected or Co-Infected Patients. <i>Viruses</i> , 2022, 14, 1811.	1.5	5
8838	Stage-specific roles of microbial dysbiosis and metabolic disorders in rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1669-1677.	0.5	20
8839	Ruminal Microbiota Determines the High-Fiber Utilization of Ruminants: Evidence from the Ruminal Microbiota Transplant. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	14
8840	<i>Lactiplantibacillus plantarum</i> Strain FLPL05 Promotes Longevity in Mice by Improving Intestinal Barrier. <i>Probiotics and Antimicrobial Proteins</i> , 2023, 15, 1193-1205.	1.9	3
8841	Low-dose IL-2 shapes a tolerogenic gut microbiota that improves autoimmunity and gut inflammation. <i>JCI Insight</i> , 2022, 7, .	2.3	8
8842	Latitudinal Dynamics of <i>Vibrio</i> along the Eastern Coastline of Australia. <i>Water (Switzerland)</i> , 2022, 14, 2510.	1.2	2
8843	Difference of microbial community and gene composition with saccharification function between Chinese <i>nongxiangxing daqu</i> and <i>jiangxiangxing daqu</i>. <i>Journal of the Science of Food and Agriculture</i> , 2023, 103, 637-647.	1.7	13
8844	Effects of frequency and amount of stover mulching on soil nitrogen and the microbial functional guilds of the endosphere and rhizosphere. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8845	Specific gut microbiota alterations in essential tremor and its difference from Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2022, 8, .	2.5	14

#	ARTICLE	IF	CITATIONS
8846	A comparison between yaks and Qaidam cattle in in vitro rumen fermentation, methane emission, and bacterial community composition with poor quality substrate. <i>Animal Feed Science and Technology</i> , 2022, 291, 115395.	1.1	9
8847	The role of the biogas slurry microbial communities in suppressing fusarium wilt of cucumber. <i>Waste Management</i> , 2022, 151, 142-153.	3.7	5
8848	Dynamic evolution of flavor substances and bacterial communities during fermentation of leaf mustard (<i>Brassica juncea</i> var. <i>multiceps</i>) and their correlation. <i>LWT - Food Science and Technology</i> , 2022, 167, 113796.	2.5	10
8849	Discrepancies among healthy, subclinical mastitic, and clinical mastitic cows in fecal microbiome and metabolome and serum metabolome. <i>Journal of Dairy Science</i> , 2022, 105, 7668-7688.	1.4	8
8850	The true picture of environmental DNA, a case study in harvested fishponds. <i>Ecological Indicators</i> , 2022, 142, 109241.	2.6	0
8851	Acid deposition at higher acidity weakens the antagonistic responses during the co-decomposition of two Asteraceae invasive plants. <i>Ecotoxicology and Environmental Safety</i> , 2022, 243, 114012.	2.9	7
8852	Molecular diversity of foraminiferal eDNA in sediments and their correlations with environmental factors from the Yellow Sea. <i>Ecological Indicators</i> , 2022, 142, 109294.	2.6	3
8853	<i>Debaryomyces nepalensis</i> reduces fungal decay by affecting the postharvest microbiome during jujube storage. <i>International Journal of Food Microbiology</i> , 2022, 379, 109866.	2.1	5
8854	Valorization of sugarcane bagasse through biofuel and value-added soluble metabolites production: Optimization of alkaline hydrothermal pretreatment. <i>Biomass and Bioenergy</i> , 2022, 165, 106564.	2.9	2
8855	Co-occurrence network of microbes linking growth and immunity parameters with the gut microbiota in Nile tilapia (<i>Oreochromis niloticus</i>) after feeding with fermented soybean meal. <i>Aquaculture Reports</i> , 2022, 26, 101280.	0.7	5
8856	Synergistic effects of straw and earthworm addition on microbial diversity and microbial nutrient limitation in a subtropical conservation farming system. <i>Soil and Tillage Research</i> , 2022, 224, 105500.	2.6	6
8857	Effects of dietary <i>Lactobacillus reuteri</i> on growth performance, nutrient retention, gut health and microbiota of the Nile tilapia (<i>Oreochromis niloticus</i>). <i>Aquaculture Reports</i> , 2022, 26, 101275.	0.7	1
8858	Group 1 phylogeny and alkenone distributions in a freshwater volcanic lake of northeastern China: Implications for paleotemperature reconstructions. <i>Organic Geochemistry</i> , 2022, 172, 104483.	0.9	3
8859	Isolation and characterization of bacteria that produce quorum sensing molecules during the fermentation and deterioration of pickles. <i>International Journal of Food Microbiology</i> , 2022, 379, 109869.	2.1	3
8860	Changes in microbial community composition drive the response of ecosystem multifunctionality to elevated ozone. <i>Environmental Research</i> , 2022, 214, 114142.	3.7	8
8861	Advancing FDSTools by integrating STRNaming 1.1. <i>Forensic Science International: Genetics</i> , 2022, 61, 102768.	1.6	1
8862	Unraveling the ecological mechanisms of bacterial succession in epiphytic biofilms on <i>Vallisneria natans</i> and <i>Hydrilla verticillata</i> during bioremediation of phenanthrene and pyrene polluted wetland. <i>Journal of Environmental Management</i> , 2022, 321, 115986.	3.8	8
8863	Sulfamox forwarding thiosulfate-driven denitrification and anammox process for nitrogen removal. <i>Environmental Research</i> , 2022, 214, 113904.	3.7	5

#	ARTICLE	IF	CITATIONS
8864	Structural variability and niche differentiation of <i>Paeonia lactiflora</i> 's root-associated microbiomes. <i>Applied Soil Ecology</i> , 2022, 180, 104632.	2.1	2
8865	Relationship between phosphorus uptake via indigenous arbuscular mycorrhizal fungi and crop response: A ³² P-labeling study. <i>Applied Soil Ecology</i> , 2022, 180, 104624.	2.1	6
8866	Nitrogen addition and warming rapidly alter microbial community compositions in the mangrove sediment. <i>Science of the Total Environment</i> , 2022, 850, 157992.	3.9	1
8867	LDPE microplastics affect soil microbial community and form a unique plastsphere on microplastics. <i>Applied Soil Ecology</i> , 2022, 180, 104623.	2.1	33
8868	Long-term soil management practices influence the rhizosphere microbial community structure and bacterial function of hilly apple orchard soil. <i>Applied Soil Ecology</i> , 2022, 180, 104627.	2.1	11
8869	Effects of dietary yeast culture on health status in digestive tract of juvenile Pacific white shrimp <i>Litopenaeus Vannamei</i> . <i>Fish and Shellfish Immunology Reports</i> , 2022, 3, 100065.	0.5	2
8870	Response of bacterial diversity and community structure to metals in mangrove sediments from South China. <i>Science of the Total Environment</i> , 2022, 850, 157969.	3.9	5
8871	Biochar increases <i>Panax notoginseng</i> 's survival under continuous cropping by improving soil properties and microbial diversity. <i>Science of the Total Environment</i> , 2022, 850, 157990.	3.9	9
8872	Increasing land-use durations enhance soil microbial deterministic processes and network complexity and stability in an ecotone. <i>Applied Soil Ecology</i> , 2023, 181, 104630.	2.1	3
8874	Uncovering the Fecal Bacterial Communities of Sympatric Sika Deer (<i>Cervus nippon</i>) and Wapiti (<i>Cervus canadensis</i>). <i>Animals</i> , 2022, 12, 2468.	1.0	1
8875	Responses of soil enzyme activities and bacterial community structure to different hydrological regimes during peatland restoration in the Changbai Mountain, northeast China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8876	IP6 reduces colorectal cancer metastasis by mediating the interaction of gut microbiota with host genes. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	6
8877	Effect of Dietary <i>Fructus mume</i> and <i>Scutellaria baicalensis</i> Georgi on the Fecal Microbiota and Its Correlation with Apparent Nutrient Digestibility in Weaned Piglets. <i>Animals</i> , 2022, 12, 2418.	1.0	1
8878	Mitochondrial cytochrome c oxidase subunit I (COI) metabarcoding of Foraminifera communities using taxon-specific primers. <i>PeerJ</i> , 0, 10, e13952.	0.9	6
8880	Different mechanisms driving increasing abundance of microbial phosphorus cycling gene groups along an elevational gradient. <i>IScience</i> , 2022, 25, 105170.	1.9	4
8881	Hedgerows increase the diversity and modify the composition of arbuscular mycorrhizal fungi in Mediterranean agricultural landscapes. <i>Mycorrhiza</i> , 2022, 32, 397-407.	1.3	4
8882	The divergent vertical pattern and assembly of soil bacterial and fungal communities in response to short-term warming in an alpine peatland. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
8883	Influence of <i>Bacillus subtilis</i> strain Z-14 on microbial communities of wheat rhizospheric soil infested with <i>Gaeumannomyces graminis</i> var. <i>tritici</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3

#	ARTICLE	IF	CITATIONS
8884	Reduced pollen activity in peanut (<i>Arachis hypogaea</i> L.) by long-term monocropping is linked to flower water deficit. <i>Plant and Soil</i> , 2023, 482, 427-450.	1.8	3
8885	Linking the bacterial microbiome between gut and habitat soil of Tibetan macaque (<i>Macaca</i>) Tj ETQq1 1 0.784314 rgBT /Qverlock 10	0.8	2
8887	Structural and compositional segregation of the gut microbiota in HCV and liver cirrhotic patients: A clinical pilot study. <i>Microbial Pathogenesis</i> , 2022, 171, 105739.	1.3	4
8888	Plant Growth-Promoting Rhizobacteria Promote Growth of Seedlings, Regulate Soil Microbial Community, and Alleviate Damping-Off Disease Caused by <i>Rhizoctonia solani</i> on <i>Pinus sylvestris</i> var. <i>mongolica</i> . <i>Plant Disease</i> , 2022, 106, 2730-2740.	0.7	4
8889	Protective effect of methionine on the intestinal oxidative stress and microbiota change induced by nickel. <i>Ecotoxicology and Environmental Safety</i> , 2022, 244, 114037.	2.9	2
8890	Enrichment of Methylosinus-dominant consortia from mangroves for polyhydroxybutyrate (PHB) production. <i>Journal of Environmental Chemical Engineering</i> , 2022, 10, 108490.	3.3	5
8891	Wastewater microorganisms impact microbial diversity and important ecological functions of stream periphyton. <i>Water Research</i> , 2022, 225, 119119.	5.3	13
8892	Body size as key trait determining aquatic metacommunity assemblies in benthonic and planktonic habitats of Dongting Lake, China. <i>Ecological Indicators</i> , 2022, 143, 109355.	2.6	2
8893	Role of gut microbiota-derived branched-chain amino acids in the pathogenesis of Parkinson's disease: An animal study. <i>Brain, Behavior, and Immunity</i> , 2022, 106, 307-321.	2.0	19
8894	Improving the safety and quality of Roucha using amine-degrading lactic acid bacteria starters. <i>Food Research International</i> , 2022, 161, 111918.	2.9	7
8895	Additional supplementation of sulfur-containing amino acids in the diets improves the intestinal health of turbot fed high-lipid diets. <i>Fish and Shellfish Immunology</i> , 2022, 130, 368-379.	1.6	4
8896	Impact of golden mussel (<i>Limnoperna fortunei</i>) colonization on bacterial communities and potential risk to water quality. <i>Ecological Indicators</i> , 2022, 144, 109499.	2.6	3
8897	Oral exposure to Ag or TiO ₂ nanoparticles perturbed gut transcriptome and microbiota in a mouse model of ulcerative colitis. <i>Food and Chemical Toxicology</i> , 2022, 169, 113368.	1.8	6
8898	Effects of replacing dietary fish meal with enzyme-treated soybean meal on growth performance, intestinal microbiota, immunity and mTOR pathway in abalone <i>Haliotis discus hannai</i> . <i>Fish and Shellfish Immunology</i> , 2022, 130, 9-21.	1.6	8
8899	Accelerated degradation of cellulose in silkworm excrement by the interaction of housefly larvae and cellulose-degrading bacteria. <i>Journal of Environmental Management</i> , 2022, 323, 116295.	3.8	6
8900	Soil depth exerts stronger impact on bacterial community than elevation in subtropical forests of Huangshan Mountain. <i>Science of the Total Environment</i> , 2022, 852, 158438.	3.9	11
8901	Implications of environmentally shaped microbial communities for insecticide resistance in <i>Sitobion miscanthi</i> . <i>Environmental Research</i> , 2022, 215, 114409.	3.7	4
8902	Field-aged biochar enhances soil organic carbon by increasing recalcitrant organic carbon fractions and making microbial communities more conducive to carbon sequestration. <i>Agriculture, Ecosystems and Environment</i> , 2022, 340, 108177.	2.5	17

#	ARTICLE	IF	CITATIONS
8903	The preharvest application of <i>Aureobasidium pullulans</i> S2 remodeled the microbiome of tomato surface and reduced postharvest disease incidence of tomato fruit. <i>Postharvest Biology and Technology</i> , 2022, 194, 112101.	2.9	5
8904	Generalists and specialists decomposing labile and aromatic biochar compounds and sequestering carbon in soil. <i>Geoderma</i> , 2022, 428, 116176.	2.3	9
8905	Microbial diversity across compartments in an aquaponic system and its connection to the nitrogen cycle. <i>Science of the Total Environment</i> , 2022, 852, 158426.	3.9	14
8906	Responses of abundant and rare prokaryotic taxa in a controlled organic contaminated site subjected to vertical pollution-induced disturbances. <i>Science of the Total Environment</i> , 2022, 853, 158625.	3.9	7
8907	Evaluation of ethylcin as a potential soil fumigant in commercial tomato production in China. <i>Science of the Total Environment</i> , 2023, 854, 158520.	3.9	7
8908	Changes in rhizosphere phosphorus fractions and phosphate-mineralizing microbial populations in acid soil as influenced by organic acid exudation. <i>Soil and Tillage Research</i> , 2023, 225, 105543.	2.6	16
8909	Positive effects of steamed <i>Polygonatum sibiricum</i> polysaccharides including a glucofructan on fatty acids and intestinal microflora. <i>Food Chemistry</i> , 2023, 402, 134068.	4.2	10
8910	Effects of resistant starch III on the serum lipid levels and gut microbiota of Kunming mice under high-fat diet. <i>Food Science and Human Wellness</i> , 2023, 12, 575-583.	2.2	6
8911	Long-Term Effective Remediation of Black-Odoriferous Water Via Calcium Nitrate Sustained-Release. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8912	Urinary Microbiota and Serum Metabolite Analysis in Patients with Diabetic Kidney Disease. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8913	Multi-Omics Eco-Surveillance of Bacterial Community Function in Legacy Contaminated Estuary Sediments. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8914	Influence of Dom and Microbes on Fe Biogeochemistry at a Riverbank Filtration Site. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8915	Characterization of the nitrogen-transforming microbial community in the biofilms of a full-scale rotating biological contactor system treating wastewater from a fresh market building. <i>Environmental Science: Water Research and Technology</i> , 2022, 8, 1845-1858.	1.2	1
8916	Complex Responses of Soil Bacterial and its Metabolites to Bio-Organic Fertilizer in Soil-Dendrocalamus Farinosus Scenarios. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8917	Different Horizontal Transfer Mechanisms of Intracellular and Extracellular Args in Sludge Compost Under Sulfamethoxazole Stress. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
8918	Microbiome dysbiosis inhibits carcinogen-induced murine oral tumorigenesis. <i>Journal of Cancer</i> , 2022, 13, 3051-3060.	1.2	2
8919	Fungal Communities across an Edaphic Gradient in Central Borneo. , 0, , .		0
8920	Combined Non-Invasive Prediction and New Biomarkers of Oral and Fecal Microbiota in Patients With Gastric and Colorectal Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	17

#	ARTICLE	IF	CITATIONS
8921	Genome-wide profiling of dysregulated piRNAs and their target genes implicated in oncogenicity of tongue squamous cell carcinoma. <i>Gene</i> , 2023, 849, 146919.	1.0	6
8922	Soil bacterial community structure in the habitats with different levels of heavy metal pollution at an abandoned polymetallic mine. <i>Journal of Hazardous Materials</i> , 2023, 442, 130063.	6.5	35
8923	Recruitment of specific microbes through exudates affects cadmium activation and accumulation in <i>Brassica napus</i> . <i>Journal of Hazardous Materials</i> , 2023, 442, 130066.	6.5	7
8924	Influence of DOM and microbes on Fe biogeochemistry at a riverbank filtration site. <i>Environmental Research</i> , 2023, 216, 114430.	3.7	9
8925	Gellan gum prevents non-alcoholic fatty liver disease by modulating the gut microbiota and metabolites. <i>Food Chemistry</i> , 2023, 400, 134038.	4.2	9
8926	Impact of Norway spruce pre-degradation stages induced by <i>GloeophyllumÂtrabeum</i> on fungal and bacterial communities. <i>Fungal Ecology</i> , 2023, 61, 101188.	0.7	2
8927	Dietary fiber konjac glucomannan exerts an antidiabetic effect via inhibiting lipid absorption and regulation of PPAR-Î³ and gut microbiome. <i>Food Chemistry</i> , 2023, 403, 134336.	4.2	10
8928	SIQ: easy quantitative measurement of mutation profiles in sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	4
8929	Analysis of endophyte diversity of <i>Gentiana officinalis</i> among different tissue types and ages and their association with four medicinal secondary metabolites. <i>PeerJ</i> , 0, 10, e13949.	0.9	5
8930	Structural Characteristics and Formation Mechanism of Microbiota Related to Fermentation Ability and Alcohol Production Ability in Nongxiang Daqu. <i>Foods</i> , 2022, 11, 2602.	1.9	8
8931	Addition of Organic Acids and <i>Lactobacillus acidophilus</i> to the Leguminous Forage <i>Chamaecrista rotundifolia</i> Improved the Quality and Decreased Harmful Bacteria of the Silage. <i>Animals</i> , 2022, 12, 2260.	1.0	6
8932	Different rhizosphere soil microbes are recruited by tomatoes with different fruit color phenotypes. <i>BMC Microbiology</i> , 2022, 22, .	1.3	6
8933	Shifts of Antibiotic Resistomes in Soil Following Amendments of Antibiotics-Contained Dairy Manure. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 10804.	1.2	1
8934	Vectors as Sentinels: Rising Temperatures Increase the Risk of <i>Xylella fastidiosa</i> Outbreaks. <i>Biology</i> , 2022, 11, 1299.	1.3	7
8935	FXR Signaling-Mediated Bile Acid Metabolism Is Critical for Alleviation of Cholesterol Gallstones by <i>Lactobacillus</i> Strains. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	17
8936	Community Dynamics in Structure and Function of Honey Bee Gut Bacteria in Response to Winter Dietary Shift. <i>MBio</i> , 2022, 13, .	1.8	17
8937	Searching for the <i>Fusarium</i> spp. Which Are Responsible for Trichothecene Contamination in Oats. Using Metataxonomy to Compare the Distribution of Toxigenic Species in Fields from Spain and the UK. <i>Toxins</i> , 2022, 14, 592.	1.5	5
8939	In Vitro Interactions between Okadaic Acid and Rat Gut Microbiome. <i>Marine Drugs</i> , 2022, 20, 556.	2.2	1

#	ARTICLE	IF	CITATIONS
8940	Effects of different harvest frequencies on microbial community and metabolomic properties of annual ryegrass silage. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	15
8941	The Comparison of Antioxidant Performance, Immune Performance, IIS Activity and Gut Microbiota Composition between Queen and Worker Bees Revealed the Mechanism of Different Lifespan of Female Casts in the Honeybee. <i>Insects</i> , 2022, 13, 772.	1.0	3
8942	Possibility of Using By-Products with High NDF Content to Alter the Fecal Short Chain Fatty Acid Profiles, Bacterial Community, and Digestibility of Lactating Dairy Cows. <i>Microorganisms</i> , 2022, 10, 1731.	1.6	6
8943	Long-Term Fertilization Strategy Impacts <i>Rhizoctonia solani</i> –Microbe Interactions in Soil and Rhizosphere and Defense Responses in Lettuce. <i>Microorganisms</i> , 2022, 10, 1717.	1.6	5
8945	Correlation in endophytic fungi community diversity and bioactive compounds of <i>Sophora alopecuroides</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
8946	Root exudates and rhizosphere soil bacterial relationships of <i>Nitraria tangutorum</i> are linked to <i>k</i> -strategists bacterial community under salt stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	12
8947	Soil fungal communities show more specificity than bacteria for plant species composition in a temperate forest in China. <i>BMC Microbiology</i> , 2022, 22, .	1.3	10
8948	<i>Treponema denticola</i> Induces Interleukin-36 β Expression in Human Oral Gingival Keratinocytes via the Parallel Activation of NF- κ B and Mitogen-Activated Protein Kinase Pathways. <i>Infection and Immunity</i> , 2022, 90, .	1.0	3
8949	Effects of fecal microbiota transplantation from yaks on weaning diarrhea, fecal microbiota composition, microbial network structure and functional pathways in Chinese Holstein calves. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
8950	Probiotics added to maternal nutrition affect \pm infantile colic symptoms and fecal microbiota profile: a single-blind randomized controlled study. <i>Clinical and Experimental Pediatrics</i> , 2022, 65, 547-554.	0.9	2
8951	Nitrogen deposition experiment mimicked with NH ₄ NO ₃ overestimates the effect on soil microbial community composition and functional potential in the Eurasian steppe. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	0
8952	Strong Linkage Between Symbiotic Bacterial Community and Host Age and Morph in a Hemipteran Social Insect. <i>Microbial Ecology</i> , 0, , .	1.4	3
8953	Comparison of Gut Bacterial Communities of <i>Locusta migratoria manilensis</i> (Meyen) Reared on Different Food Plants. <i>Biology</i> , 2022, 11, 1347.	1.3	6
8954	Effects of sodium humate and probiotics on growth performance enzyme activity and microbial environment of <i>Litopenaeus vannamei</i> in high-density zero-water exchange systems. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	3
8956	Relationship between Changes in Intestinal Microorganisms and Effect of High Temperature on the Growth and Development of <i>Bombyx mori</i> Larvae. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10289.	1.8	4
8957	<i>Strongyloides stercoralis</i> infection induces gut dysbiosis in chronic kidney disease patients. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010302.	1.3	5
8958	Sheep fecal transplantation affects growth performance in mouse models by altering gut microbiota. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	1
8959	Effect of continuous cropping of konjac (<i>Amorphophallus konjac</i>) on soil bacterial communities as evaluated by Illumina high-throughput sequencing. <i>Archives of Agronomy and Soil Science</i> , 0, , 1-15.	1.3	0

#	ARTICLE	IF	CITATIONS
8960	The evolutionary potential of influenza A virus hemagglutinin is highly constrained by epistatic interactions with neuraminidase. <i>Cell Host and Microbe</i> , 2022, 30, 1363-1369.e4.	5.1	11
8961	Root-Associated Microbiomes of <i>Panax notoginseng</i> under the Combined Effect of Plant Development and <i>Alpinia officinarum</i> Hance Essential Oil. <i>Molecules</i> , 2022, 27, 6014.	1.7	1
8962	Comparison of gut microflora of donkeys in high and low altitude areas. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8963	Altered Gut Microbiota and Its Clinical Relevance in Mild Cognitive Impairment and Alzheimer's Disease: Shanghai Aging Study and Shanghai Memory Study. <i>Nutrients</i> , 2022, 14, 3959.	1.7	16
8964	Planktonic microbial communities from microbialite-bearing lakes sampled along a salinity-alkalinity gradient. <i>Limnology and Oceanography</i> , 2022, 67, 2718-2733.	1.6	7
8965	Effects of Water Loss Stress under Tidal Effects on the Epiphytic Bacterial Community of <i>Sargassum thunbergii</i> in the Intertidal Zone. <i>MSphere</i> , 2022, 7, .	1.3	1
8966	Long-term cultivation alter soil bacterial community in a forest-grassland transition zone. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8967	Diversity and assembly processes of microbial eukaryotic communities in Fildes Peninsula Lakes (West) Tj ETQq1 1 0,784314,rgBT /Over	1.3	4
8968	Dietary Antimicrobial Peptides Improve Intestinal Function, Microbial Composition and Oxidative Stress Induced by <i>Aeromonas hydrophila</i> in Pengze Crucian Carp (<i>Carassius auratus</i> var. Pengze). <i>Antioxidants</i> , 2022, 11, 1756.	2.2	3
8969	Biogeographical Patterns and Assembly of Bacterial Communities in Saline Soils of Northeast China. <i>Microorganisms</i> , 2022, 10, 1787.	1.6	4
8970	Pyrolyzed or Composted Sewage Sludge Application Induces Short-Term Changes in the Terra Rossa Soil Bacterial and Fungal Communities. <i>Sustainability</i> , 2022, 14, 11382.	1.6	1
8971	Impact of <i>Litsea cubeba</i> inter-row cover on the structure of bacterial community in the tea plantation. <i>Annals of Microbiology</i> , 2022, 72, .	1.1	1
8972	Delayed application of N fertilizer mitigates the carbon emissions of pea/maize intercropping via altering soil microbial diversity. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8973	Differential Response of Ileal and Colonic Microbiota in Rats with High-Fat Diet-Induced Atherosclerosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11154.	1.8	2
8974	High replacement of fishmeal by <i>Chlorella</i> meal affects intestinal microbiota and the potential metabolic function in largemouth bass (<i>Micropterus salmoides</i>). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	10
8975	Effects of continuous and rotational cropping practices on soil fungal communities in pineapple cultivation. <i>PeerJ</i> , 0, 10, e13937.	0.9	1
8976	Comparison and interpretation of freshwater bacterial structure and interactions with organic to nutrient imbalances in restored wetlands. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
8977	In-Forest Planting of High-Value Herb <i>Sarcandra glabra</i> Enhances Soil Carbon Storage without Affecting the Diversity of the Arbuscular Mycorrhiza Fungal Community and Composition of <i>Cunninghamia lanceolata</i> . <i>Microorganisms</i> , 2022, 10, 1844.	1.6	1

#	ARTICLE	IF	CITATIONS
8978	Expansion of Opportunistic Enteric Fungal Pathogens and Occurrence of Gut Inflammation in Human Liver Echinococcosis. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
8980	Occurrence and driving mechanism of antibiotic resistance genes in marine recreational water around Qinhuangdao, China. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	4
8981	Effects of various logistics packaging on the quality and microbial variation of bigeye tuna (<i>Thunnus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf .	1.6	2
8982	5300â€Yearâ€old soil carbon is less primed than young soil organic matter. <i>Global Change Biology</i> , 2023, 29, 260-275.	4.2	13
8983	Uncovering the biogeography of the microbial community and its association with nutrient metabolism in the intestinal tract using a pig model. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	1
8984	The impact of pelvic floor electrical stimulation on vaginal microbiota and immunity. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
8986	Effects of Feed Composition in Different Growth Stages on Rumen Fermentation and Microbial Diversity of Hanwoo Steers. <i>Animals</i> , 2022, 12, 2606.	1.0	0
8988	Abscisic acid-polyacrylamide (ABA-PAM) treatment enhances forage grass growth and soil microbial diversity under drought stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
8989	Impacts of Japanese Larch Invasion on Soil Bacterial Communities of the Giant Panda Habitat in the Qinling Mountains. <i>Microorganisms</i> , 2022, 10, 1807.	1.6	2
8990	Bacterial and fungal communities within and among geographic samples of the hemp pest <i>Psylliodes attenuata</i> from China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8992	Changes in soil bacterial community and functions by substituting chemical fertilizer with biogas slurry in an apple orchard. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
8993	Histamine Signaling Is Essential for Tissue Macrophage Differentiation and Suppression of Bacterial Overgrowth in the Stomach. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2023, 15, 213-236.	2.3	2
8994	Oil-degrading bacterial consortium from Gulf of Mexico designed by a factorial method, reveals stable population dynamics. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
8995	Reducing Carbon Input Improved the Diversity of Bacterial Community in Large-Scale Biofloc Shrimp Culture Facilities. <i>Diversity</i> , 2022, 14, 778.	0.7	2
8996	Characteristics of soil microbiota and organic carbon distribution in jackfruit plantation under different fertilization regimes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
8997	The effect of "Fishery-PV Integration" on <i>Penaeus monodon</i> culture and research on the micro-ecological environment. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
8998	Exploring a Possible Link between the Fecal Microbiota and the Production Performance of Pigs. <i>Veterinary Sciences</i> , 2022, 9, 527.	0.6	1
8999	Efficacy and Safety of Fecal Microbiota Transplantation for Clearance of Multidrug-Resistant Organisms under Multiple Comorbidities: A Prospective Comparative Trial. <i>Biomedicines</i> , 2022, 10, 2404.	1.4	2

#	ARTICLE	IF	CITATIONS
9000	The Intratumoral Bacterial Metataxonomic Signature of Hepatocellular Carcinoma. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	15
9001	Paleogenomes Reveal a Complex Evolutionary History of Late Pleistocene Bison in Northeastern China. <i>Genes</i> , 2022, 13, 1684.	1.0	1
9002	A physicochemical double-cross-linked gelatin hydrogel with enhanced antibacterial and anti-inflammatory capabilities for improving wound healing. <i>Journal of Nanobiotechnology</i> , 2022, 20, .	4.2	22
9003	Regionalization and Shaping Factors for Microbiomes and Core Resistomes in Atmospheric Particulate Matters. <i>MSystems</i> , 2022, 7, .	1.7	1
9004	Changes in the gut microbiota of forest musk deer (<i>Moschus berezovskii</i>) during ex situ conservation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9005	Bacterial diversity in surface sediments of collapsed lakes in Huaibei, China. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
9006	Human umbilical cord-derived mesenchymal stem cells ameliorate experimental colitis by normalizing the gut microbiota. <i>Stem Cell Research and Therapy</i> , 2022, 13, .	2.4	12
9007	Differences in Intestinal Microbial Composition between Red Claw Crayfish (<i>Cherax quadricarinatus</i>) and Red Swamp Crayfish (<i>Procambarus clarkii</i>) Cultured in Pond. <i>Fishes</i> , 2022, 7, 241.	0.7	4
9008	Effects of g-C3N4 on bacterial community and tetracycline resistance genes in two typical sediments in tetracycline pollution remediation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9009	Watershed-scale Variation in Potential Fungal Community Contributions to Ectomycorrhizal Biogeochemical Syndromes. <i>Ecosystems</i> , 2023, 26, 724-739.	1.6	1
9010	Gut microbiome and metabolic activity in type 1 diabetes: An analysis based on the presence of GADA. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
9011	Comparative study of the function and structure of the gut microbiota in Siberian musk deer and Forest musk deer. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 6799-6817.	1.7	3
9012	The Effect of Rotational Cropping of Industrial Hemp (<i>Cannabis sativa</i> L.) on Rhizosphere Soil Microbial Communities. <i>Agronomy</i> , 2022, 12, 2293.	1.3	1
9013	Insights into the deriving of rhizosphere microenvironments and its effects on the growth of authentic <i>Angelica sinensis</i> seedlings under continuous monoculture. <i>Annals of Microbiology</i> , 2022, 72, .	1.1	0
9014	Differences in microbial diversity and environmental factors in ploughing-treated tobacco soil. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
9015	<i>Epidendrum radicans</i> Fungal Community during Ex Situ Germination and Isolation of Germination-Enhancing Fungi. <i>Microorganisms</i> , 2022, 10, 1841.	1.6	0
9016	Metabarcoding and Metabolome Analyses Reveal Mechanisms of <i>Leymus chinensis</i> Growth Promotion by Fairy Ring of <i>Leucocalocybe mongolica</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 944.	1.5	6
9017	Effects of Dietary Supplementation of Solubles from Shredded, Steam-Exploded Pine Particles on the Performance and Cecum Microbiota of Acute Heat-Stressed Broilers. <i>Microorganisms</i> , 2022, 10, 1795.	1.6	6

#	ARTICLE	IF	CITATIONS
9018	Factors structuring microbial communities in highly impacted coastal marine sediments (Mar Menor). <i>Journal of Applied Microbiology</i> , 2022, 124, 1-15.	1.5	4
9019	Long-term no-tillage and rye cover crop affect soil biological indicators on Andosols in a humid, subtropical climate. <i>European Journal of Soil Science</i> , 0, , .	1.8	0
9020	Development and characterization of microsatellite markers in the African timber tree species <i>Cylicodiscus gabunensis</i> (Fabaceae). <i>Molecular Biology Reports</i> , 2022, 49, 11209-11214.	1.0	1
9022	Effects of simulated acid rain on rhizosphere microorganisms of invasive <i>Alternanthera philoxeroides</i> and native <i>Alternanthera sessilis</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9023	Microbiological characteristics of different tongue coatings in adults. <i>BMC Microbiology</i> , 2022, 22, .	1.3	3
9024	Effects of feed transition on digestive tract digestive enzyme, morphology and intestinal community in cuttlefish (<i>Sepia pharaonis</i>). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
9025	The microbiota changes of the brown dog tick, <i>Rhipicephalus sanguineus</i> under starvation stress. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	2
9026	<i>Mikania</i> sesquiterpene lactones enhance soil bacterial diversity and fungal and bacterial activities. <i>Biological Invasions</i> , 0, , .	1.2	0
9027	Microbial community starters affect the profiles of volatile compounds in traditional Chinese Xiaoqu rice wine: Assessment via high-throughput sequencing and gas chromatography-ion mobility spectrometry. <i>LWT - Food Science and Technology</i> , 2022, 170, 114000.	2.5	10
9028	Environmental DNA Metabarcoding Reflects Fish DNA Dynamics in Lentic Ecosystems: A Case Study of Freshwater Ponds. <i>Fishes</i> , 2022, 7, 257.	0.7	4
9029	Oral and fecal microbiome of confiscated Bengal slow lorises in response to confinement duration. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9030	A Preliminary Study of Bacterioplankton Community Structure in the Taiyangshan Wetland in Ningxia and Its Driving Factors. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 12224.	1.2	0
9031	Functional changes in the oral microbiome after use of fluoride and arginine containing dentifrices: a metagenomic and metatranscriptomic study. <i>Microbiome</i> , 2022, 10, .	4.9	11
9032	High fat diet-induced hyperlipidemia and tissue steatosis in rabbits through modulating ileal microbiota. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 7187-7207.	1.7	5
9034	Impact of high pressure treatment on shelf life and microbial profile of wild harvested <i>Ascophyllum nodosum</i> and aquacultured <i>Alaria esculenta</i> during storage. <i>LWT - Food Science and Technology</i> , 2022, 170, 114022.	2.5	4
9035	Comparative Analysis of In Situ Eukaryotic Food Sources in Three Tropical Sea Cucumber Species by Metabarcoding. <i>Animals</i> , 2022, 12, 2303.	1.0	2
9036	Modulating effect of Xuanfei Baidu granule on host metabolism and gut microbiome in rats. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
9037	A comprehensive map of microbial biomarkers along the gastrointestinal tract for celiac disease patients. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7

#	ARTICLE	IF	CITATIONS
9038	Changes in Microbial Diversity, Soil Function, and Plant Biomass of Cotton Rhizosphere Soil Under the Influence of Chlorpyrifos. <i>Current Microbiology</i> , 2022, 79, .	1.0	3
9039	Anthocyanin Addition to Kefir: Metagenomic Analysis of Microbial Community Structure. <i>Current Microbiology</i> , 2022, 79, .	1.0	4
9040	Apex Predators Enhance Environmental Adaptation but Reduce Community Stability of Bacterioplankton in Crustacean Aquaculture Ponds. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10785.	1.8	4
9041	Diversity of bacterial community in Jerusalem artichoke (<i>Helianthus tuberosus</i> L.) during storage is associated with the genotype and carbohydrates. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9042	Metabolome, microbiome, and gene expression alterations in the colon of newborn piglets with intrauterine growth restriction. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9044	Energy consumption and intestinal microbiome disorders of yellow catfish (<i>Pelteobagrus fulvidraco</i>) under cold stress. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	6
9045	The rhizosphere bacterial community contributes to the nutritional competitive advantage of weedy rice over cultivated rice in paddy soil. <i>BMC Microbiology</i> , 2022, 22, .	1.3	5
9046	<i>Bifidobacterium longum</i> 070103 Fermented Milk Improve Glucose and Lipid Metabolism Disorders by Regulating Gut Microbiota in Mice. <i>Nutrients</i> , 2022, 14, 4050.	1.7	6
9047	nifH gene expression and diversity in geothermal springs of Tengchong, China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9048	Horizontal and vertical heterogeneity of sediment microbial community in Site F cold seep, the South China Sea. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	7
9049	Short-term application of chicken manure under different nitrogen rates alters structure and co-occurrence pattern but not diversity of soil microbial community in wheat field. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9050	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. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	24
9051	The evaluation of fecal microbiota transplantation vs vancomycin in a <i>Clostridioides difficile</i> infection model. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 6689-6700.	1.7	3
9054	Comparison of assembly process and co-occurrence pattern between planktonic and benthic microbial communities in the Bohai Sea. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
9055	Inulin accelerates weight loss in obese mice by regulating gut microbiota and serum metabolites. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	6
9056	The Study of Soil Bacterial Diversity and the Influence of Soil Physicochemical Factors in Meltwater Region of Ny-Å..lesund, Arctic. <i>Microorganisms</i> , 2022, 10, 1913.	1.6	3
9057	Changes in Soil Properties, Bacterial Communities and Wheat Roots Responding to Subsoiling in South Loess Plateau of China. <i>Agronomy</i> , 2022, 12, 2288.	1.3	4
9058	Influence of planting yellowhorn (<i>Xanthoceras sorbifolium</i> Bunge) on the bacterial and fungal diversity of fly ash. <i>PeerJ</i> , 0, 10, e14015.	0.9	0

#	ARTICLE	IF	CITATIONS
9060	Investigating genetic diversity within the most abundant and prevalent non-pathogenic leaf-associated bacteria interacting with <i>Arabidopsis thaliana</i> in natural habitats. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9061	Simulated seasonal diets alter yak rumen microbiota structure and metabolic function. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9062	Different outer membrane c-type cytochromes are involved in direct interspecies electron transfer to <i>Geobacter</i> or <i>Methanosarcina</i> species. , 2022, 1, 272-286.		15
9063	The mediating role of the gut microbiome in the association between ambient air pollution and autistic traits. <i>International Journal of Hygiene and Environmental Health</i> , 2022, 246, 114047.	2.1	4
9064	Schisantherin A alleviates non-alcoholic fatty liver disease by restoring intestinal barrier function. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
9065	Community assembly of plant, soil bacteria, and fungi vary during the restoration of an ecosystem threatened by desertification. <i>Journal of Soils and Sediments</i> , 2023, 23, 459-472.	1.5	3
9066	Dietary supplementation with <i>Cyberlindnera jadinii</i> improved growth performance, serum biochemical indices, antioxidant status, and intestinal health in growing raccoon dogs (<i>Nyctereutes</i>) <i>TJ ETQq0 0 0 rgBT /Overlocks10 Tf 50497 Td (p</i>		4
9067	Supplementation with paraformic acid in the diet improved intestinal development through modulating intestinal inflammation and microbiota in broiler chickens. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
9068	The effects of <i>Clostridium butyricum</i> on Ira rabbit growth performance, cecal microbiota and plasma metabolome. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9069	Horizontal gene transfer enables programmable gene stability in synthetic microbiota. <i>Nature Chemical Biology</i> , 2022, 18, 1245-1252.	3.9	12
9070	Microbial community structure and niche differentiation under different health statuses of <i>Pinus bungeana</i> in the Xiong'an New Area in China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9071	Management-induced shifts in rhizosphere bacterial communities contribute to the control of pathogen causing citrus greening disease. , 2022, 1, 275-286.		4
9072	Features of gut microbiota in patients with anorexia nervosa. <i>Chinese Medical Journal</i> , 2022, 135, 1993-2002.	0.9	8
9073	Soil microbial diversity and functional capacity associated with the production of edible mushroom <i>Stropharia rugosoannulata</i> in croplands. <i>PeerJ</i> , 0, 10, e14130.	0.9	3
9074	Alterations in the Gut Microbiota and Metabolomics of Seafarers after a Six-Month Sea Voyage. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
9075	Tissue-specific Grb10/Ddc insulator drives allelic architecture for cardiac development. <i>Molecular Cell</i> , 2022, 82, 3613-3631.e7.	4.5	9
9076	Soil bacterial community structure as affected by stand age in Chinese fir plantations: Insights at the aggregate scale. <i>Land Degradation and Development</i> , 2023, 34, 389-402.	1.8	2
9077	The <i>Aurantii Fructus Immaturus</i> flavonoid extract alleviates inflammation and modulate gut microbiota in DSS-induced colitis mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	3

#	ARTICLE	IF	CITATIONS
9079	Comparative analysis of the fecal microbiome and metabolomics of healthy versus captive South China tigers with mild diarrhea. <i>Canadian Journal of Microbiology</i> , 2022, 68, 758-768.	0.8	1
9080	Effect of dioscorea opposite waste on growth performance, blood parameters, rumen fermentation and rumen bacterial community in weaned lambs. <i>Journal of Integrative Agriculture</i> , 2023, 22, 1833-1846.	1.7	2
9081	Effects of rice-prawn (<i>Macrobrachium nipponense</i>) co-culture on the microbial community of soil. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 7361-7372.	1.7	1
9082	Correlation of characteristic flavor and microbial community in Jinhua ham during the post-ripening stage. <i>LWT - Food Science and Technology</i> , 2022, 171, 114067.	2.5	11
9083	Deterministic processes shape bacterial community assembly in a karst river across dry and wet seasons. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9084	Dietary fiber and probiotics based on gut microbiota targeting for functional constipation in children with cerebral palsy. <i>Frontiers in Pediatrics</i> , 0, 10, .	0.9	3
9085	Metatranscriptomic and metataxonomic insights into the ultra-small microbiome of the Korean fermented vegetable, kimchi. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9086	Soil microbial community assembly and stability are associated with potato (<i>Solanum tuberosum</i> L.) fitness under continuous cropping regime. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	12
9087	Phylogenomic analysis of the bowfin (<i>Amia calva</i>) reveals unrecognized species diversity in a living fossil lineage. <i>Scientific Reports</i> , 2022, 12, .	1.6	11
9088	Structure and diversity of mycorrhizal fungi communities of different part of <i>Bulbophyllum tianguii</i> in three terrestrial environments. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
9089	The rhizosphere microbiome improves the adaptive capabilities of plants under high soil cadmium conditions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
9090	Spatiotemporal distribution of size-fractioned phytoplankton in the Yalu River Estuary, China. <i>Ecosystem Health and Sustainability</i> , 2022, 8, .	1.5	2
9091	<i>Cornus officinalis</i> prior and post-processing: Regulatory effects on intestinal flora of diabetic nephropathy rats. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	8
9092	Sustainable management of the potato cyst nematode, <i>Globodera rostochiensis</i> , with two microbial fermentation products. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
9094	Fast-tracking antibody maturation using a B cell-based display system. <i>MAbs</i> , 2022, 14, .	2.6	0
9095	Response of soil microbial communities to natural radionuclides along specific-activity gradients. <i>Ecotoxicology and Environmental Safety</i> , 2022, 246, 114156.	2.9	6
9096	Distinct distribution patterns of planktonic ciliate communities along environmental gradients in a semi-enclosed bay. <i>Ecological Indicators</i> , 2022, 144, 109513.	2.6	1
9097	Diversity analysis and gene function prediction of bacteria and fungi of Bactrian camel milk and naturally fermented camel milk from Alxa in Inner Mongolia. <i>LWT - Food Science and Technology</i> , 2022, 169, 114001.	2.5	4

#	ARTICLE	IF	CITATIONS
9098	Microbiome and metabolome dysbiosis of the gut-lung axis in pulmonary hypertension. <i>Microbiological Research</i> , 2022, 265, 127205.	2.5	5
9099	Stuck or sluggish fermentations in home-made beers: Beyond the surface. <i>International Journal of Food Microbiology</i> , 2022, 383, 109956.	2.1	1
9100	Electron acceptors determine the BTEX degradation capacity of anaerobic microbiota via regulating the microbial community. <i>Environmental Research</i> , 2022, 215, 114420.	3.7	7
9101	Co-infection of porcine deltacoronavirus and porcine epidemic diarrhoea virus alters gut microbiota diversity and composition in the colon of piglets. <i>Virus Research</i> , 2022, 322, 198954.	1.1	5
9102	Data supporting a saturation mutagenesis assay for Tat-driven transcription with the GigaAssay. <i>Data in Brief</i> , 2022, 45, 108641.	0.5	2
9103	Linking microbial body size to community co-occurrences and stability at multiple geographical scales in agricultural soils. <i>Advances in Ecological Research</i> , 2022, , 1-26.	1.4	1
9104	An exploratory to analysis the effects of the different roles of mathca on lipid metabolism and intestinal flora regulation between normal and diabetic mice fed a high-fat diet. <i>Food Science and Technology</i> , 0, 42, .	0.8	0
9105	Analysis of microbial diversity in the root of <i>Astragalus mongholicus</i> . <i>Brazilian Journal of Biology</i> , 0, 82, .	0.4	0
9106	Genistein improves glucose metabolism and promotes adipose tissue browning through modulating gut microbiota in mice. <i>Food and Function</i> , 2022, 13, 11715-11732.	2.1	9
9107	Response of Carbon Emissions and the Bacterial Community to Freeze-Thaw Cycles in a Permafrost-Affected Forest-Wetland Ecotone in Northeast China. <i>Microorganisms</i> , 2022, 10, 1950.	1.6	3
9108	Microbiome-metabolome analysis reveals cervical lesion alterations. <i>Acta Biochimica Et Biophysica Sinica</i> , 2022, 54, 1552-1560.	0.9	1
9109	Bacterial communities in co-cultured fish intestines and rice field soil irrigated with aquaculture wastewater. <i>AMB Express</i> , 2022, 12, .	1.4	1
9110	<i>Paeoniae Radix Rubra</i> can enhance fatty acid β -oxidation and alleviate gut microbiota disorder in β -naphthyl isothiocyanate induced cholestatic model rats. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
9111	Humification improvement by optimizing particle size of bulking agent and relevant mechanisms during swine manure composting. <i>Bioresource Technology</i> , 2023, 367, 128191.	4.8	5
9112	Impact of Sulfoxaflo Exposure on Bacterial Community and Developmental Performance of the Predatory Ladybeetle <i>Propylea japonica</i> . <i>Microbial Ecology</i> , 2023, 86, 1226-1239.	1.4	0
9113	Rhizospheric microbial consortium of <i>Lilium lancifolium</i> Thunb. causes lily root rot under continuous cropping system. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9114	Effect of Environmental Heterogeneity and Trophic Status in Sampling Strategy on Estimation of Small-Scale Regional Biodiversity of Microorganisms. <i>Microorganisms</i> , 2022, 10, 2119.	1.6	1
9115	Potential Contribution of Coastal Upwelling to Carbon Sink through Interaction between Cyanobacteria and Microbial Eukaryotes. <i>Water (Switzerland)</i> , 2022, 14, 3097.	1.2	2

#	ARTICLE	IF	CITATIONS
9116	Manual acupuncture benignly regulates blood-brain barrier disruption and reduces lipopolysaccharide loading and systemic inflammation, possibly by adjusting the gut microbiota. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	13
9117	The responses to long-term nitrogen addition of soil bacterial, fungal, and archaeal communities in a desert ecosystem. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9118	Long-Term Protein Restriction Modulates Lipid Metabolism in White Adipose Tissues and Alters Colonic Microbiota of Shaziling Pigs. <i>Animals</i> , 2022, 12, 2944.	1.0	1
9119	Single-base resolution mapping of 2â€²-O-methylation sites by an exoribonuclease-enriched chemical method. <i>Science China Life Sciences</i> , 2023, 66, 800-818.	2.3	3
9120	Effects of Insect-Resistant Maize HGK60 on Community Diversity of Bacteria and Fungi in Rhizosphere Soil. <i>Plants</i> , 2022, 11, 2824.	1.6	2
9121	Isolation and Molecular Characterization of Two Novel Lytic Bacteriophages for the Biocontrol of <i>Escherichia coli</i> in Uterine Infections: In Vitro and Ex Vivo Preliminary Studies in Veterinary Medicine. <i>Pharmaceutics</i> , 2022, 14, 2344.	2.0	8
9122	Effects of Intercropping <i>Pandanus amaryllifolius</i> on Soil Properties and Microbial Community Composition in Areca Catechu Plantations. <i>Forests</i> , 2022, 13, 1814.	0.9	3
9123	Effect of Aerated Irrigation on the Growth and Rhizosphere Soil Fungal Community Structure of Greenhouse Grape Seedlings. <i>Sustainability</i> , 2022, 14, 12719.	1.6	1
9124	Hole Application of Urea Inhibited Nitrification in the Zone around the Fertilizer Point by Reducing the Abundance of Nitrification Genes. <i>Agriculture (Switzerland)</i> , 2022, 12, 1771.	1.4	1
9125	Differential Influences of Wind-Blown Sand Burial on Bacterial and Fungal Communities Inhabiting Biological Soil Crusts in a Temperate Desert, China. <i>Microorganisms</i> , 2022, 10, 2010.	1.6	0
9126	Macroporous Silicone Chips for Decoding Microbial Dark Matter in Environmental Microbiomes. <i>ACS Applied Materials & Interfaces</i> , 2022, 14, 49592-49603.	4.0	3
9127	Sexual Dimorphism of the Gut Microbiota in the Chinese Alligator and Its Convergence in the Wild Environment. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12140.	1.8	1
9129	The Effect of Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> (Steiner and Buhner) Nickle on Intestinal Bacterial Community of Insect Vector <i>Monochamus saltuarius</i> (Coleoptera: Cerambycidae). <i>Forests</i> , 2022, 13, 1673.	0.9	0
9130	Nitrogen addition alters plant growth in Chinaâ€™s Yellow River Delta coastal wetland through direct and indirect effects. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
9131	Gut microbiota modulation by plant polyphenols in koi carp (<i>Cyprinus carpio</i> L.). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
9132	Ecological niche selection shapes the assembly and diversity of microbial communities in <i>Casuarina equisetifolia</i> L.. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
9134	Effects of autochthonous strains mixture on gut microbiota and metabolic profile in cobia (<i>Rachycentron canadum</i>). <i>Scientific Reports</i> , 2022, 12, .	1.6	11
9135	Assessing the Bacterial Communities Composition from Differently Treated Agarwood via 16S rRNA Gene Metabarcoding. <i>Life</i> , 2022, 12, 1697.	1.1	1

#	ARTICLE	IF	CITATIONS
9136	Maternal supplementation with a casein hydrolysate and yeast beta-glucan from late gestation through lactation improves gastrointestinal health of piglets at weaning. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
9137	Saline-alkali stress reduces soil bacterial community diversity and soil enzyme activities. <i>Ecotoxicology</i> , 2022, 31, 1356-1368.	1.1	7
9138	Effects of trunk injection with emamectin benzoate on arthropod diversity. <i>Pest Management Science</i> , 2023, 79, 935-946.	1.7	4
9139	Transmission of tetracycline resistance genes and microbiomes from manure-borne black soldier fly larvae frass to rhizosphere soil and pakchoi endophytes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9140	»Cecinothofagus Nieves-Aldrey & Liljeblad (Hymenoptera, Cynipidae) is likely an endoparasitoid of the gall-maker genus Aditrochus R¼bsaamen (Hymenoptera, Pteromalidae). <i>Journal of Hymenoptera Research</i> , 0, 93, 33-42.	0.8	2
9141	Incubation determines favorable microbial communities in Chinese alligator nests. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9142	Effects of captive and primate-focused tourism on the gut microbiome of Tibetan macaques. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9143	Characteristics of Bacterial Community in Pelteobagrus fulvidraco Integrated Multi-Trophic Aquaculture System. <i>Water (Switzerland)</i> , 2022, 14, 3192.	1.2	2
9144	Evaluating the fermentation characteristics, bacterial community, and predicted functional profiles of native grass ensiled with different additives. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9145	A comparison of microbial composition under three tree ecosystems using the stochastic process and network complexity approaches. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	13
9146	Root-associated fungal microbiota of the perennial sweet sorghum cultivar under field growth. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9147	Partial Replacement of Oat Hay with Whole-Plant Hydroponic Barley Seedlings Modulates Ruminant Microbiota and Affects Growth Performance of Holstein Heifers. <i>Microorganisms</i> , 2022, 10, 2000.	1.6	2
9149	The Endophytic Fungi Diversity, Community Structure, and Ecological Function Prediction of Sophora alopecuroides in Ningxia, China. <i>Microorganisms</i> , 2022, 10, 2099.	1.6	8
9150	Association between Gut Microbiota and Emotional-Behavioral Symptoms in Children with Attention-Deficit/Hyperactivity Disorder. <i>Journal of Personalized Medicine</i> , 2022, 12, 1634.	1.1	3
9151	Microbial assemblages of Schisandraceae plants and the correlations between endophytic species and the accumulation of secondary metabolites. <i>Plant and Soil</i> , 2023, 483, 85-107.	1.8	4
9152	PotatoMASHâ€”A Low Cost, Genome-Scanning Marker System for Use in Potato Genomics and Genetics Applications. <i>Agronomy</i> , 2022, 12, 2461.	1.3	5
9153	Supplemental dietary Selenohomolanthionine affects growth and rumen bacterial population of Shaanbei white cashmere wether goats. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
9154	Determination of physiological, biochemical and molecular interactions between Fraserâ€™s Photinia (Photinia Å— fraseri Dress.) and its endophytic bacterium PGB_invit. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 151, 631-649.	1.2	2

#	ARTICLE	IF	CITATIONS
9155	Elemental sulphur recovery from a sulphate-rich aqueous stream in a single hybrid linear flow channel reactor is mediated through microbial community dynamics and adaptation to reactor zones. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	0
9156	Evaluation of Genetic Diversity and Parasite-Mediated Selection of MHC Class I Genes in <i>Emberiza godlewskii</i> (Passeriformes: Emberizidae). <i>Diversity</i> , 2022, 14, 925.	0.7	0
9157	Agroforestry alters the fluxes of greenhouse gases of Moso bamboo plantation soil. <i>Environmental Research Letters</i> , 2022, 17, 115003.	2.2	2
9158	Effects of Plant Growth-Promoting Rhizobacteria on the Growth and Soil Microbial Community of <i>Carya illinoensis</i> . <i>Current Microbiology</i> , 2022, 79, .	1.0	7
9159	Toward efficient and high-fidelity metagenomic data from sub-nanogram DNA: evaluation of library preparation and decontamination methods. <i>BMC Biology</i> , 2022, 20, .	1.7	1
9160	Changes in antibiotic residues and the gut microbiota during ciprofloxacin administration throughout Silkie chicken development. <i>Poultry Science</i> , 2023, 102, 102267.	1.5	3
9161	Genomic insights into the physiology of <i>Quinella</i> , an iconic uncultured rumen bacterium. <i>Nature Communications</i> , 2022, 13, .	5.8	10
9162	Variations in nano- and pico-eukaryotic phytoplankton assemblages in the Qinhuangdao green-tide area. <i>Journal of Oceanology and Limnology</i> , 0, , .	0.6	1
9163	Effects of Lysophosphatidylcholine on Intestinal Health of Turbot Fed High-Lipid Diets. <i>Nutrients</i> , 2022, 14, 4398.	1.7	5
9164	High-Density Lipoprotein Cholesterol as a Potential Medium between Depletion of <i>Lachnospiraceae</i> Genera and Hypertension under a High-Calorie Diet. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
9165	Deep mutational scanning and machine learning reveal structural and molecular rules governing allosteric hotspots in homologous proteins. <i>ELife</i> , 0, 11, .	2.8	17
9166	TangNaiKang, herbal formulation, alleviates obesity in diabetic SHR/cp rats through modulation of gut microbiota and related metabolic functions. <i>Pharmaceutical Biology</i> , 2022, 60, 2002-2010.	1.3	1
9167	Fermented soybean meal modified the rumen microbiome to enhance the yield of milk components in Holstein cows. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 7627-7642.	1.7	5
9168	SCRAP: a bioinformatic pipeline for the analysis of small chimeric RNA-seq data. <i>Rna</i> , 0, , rna.079240.122.	1.6	2
9169	Fecal fungal microbiota alterations associated with clinical phenotypes in Crohn's disease in southwest China. <i>PeerJ</i> , 0, 10, e14260.	0.9	4
9170	Metabarcoding assessment of fungal diversity in brown algae and sponges of Mauritius. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9171	Plastic mulch stimulates denitrification by interaction between soil environment and denitrifying bacteria. <i>Plant and Soil</i> , 0, , .	1.8	1
9172	The Threat of Potentially Pathogenic Bacteria in the Feces of Bats. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4

#	ARTICLE	IF	CITATIONS
9173	Regulation of viable/inactivated/lysed probiotic <i>Lactobacillus plantarum</i> H6 on intestinal microbiota and metabolites in hypercholesterolemic mice. <i>Npj Science of Food</i> , 2022, 6, .	2.5	17
9174	The long-acting herbicide mesosulfuron-methyl inhibits soil microbial community assembly mediating nitrogen cycling. <i>Journal of Hazardous Materials</i> , 2023, 443, 130293.	6.5	6
9175	Electrochemical Responses and Microbial Community Shift of Electroactive Biofilm to Acidity Stress in Microbial Fuel Cells. <i>Minerals (Basel, Switzerland)</i> , 2022, 12, 1268.	0.8	0
9176	Effects of land-use patterns on the biogeography of the sediment bacteria in the Yarlung Tsangpo River. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
9177	Pretreatment with probiotics <i>Enterococcus faecium</i> NCIMB 11181 attenuated <i>Salmonella</i> Typhimurium-induced gut injury through modulating intestinal microbiome and immune responses with barrier function in broiler chickens. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	12
9178	Exploratory studies of oral and fecal microbiome in healthy human aging. <i>Frontiers in Aging</i> , 0, 3, .	1.2	5
9179	Bacterial Community Shifts in Casing Soil Before and After the Cultivation of <i>Oudemansiella raphanipes</i> . <i>Journal of Soil Science and Plant Nutrition</i> , 2022, 22, 4116-4126.	1.7	1
9180	Effects of Variety, Plant Location, and Season on the Phyllosphere Bacterial Community Structure of Alfalfa (<i>Medicago sativa</i> L.). <i>Microorganisms</i> , 2022, 10, 2023.	1.6	5
9181	Hyperbaric oxygen improves depression-like behaviors in chronic stress model mice by remodeling gut microbiota and regulating host metabolism. <i>CNS Neuroscience and Therapeutics</i> , 2023, 29, 239-255.	1.9	7
9182	Response of Soil Bacterial Diversity, Predicted Functions and Co-Occurrence Patterns to Nanoceria and Ionic Cerium Exposure. <i>Microorganisms</i> , 2022, 10, 1982.	1.6	1
9183	Genotype-to-Protein Map and Collective Adaptation in a Viral Population. <i>Biophysica</i> , 2022, 2, 381-399.	0.6	2
9184	Amoxicillin modulates gut microbiota to improve short-term high-fat diet induced pathophysiology in mice. <i>Gut Pathogens</i> , 2022, 14, .	1.6	2
9185	The Combined Use of Medium- and Short-Chain Fatty Acids Improves the Pregnancy Outcomes of Sows by Enhancing Ovarian Steroidogenesis and Endometrial Receptivity. <i>Nutrients</i> , 2022, 14, 4405.	1.7	3
9186	Coal Mining Activities Driving the Changes in Microbial Community and Hydrochemical Characteristics of Underground Mine Water. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 13359.	1.2	6
9187	Functional organic fertilizers can alleviate tobacco (<i>Nicotiana tabacum</i> L.) continuous cropping obstacle via ameliorating soil physicochemical properties and bacterial community structure. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	3
9188	Long-term nitrogen fertilization alters phylogenetic structure of arbuscular mycorrhizal fungal community in plant roots across fine spatial scales. <i>Plant and Soil</i> , 2023, 483, 427-440.	1.8	2
9189	Changes in soil fungal communities after onset of wheat yellow mosaic virus disease. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	4
9190	Dephenolization pyrolysis fluid improved physicochemical properties and microbial community structure of saline-alkali soils. <i>Environmental Science and Pollution Research</i> , 0, , .	2.7	0

#	ARTICLE	IF	CITATIONS
9191	Mitochondrial Transport from Mesenchymal Stromal Cells to Chondrocytes Increases DNA Content and Proteoglycan Deposition <i>In Vitro</i> in 3D Cultures. <i>Cartilage</i> , 2022, 13, 133-147.	1.4	6
9192	Divergent Changes in Bacterial Functionality as Affected by Root-Zone Ecological Restoration in an Aged Peach Orchard. <i>Microorganisms</i> , 2022, 10, 2127.	1.6	2
9193	Effect of Unsaturated Fatty Acid Ratio <i>In Vitro</i> on Rumen Fermentation, Methane Concentration, and Microbial Profile. <i>Fermentation</i> , 2022, 8, 540.	1.4	5
9194	Expression Analysis and the Roles of the Sec1 Gene in Regulating the Composition of Mouse Gut Microbiota. <i>Genes</i> , 2022, 13, 1858.	1.0	3
9195	Proportions of Pacific white shrimp, <i>Litopenaeus vannamei</i> , gut microbiota from ambient microbiota increased with aquaculture process. <i>Journal of the World Aquaculture Society</i> , 2023, 54, 982-993.	1.2	1
9196	A Novel Inovirus Reprograms Metabolism and Motility of Marine <i>Alteromonas</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
9198	Effects of heat stress on 16S rDNA, metagenome and metabolome in Holstein cows at different growth stages. <i>Scientific Data</i> , 2022, 9, .	2.4	1
9199	Organic matter degradation and bacterial communities in surface sediment influenced by <i>Procambarus clarkia</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9200	Multi-omics association analysis reveals interactions between the oropharyngeal microbiome and the metabolome in pediatric patients with influenza A virus pneumonia. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
9201	Effects of <i>Allium mongolicum</i> regel essential oil supplementation on growth performance, nutrient digestibility, rumen fermentation, and bacterial communities in sheep. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	3
9202	Effects of <i>Rhizophagus intraradices</i> on soybean yield and the composition of microbial communities in the rhizosphere soil of continuous cropping soybean. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
9203	Sodium humate alters the intestinal microbiome, short-chain fatty acids, eggshell ultrastructure, and egg performance of old laying hens. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
9204	Comprehensive analysis and accurate quantification of unintended large gene modifications induced by CRISPR-Cas9 gene editing. <i>Science Advances</i> , 2022, 8, .	4.7	25
9205	Effects of combined aerobic and resistance training on gut microbiota and cardiovascular risk factors in physically active elderly women: A randomized controlled trial. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	5
9206	Distinct B-Cell Specific Transcriptional Contexts of the BCL2 Oncogene Impact Pre-Malignant Development in Mouse Models. <i>Cancers</i> , 2022, 14, 5337.	1.7	2
9207	Vanadate reducing bacteria and archaea may use different mechanisms to reduce vanadate in vanadium contaminated riverine ecosystems as revealed by the combination of DNA-SIP and metagenomic-binning. <i>Water Research</i> , 2022, 226, 119247.	5.3	9
9208	Geographic patterns and determinants of antibiotic resistomes in coastal sediments across complex ecological gradients. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9209	Effects of rice-crayfish co-culture on ammonia-oxidizing microbial abundance and community structure. <i>Aquatic Ecology</i> , 0, , .	0.7	0

#	ARTICLE	IF	CITATIONS
9212	Comparison of epiphytic and intestinal bacterial communities in freshwater snails (<i>Bellamya</i>) Tj ETQq0 0 0 rgBT /Overlock 1 Tf 50 74	0.9	1
9213	The relationship between pelvic floor functions and vaginal microbiota in 6–8 weeks postpartum women. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9214	Effects of Microbial Transfer during Food-Gut-Feces Circulation on the Health of <i>Bombyx mori</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
9215	Uncovering the characteristics of the gut microbiota in patients with acute ischemic stroke and phlegm-heat syndrome. <i>PLoS ONE</i> , 2022, 17, e0276598.	1.1	2
9216	The addition of biochar and nitrogen alters the microbial community and their cooccurrence network by affecting soil properties. <i>Chemosphere</i> , 2023, 312, 137101.	4.2	9
9217	Blue Turns to Gray: Paleogenomic Insights into the Evolutionary History and Extinction of the Blue Antelope (<i>Hippotragus leucophaeus</i>). <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
9218	The impact of genetic modified Ma bamboo on soil microbiome. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9219	Unraveling potential enzymes and their functional role in fine cocoa beans fermentation using temporal shotgun metagenomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9220	Lake sediments from littoral and profundal zones are heterogeneous but equivalent sources of methane produced by distinct methanogenic communities – a case study from Lake Remoray. <i>Journal of Geophysical Research G: Biogeosciences</i> , 0, , .	1.3	0
9221	Response of soil microbes to <i>Carex meyeriana</i> meadow degeneration caused by overgrazing in inner Mongolia. <i>Acta Oecologica</i> , 2022, 117, 103860.	0.5	3
9222	Microbial community structures and important taxa across oxygen gradients in the Andaman Sea and eastern Bay of Bengal epipelagic waters. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9223	Nitrogen fertilizer amount has minimal effect on rhizosphere bacterial diversity during different growth stages of peanut. <i>PeerJ</i> , 0, 10, e13962.	0.9	0
9224	Gut content metabarcoding and citizen science reveal the earthworm prey of the exotic terrestrial flatworm, <i>Obama nungara</i> . <i>European Journal of Soil Biology</i> , 2022, 113, 103449.	1.4	2
9225	Rescue of social deficits by early-life melatonin supplementation through modulation of gut microbiota in a murine model of autism. <i>Biomedicine and Pharmacotherapy</i> , 2022, 156, 113949.	2.5	5
9226	Change of the structure and assembly of bacterial and photosynthetic communities by the ecological engineering practices in Dianchi Lake. <i>Environmental Pollution</i> , 2022, 315, 120386.	3.7	2
9227	Environmental DNA metabarcoding effectively monitors terrestrial species by using urban green spaces. <i>Urban Forestry and Urban Greening</i> , 2022, 78, 127782.	2.3	1
9228	Nutrient enrichment decreases dissolved organic carbon sequestration potential of tropical seagrass meadows by mediating bacterial activity. <i>Ecological Indicators</i> , 2022, 145, 109576.	2.6	4
9229	The toxicity of the monoterpenes from lemongrass is mitigated by the detoxifying symbiosis of bacteria and fungi in the tick <i>Haemaphysalis longicornis</i> . <i>Ecotoxicology and Environmental Safety</i> , 2022, 247, 114261.	2.9	2

#	ARTICLE	IF	CITATIONS
9230	Emission mitigation of CH ₄ and N ₂ O during semi-permeable membrane covered hyperthermophilic aerobic composting of livestock manure. <i>Journal of Cleaner Production</i> , 2022, 379, 134850.	4.6	18
9231	Changes in the gut microbial community of larvae of the harlequin lady beetle in response to cannibalism and intraguild predation. <i>Biological Control</i> , 2022, 176, 105090.	1.4	3
9232	Effects of ethanamizuril, sulfachlorpyridazine or their combination on cecum microbial community and metabolomics in chickens infected with <i>Eimeria tenella</i> . <i>Microbial Pathogenesis</i> , 2022, 173, 105823.	1.3	1
9233	Contrasting diversity patterns and community assembly mechanisms of bacterioplankton among different aquatic habitats in Lake Taihu, a large eutrophic shallow lake in China. <i>Environmental Pollution</i> , 2022, 315, 120342.	3.7	4
9234	Abundant bacteria and fungi attached to airborne particulates in vegetable plastic greenhouses. <i>Science of the Total Environment</i> , 2023, 857, 159507.	3.9	8
9235	Influence of low-energy electron beam irradiation on the quality and shelf-life of vacuum-packaged pork stored under chilled and superchilled conditions. <i>Meat Science</i> , 2023, 195, 109019.	2.7	5
9236	Removal performance and inhibitory effects of combined tetracycline, oxytetracycline, sulfadiazine, and norfloxacin on anaerobic digestion process treating swine manure. <i>Science of the Total Environment</i> , 2023, 857, 159536.	3.9	13
9237	Oral vaccination with feed-based live attenuated vaccine protects large yellow croaker against <i>Pseudomonas plecoglossicida</i> infection. <i>Aquaculture</i> , 2023, 563, 738932.	1.7	1
9238	Acute polyethylene microplastic (PE-MPs) exposure activates the intestinal mucosal immune network pathway in adult zebrafish (<i>Danio rerio</i>). <i>Chemosphere</i> , 2023, 311, 137048.	4.2	9
9239	Rhizosphere soil microbes benefit carbon and nitrogen sinks under long-term afforestation on the Tibetan Plateau. <i>Catena</i> , 2023, 220, 106705.	2.2	5
9240	Quorum sensing responses of r-/K-strategists <i>Nitrospira</i> in continuous flow and sequencing batch nitrifying biofilm reactors. <i>Science of the Total Environment</i> , 2023, 857, 159328.	3.9	1
9241	Joint role of land cover types and microbial processing on molecular composition of dissolved organic matter in inland lakes. <i>Science of the Total Environment</i> , 2023, 857, 159522.	3.9	4
9242	Arsenic shapes the microbial community structures in tungsten mine waste rocks. <i>Environmental Research</i> , 2023, 216, 114573.	3.7	2
9243	Eukaryotic plankton community assembly and influencing factors between continental shelf and slope sites in the northern South China Sea. <i>Environmental Research</i> , 2023, 216, 114584.	3.7	3
9244	Effects of hyperosmotic stress on the intestinal microbiota, transcriptome, and immune function of mandarin fish (<i>Siniperca chuatsi</i>). <i>Aquaculture</i> , 2023, 563, 738901.	1.7	6
9245	Nitrogen addition weakens the biodiversity multifunctionality relationships across soil profiles in a grassland assemblage. <i>Agriculture, Ecosystems and Environment</i> , 2023, 342, 108241.	2.5	12
9246	A novel endophytic bacterial strain improves potato storage characteristics by degrading glycoalkaloids and regulating microbiota. <i>Postharvest Biology and Technology</i> , 2023, 196, 112176.	2.9	1
9247	Is there a significant difference in microbiota between water and microplastic surfaces in winter? The possibility of spreading offshore into the ocean. <i>Science of the Total Environment</i> , 2023, 858, 159769.	3.9	2

#	ARTICLE	IF	CITATIONS
9248	Horizontal transfer of intracellular and extracellular ARGs in sludge compost under sulfamethoxazole stress. <i>Chemical Engineering Journal</i> , 2023, 454, 139968.	6.6	14
9249	Dietary selenium regulates the diversity and stability of microbial communities in stomach and intestine of rabbitfish (<i>Siganus oramin</i>). <i>Aquaculture</i> , 2023, 563, 738979.	1.7	2
9250	Effects of secondary release of chromium and vanadium on soil properties, nutrient cycling and bacterial communities in contaminated acidic paddy soil. <i>Journal of Environmental Management</i> , 2023, 326, 116725.	3.8	4
9251	Adaptive bacterial and fungal matching between a parasitic plant and its host: A case of <i>Cistanche deserticola</i> and <i>Haloxylon ammodendron</i> . <i>Industrial Crops and Products</i> , 2023, 191, 115932.	2.5	2
9252	Distribution and migration of antibiotic resistance genes, as well as their correlation with microbial communities in swine farm and its surrounding environments. <i>Environmental Pollution</i> , 2023, 316, 120618.	3.7	6
9253	Biochar reduces bioavailability of phosphorus during swine manure composting: Roles of phoD-harboring bacterial community. <i>Science of the Total Environment</i> , 2023, 858, 159926.	3.9	13
9254	Intestinal microbiota perturbations in the gastropod <i>Trochus niloticus</i> concurrently exposed to ocean acidification and environmentally relevant concentrations of sulfamethoxazole. <i>Chemosphere</i> , 2023, 311, 137115.	4.2	1
9255	Long-acting mechanisms of concentrated urea application “ High urea concentrations are biological inhibitors. <i>Applied Soil Ecology</i> , 2023, 182, 104723.	2.1	2
9256	Organic fertilizer substitution over six years improves the productivity of garlic, bacterial diversity, and microbial communities network complexity. <i>Applied Soil Ecology</i> , 2023, 182, 104718.	2.1	10
9257	Soil microbial communities and their co-occurrence networks in response to long-term Pb“Zn contaminated soil in southern China. <i>Environmental Science and Pollution Research</i> , 0, , .	2.7	0
9258	A comprehensive assessment of fungal communities in various habitats from an ice-free area of maritime Antarctica: diversity, distribution, and ecological trait. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	2
9259	Amoxicillin impact on pathophysiology induced by short term high salt diet in mice. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
9260	Diversity of soil faunal community as influenced by crop straw combined with different synthetic fertilizers in upland purple soil. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
9261	Cysteamine Supplementation In Vitro Remarkably Promoted Rumen Fermentation Efficiency towards Propionate Production via <i>Prevotella</i> Enrichment and Enhancing Antioxidant Capacity. <i>Antioxidants</i> , 2022, 11, 2233.	2.2	5
9262	Linking bacterial and fungal assemblages to soil nutrient cycling within different aggregate sizes in agroecosystem. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9263	Changes in the Physical, Chemical, and Bacterial Community Characteristics of Soil in Response to Short-Term Combined Organic“Inorganic Fertilizers in a Dry Direct-Seeded Paddy Field. <i>Agronomy</i> , 2022, 12, 2808.	1.3	2
9264	Gut Microbiota Mediates Skin Ulceration Syndrome Outbreak by Readjusting Lipid Metabolism in <i>Apostichopus japonicus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13583.	1.8	5
9265	Association of intestinal microbiota markers and dietary pattern in Chinese patients with type 2 diabetes: The Henan rural cohort study. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	2

#	ARTICLE	IF	CITATIONS
9266	Assessment of the rhizosphere fungi and bacteria recruited by sugarcane during smut invasion. <i>Brazilian Journal of Microbiology</i> , 0, , .	0.8	6
9267	Wild Boar (<i>Sus scrofa</i>)â€™Fascioloides magna Interaction from the Perspective of the MHC Genes. <i>Pathogens</i> , 2022, 11, 1359.	1.2	1
9269	Chalcone-1-Deoxynojirimycin Heterozygote Reduced the Blood Glucose Concentration and Alleviated the Adverse Symptoms and Intestinal Flora Disorder of Diabetes Mellitus Rats. <i>Molecules</i> , 2022, 27, 7583.	1.7	2
9270	Diversity and Distribution Characteristics of Soil Microbes across Forestâ€™Peatland Ecotones in the Permafrost Regions. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 14782.	1.2	3
9271	Short-term head-down bed rest microgravity simulation alters salivary microbiome in young healthy men. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9272	Dietary shredded steam-exploded pine particle supplementation as a strategy to mitigate chronic cyclic heat stress by modulating gut microbiota in broilers. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
9273	<i>Lactobacillus rhamnosus</i> GG protects against atherosclerosis by improving ketone body synthesis. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 8233-8243.	1.7	2
9274	Plant sex affects plant-microbiome assemblies of dioecious <i>Populus cathayana</i> trees under different soil nitrogen conditions. <i>Microbiome</i> , 2022, 10, .	4.9	16
9275	Effects of different grains on bacterial diversity and enzyme activity associated with digestion of starch in the foal stomach. <i>BMC Veterinary Research</i> , 2022, 18, .	0.7	2
9276	Beneficial effect of the short-chain fatty acid propionate on vascular calcification through intestinal microbiota remodelling. <i>Microbiome</i> , 2022, 10, .	4.9	22
9277	Mapping responsive genomic elements to heat stress in a maize diversity panel. <i>Genome Biology</i> , 2022, 23, .	3.8	5
9278	Community distribution of rhizosphere and endophytic bacteria of ephemeral plants in desertâ€™oasis ecotone and analysis of environmental driving factors. <i>Land Degradation and Development</i> , 0, , .	1.8	0
9279	Response of rice growth to soil microorganisms and soil properties in different soil types. <i>Agronomy Journal</i> , 2023, 115, 197-207.	0.9	3
9280	Arbuscular Mycorrhiza Support Plant Sulfur Supply through Organosulfur Mobilizing Bacteria in the Hypo- and Rhizosphere. <i>Plants</i> , 2022, 11, 3050.	1.6	5
9281	Phyllosphere microbial community of cigar tobacco and its corresponding metabolites. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
9282	The Impact of <i>Vairimorpha (Nosema) ceranae</i> Natural Infection on Honey Bee (<i>Apis mellifera</i>) and Bee Bread Microbiota. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 11476.	1.3	2
9283	Effect of Mulberry Leaf Powder of Varying Levels on Growth Performance, Immuno-Antioxidant Status, Meat Quality and Intestinal Health in Finishing Pigs. <i>Antioxidants</i> , 2022, 11, 2243.	2.2	2
9284	Dynamics of extracellular polymeric substances and soil organic carbon with mangrove zonation along a continuous tidal gradient. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1

#	ARTICLE	IF	CITATIONS
9285	Climate-induced salinization may lead to increased lake nitrogen retention. <i>Water Research</i> , 2023, 228, 119354.	5.3	8
9286	Freshwater trophic status mediates microbial community assembly and interdomain network complexity. <i>Environmental Pollution</i> , 2023, 316, 120690.	3.7	6
9287	Synergistic PAH biodegradation by a mixed bacterial consortium: based on a multi-substrate enrichment approach. <i>Environmental Science and Pollution Research</i> , 2023, 30, 24606-24616.	2.7	1
9288	Long-term atorvastatin improves cognitive decline by regulating gut function in naturally ageing rats. <i>Immunity and Ageing</i> , 2022, 19, .	1.8	2
9289	Composition and diversity of root-inhabiting bacterial microbiota in the perennial sweet sorghum cultivar at the maturing stage. <i>Plant Growth Regulation</i> , 0, , .	1.8	0
9290	Identification and characterization of mixed infections of <i>Chlamydia trachomatis</i> via high-throughput sequencing. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9291	Interplay of Lymphocytes with the Intestinal Microbiota in Children with Nonalcoholic Fatty Liver Disease. <i>Nutrients</i> , 2022, 14, 4641.	1.7	4
9292	Developmental stage variation in the gut microbiome of South China tigers. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9293	Respiratory Microbiome Profile of Pediatric Pulmonary Hypertension Patients Associated With Congenital Heart Disease. <i>Hypertension</i> , 2023, 80, 214-226.	1.3	1
9294	Bacterial Community Diversity and Bacterial Interaction Network in Eight Mosquito Species. <i>Genes</i> , 2022, 13, 2052.	1.0	1
9295	The incorporation of straw into the subsoil increases C, N, and P enzyme activities and nutrient supply by enriching distinctive functional microorganisms. <i>Land Degradation and Development</i> , 2023, 34, 1297-1310.	1.8	3
9296	Linking Microbial Functional Gene Abundance and Daqu Extracellular Enzyme Activity: Implications for Carbon Metabolism during Fermentation. <i>Foods</i> , 2022, 11, 3623.	1.9	4
9297	Washed microbiota transplantation improves patients with metabolic syndrome in South China. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	9
9298	Bioâ€Functionalized Manganese Nanoparticles Suppress Fusarium Wilt in Watermelon (<i>Citrullus</i> Tj ETQq1 1 0.784314 rgBT /Over Community Modulation. <i>Small</i> , 2023, 19, .	5.2	22
9299	Prokaryotic communities adapted to microhabitats on the Indian lotus (<i>Nelumbo nucifera</i>) growing in the high-altitude urban Dal Lake. <i>International Microbiology</i> , 2023, 26, 257-267.	1.1	2
9300	Effects of Drying and Rewetting Cycles on Carbon Dioxide Emissions and Soil Microbial Communities. <i>Forests</i> , 2022, 13, 1916.	0.9	2
9301	Effects of Softening Dry Food with Water on Stress Response, Intestinal Microbiome, and Metabolic Profile in Beagle Dogs. <i>Metabolites</i> , 2022, 12, 1124.	1.3	2
9302	Alteration of gut microbiota in migraine patients with irritable bowel syndrome in a Chinese Han population. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	0

#	ARTICLE	IF	CITATIONS
9303	SARS-CoV-2 variant Alpha has a spike-dependent replication advantage over the ancestral B.1 strain in human cells with low ACE2 expression. <i>PLoS Biology</i> , 2022, 20, e3001871.	2.6	11
9304	Explore the interaction between root metabolism and rhizosphere microbiota during the growth of <i>Angelica sinensis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
9305	Genetic mutation and tumor microbiota determine heterogeneity of tumor immune signature: Evidence from gastric and colorectal synchronous cancers. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
9306	Microbial Community Structure of Colostrum in Women with Antibiotic Exposure Immediately After Delivery. <i>Breastfeeding Medicine</i> , 2022, 17, 940-946.	0.8	0
9308	Effects of combined addition of 3-nitrooxypropanol and vitamin B12 on methane and propionate production in dairy cows by in vitro-simulated fermentation. <i>Journal of Dairy Science</i> , 2023, 106, 219-232.	1.4	2
9309	Effects of Two <i>Bacillus Velezensis</i> Microbial Inoculants on the Growth and Rhizosphere Soil Environment of <i>Prunus davidiana</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13639.	1.8	8
9310	Correlation between microbial communities and key odourants in fermented capsicum inoculated with <i>Pediococcus pentosaceus</i> and <i>Cyberlindnera rhodanensis</i> . <i>Journal of the Science of Food and Agriculture</i> , 2023, 103, 1139-1151.	1.7	3
9311	Variation in Community Structure of the Root-Associated Fungi of <i>Cinnamomum camphora</i> Forest. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1210.	1.5	2
9312	Significant Shifts in Microbial Communities Associated with Scleractinian Corals in Response to Algae Overgrowth. <i>Microorganisms</i> , 2022, 10, 2196.	1.6	3
9313	Maize-soybean intercropping facilitates chemical and microbial transformations of phosphorus fractions in a calcareous soil. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9314	Short-term application of organic fertilization impacts phosphatase activity and phosphorus-mineralizing bacterial communities of bulk and rhizosphere soils of maize in acidic soil. <i>Plant and Soil</i> , 2023, 484, 95-113.	1.8	7
9316	Differential patterns and assembly processes of bacterial communities from distinct microhabitats in a subtropical estuary. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
9317	Responses of soil microbial diversity, network complexity and multifunctionality to three land-use changes. <i>Science of the Total Environment</i> , 2023, 859, 160255.	3.9	21
9318	Linking Bacterial Rhizosphere Communities of Two Pioneer Species, <i>Brachystegia boehmii</i> and <i>B. spiciformis</i> , to the Ecological Processes of Miombo Woodlands. <i>Forests</i> , 2022, 13, 1840.	0.9	1
9319	Microbiome Analysis of Traditional Grain Vinegar Produced under Different Fermentation Conditions in Various Regions in Korea. <i>Foods</i> , 2022, 11, 3573.	1.9	3
9320	Coupling of leaf elemental traits with root fungal community composition reveals a plant resource acquisition strategy in a desert ecosystem. <i>Plant and Soil</i> , 2023, 484, 115-131.	1.8	1
9321	Functional analysis of intergenic regulatory regions of genes encoding surface adhesins in <i>Staphylococcus aureus</i> isolates from periprosthetic joint infections. <i>Biofilm</i> , 2022, 4, 100093.	1.5	0
9322	Translucent disease outbreak in <i>Penaeus vannamei</i> post-larva accompanies the imbalance of pond water and shrimp gut microbiota homeostasis. <i>Aquaculture Reports</i> , 2022, 27, 101410.	0.7	1

#	ARTICLE	IF	CITATIONS
9323	Lactobacillus reuteri normalizes altered fear memory in male Cntnap4 knockout mice. EBioMedicine, 2022, 86, 104323.	2.7	6
9324	Relationships between rumen microbes, short-chain fatty acids, and markers of white adipose tissue browning during the cold season in grazing Mongolian sheep (Ovis aries). Journal of Thermal Biology, 2022, 110, 103386.	1.1	3
9325	A new potential risk: The impacts of Klebsiella pneumoniae infection on the histopathology, transcriptome and metagenome of Chinese mitten crab (Eriocheir sinensis). Fish and Shellfish Immunology, 2022, 131, 918-928.	1.6	1
9326	Citrus Huanglongbing correlated with incidence of Diaphorina citri carrying Candidatus Liberibacter asiaticus and citrus phyllosphere microbiome. Frontiers in Plant Science, 0, 13, .	1.7	1
9327	Effects of dietary β -1,3-glucan addition on the growth performance, mRNA expression in jejunal barrier, and cecal microflora of broilers challenged with Clostridium perfringens. Poultry Science, 2023, 102, 102349.	1.5	1
9328	Dynamics of Microbial Community and Removal of Hydrogen Sulfide (H ₂ S) Using a Bio-Inhibitor and Its Application under the Oil Reservoir Condition. Energy & Fuels, 2022, 36, 14128-14135.	2.5	3
9329	Variations in leaf phyllosphere microbial communities and development of tobacco brown spot before and after fungicide application. Frontiers in Microbiology, 0, 13, .	1.5	3
9330	Gut microbiota is correlated with gastrointestinal adverse events of metformin in patients with type 2 diabetes. Frontiers in Endocrinology, 0, 13, .	1.5	5
9331	Mycorrhizal diversity and community composition in co-occurring Cypripedium species. Mycorrhiza, 0, , .	1.3	0
9332	A less complex but more specialized microbial network resulted in faster fine-root decomposition in young stands of Robinia pseudoacacia. Applied Soil Ecology, 2023, 182, 104735.	2.1	5
9333	Crop rotation-driven change in physicochemical properties regulates microbial diversity, dominant components, and community complexity in paddy soils. Agriculture, Ecosystems and Environment, 2023, 343, 108278.	2.5	16
9334	Hypoxia triggers the proliferation of antibiotic resistance genes in a marine aquaculture system. Science of the Total Environment, 2023, 859, 160305.	3.9	4
9335	Characterization of AMF-diversity of endosphere versus rhizosphere of tea (Camellia sinensis) crops. , 2019, 89, .		3
9336	Akkermansia muciniphila ameliorates chronic kidney disease interstitial fibrosis via the gut-renal axis. Microbial Pathogenesis, 2023, 174, 105891.	1.3	6
9337	Rhizosphere bacterial and fungal communities of healthy and wilted pepper (Capsicum annuum L.) in an organic farming system. Ciencia Rural, 2023, 53, .	0.3	2
9338	Fate of antibiotic resistance genes in cultivation substrate and its association with bacterial communities throughout commercial production of Agaricus bisporus. Ecotoxicology and Environmental Safety, 2023, 249, 114360.	2.9	2
9339	Deciphering soil amendments and actinomycetes for remediation of cadmium (Cd) contaminated farmland. Ecotoxicology and Environmental Safety, 2023, 249, 114388.	2.9	7
9340	Pollen meta-barcoding reveals different community structures of foraged plants by honeybees (Apis Tj ETQq1 1 0.784314 rgBT /Overbo	2.3	2

#	ARTICLE	IF	CITATIONS
9341	Host's P851± genotype restructures the gut microbiota and regulates fat metabolism in gibel carp. <i>Aquaculture</i> , 2023, 565, 739160.	1.7	0
9342	Multi-omics eco-surveillance of bacterial community function in legacy contaminated estuary sediments. <i>Environmental Pollution</i> , 2023, 318, 120857.	3.7	5
9343	Effect of <i>Massa Medicata Fermentata</i> on the intestinal flora of rats with functional dyspepsia. <i>Microbial Pathogenesis</i> , 2023, 174, 105927.	1.3	3
9344	Different sulfide to arsenic ratios driving arsenic speciation and microbial community interactions in two alkaline hot springs. <i>Environmental Research</i> , 2023, 218, 115033.	3.7	2
9345	Ecological toxicity of Cd, Pb, Zn, Hg and regulation mechanism in <i>Solanum nigrum</i> L.. <i>Chemosphere</i> , 2023, 313, 137447.	4.2	14
9346	Tilapia processing byproduct treated with enzymatic hydrolysis and <i>Rhodopseudomonas palustris</i> is feasible for live feed culturing: Pathogen inhibition in vitro, live feeds microbiota, and <i>Bidyanus bidyanus</i> larviculture. <i>Aquaculture Reports</i> , 2023, 28, 101439.	0.7	0
9347	Variations in antibiotic resistance genes and microbial community in sludges passing through biological nutrient removal and anaerobic digestion processes in municipal wastewater treatment plants. <i>Chemosphere</i> , 2023, 313, 137362.	4.2	10
9348	Effect of substituting steam-flaked corn for coarse ground corn on in vitro digestibility, average daily gain, serum metabolites and ruminal volatile fatty acids, and bacteria diversity in growing yaks. <i>Animal Feed Science and Technology</i> , 2023, 296, 115553.	1.1	2
9349	Composition and function of viruses in sauce-flavor baijiu fermentation. <i>International Journal of Food Microbiology</i> , 2023, 387, 110055.	2.1	4
9350	Ancient and modern mitogenomes of red deer reveal its evolutionary history in northern China. <i>Quaternary Science Reviews</i> , 2023, 301, 107924.	1.4	2
9351	The protective effect of 2â€™-Fucosyllactose on LPS-induced colitis suckling mice by ameliorating intestinal inflammation and modulating gut microbiota. <i>Food Bioscience</i> , 2023, 51, 102317.	2.0	2
9352	Transient nitrite accumulation explains the variation of N ₂ O emissions to N fertilization in upland agricultural soils. <i>Soil Biology and Biochemistry</i> , 2023, 177, 108917.	4.2	11
9353	Integrated effects of residual plastic films on soil-rhizosphere microbe-plant ecosystem. <i>Journal of Hazardous Materials</i> , 2023, 445, 130420.	6.5	14
9354	Co-variance between free-living bacteria and <i>Cochlodinium polykrikoides</i> (Dinophyta) harmful algal blooms, South Korea. <i>Harmful Algae</i> , 2023, 122, 102371.	2.2	3
9355	Microbial community assembly of the hyperaccumulator plant <i>Sedum plumbizincicola</i> in two contrasting soil types with three levels of cadmium contamination. <i>Science of the Total Environment</i> , 2023, 863, 160917.	3.9	9
9356	Microscale dynamics of dark zone alterations in anthropized karstic cave shows abrupt microbial community switch. <i>Science of the Total Environment</i> , 2023, 862, 160824.	3.9	2
9357	The biodeterioration outbreak in Dunhuang Mogao Grottoes analyzed for the microbial communities and the occurrence time by C-14 dating. <i>International Biodeterioration and Biodegradation</i> , 2023, 178, 105533.	1.9	6
9358	Prediction of functional proteins associated with the gut microbiome of an adult population in Lagos State, Nigeria. <i>Scientific African</i> , 2023, 19, e01445.	0.7	0

#	ARTICLE	IF	CITATIONS
9359	Abundant culturable diazotrophs within Actinomycetia rather than rare taxa are underlying inoculants for nitrogen promotion in desert soil. <i>Applied Soil Ecology</i> , 2023, 184, 104774.	2.1	2
9360	Lead and copper influenced bile acid metabolism by changing intestinal microbiota and activating farnesoid X receptor in <i>Bufo gargarizans</i> . <i>Science of the Total Environment</i> , 2023, 863, 160849.	3.9	2
9361	Soil nutrients shape the composition and function of fungal communities in abandoned ancient rice terraces. <i>Journal of Environmental Management</i> , 2023, 329, 117064.	3.8	7
9362	Evaluation of a subtropical maize-rice rotation system maintained under long-term fertilizer inputs for sustainable intensification of agriculture. <i>Applied Soil Ecology</i> , 2023, 184, 104772.	2.1	2
9363	Nitrogen loss from anaerobic ammonium oxidation coupled to Iron(III) reduction activity across estuarine and coastal wetlands of China: Spatial variations, controlling factors, and environmental implications. <i>Catena</i> , 2023, 222, 106805.	2.2	5
9364	Microbial community diversity and enzyme activity varies in response to long-term fertilisation in a continuous potato (<i>Solanum tuberosum</i> L.) cropping system. <i>Soil Research</i> , 2022, , .	0.6	0
9365	ä,â>1/2â,æ°”ä€™äCE²â†-âä,â£ä1/2â®...â®â†...â¾®ç”ÿç%©ç%¹â¾4. <i>Chinese Science Bulletin</i> , 2022, , .	0.4	0
9366	Seasonal patterns of rhizosphere microorganisms suggest carbohydrate-degrading and nitrogen-fixing microbes contribute to the attribute of full-year shooting in woody bamboo <i>Cephalostachyum pingbianense</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9367	Organomineral fertilizer application enhances <i>Perilla frutescens</i> nutritional quality and rhizosphere microbial community stability in karst mountain soils. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9368	Vaginal <i>Lactobacillus iners</i> abundance is associated with outcome in antibiotic treatment of bacterial vaginosis and capable of inhibiting <i>Gardnerella</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	6
9369	<i>Brevibacillus laterosporus</i> BL1, a promising probiotic, prevents obesity and modulates gut microbiota in mice fed a high-fat diet. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	3
9370	Chitin amendments eliminate the negative impacts of continuous cropping obstacles on soil properties and microbial assemblage. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
9372	Airway microecology in rifampicin-resistant and rifampicin-sensitive pulmonary tuberculosis patients. <i>BMC Microbiology</i> , 2022, 22, .	1.3	1
9373	<scp>COI</scp> metabarcoding of large benthic Foraminifera: Method validation for application in ecological studies. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	0
9374	Method comparison for Japanese encephalitis virus detection in samples collected from the Indo-Pacific region. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	1
9375	Timing matters: age-dependent impacts of the social environment and host selection on the avian gut microbiota. <i>Microbiome</i> , 2022, 10, .	4.9	3
9376	Heterosis in root microbiota inhibits growth of soilâ€borne fungal pathogens in hybrid rice. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1059-1076.	4.1	1
9378	Siamese Fighting Fish (<i>Betta splendens</i> Regan) Gut Microbiota Associated with Age and Gender. <i>Fishes</i> , 2022, 7, 347.	0.7	1

#	ARTICLE	IF	CITATIONS
9379	Soil Microbial Communities in Desert Grassland around Rare Earth Mine: Diversity, Variation, and Response Patterns. <i>Sustainability</i> , 2022, 14, 15629.	1.6	2
9380	The effect of tuina on ulcerative colitis model mice analyzed by gut microbiota and proteomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9381	Microbiome and metabolome analysis to clarify the interaction between the urine microbiota and serum metabolites in Chinese patients with immunoglobulin A nephropathy. <i>Annals of Translational Medicine</i> , 2022, 10, 1230-1230.	0.7	1
9382	Isolation and Characterization of Ruminal Yeast Strain with Probiotic Potential and Its Effects on Growth Performance, Nutrients Digestibility, Rumen Fermentation and Microbiota of Hu Sheep. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1260.	1.5	2
9383	<i>Saussurea involucrata</i> oral liquid regulates gut microbiota and serum metabolism during alleviation of collagen-induced arthritis in rats. <i>Phytotherapy Research</i> , 2023, 37, 1242-1259.	2.8	5
9384	Dynamic Changes of Bacterial Communities and Microbial Association Networks in Ready-to-Eat Chicken Meat during Storage. <i>Foods</i> , 2022, 11, 3733.	1.9	7
9385	Metagenome-Based Exploration of Bacterial Communities Associated with Cyanobacteria Strains Isolated from Thermal Muds. <i>Microorganisms</i> , 2022, 10, 2337.	1.6	3
9386	Analysis of the gut microbiome in obese native Tibetan children living at different altitudes: A case-control study. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	4
9387	A comparative study to determine the association of gut microbiome with schizophrenia in Zhejiang, China. <i>BMC Psychiatry</i> , 2022, 22, .	1.1	3
9388	Potential for Polyethylene Terephthalate (PET) Degradation Revealed by Metabarcoding and Bacterial Isolates from Soil Around a Bitumen Source in Southwestern Iran. <i>Journal of Polymers and the Environment</i> , 2023, 31, 1279-1291.	2.4	5
9389	Effects of Circadian Rhythm and Feeding Modes on Rumen Fermentation and Microorganisms in Hu Sheep. <i>Microorganisms</i> , 2022, 10, 2308.	1.6	3
9390	Analysis of gut microbiome composition, function, and phenotype in patients with osteoarthritis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9391	Short- and Long-Term Effects of Different Antibiotics on the Gut Microbiota and Cytokines Level in Mice. <i>Infection and Drug Resistance</i> , 0, Volume 15, 6785-6797.	1.1	5
9392	TDP-43 safeguards the embryo genome from L1 retrotransposition. <i>Science Advances</i> , 2022, 8, .	4.7	9
9393	Polysaccharides from <i>Pseudostellaria heterophylla</i> modulate gut microbiota and alleviate syndrome of spleen deficiency in rats. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
9394	The effects of elemene emulsion injection on rat fecal microbiota and metabolites: Evidence from metagenomic exploration and liquid chromatography-mass spectrometry. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9395	Diversity, structure, and distribution of bacterioplankton and diazotroph communities in the Bay of Bengal during the winter monsoon. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9396	Diversity of growth performance and rumen microbiota vary with feed types. <i>Frontiers in Sustainable Food Systems</i> , 0, 6, .	1.8	1

#	ARTICLE	IF	CITATIONS
9397	Quasispecies Fitness Partition to Characterize the Molecular Status of a Viral Population. Negative Effect of Early Ribavirin Discontinuation in a Chronically Infected HEV Patient. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14654.	1.8	4
9398	Forest succession improves the complexity of soil microbial interaction and ecological stochasticity of community assembly: Evidence from <i>Phoebe bournei</i> -dominated forests in subtropical regions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
9399	Impact of Biochar and Bioorganic Fertilizer on Rhizosphere Bacteria in Saline Alkali Soil. <i>Microorganisms</i> , 2022, 10, 2310.	1.6	8
9400	AMF colonization affects allelopathic effects of <i>Zea mays</i> L. root exudates and community structure of rhizosphere bacteria. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
9401	Altered functional connectivity strength in chronic insomnia associated with gut microbiota composition and sleep efficiency. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	3
9402	Biodiversity of freshwater ciliates (Protista, Ciliophora) in the Lake Weishan Wetland, China: the state of the art. <i>Marine Life Science and Technology</i> , 2022, 4, 429-451.	1.8	31
9404	Dietary Supplementation of Fruit from <i>Nitraria tangutorum</i> Improved Immunity and Abundance of Beneficial Ruminant Bacteria in Hu Sheep. <i>Animals</i> , 2022, 12, 3211.	1.0	3
9405	Characterization and Dynamics of the Gut Microbiota in Rice Fishes at Different Developmental Stages in Rice-Fish Coculture Systems. <i>Microorganisms</i> , 2022, 10, 2373.	1.6	3
9406	Natural Cross-Kingdom Spread of Apple Scar Skin Viroid from Apple Trees to Fungi. <i>Cells</i> , 2022, 11, 3686.	1.8	9
9408	Changes in soil fungal community composition and functional groups during the succession of Alpine grassland. <i>Plant and Soil</i> , 2023, 484, 201-216.	1.8	5
9409	Effects of Dietary Quinoa Seeds on Cecal Microorganisms and Muscle Fatty Acids of Female Luhua Chickens. <i>Animals</i> , 2022, 12, 3334.	1.0	1
9410	River damming enhances ecological functional stability of planktonic microorganisms. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9411	Remodeling of the microbiota improves the environmental adaptability and disease resistance in Tibetan pigs. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9412	Distribution Patterns of Antibiotic Resistance Genes and Their Bacterial Hosts in a Manure Lagoon of a Large-Scale Swine Finishing Facility. <i>Microorganisms</i> , 2022, 10, 2301.	1.6	5
9413	Effects of Dietary Oregano Essential Oil on Cecal Microorganisms and Muscle Fatty Acids of Luhua Chickens. <i>Animals</i> , 2022, 12, 3215.	1.0	4
9414	First report of ectomycorrhizae in <i>Prunus serotina</i> in the exotic range. <i>Plant and Soil</i> , 2023, 484, 171-181.	1.8	2
9415	Biodissolution of pyrite and bornite by moderate thermophiles. <i>Journal of Central South University</i> , 2022, 29, 3630-3644.	1.2	4
9416	Exploring variation in the fecal microbial communities of Kasaragod Dwarf and Holstein crossbred cattle. <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 53-65.	0.7	3

#	ARTICLE	IF	CITATIONS
9417	Drought stress modifies the community structure of root-associated microbes that improve <i>Attractylodes lancea</i> growth and medicinal compound accumulation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
9418	Analysis of endophyte diversity of <i>Rheum palmatum</i> among different tissues and ages. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	4
9419	Community Composition Specificities of Cyanobacteria in Paddy Soil under Different Ecological Conditions. <i>Agronomy</i> , 2022, 12, 3090.	1.3	3
9420	Effects of Dietary L-TRP on Immunity, Antioxidant Capacity and Intestinal Microbiota of the Chinese Mitten Crab (<i>Eriocheir Sinensis</i>) in Pond Culture. <i>Metabolites</i> , 2023, 13, 1.	1.3	3
9421	Comparative analysis of fungal communities between herbicide-resistant and -susceptible <i>Alopecurus aequalis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
9422	Whole-genome sequencing (WGS) analysis of <i>Brucella suis</i> biovar 2 isolated from domestic pigs in Egypt for epidemiological and genetic diversity tracing. <i>Veterinary Microbiology</i> , 2023, 277, 109637.	0.8	1
9423	Quantification of Marine Picocyanobacteria on Water Column Particles and in Sediments Using Real-Time PCR Reveals Their Role in Carbon Export. <i>MSphere</i> , 2022, 7, .	1.3	0
9424	Characteristics of intestinal microbiota in C57BL/6 mice with non-alcoholic fatty liver induced by high-fat diet. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9425	Microbiota of preterm infant develops over time along with the first teeth eruption. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9426	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. <i>PeerJ</i> , 0, 10, e14459.	0.9	2
9427	Nodule-associated diazotrophic community succession is driven by developmental phases combined with microhabitat of <i>Sophora davidii</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9428	Characterizing corn-straw-degrading actinomycetes and evaluating application efficiency in straw-returning experiments. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
9429	<i>In Vitro</i> Modulation of Rumen Fermentation by Microbiota from the Recombination of Rumen Fluid and Solid Phases. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	15
9430	Morphology, phylogeny, mitogenomics and metagenomics reveal a new entomopathogenic fungus <i>Ophiocordyceps nujiangensis</i> (Hypocreales, Ophiocordycipitaceae) from Southwestern China. <i>MycKeys</i> , 0, 94, 91-108.	0.8	1
9431	Gut bacteria reflect the adaptation of <i>Diestrammena japonica</i> (Orthoptera: Rhaphidophoridae) to the cave. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9432	Glycyrrhizic Acid and Compound Probiotics Supplementation Alters the Intestinal Transcriptome and Microbiome of Weaned Piglets Exposed to Deoxynivalenol. <i>Toxins</i> , 2022, 14, 856.	1.5	2
9433	Sex Differences in Fecal Microbiome Composition and Function of Dromedary Camels in Saudi Arabia. <i>Animals</i> , 2022, 12, 3430.	1.0	2
9435	<i>Bacteroides fragilis</i> participates in the therapeutic effect of methotrexate on arthritis through metabolite regulation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7

#	ARTICLE	IF	CITATIONS
9436	Promotion of Deoxycholic Acid Effect on Colonic Cancer Cell Lines In Vitro by Altering the Mucosal Microbiota. <i>Microorganisms</i> , 2022, 10, 2486.	1.6	3
9437	Photovoltaic panels have altered grassland plant biodiversity and soil microbial diversity. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
9438	Comparison between <i>Lactobacillus rhamnosus</i> GG and LuxS-deficient strain in regulating gut barrier function and inflammation in early-weaned piglets. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
9439	Virulence potential of antimicrobial-resistant extraintestinal pathogenic <i>Escherichia coli</i> from retail poultry meat in a <i>Caenorhabditis elegans</i> model. <i>Journal of Food Protection</i> , 2023, 86, 100008.	0.8	0
9440	Evidence of Residual Ongoing Viral Replication in Chronic Hepatitis B Patients Successfully Treated with Nucleos(t)ide Analogues. <i>Journal of Infectious Diseases</i> , 0, , .	1.9	3
9441	Elevated estuary water temperature drives fish gut dysbiosis and increased loads of pathogenic vibronaceae. <i>Environmental Research</i> , 2023, 219, 115144.	3.7	8
9442	Protein fractionation and shotgun proteomics analysis of enriched bacterial cultures shed new light on the enzymatically catalyzed degradation of acesulfame. <i>Water Research</i> , 2023, 230, 119535.	5.3	4
9443	Integrated Transcriptome and Microbiota Reveal the Regulatory Effect of 25-Hydroxyvitamin D Supplementation in Antler Growth of Sika Deer. <i>Animals</i> , 2022, 12, 3497.	1.0	0
9444	Diversity and antibacterial potential of the Actinobacteria associated with <i>Apis mellifera ligustica</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9445	Microbiome analysis and biocontrol bacteria isolation from rhizosphere soils associated with different sugarcane root rot severity. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	4
9446	Disproportionation of Inorganic Sulfur Compounds by Mesophilic Chemolithoautotrophic <i>Campylobacterota</i> . <i>MSystems</i> , 2023, 8, .	1.7	5
9448	Increasing buffering capacity enhances rumen fermentation characteristics and alters rumen microbiota composition of high-concentrate fed Hanwoo steers. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
9449	Contrasting relationships between plant-soil microbial diversity are driven by geographic and experimental precipitation changes. <i>Science of the Total Environment</i> , 2023, 861, 160654.	3.9	9
9450	<i>Lactobacillus</i> spp. in the reproductive system of female moths and mating induced changes and possible transmission. <i>BMC Microbiology</i> , 2022, 22, .	1.3	1
9451	Insights into Bacterial Communities and Diversity of Mangrove Forest Soils along the Upper Gulf of Thailand in Response to Environmental Factors. <i>Biology</i> , 2022, 11, 1787.	1.3	5
9452	Effects of on- and off-year management practices on the soil organic C fractions and microbial community in a Moso bamboo (<i>Phyllostachys edulis</i>) forest in subtropical China. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
9453	Exploring the mechanism of a novel recirculating aquaculture system based on water quality parameters and bacterial communities. <i>Environmental Science and Pollution Research</i> , 2023, 30, 34760-34774.	2.7	3
9454	Effects of rearing system and antibiotic treatment on immune function, gut microbiota and metabolites of broiler chickens. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	4

#	ARTICLE	IF	CITATIONS
9455	Over-expression of miR-183-5p or miR-492 triggers invasion and proliferation and loss of polarity in non-neoplastic breast epithelium. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
9456	Differential responding patterns of the nirK-type and nirS-type denitrifying bacterial communities to an <i>Ulva prolifera</i> green tide in coastal Qingdao areas. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
9457	Intratumor microbiome features reveal antitumor potentials of intrahepatic cholangiocarcinoma. <i>Gut Microbes</i> , 2023, 15, .	4.3	19
9459	High-throughput sequencing reveals omnivorous and preferential diets of the rotifer <i>Polyarthra</i> in situ. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9460	Changes of bacterial and fungal communities and relationship between keystone taxon and physicochemical factors during dairy manure ectopic fermentation. <i>PLoS ONE</i> , 2022, 17, e0276920.	1.1	0
9461	Evaluating the Effect on Cultivation of Replacing Soil with Typical Soilless Growing Media: A Microbial Perspective. <i>Agronomy</i> , 2023, 13, 6.	1.3	0
9462	Soil properties and root traits are important factors driving rhizosphere soil bacterial and fungal community variations in alpine <i>Rhododendron nitidulum</i> shrub ecosystems along an altitudinal gradient. <i>Science of the Total Environment</i> , 2023, 864, 161048.	3.9	11
9463	Characterization of Intestinal Microbiota in Lambs with Different Susceptibility to <i>Escherichia coli</i> F17. <i>Veterinary Sciences</i> , 2022, 9, 670.	0.6	2
9464	<i>Phyllanthus emblica</i> (Amla) Fruit Powder as a Supplement to Improve Preweaning Dairy Calves' Health: Effect on Antioxidant Capacity, Immune Response, and Gut Bacterial Diversity. <i>Biology</i> , 2022, 11, 1753.	1.3	3
9465	Geological History and Forest Mycorrhizal Dominance Effects on Soil Fungal Diversity in Chilean Temperate Rainforests. <i>Journal of Soil Science and Plant Nutrition</i> , 2023, 23, 734-745.	1.7	2
9466	Influence of group B <i>Streptococcus</i> and vaginal cleanliness on the vaginal microbiome of pregnant women. <i>World Journal of Clinical Cases</i> , 0, 10, 12578-12586.	0.3	1
9467	Composition and assembly of the bacterial community in the overlying waters of the coral reef of China's Xisha Islands. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9468	Pectin supplement alleviates gut injury potentially through improving gut microbiota community in piglets. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
9469	STAT3 gain-of-function mutations connect leukemia with autoimmune disease by pathological NKG2Dhi CD8+ T cell dysregulation and accumulation. <i>Immunity</i> , 2022, 55, 2386-2404.e8.	6.6	20
9470	<i>Bacteroides plebeius</i> improves muscle wasting in chronic kidney disease by modulating the gut-renal muscle axis. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 6066-6078.	1.6	6
9471	Impacts of maize hybrids with different nitrogen use efficiency on root-associated microbiota based on distinct rhizosphere soil metabolites. <i>Environmental Microbiology</i> , 2023, 25, 473-492.	1.8	1
9473	The role of upper and lower genital tract microbiota alterations in term chorionamnionitis: A prospective study. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9474	High-Throughput DNA Metabarcoding as an Approach for Ichthyoplankton Survey in Oujiang River Estuary, China. <i>Diversity</i> , 2022, 14, 1111.	0.7	4

#	ARTICLE	IF	CITATIONS
9475	Home-field advantage meets priming effect in root decomposition: Implications for belowground carbon dynamics. <i>Functional Ecology</i> , 2023, 37, 676-689.	1.7	7
9476	Changes in Soil Microbial Communities under Mixed Organic and Inorganic Nitrogen Addition in Temperate Forests. <i>Forests</i> , 2023, 14, 21.	0.9	3
9477	Probiotic <i>Bifidobacterium longum</i> BB68S Improves Cognitive Functions in Healthy Older Adults: A Randomized, Double-Blind, Placebo-Controlled Trial. <i>Nutrients</i> , 2023, 15, 51.	1.7	9
9478	Land use intensity constrains the positive relationship between soil microbial diversity and multifunctionality. <i>Plant and Soil</i> , 0, .	1.8	1
9479	Community structure and antifungal activity of actinobacteria in a fungus-growing termite. <i>Ecological Entomology</i> , 2023, 48, 251-262.	1.1	3
9480	Diversity of bacterial communities in the plasmodia of myxomycetes. <i>BMC Microbiology</i> , 2022, 22, .	1.3	1
9481	Dietary Intake of Monosaccharides from Foods is Associated with Characteristics of the Gut Microbiota and Gastrointestinal Inflammation in Healthy US Adults. <i>Journal of Nutrition</i> , 2023, 153, 106-119.	1.3	4
9482	Microbiota-host crosstalk in the newborn and adult rumen at single-cell resolution. <i>BMC Biology</i> , 2022, 20, .	1.7	6
9483	Benthic Microbial Communities and Environmental Parameters of Estuary and Hypoxic Zone in the Bohai Sea, China. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1862.	1.2	2
9484	Whether interstitial space features were the main factors affecting sediment microbial community structures in Chaohu Lake. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9485	Compound Probiotic Ameliorates Acute Alcoholic Liver Disease in Mice by Modulating Gut Microbiota and Maintaining Intestinal Barrier. <i>Probiotics and Antimicrobial Proteins</i> , 2023, 15, 185-201.	1.9	4
9486	Broad host range may be a key to long-term persistence of bacteriophages infecting intestinal <i>Bacteroidaceae</i> species. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
9487	Analysis of bronchoalveolar lavage fluid metatranscriptomes among patients with COVID-19 disease. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
9488	Role of bacterial community succession in flavor formation during Sichuan sun vinegar grain (Cupei) fermentation. <i>Journal of Bioscience and Bioengineering</i> , 2023, 135, 109-117.	1.1	7
9489	Biocontrol and plant growth promotion by combined <i>Bacillus</i> spp. inoculation affecting pathogen and AMF communities in the wheat rhizosphere at low salt stress conditions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
9490	Metatranscriptomes reveal the diverse responses of <i>Thaumarchaeota</i> ecotypes to environmental variations in the northern slope of the South China Sea. <i>Environmental Microbiology</i> , 0, .	1.8	2
9491	Next-generation sequencing and metabarcoding to understand the ecology of benthic foraminiferal community in the Bering Sea. <i>Journal of Sea Research</i> , 2022, , 102321.	0.6	0
9493	Dynamics of symbiotic bacterial community in whole life stage of <i>Harmonia axyridis</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overloc	1.5	4

#	ARTICLE	IF	CITATIONS
9495	<scp>Peptidoglycan recognition protein SC (PGRPâ€šC)</scp> shapes gut microbiota richness, diversity and composition by modulating immunity in the house fly <i>Musca domestica</i>. <i>Insect Molecular Biology</i> , 2023, 32, 200-212.	1.0	4
9496	Effects of Dietary Protein Restriction on Colonic Microbiota of Finishing Pigs. <i>Animals</i> , 2023, 13, 9.	1.0	2
9497	Spatial patterns of dominant bacterial community components and their influential factors in the southern Qinling Mountains, China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9498	Effect and mechanism of the improvement of coastal silt soil by application of organic fertilizer and gravel combined with <i>Sesbania cannabina</i> cultivation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
9499	Continuous Wheat/Soybean Cropping Influences Soybean Yield and Rhizosphere Microbial Community Structure and Function. <i>Agronomy</i> , 2023, 13, 28.	1.3	6
9500	Effect of Biochar on Soil Physiochemical Properties and Bacterial Diversity in Dry Direct-Seeded Rice Paddy Fields. <i>Agronomy</i> , 2023, 13, 4.	1.3	9
9501	Dietary Association with Midgut Microbiota Components of <i>Eocanthecona furcellata</i> (Wolff). <i>Diversity</i> , 2022, 14, 1130.	0.7	0
9502	High resolution 16S rRNA gene Next Generation Sequencing study of brain areas associated with Alzheimerâ€™s and Parkinsonâ€™s disease. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	4
9504	30-Month Pot Experiment: Biochar Alters Soil Potassium Forms, Soil Properties and Soil Fungal Diversity and Composition in Acidic Soil of Southern China. <i>Plants</i> , 2022, 11, 3442.	1.6	1
9505	Bacterial dynamics during the burial of starch-based bioplastic and oxo-low-density-polyethylene in compost soil. <i>BMC Microbiology</i> , 2022, 22, .	1.3	5
9506	Potential Efficacy of <i>Bacillus coagulans</i> BACO-17 to Modulate Gut Microbiota in Rats Fed High-Fat Diet. <i>Processes</i> , 2022, 10, 2692.	1.3	1
9507	Effects of the Application of Nutrients on Soil Bacterial Community Composition and Diversity in a <i>Larix olgensis</i> Plantation, Northeast China. <i>Sustainability</i> , 2022, 14, 16759.	1.6	3
9509	Identification and antibacterial activity of <i>Thamnia vermicularis</i> and <i>Thamnia subuliformis</i> . <i>Journal of Microbiological Methods</i> , 2022, 203, 106628.	0.7	1
9510	Positive Effects of Organic Substitution in Reduced-Fertilizer Regimes on Bacterial Diversity and N-Cycling Functionality in Greenhouse Ecosystem. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 16954.	1.2	2
9511	Effects of microbiota-directed supplementary foods on gut microbiota in fecal colonized mice of healthy infants. <i>Journal of Functional Foods</i> , 2022, 99, 105346.	1.6	0
9512	Characterizing potential pathogens from intracellular bacterial community of protists in wastewater treatment plants. <i>Environment International</i> , 2023, 171, 107723.	4.8	3
9513	Analysis of gut microbiota diversity in Hashimotoâ€™s thyroiditis patients. <i>BMC Microbiology</i> , 2022, 22, .	1.3	10
9514	Plant and fungal species interactions differ between aboveground and belowground habitats in mountain forests of eastern China. <i>Science China Life Sciences</i> , 2023, 66, 1134-1150.	2.3	10

#	ARTICLE	IF	CITATIONS
9515	CRISPRi-microfluidics screening enables genome-scale target identification for high-titer protein production and secretion. <i>Metabolic Engineering</i> , 2023, 75, 192-204.	3.6	12
9516	Microbiome Analysis of New, Insidious Cave Wall Alterations in the Apse of Lascaux Cave. <i>Microorganisms</i> , 2022, 10, 2449.	1.6	2
9517	Potential binding modes of the gut bacterial metabolite, 5-hydroxyindole, to the intestinal L-type calcium channels and its impact on the microbiota in rats. <i>Gut Microbes</i> , 2023, 15, .	4.3	3
9519	Whole-genome functional characterization of RE1 silencers using a modified massively parallel reporter assay. <i>Cell Genomics</i> , 2023, 3, 100234.	3.0	0
9521	Microcystin-LR exposure interfered maintenance of colonic microenvironmental homeostasis in rat. <i>Food and Chemical Toxicology</i> , 2023, 173, 113611.	1.8	5
9522	Gut microbial community structure and function of Przewalski's horses varied across reintroduced sites in China. <i>Integrative Zoology</i> , 2023, 18, 1027-1040.	1.3	1
9523	Age- and Microbiota-Dependent Cell Stemness Plasticity Revealed by Cattle Cell Landscape. <i>Research</i> , 2023, 6, .	2.8	0
9525	Linkages between the molecular composition of dissolved organic matter and soil microbial community in a boreal forest during freeze-thaw cycles. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9526	Effects of growth stage on the fermentation quality, microbial community, and metabolomic properties of Italian ryegrass (<i>Lolium multiflorum</i> Lam.) silage. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9527	Divergent Effects of Fertilizer Regimes on Taxonomic and Functional Compositions of Rhizosphere Bacteria and Fungi in <i>Phoebe bournei</i> Young Plantations Are Associated with Root Exudates. <i>Forests</i> , 2023, 14, 126.	0.9	2
9529	Gut microbiota signatures in tissues of the colorectal polyp and normal colorectal mucosa, and faeces. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
9530	Fungal Diversity and Its Relationship with Environmental Factors in Coastal Sediments from Guangdong, China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 101.	1.5	5
9531	Effect of Energy Provision Strategy on Rumen Fermentation Characteristics, Bacterial Diversity and Community Composition. <i>Bioengineering</i> , 2023, 10, 107.	1.6	1
9532	The effects of dietary supplementation with mushroom or selenium enriched mushroom powders on the growth performance and intestinal health of post-weaned pigs. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	6
9533	The spliceophilin CYP18A2 is mainly involved in the splicing of retained introns under heat stress in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1113-1133.	4.1	4
9534	Dietary supplementation of solubles from shredded, steam-exploded pine particles modifies gut length and cecum microbiota in cyclic heat-stressed broilers. <i>Poultry Science</i> , 2023, 102, 102498.	1.5	4
9535	A deep continental aquifer downhole sampler for microbiological studies. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9536	Synergic mitigation of saline-alkaline stress in wheat plant by silicon and <i>Enterobacter</i> sp. FN0603. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3

#	ARTICLE	IF	CITATIONS
9537	Comparative analysis of <i>Penicillium</i> genomes reveals the absence of a specific genetic basis for biocontrol in <i>Penicillium rubens</i> strain 212. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9538	Modelling, Characterization of Data-Dependent and Process-Dependent Errors in DNA Data Storage. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 2147-2158.	1.9	2
9539	Prolonged High-Fat Diet Consumption throughout Adulthood in Mice Induced Neurobehavioral Deterioration via Gut-Brain Axis. <i>Nutrients</i> , 2023, 15, 392.	1.7	7
9541	Polycomb repressive complexes 1 and 2 are each essential for maintenance of X inactivation in extra-embryonic lineages. <i>Nature Cell Biology</i> , 2023, 25, 134-144.	4.6	5
9542	Metagenomic data reveals microbiome characteristics of culture-negative brain abscess samples. <i>Data in Brief</i> , 2023, , 108893.	0.5	0
9543	The characters of root-derived fungi from <i>Gentiana scabra</i> Bunge and the relations with their habitats. <i>Plant and Soil</i> , 2023, 486, 391-408.	1.8	0
9544	Treatment Success Following Standard Antibiotic Treatment for Bacterial Vaginosis Is Not Associated With Pretreatment Genital Immune or Microbial Parameters. <i>Open Forum Infectious Diseases</i> , 2023, 10, .	0.4	3
9545	Different Geographic Strains of Dinoflagellate <i>Karlodinium veneficum</i> Host Highly Diverse Fungal Community and Potentially Serve as Possible Niche for Colonization of Fungal Endophytes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1672.	1.8	2
9546	Soil amendment with sorbitol and mannitol changes the soil microbial community and its enzymatic activities. <i>Journal of Soils and Sediments</i> , 2023, 23, 1857-1876.	1.5	3
9547	Changes in vaginal microbiome after focused ultrasound treatment of high-risk human papillomavirus infection-related low-grade cervical lesions. <i>BMC Infectious Diseases</i> , 2023, 23, .	1.3	4
9549	6His-tatritin promotes antimicrobial defense via regulating immune ability and intestinal microbial community in grass carp (<i>Ctenopharyngodon idella</i>). <i>Fish and Shellfish Immunology</i> , 2023, , 108532.	1.6	0
9550	Grazing lowers soil multifunctionality but boosts soil microbial network complexity and stability in a subtropical grassland of China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	11
9551	Covariance of Marine Nucleocytoplasmic Large DNA Viruses with Eukaryotic Plankton Communities in the Sub-Arctic Kongsfjorden Ecosystem: A Metagenomic Analysis of Marine Microbial Ecosystems. <i>Microorganisms</i> , 2023, 11, 169.	1.6	5
9552	Bioleaching of uranium from low-grade uranium ore with a high fluorine content by indigenous microorganisms and their community structure analysis. <i>Journal of Radioanalytical and Nuclear Chemistry</i> , 2023, 332, 387-398.	0.7	2
9553	Effects of Zhishi Daozhi Decoction on the intestinal flora of nonalcoholic fatty liver disease mice induced by a high-fat diet. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
9554	<i>Akkermansia muciniphila</i> protects mice against an emerging tick-borne viral pathogen. <i>Nature Microbiology</i> , 2023, 8, 91-106.	5.9	22
9555	Characteristics of the soil arbuscular mycorrhizal fungal community along succession stages in tropical forest and its driving factors. <i>Frontiers in Environmental Science</i> , 0, 10, .	1.5	1
9556	Effects of the Continuous Cropping and Soilborne Diseases of <i>Panax Ginseng</i> C. A. Meyer on Rhizosphere Soil Physicochemical Properties, Enzyme Activities, and Microbial Communities. <i>Agronomy</i> , 2023, 13, 210.	1.3	4

#	ARTICLE	IF	CITATIONS
9557	Effects of Two Different Straw Pellets on Yak Growth Performance and Ruminal Microbiota during Cold Season. <i>Animals</i> , 2023, 13, 335.	1.0	4
9558	Microbial community and predictive functionalities associated with the marine sediment of Coastal Gujarat. <i>Environmental Science and Pollution Research</i> , 2023, 30, 43245-43266.	2.7	2
9559	Spatiotemporal biocontrol and rhizosphere microbiome analysis of Fusarium wilt of banana. <i>Communications Biology</i> , 2023, 6, .	2.0	9
9560	Characterization of highly polymorphic microsatellite markers for the chinese monal (Lophophorus) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0	1.0	2
9561	New Insights from Soil Microorganisms for Sustainable Double Rice-Cropping System with 37-Year Manure Fertilization. <i>Agronomy</i> , 2023, 13, 261.	1.3	9
9563	Microbial community structure and biogenic amines content variations in chilled chicken during storage. <i>Food Science and Nutrition</i> , 2023, 11, 627-638.	1.5	4
9564	The structural discrepancy between the small and large gut microbiota of Asiatic toad (Bufo) Tj ETQq0 0 0 rgBT /Overlock 1.1 Tf 50 502 T	1.1	2
9565	Biodegradation of chemicals tested in mixtures and individually: mixture effects on biodegradation kinetics and microbial composition. <i>Biodegradation</i> , 2023, 34, 139-153.	1.5	4
9566	Partial Substitution of Fish Meal with Soy Protein Concentrate on Growth, Liver Health, Intestinal Morphology, and Microbiota in Juvenile Large Yellow Croaker (<i>Larimichthys crocea</i>). <i>Aquaculture Nutrition</i> , 2023, 2023, 1-15.	1.1	3
9567	Diversifying selection and climatic effects on major histocompatibility complex class II gene diversity in the greater horseshoe bat. <i>Evolutionary Applications</i> , 2023, 16, 688-704.	1.5	4
9568	Continuous-cropping-tolerant soybean cultivars alleviate continuous cropping obstacles by improving structure and function of rhizosphere microorganisms. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9569	Changes in the Ixodes ricinus microbiome associated with artificial tick feeding. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
9570	Exacerbation of allergic rhinitis by the commensal bacterium <i>Streptococcus salivarius</i> . <i>Nature Microbiology</i> , 2023, 8, 218-230.	5.9	10
9571	Response of Intestinal Microbiota of Tiger Puffer (<i>Takifugu rubripes</i>) to the Fish Oil Finishing Strategy. <i>Microorganisms</i> , 2023, 11, 208.	1.6	2
9572	Increasing precipitation weakened the negative effects of simulated warming on soil microbial community composition in a semi-arid sandy grassland. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9573	Correlational Analysis of the Physicochemical Indexes, Volatile Flavor Components, and Microbial Communities of High-Temperature Daqu in the Northern Region of China. <i>Foods</i> , 2023, 12, 326.	1.9	4
9574	Integration of Grape-Duck Production Pattern Boosts Duck Behavior, Meat Quality, Fecal Microbiota and Soil Microorganisms. <i>Agriculture (Switzerland)</i> , 2023, 13, 218.	1.4	0
9575	<i>Poria cocos</i> Polysaccharide Ameliorated Antibiotic-Associated Diarrhea in Mice via Regulating the Homeostasis of the Gut Microbiota and Intestinal Mucosal Barrier. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1423.	1.8	12

#	ARTICLE	IF	CITATIONS
9576	A symbiotic bacterium of Antarctic fish reveals environmental adaptability mechanisms and biosynthetic potential towards antibacterial and cytotoxic activities. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9577	Insertions and deletions in the hypervariable region of the hepatitis E virus genome in individuals with acute and chronic infection. <i>Liver International</i> , 0, , .	1.9	0
9578	Deep mowing rather than fire restrains grassland <i>Miscanthus</i> growth via affecting soil nutrient loss and microbial community redistribution. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
9579	Alterations of gut mycobiota profiles in intrahepatic cholangiocarcinoma. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9580	Microbial community composition and function in an urban waterway with combined sewer overflows before and after implementation of a stormwater storage pipe. <i>PeerJ</i> , 0, 11, e14684.	0.9	1
9582	Bacteroides-derived isovaleric acid enhances mucosal immunity by facilitating intestinal IgA response in broilers. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	7
9583	The root enrichment of bacteria is consistent across different stress-resistant plant species. <i>PeerJ</i> , 0, 11, e14683.	0.9	1
9584	Microbial community analyses provide a differential diagnosis for the antemortem and postmortem injury of decayed cadaver: An animal model. <i>Journal of Clinical Forensic and Legal Medicine</i> , 2023, 93, 102473.	0.5	1
9585	Microbial survival mechanisms within serpentinizing Mariana forearc sediments. <i>FEMS Microbiology Ecology</i> , 2023, 99, .	1.3	0
9586	Mutualistic Interactions between Dinoflagellates and Pigmented Bacteria Mitigate Environmental Stress. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	6
9587	Functional insights into succession in a phyllospheric microbial community across a full stage of plant litter decomposition in wetlands. <i>Freshwater Science</i> , 0, , .	0.9	2
9588	Mutational fitness landscape of human influenza H3N2 neuraminidase. <i>Cell Reports</i> , 2023, 42, 111951.	2.9	5
9589	Phylogenetic group-based assembly and co-occurrence pattern of the microbial community in full-scale wastewater treatment plants during the Chinese spring festival. <i>Chemosphere</i> , 2023, , 137775.	4.2	0
9590	Functional immune diversity in reindeer reveals a high Arctic population at risk. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0
9593	Landscape structure is a key driver of soil protist diversity in meadows in the Swiss Alps. <i>Landscape Ecology</i> , 2023, 38, 949-965.	1.9	2
9594	Mucus-associated microbiotas among different body sites of wild tuna from the South China Sea. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
9595	Ecological influence by colonization of fluoride-resistant <i>Streptococcus mutans</i> in oral biofilm. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
9596	Effects of citrus pulp on the composition and diversity of broiler cecal microbes. <i>Poultry Science</i> , 2023, 102, 102454.	1.5	4

#	ARTICLE	IF	CITATIONS
9597	The Co-Association of Enterobacteriaceae and Pseudomonas with Specific Resistant Cucumber against Fusarium Wilt Disease. <i>Biology</i> , 2023, 12, 143.	1.3	6
9598	Characteristics and Correlation of the Microbial Communities and Flavor Compounds during the First Three Rounds of Fermentation in Chinese Sauce-Flavor Bajiu. <i>Foods</i> , 2023, 12, 207.	1.9	18
9599	Replacing starch with resistant starch (<i>Laminaria japonica</i>) improves water quality, nitrogen and phosphorus budget and microbial community in hybrid snakehead (<scp><i>Channa</i>) Tj ETQq0 0 0 rgBT /Overlook 10 Tf 50 657 Td		
9600	Gut bacterial species in late trimester of pregnant sows influence the occurrence of stillborn piglet through pro-inflammation response. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
9601	Prediction and validation of microbial community function from normal pulp to pulpitis caused by deep dental caries. <i>International Endodontic Journal</i> , 2023, 56, 608-621.	2.3	0
9602	Microbial Enterotypes Shape the Divergence in Gut Fermentation, Host Metabolism, and Growth Rate of Young Goats. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
9603	Fungi and cercozoa regulate methane-associated prokaryotes in wetland methane emissions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9604	The synergistic synbiotic potential of 1-kestose and Bifidobacterium longum in the mouse gut. <i>Journal of Functional Foods</i> , 2023, 101, 105403.	1.6	0
9605	Comparative metabarcoding analysis of phytoplankton community composition and diversity in aquaculture water and the stomach contents of Tegillarca granosa during months of growth. <i>Marine Pollution Bulletin</i> , 2023, 187, 114556.	2.3	4
9606	Mixed organic and inorganic amendments enhance soil microbial interactions and environmental stress resistance of Tibetan barley on plateau farmland. <i>Journal of Environmental Management</i> , 2023, 330, 117137.	3.8	4
9607	Elevated antimony concentration stimulates rare taxa of potential autotrophic bacteria in the Xikuangshan groundwater. <i>Science of the Total Environment</i> , 2023, 864, 161105.	3.9	6
9608	Contrasting responses of microbial diversity and community structure in decaying root bark and xylem to N addition in an alpine shrubland. <i>Soil Biology and Biochemistry</i> , 2023, 178, 108937.	4.2	0
9609	Biotransformation kinetics and pathways of typical synthetic progestins in soil microcosms. <i>Journal of Hazardous Materials</i> , 2023, 446, 130684.	6.5	5
9610	Integrated analysis of the digestive tract bacterial community on individual growth in sibling generation of Swamp Eels (<i>Monopterus albus</i>). <i>Aquaculture</i> , 2023, 566, 739228.	1.7	0
9611	Antibiotic and heavy metal resistance genes in sewage sludge survive during aerobic composting. <i>Science of the Total Environment</i> , 2023, 866, 161386.	3.9	10
9612	Interaction among biofilter microbiome, fecal metabolome and water quality and regulation of sewage discharge in the recirculating aquaculture system of <i>Apostichopus japonicus</i> . <i>Journal of Environmental Management</i> , 2023, 330, 117100.	3.8	1
9613	Characterization of root microbial communities associated with <i>Astragalus membranaceus</i> and their correlation with soil environmental factors. <i>Rhizosphere</i> , 2023, 25, 100656.	1.4	4
9614	Seawater intrusion alters nitrogen cycling patterns through hydrodynamic behavior and biochemical reactions: Based on Bayesian isotope mixing model and microbial functional network. <i>Science of the Total Environment</i> , 2023, 867, 161368.	3.9	6

#	ARTICLE	IF	CITATIONS
9615	Arbuscular mycorrhizal fungi increase the interspecific competition between two forage plant species and stabilize the soil microbial network during a drought event: Evidence from the field. <i>Applied Soil Ecology</i> , 2023, 185, 104805.	2.1	5
9616	Soil warming decreases carbon availability and reduces metabolic functions of bacteria. <i>Catena</i> , 2023, 223, 106913.	2.2	3
9617	Soil microbiota impact on <i>Boletus edulis</i> mycelium in chestnut orchards of different ages. <i>Applied Soil Ecology</i> , 2023, 185, 104790.	2.1	1
9618	A special drop: Characterising yeast isolates associated with fermented beverages produced by Australia's indigenous peoples. <i>Food Microbiology</i> , 2023, 112, 104216.	2.1	2
9619	Metabolism of resistant starch RS3 administered in combination with <i>Lactiplantibacillus plantarum</i> strain 84-3 by human gut microbiota in simulated fermentation experiments in vitro and in a rat model. <i>Food Chemistry</i> , 2023, 411, 135412.	4.2	10
9620	Total flavonoids of <i>Tetrastigma hemsleyanum</i> Diels et Gilg inhibits colorectal tumor growth by modulating gut microbiota and metabolites. <i>Food Chemistry</i> , 2023, 410, 135361.	4.2	9
9621	Soil bacterial community structure and functions but not assembly processes are affected by the conversion from monospecific <i>Cunninghamia lanceolata</i> plantations to mixed plantations. <i>Applied Soil Ecology</i> , 2023, 185, 104775.	2.1	4
9622	Continuous cropping of cut chrysanthemum reduces rhizospheric soil bacterial community diversity and co-occurrence network complexity. <i>Applied Soil Ecology</i> , 2023, 185, 104801.	2.1	6
9623	Sludge composition and characteristics shaped microbial community and further determined process performance: A study on full-scale thermal hydrolysis-anaerobic digestion processes. <i>Journal of Environmental Sciences</i> , 2022, , .	3.2	3
9624	Effects of Dietary Capsaicin and <i>Yucca schidigera</i> Extracts as Feed Additives on Rumen Fermentation and Microflora of Beef Cattle Fed with a Moderate-Energy Diet. <i>Fermentation</i> , 2023, 9, 30.	1.4	3
9625	Genomic diversification of the specialized parasite of the fungus-growing ant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
9626	Long-term egret (<i>Egretta garzetta</i>) habitation alters topsoil and subsoil phosphorus fractions and bacterial communities in coastal wetlands. <i>Biology and Fertility of Soils</i> , 2023, 59, 179-190.	2.3	1
9627	Seasonal Changes Modulate the Rhizosphere of Desert Plant Species. <i>Agronomy</i> , 2023, 13, 57.	1.3	0
9628	Exogenous antibiotic resistance gene contributes to intestinal inflammation by modulating the gut microbiome and inflammatory cytokine responses in mouse. <i>Gut Microbes</i> , 2023, 15, .	4.3	1
9629	Genome Resources of <i>Verticillium dahliae</i> VdGL16: The Causal Agent of Vascular Wilt on the Invasive Species <i>Ailanthus altissima</i> . <i>Plant Disease</i> , 2023, 107, 1207-1209.	0.7	2
9630	Antimicrobial Resistance and Genetic Diversity of <i>Pseudomonas aeruginosa</i> Strains Isolated from Equine and Other Veterinary Samples. <i>Pathogens</i> , 2023, 12, 64.	1.2	4
9632	The ground beetle <i>Pseudoophonus rufipes</i> gut microbiome is influenced by the farm management system. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
9633	Discovery of antibodies and cognate surface targets for ovarian cancer by surface profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	0

#	ARTICLE	IF	CITATIONS
9634	Application of DNA Metabarcoding for Identifying the Diet of Asian Clam (<i>Corbicula fluminea</i> , MÅ¼ller,) Tj ETQq0 0,0 rgBT /Qverlock 10	1.6	1
9635	Host niche, genotype, and field location shape the diversity and composition of the soybean microbiome. <i>Journal of Integrative Agriculture</i> , 2023, 22, 2412-2425.	1.7	6
9636	Gut Microbial Succession Patterns and Metabolic Profiling during Pregnancy and Lactation in a Goat Model. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
9637	Phytoplankton community structure in the Western Subarctic Gyre of the Pacific Ocean during summer determined by a combined approach of HPLC-pigment CHEMTAX and metabarcoding sequencing. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
9638	Diagnosis and functional prediction of microbial markers in tumor tissues of sporadic colorectal cancer patients associated with the MLH1 protein phenotype. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
9639	Structure and Function Analysis of Cultivated <i>Meconopsis integrifolia</i> Soil Microbial Community Based on High-Throughput Sequencing and Culturability. <i>Biology</i> , 2023, 12, 160.	1.3	2
9640	A fifty-locus phylogenetic analysis provides deep insights into the phylogeny of <i>Tricholoma</i> (<i>Tricholomataceae</i> , <i>Agaricales</i>). <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2023, 50, 1-26.	1.6	1
9641	The effect of short-term fallowing on the microbial communities in forest soil cultivated with ginseng: Preliminary research. <i>PeerJ</i> , 0, 11, e14758.	0.9	0
9642	Analysis of serum antioxidant capacity and gut microbiota in calves at different growth stages in Tibet. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
9643	Contrasting effects of elevated CO ₂ on autotrophic prokaryotes with different CO ₂ fixation strategies in tea plantation soil. <i>Biology and Fertility of Soils</i> , 2023, 59, 205-215.	2.3	3
9644	Effect of Methionine Hydroxy Analog on Hu Sheep Digestibility, Rumen Fermentation, and Rumen Microbial Community In Vitro. <i>Metabolites</i> , 2023, 13, 169.	1.3	2
9645	<i>Luteibacter flocculans</i> sp. nov., Isolated from a Eutrophic Pond and Isolation and Characterization of <i>Luteibacter</i> Phage vB_LfIM-Pluto. <i>Microorganisms</i> , 2023, 11, 307.	1.6	4
9647	<i>Candida albicans</i> enriched in orthodontic derived white spot lesions and shaped focal supragingival bacteriome. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9648	Litter size influences rumen microbiota and fermentation efficiency, thus determining host early growth in goats. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9649	Deciphering pH-dependent microbial taxa and functional gene co-occurrence in the coral <i>Galaxea fascicularis</i> . <i>Microbial Ecology</i> , 0, , .	1.4	1
9650	High throughput analysis of <i>MHC</i> class I and class II diversity of Zambian indigenous cattle populations. <i>Hla</i> , 2023, 101, 458-483.	0.4	3
9651	Combining vertebrate mitochondrial 12S rRNA gene sequencing and shotgun metagenomic sequencing to investigate the diet of the leopard cat (<i>Prionailurus bengalensis</i>) in Korea. <i>PLoS ONE</i> , 2023, 18, e0281245.	1.1	1
9652	Grass-microbial inter-domain ecological networks associated with alpine grassland productivity. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5

#	ARTICLE	IF	CITATIONS
9653	Dynamic Changes in the Gut Microbiota and Metabolites during the Growth of Hainan Wenchang Chickens. <i>Animals</i> , 2023, 13, 348.	1.0	3
9654	Assessment of the impact of intravenous antibiotics treatment on gut microbiota in patients: Clinical data from pre-and post-cardiac surgery. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
9655	Identifying rare genetic variants in 21 highly multiplex autism families: the role of diagnosis and autistic traits. <i>Molecular Psychiatry</i> , 2023, 28, 2148-2157.	4.1	4
9656	Strengthening and microbial regulation mechanism of <i>Bacillus</i> on purification device for grass carp culture wastewater. <i>Frontiers in Environmental Science</i> , 0, 11, .	1.5	1
9657	T-2 toxin-induced intestinal damage with dysregulation of metabolism, redox homeostasis, inflammation, and apoptosis in chicks. <i>Archives of Toxicology</i> , 2023, 97, 805-817.	1.9	8
9658	Probiotic mediated intestinal microbiota and improved performance, egg quality and ovarian immune function of laying hens at different laying stage. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	7
9660	Mycorrhiza-feeding soil invertebrates in two coniferous forests traced with ¹³ C labelling. <i>Mycorrhiza</i> , 2023, 33, 59-68.	1.3	1
9661	Biogeography and potential ecological functions of prokaryotes in the hydrothermal and non-hydrothermal field sediments of the Indian Ocean Ridges. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
9663	Biogeochemical Activity of Methane-Related Microbial Communities in Bottom Sediments of Cold Seeps of the Laptev Sea. <i>Microorganisms</i> , 2023, 11, 250.	1.6	6
9664	PhoD Harboring Microbial Community and Alkaline Phosphatase as Affected by Long Term Fertilization Regimes on a Calcareous Soil. <i>Agronomy</i> , 2023, 13, 363.	1.3	3
9665	Effect of Dietary Supplemented with Mulberry Leaf Powder on Growth Performance, Serum Metabolites, Antioxidant Property and Intestinal Health of Weaned Piglets. <i>Antioxidants</i> , 2023, 12, 307.	2.2	4
9666	The effects of native lactic acid bacteria on the microbiome, fermentation profile, and nutritive value of Napier grass silage prepared with different legume ratios. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
9667	Multi-Omic Profiling, Structural Characterization, and Potent Inhibitor Screening of Evasion-Related Proteins of a Parasitic Nematode, <i>Haemonchus contortus</i> , Surviving Vaccine Treatment. <i>Biomedicines</i> , 2023, 11, 411.	1.4	1
9668	Effects of taurine on rumen fermentation, nutrient digestion, rumen bacterial community and metabolomics and nitrogen metabolism in beef steers. <i>Journal of the Science of Food and Agriculture</i> , 0, , .	1.7	4
9669	Average Daily Gain in Lambs Weaned at 60 Days of Age Is Correlated with Rumen and Rectum Microbiota. <i>Microorganisms</i> , 2023, 11, 348.	1.6	1
9671	Global diversity and distribution of nitrogen-fixing bacteria in the soil. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	10
9672	Influence of neo-adjuvant radiotherapy on the intestinal microbiota of rectal cancer patients. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 6085-6096.	1.2	0
9673	Artisanal and farmer bread making practices differently shape fungal species community composition in French sourdoughs. , 0, 3, .		4

#	ARTICLE	IF	CITATIONS
9675	Sugarcane Wax Metabolites and Their Toxicity to Silkworms. <i>Life</i> , 2023, 13, 286.	1.1	0
9676	Association of gut microbiota and SCFAs with finishing weight of Diannan small ear pigs. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	6
9677	Effects of <i>Cinnamomum camphora</i> coppice planting on soil fertility, microbial community structure and enzyme activity in subtropical China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9678	Warming changes the composition and diversity of fungal communities in permafrost. <i>Annals of Microbiology</i> , 2023, 73, .	1.1	3
9679	Distinct responses of abundant and rare foraminifera to environmental variables in the Antarctic region revealed by DNA metabarcoding. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
9680	Characteristics of key microorganisms and metabolites in irradiated marbled beef. <i>Meat Science</i> , 2023, 199, 109121.	2.7	3
9681	Replacing alfalfa hay with industrial hemp ethanol extraction byproduct and Chinese wildrye hay: Effects on lactation performance, plasma metabolites, and bacterial communities in Holstein cows. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	8
9682	Gamma aminobutyric acid production by commercially available probiotic strains. <i>Journal of Applied Microbiology</i> , 2023, 134, .	1.4	5
9683	Deciphering microeukaryoticâ€”bacterial co-occurrence networks in coastal aquaculture ponds. <i>Marine Life Science and Technology</i> , 2023, 5, 44-55.	1.8	5
9684	Three-way relationships between gut microbiota, helminth assemblages and bacterial infections in wild rodent populations. , 0, 3, .		2
9685	Bacterial Community Drives the Carbon Source Degradation during the Composting of <i>Cinnamomum camphora</i> Leaf Industrial Extracted Residues. <i>Microbiology Research</i> , 2023, 14, 229-242.	0.8	2
9686	Interaction between Microbes and Host in Sow Vaginas in Early Pregnancy. <i>MSystems</i> , 0, , .	1.7	1
9687	Effects of Italian ryegrass silage-based total mixed ration on rumen fermentation, growth performance, blood metabolites, and bacterial communities of growing Hanwoo heifers. <i>Journal of Animal Science and Technology</i> , 2023, 65, 951-970.	0.8	1
9688	Plantation rhizosphere soil microbes promote soilâ€™ plant phosphorus feedback on the Tibetan Plateau. <i>Plant and Soil</i> , 0, , .	1.8	1
9691	Do commercial arbuscular mycorrhizal inoculants contain the species that they claim?. <i>Mycorrhiza</i> , 2023, 33, 211-220.	1.3	5
9692	Dynamics and diversity of symbiotic bacteria in <i>Apolygus lucorum</i> at different developmental stages. <i>Journal of Cotton Research</i> , 2023, 6, .	1.0	1
9693	Fecal microbiota from MRL/lpr mice exacerbates pristane-induced lupus. <i>Arthritis Research and Therapy</i> , 2023, 25, .	1.6	0
9694	Plant species shape the bacterial communities on the phyllosphere in a hyper-arid desert. <i>Microbiological Research</i> , 2023, 269, 127314.	2.5	4

#	ARTICLE	IF	CITATIONS
9695	Effects of different fertilization methods on <i>Lolium multiflorum</i> Lam. growth and bacterial community in waste slag. <i>Environmental Science and Pollution Research</i> , 2023, 30, 60538-60551.	2.7	0
9696	First report on the bacterial community composition, diversity, and functions in Ramsar site of Central Himalayas, Nepal. <i>Environmental Monitoring and Assessment</i> , 2023, 195, .	1.3	1
9697	Fecal microbiota transplantation from <i>Suncus murinus</i> , an obesity-resistant animal, to C57BL/6NCrSlc mice, and the antibiotic effects in the approach. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
9698	Microbial Communities of Flor Velums and the Genetic Stability of Flor Yeasts Used for a Long Time for the Industrial Production of Sherry-like Wines. <i>Fermentation</i> , 2023, 9, 367.	1.4	2
9699	Micro-aeration assisted with electrogenic respiration enhanced the microbial catabolism and ammonification of aromatic amines in industrial wastewater. <i>Journal of Hazardous Materials</i> , 2023, 448, 130943.	6.5	6
9700	The effect of C/N ratio and its frequent addition on commensal and pathogenic bacterial abundances in shrimp <i>Litopenaeus vannamei</i> gut in a biofloc system: Ratio and frequent addition interaction matters. <i>PLoS ONE</i> , 2023, 18, e0283841.	1.1	0
9701	Composition and function of the skin microbiota were altered of red leg syndrome in cultured bullfrog (<i>Rana catesbeiana</i>). <i>Aquaculture Reports</i> , 2023, 29, 101487.	0.7	2
9702	Effects of bile acids supplemented into low fishmeal diet on growth, molting, and intestinal health of Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Aquaculture Reports</i> , 2023, 29, 101491.	0.7	2
9703	Plant growth stages covered the legacy effect of rotation systems on microbial community structure and function in wheat rhizosphere. <i>Environmental Science and Pollution Research</i> , 2023, 30, 59632-59644.	2.7	1
9704	Insights into the Gut Microbiota of the Freshwater Crab <i>Sinopotamon planum</i> across Three Seasons and Its Associations with the Surrounding Aquatic Microbiota. <i>Diversity</i> , 2023, 15, 519.	0.7	2
9705	Environmental Factors Affect the Bacterial Community in <i>Diaphorina citri</i> , an Important Vector of <i>Candidatus Liberibacter asiaticus</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
9706	Acute temperature stresses trigger liver transcriptome and microbial community remodeling in largemouth bass (<i>Micropterus salmoides</i>). <i>Aquaculture</i> , 2023, 573, 739573.	1.7	7
9707	Biodiversity of Basidiomycetous Yeasts Associated with <i>Cladonia rei</i> Lichen in Japan, with a Description of <i>Microsporomyces cladoniophilus</i> sp. nov. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 473.	1.5	0
9708	Interrogating the performance and microbial ecology of an enhanced biological phosphorus removal/post-anoxic denitrification process at bench and pilot scales. <i>Water Environment Research</i> , 2023, 95, .	1.3	0
9709	An Integrative Study of Mycobiome in Different Habitats from a High Arctic Region: Diversity, Distribution, and Functional Role. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 437.	1.5	3
9710	Combined treatment with glucosamine and chondroitin sulfate improves rheumatoid arthritis in rats by regulating the gut microbiota. <i>Nutrition and Metabolism</i> , 2023, 20, .	1.3	6
9711	Hydrogen inhalation ameliorates hepatic inflammation and modulates gut microbiota in rats with high-fat diet-induced non-alcoholic fatty liver disease. <i>European Journal of Pharmacology</i> , 2023, 947, 175698.	1.7	3
9712	Germline-targeting HIV-1 Env vaccination induces VRC01-class antibodies with rare insertions. <i>Cell Reports Medicine</i> , 2023, 4, 101003.	3.3	7

#	ARTICLE	IF	CITATIONS
9713	Fecal microbiota transplantation affects the recovery of AD-skin lesions and enhances gut microbiota homeostasis. <i>International Immunopharmacology</i> , 2023, 118, 110005.	1.7	5
9714	Sustained detoxification of 1,2-dichloroethane to ethylene by a symbiotic consortium containing <i>Dehalococcoides</i> species. <i>Environmental Pollution</i> , 2023, 325, 121443.	3.7	3
9715	Multi-factor correlation analysis of the effect of root-promoting practices on tobacco rhizosphere microecology in growth stages. <i>Microbiological Research</i> , 2023, 270, 127349.	2.5	1
9716	Forced treadmill running modifies gut microbiota with alleviations of cognitive impairment and Alzheimer's disease pathology in 3xTg-AD mice. <i>Physiology and Behavior</i> , 2023, 264, 114145.	1.0	1
9717	Jiang-Tang-San-Huang pill alleviates type 2 diabetes mellitus through modulating the gut microbiota and bile acids metabolism. <i>Phytomedicine</i> , 2023, 113, 154733.	2.3	7
9718	Gut microbial and metabolic characterization of Atlantic salmon (<i>Salmon salar</i>) challenged with <i>Aeromonas salmonicida</i> . <i>Aquaculture</i> , 2023, 570, 739420.	1.7	0
9719	Effects of salinity on growth, physiology, biochemistry and gut microbiota of juvenile grass carp (<i>Ctenopharyngodon idella</i>). <i>Aquatic Toxicology</i> , 2023, 258, 106482.	1.9	5
9720	A reverse genetic approach in geckos with the CRISPR/Cas9 system by oocyte microinjection. <i>Developmental Biology</i> , 2023, 497, 26-32.	0.9	5
9721	Stress-buster <i>Enterobacter</i> sp. alleviates salinity stress in <i>Cajanus cajan</i> together with impacting its rhizospheric microbiome. <i>South African Journal of Botany</i> , 2023, 156, 202-212.	1.2	3
9722	Mammalian carcass decay increases carbon storage and temporal turnover of carbon-fixing microbes in alpine meadow soil. <i>Environmental Research</i> , 2023, 225, 115653.	3.7	2
9723	Bacterial diversity and its correlation with sensory quality of two types of zha-chili from Shennongjia region, China. <i>Food Research International</i> , 2023, 168, 112789.	2.9	6
9724	Co-occurrence patterns and assembly processes of abundant and rare bacterioplankton in plain river network areas of eastern China. <i>Ecological Indicators</i> , 2023, 150, 110204.	2.6	1
9725	Straw is more effective than biochar in mobilizing soil organic phosphorus mineralization in saline-alkali paddy soil. <i>Applied Soil Ecology</i> , 2023, 186, 104848.	2.1	3
9726	Effects of microplastics and nitrogen deposition on soil multifunctionality, particularly C and N cycling. <i>Journal of Hazardous Materials</i> , 2023, 451, 131152.	6.5	29
9727	The first genomic insight into <i>Chlamydia psittaci</i> sequence type (ST)24 from a healthy captive psittacine host in Australia demonstrates evolutionary proximity with strains from psittacine, human, and equine hosts. <i>Veterinary Microbiology</i> , 2023, 280, 109704.	0.8	2
9728	Promotion of astrocyte-neuron glutamate-glutamine shuttle by SCFA contributes to the alleviation of Alzheimer's disease. <i>Redox Biology</i> , 2023, 62, 102690.	3.9	14
9729	The effects of flow field on the succession of the microbial community on artificial reefs. <i>Marine Pollution Bulletin</i> , 2023, 191, 114920.	2.3	1
9730	Nitrite-resistance mechanisms on wastewater treatment in denitrifying phosphorus removal process revealed by machine learning, co-occurrence, and metagenomics analysis. <i>Environmental Pollution</i> , 2023, 327, 121549.	3.7	3

#	ARTICLE	IF	CITATIONS
9731	Lignite bioorganic fertilizer enhanced microbial co-occurrence network stability and plant-microbe interactions in saline-sodic soil. <i>Science of the Total Environment</i> , 2023, 879, 163113.	3.9	6
9732	Shaoyao-Gancao-Tang regulates the T-helper-type 1/T-helper-type 2 ratio in the lung and gut and alters gut microbiota in rats with ovalbumin-induced asthma. <i>Journal of Ethnopharmacology</i> , 2023, 309, 116300.	2.0	8
9733	Effects of poultry by-product meal replacing fish meal on growth performance, feed utilization, intestinal morphology and microbiota communities in juvenile large yellow croaker (<i>Larimichthys tjingitensis</i>). <i>Journal of Applied Microbiology</i> , 2023, 125, 107107.	3.9	10
9734	Evaluation of the effects of dietary mycotoxin-degrading adsorbent on juvenile turbot (<i>Scophthalmus maximus</i> L.) fed aflatoxin B1-contaminated diets. <i>Aquaculture Reports</i> , 2023, 30, 101539.	0.7	0
9735	RNA outperforms DNA-based metabarcoding in assessing the diversity and response of microeukaryotes to environmental variables in the Arctic Ocean. <i>Science of the Total Environment</i> , 2023, 876, 162608.	3.9	4
9736	Depth-dependent effects of tree species identity on soil microbial community characteristics and multifunctionality. <i>Science of the Total Environment</i> , 2023, 878, 162972.	3.9	12
9737	Mariculture affects antibiotic resistome and microbiome in the coastal environment. <i>Journal of Hazardous Materials</i> , 2023, 452, 131208.	6.5	14
9738	Impact of aged and virgin microplastics on sedimentary nitrogen cycling and microbial ecosystems in estuaries. <i>Science of the Total Environment</i> , 2023, 878, 162977.	3.9	7
9739	Metagenomics and network analysis decipher profiles and co-occurrence patterns of bacterial taxa in soils amended with biogas slurry. <i>Science of the Total Environment</i> , 2023, 877, 162911.	3.9	3
9740	<i>Dendrobium officinale</i> aqueous extract influences the immune response following vaccination against SARS-CoV-2. <i>Biomedicine and Pharmacotherapy</i> , 2023, 162, 114702.	2.5	1
9741	Molecular characterisation of a rabbit Hepatitis E Virus strain detected in a chronically HEV-infected individual from Germany. <i>One Health</i> , 2023, 16, 100528.	1.5	1
9742	Dietary yeast cell wall enhanced intestinal health of broiler chickens by modulating intestinal integrity, immune responses, and microbiota. <i>Poultry Science</i> , 2023, 102, 102660.	1.5	2
9743	Soil nutrients and the responses of microbial community structure to pine bark and vinegar residues in blueberry cultivation. <i>Applied Soil Ecology</i> , 2023, 189, 104907.	2.1	2
9744	Biogeographic distribution, ecotype partitioning and controlling factors of <i>Chloroflexi</i> in the sediments of six hadal trenches of the Pacific Ocean. <i>Science of the Total Environment</i> , 2023, 880, 163323.	3.9	4
9745	The composition, function and assembly mechanism of epiphytic microbial communities on <i>Gracilariopsis lemaneiformis</i> . <i>Journal of Experimental Marine Biology and Ecology</i> , 2023, 564, 151909.	0.7	1
9746	Shifts of soil archaeal nitrification and methanogenesis with elevation in water level fluctuation zone of the three Gorges Reservoir, China. <i>Journal of Environmental Management</i> , 2023, 339, 117871.	3.8	3
9747	Environmental sponge sampling: We are only scraping the surface. , 2023, 1, 13-21.		0
9748	Demultiplexing Ig repertoires by parallel mRNA/DNA sequencing shows major differential alterations in severe COVID-19. <i>IScience</i> , 2023, 26, 106260.	1.9	1

#	ARTICLE	IF	CITATIONS
9749	Impacts of three feeding modes on the diet composition and contribution ratios for juvenile Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Aquaculture Reports</i> , 2023, 29, 101516.	0.7	1
9750	Plant-soil-microbial interactions mediate vegetation succession in retreating glacial forefields. <i>Science of the Total Environment</i> , 2023, 873, 162393.	3.9	2
9751	Long-term integrated rice-crayfish culture disrupts the microbial communities in paddy soil. <i>Aquaculture Reports</i> , 2023, 29, 101515.	0.7	1
9752	Soil bacterial communities of paddy are dependent on root compartment niches but independent of growth stages from Mollisols of Northeast China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9753	Nitrogen application influences the effect of bacteria on the belowground allocation of photosynthesized carbon under elevated CO ₂ . <i>Soil Biology and Biochemistry</i> , 2023, 180, 109021.	4.2	1
9754	Assembly processes of bacterial and fungal communities in metal(loid)s smelter soil. <i>Journal of Hazardous Materials</i> , 2023, 451, 131153.	6.5	9
9755	<i>Bacillus amyloliquefaciens</i> FG14 as a potential biocontrol strain against rusty root rot of <i>Panax ginseng</i> , and its impact on the rhizosphere microbial community. <i>Biological Control</i> , 2023, 182, 105221.	1.4	5
9756	Anthropogenic land-use activities within watersheds reduce comammox activity and diversity in rivers. <i>Journal of Environmental Management</i> , 2023, 338, 117841.	3.8	0
9766	Effect of edible bird's nest and N-acetylneuraminic acid on gut microbiota in different stages of pregnant rats fed with zinc deficient diet. <i>Food Bioscience</i> , 2023, 52, 102398.	2.0	1
9767	(Meta)genomics -assisted screening of novel antibacterial lactic acid bacteria strains from traditional fermented milk from Western China and their bioprotective effects on cheese. <i>LWT - Food Science and Technology</i> , 2023, 175, 114507.	2.5	2
9768	Ammonia-oxidizing archaea and comammox <i>Nitrospira</i> clade B as freeze-thaw resistant nitrifiers in wetland soils. <i>International Biodeterioration and Biodegradation</i> , 2023, 178, 105570.	1.9	2
9769	Characterization and Hydrocarbon Degradation Potential of <i>Variovorax</i> sp. Strain N23 Isolated from the Antarctic Soil. <i>Microbiology Research</i> , 2023, 14, 91-103.	0.8	1
9770	Two for the price of one: eDNA metabarcoding reveals temporal and spatial variability of mussel and fish co-distributions in Michigan riverine systems. <i>Environmental DNA</i> , 0, , .	3.1	1
9771	Fate, uptake and gut toxicity of two colloidal silver products in mice: how micro X-ray fluorescence, micro X-ray absorption spectroscopy and near-infrared spectroscopy provide new insights in food nanotoxicology. <i>Environmental Science: Nano</i> , 2023, 10, 902-921.	2.2	0
9772	Early warning of MIB episode based on gene abundance and expression in drinking water reservoirs. <i>Water Research</i> , 2023, 231, 119667.	5.3	1
9773	Selection, Identification and Functional Performance of Ammonia-Degrading Microbial Communities from an Activated Sludge for Landfill Leachate Treatment. <i>Microorganisms</i> , 2023, 11, 311.	1.6	1
9774	Soil bacterial community response to continuous cropping of cotton. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9775	Effects of Continuous Straw Returning on Soil Functional Microorganisms and Microbial Communities. <i>Journal of Microbiology</i> , 2023, 61, 49-62.	1.3	3

#	ARTICLE	IF	CITATIONS
9776	Microplastics affect soybean rhizosphere microbial composition and function during vegetative and reproductive stages. <i>Ecotoxicology and Environmental Safety</i> , 2023, 252, 114577.	2.9	10
9777	Comparison of network connectivity and environmental driving factors of root-associated fungal communities of desert ephemeral plants in two habitat soils. <i>Journal of Environmental Management</i> , 2023, 332, 117375.	3.8	8
9778	Characterization of a pollen-part self-compatible apple (<i>Malus domestica</i> Borkh.) mutant induced by β -ray mutagenesis. <i>Scientia Horticulturae</i> , 2023, 312, 111867.	1.7	2
9779	Linking soil microbial community to the chemical composition of dissolved organic matter in a boreal forest during freeze-thaw cycles. <i>Geoderma</i> , 2023, 431, 116359.	2.3	5
9780	Correlation of microbiomes in "plant-insect-soil" ecosystem. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9781	Co-treatment with free nitrous acid and calcium peroxide regulates microbiome and metabolic functions of acidogenesis and methanogenesis in sludge anaerobic digestion. <i>Science of the Total Environment</i> , 2023, 870, 161924.	3.9	12
9782	Understory ferns promote the restoration of soil microbial diversity and function in previously degraded lands. <i>Science of the Total Environment</i> , 2023, 870, 161934.	3.9	3
9783	Composting reduces the risks of antibiotic resistance genes in maize seeds posed by gentamicin fermentation waste. <i>Science of the Total Environment</i> , 2023, 870, 161785.	3.9	5
9784	Crop diversity promotes the recovery of fungal communities in saline-alkali areas of the Western Songnen Plain. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9785	Diverse logics and grammar encode notochord enhancers. <i>Cell Reports</i> , 2023, 42, 112052.	2.9	9
9786	Root Endophyte Shift and Key Genera Discovery in Rice under Barnyardgrass Stress. <i>Rice Science</i> , 2023, 30, 160-170.	1.7	1
9787	Specific suppression of vascular wilt disease of onion is linked with fungal soil community structure. <i>Rhizosphere</i> , 2023, 25, 100671.	1.4	1
9788	PGPR Promotes the Recovery of Submerged Macrophytes via Indigenous Microbiome Modulations under Combined Abiotic Stress. <i>Water (Switzerland)</i> , 2023, 15, 590.	1.2	1
9789	The ecology of bacterial communities in groundwater of industrial areas: Diversity, composition, network, and assembly. <i>Environmental Pollution</i> , 2023, 322, 121207.	3.7	3
9790	Microbial Taxonomical and Functional Diversities Increased with Wetland Productivity at Initial Stages of Vegetation Restoration on Denuded Tidal Flats. <i>Estuaries and Coasts</i> , 2023, 46, 829-843.	1.0	0
9791	Responses of Soil Bacterial Communities and Enzyme Activities to Straw Return and Potassium Fertilization with Two Soils Under Soil Potassium Balance Condition in Rice-Wheat System. <i>Journal of Soil Science and Plant Nutrition</i> , 2023, 23, 1845-1859.	1.7	1
9792	Short-term effects of Chlorhexidine mouthwash and Listerine on oral microbiome in hospitalized patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	4
9793	Identification of quorum sensing-regulated <i>Vibrio fortis</i> as potential pathogenic bacteria for coral bleaching and the effects on the microbial shift. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	7

#	ARTICLE	IF	CITATIONS
9794	Gut microbiome variations in <i>Rhinopithecus roxellanae</i> caused by changes in the environment. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
9795	Microbial community stratification in scale-up Anaerobic Fluidized Bed Reactor applied for 4-Nonylphenol degradation. <i>Bioresource Technology Reports</i> , 2023, 21, 101359.	1.5	0
9796	Microbial density-dependent viral dynamics and low activity of temperate phages in the activated sludge process. <i>Water Research</i> , 2023, 232, 119709.	5.3	4
9797	Gut Microbiota Deficiency Exacerbates Liver Injury in Bile Duct Ligated Mice via Inflammation and Lipid Metabolism. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3180.	1.8	3
9799	A highly multiplexed assay to monitor pathogenicity, fungicide resistance and gene flow in the fungal wheat pathogen <i>Zygomoseptoria tritici</i> . <i>PLoS ONE</i> , 2023, 18, e0281181.	1.1	3
9800	Effects of Salinity on Assembly Characteristics and Function of Microbial Communities in the Phyllosphere and Rhizosphere of Salt-Tolerant <i>Avicennia marina</i> Mangrove Species. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
9801	Soil nitrification process played a key role in alleviating continuous cropping limitation induced by fumigation. <i>Plant and Soil</i> , 2023, 487, 157-171.	1.8	0
9802	Active Sulfate-Reducing Bacterial Community in the Camel Gut. <i>Microorganisms</i> , 2023, 11, 401.	1.6	2
9803	<i>Candidatus Liberibacter asiaticus</i> : An important factor affecting bacterial community composition and <i>Wolbachia</i> titers in Asian citrus psyllid. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
9804	Gut Microbiota and Metabolites may Play a Crucial Role in Sea Cucumber <i>Apostichopus Japonicus</i> Aestivation. <i>Microorganisms</i> , 2023, 11, 416.	1.6	6
9806	Analysis of Changes in Herbaceous Peony Growth and Soil Microbial Diversity in Different Growing and Replanting Years Based on High-Throughput Sequencing. <i>Horticulturae</i> , 2023, 9, 220.	1.2	0
9808	Response and recovery mechanisms of river microorganisms to gradient concentrations of estrogen. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9809	Warmer winters result in reshaping of the European beech forest soil microbiome (bacteria, archaea) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i> 2023, 25, 1118-1135.	1.8	1
9811	Seasonal Shifts in Bacterial Community Structures in the Lateral Root of Sugar Beet Grown in an Andosol Field in Japan. <i>Microbes and Environments</i> , 2023, 38, n/a.	0.7	5
9812	Analysis of Dynamics and Diversity of Microbial Community during Production of Germinated Brown Rice. <i>Foods</i> , 2023, 12, 755.	1.9	2
9814	<i>Rhodopseudomonas palustris</i> PSB06 agent enhance pepper yield and regulating the rhizosphere microecological environment. <i>Frontiers in Sustainable Food Systems</i> , 0, 7, .	1.8	1
9815	Bioorganic fertilizers improve the adaptability and remediation efficiency of <i>Puccinellia distans</i> in multiple heavy metals-contaminated saline soil by regulating the soil microbial community. <i>Journal of Hazardous Materials</i> , 2023, 448, 130982.	6.5	3
9817	The Intestinal Microbiota Involves in the Deterioration of Live Sea Cucumber During Storage. <i>Journal of Aquatic Food Product Technology</i> , 2023, 32, 129-141.	0.6	0

#	ARTICLE	IF	CITATIONS
9818	Regulatory dissection of the severe COVID-19 risk locus introgressed by Neanderthals. <i>ELife</i> , 0, 12, .	2.8	7
9819	Regulatory effect of moderate Jiang-flavour baijiu (Chinese liquor) dosage on organ function and gut microbiota in mice. <i>Journal of Bioscience and Bioengineering</i> , 2023, 135, 298-305.	1.1	1
9820	An overlooked influence of reactive oxygen species on ammonia-oxidizing microbial communities in redox-fluctuating aquifers. <i>Water Research</i> , 2023, 233, 119734.	5.3	5
9821	Gut microbiota of white-headed black langurs (<i>Trachypithecus leucocephalus</i>) in responses to habitat fragmentation. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9822	Microbiome Composition and Microbial Community Structure in Mosquito Vectors <i>Aedes aegypti</i> and <i>Aedes albopictus</i> in Northeastern Thailand, a Dengue-Endemic Area. <i>Insects</i> , 2023, 14, 184.	1.0	2
9823	Genomic insights into antibiotic resistance and mobilome of lactic acid bacteria and bifidobacteria. <i>Life Science Alliance</i> , 2023, 6, e202201637.	1.3	2
9824	Carbon allocation mediated by arbuscular mycorrhizal fungi alters the soil microbial community under various phosphorus levels. <i>Fungal Ecology</i> , 2023, 62, 101227.	0.7	4
9825	A bacteriocyte symbiont determines whitefly sex ratio by regulating mitochondrial function. <i>Cell Reports</i> , 2023, 42, 112102.	2.9	3
9826	Effects of phosphorus application on soil phosphorus forms and <i>phoD</i> -harboring microbial communities in an alpine grassland on the Qinghai-Tibetan Plateau. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	2
9827	IMperm: a fast and comprehensive IMMune Paired-End Reads Merger for sequencing data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	0
9828	The relationship between shifts in the rhizosphere microbial community and root rot disease in a continuous cropping American ginseng system. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
9829	Confirmation and detection of novel acetolactate synthase- and protoporphyrinogen oxidase-â€inhibiting herbicide-resistant redroot pigweed (<i>Amaranthus retroflexus</i>) populations in North Carolina. <i>Weed Science</i> , 2023, 71, 84-94.	0.8	3
9830	Gut Microbiota in Patients with Postoperative Atrial Fibrillation Undergoing Off-Pump Coronary Bypass Graft Surgery. <i>Journal of Clinical Medicine</i> , 2023, 12, 1493.	1.0	1
9831	Bio-organic fertilizers improve <i>Dendrocalamus farinosus</i> growth by remodeling the soil microbiome and metabolome. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
9832	Changes in Physicochemical Characteristics and Microbial Diversity of Traditional Fermented Vinasse Hairtail. <i>Fermentation</i> , 2023, 9, 173.	1.4	2
9833	Intestinal Microbiota Differences in <i>Litopenaeus vannamei</i> Shrimp between Greenhouse and Aquaponic Rearing. <i>Life</i> , 2023, 13, 525.	1.1	3
9835	Interspecific plant-plant interactions increase the soil microbial network stability, shift keystone microbial taxa, and enhance their functions in mixed stands. <i>Forest Ecology and Management</i> , 2023, 533, 120851.	1.4	11
9836	Monthly dynamics of microbial communities and variation of nitrogen-cycling genes in an industrial-scale expanded granular sludge bed reactor. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1

#	ARTICLE	IF	CITATIONS
9837	Metagenomic 16S rRNA amplicon data of gut microbial diversity in three species of subterranean termites (<i>Coptotermes gestroi</i> , <i>Globitermes sulphureus</i> and <i>Macrotermes gilvus</i>). <i>Data in Brief</i> , 2023, 47, 108993.	0.5	1
9838	Evaluation of efficacy and mechanism of <i>Bacillus velezensis</i> CB13 for controlling peanut stem rot caused by <i>Sclerotium rolfsii</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
9839	The influences of acidic electrolyzed water on quality and bacteria community of fresh-cut jackfruit in storage. <i>International Journal of Food Engineering</i> , 2023, 19, 27-36.	0.7	0
9840	Metagenomic mapping of cyanobacteria and potential cyanotoxin producing taxa in large rivers of the United States. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
9841	The shift of soil microbial community induced by cropping sequence affect soil properties and crop yield. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9842	New perspective: Symbiotic pattern and assembly mechanism of <i>Cantharellus cibarius</i> -associated bacteria. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9843	Disrupted diurnal oscillations of the gut microbiota in patients with alcohol dependence. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	2
9844	Selection of rhizosphere communities of diverse rotation crops reveals unique core microbiome associated with reduced banana <i>Fusarium</i> wilt disease. <i>New Phytologist</i> , 2023, 238, 2194-2209.	3.5	18
9845	Bidirectional Effects of Mao Jian Green Tea and Its Flavonoid Glycosides on Gastrointestinal Motility. <i>Foods</i> , 2023, 12, 854.	1.9	5
9846	Active dry yeast supplementation benefits ruminal fermentation, bacterial community, blood immunoglobulins, and growth performance in young dairy goats, but not for intermittent supplementation. <i>Animal Nutrition</i> , 2023, 13, 289-301.	2.1	4
9847	Structural characteristics and diversity of the rhizosphere bacterial communities of wild <i>Fritillaria przewalskii</i> Maxim. in the northeastern Tibetan Plateau. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9848	Relationship between the effects of heat pre-treatment on anaerobic performance of pig manure and the microbial variation within reactors. <i>Chemical Engineering Journal</i> , 2023, 461, 141991.	6.6	2
9849	Large effective population size masks population genetic structure in <i>Hirondellea</i> amphipods within the deepest marine ecosystem, the Mariana Trench. <i>Molecular Ecology</i> , 2023, 32, 2206-2218.	2.0	0
9850	Effects of different starch diets on growth performance, intestinal health and faecal microbiota of growing pigs. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2023, 107, 1043-1053.	1.0	0
9851	Seasonal variations in the gut microbiota of white-headed black langur (<i>Trachypithecus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (le Evolution, 0, 11, .	1.1	0
9852	The gut microbiota correlate with the disease characteristics and immune status of patients with untreated diffuse large B-cell lymphoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
9853	Roe Deer Produce Less Methane and Harbor Distinct Gut Microbiota. <i>Fermentation</i> , 2023, 9, 186.	1.4	0
9854	Effect of Microwave Treatment at 2.45 GHz on Soil Physicochemical Properties and Bacterial Community Characteristics in Phaeozems of Northeast China. <i>Agronomy</i> , 2023, 13, 600.	1.3	0

#	ARTICLE	IF	CITATIONS
9855	Water column dynamics control nitrite-dependent anaerobic methane oxidation by <i>Candidatus</i> <i>Methyloiridis</i> in stratified lake basins. <i>ISME Journal</i> , 2023, 17, 693-702.	4.4	7
9856	Biofouling mitigation by D-tyrosine in membrane bioreactor: Short-term performance. <i>Journal of Environmental Chemical Engineering</i> , 2023, 11, 109554.	3.3	1
9857	Characteristics of Microbiota in Different Segments of the Digestive Tract of <i>Lycodon rufozonatus</i> . <i>Animals</i> , 2023, 13, 731.	1.0	1
9858	Dynamics of Functional Genes and Bacterial Community during Bioremediation of Diesel-Contaminated Soil Amended with Compost. <i>Journal of Microbiology and Biotechnology</i> , 2023, , .	0.9	0
9859	Saliva microbiome alterations in dental fluorosis population. <i>Journal of Oral Microbiology</i> , 2023, 15, .	1.2	1
9860	MetaGenePipe: An Automated, Portable Pipeline for Contig-based Functional and Taxonomic Analysis. <i>Journal of Open Source Software</i> , 2023, 8, 4851.	2.0	1
9862	Changes of In Situ Prokaryotic and Eukaryotic Communities in the Upper Sanya River to the Sea over a Nine-Hour Period. <i>Microorganisms</i> , 2023, 11, 536.	1.6	1
9863	Impacts of dietary supplementation of bamboo vinegar and charcoal powder on growth performance, intestinal morphology, and gut microflora of large-scale loach <i>Paramisgurnus dabryanus</i> . <i>Journal of Oceanology and Limnology</i> , 2023, 41, 1187-1196.	0.6	1
9864	Shift of Feeding Strategies from Grazing to Different Forage Feeds Reshapes the Rumen Microbiota To Improve the Ability of Tibetan Sheep (<i>Ovis aries</i>) To Adapt to the Cold Season. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	7
9865	Warming affects herbaceous germination, early survival, and growth by shifting plant-soil microbe interactions in an alpine ecosystem. <i>Plant and Soil</i> , 0, , .	1.8	2
9866	Dietary butyrate ameliorates metabolic health associated with selective proliferation of gut <i>Lachnospiraceae</i> bacterium 28-4. <i>JCI Insight</i> , 2023, 8, .	2.3	3
9867	Influence of Parturition on Rumen Bacteria and SCFAs in Holstein Cows Based on 16S rRNA Sequencing and Targeted Metabolomics. <i>Animals</i> , 2023, 13, 782.	1.0	3
9868	Characterizing Free-Living and Particle-Attached Bacterial Communities of a Shallow Lake on the Inner Mongolia-Xinjiang Plateau, China. <i>Water (Switzerland)</i> , 2023, 15, 836.	1.2	0
9869	Extracellular DNA includes an important fraction of high-risk antibiotic resistance genes in treated wastewaters. <i>Environmental Pollution</i> , 2023, 323, 121325.	3.7	5
9870	Phagotrophic Protists Modulate Copper Resistance of the Bacterial Community in Soil. <i>Environmental Science & Technology</i> , 2023, 57, 3590-3601.	4.6	4
9871	Characteristics of groundwater microbial communities and the correlation with the environmental factors in a decommissioned acid in-situ uranium mine. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9872	Fermented Wheat Germ Alleviates Depression-like Behavior in Rats with Chronic and Unpredictable Mild Stress. <i>Foods</i> , 2023, 12, 920.	1.9	2
9873	From guest to host: parasite <i>Cistanche deserticola</i> shapes and dominates bacterial and fungal community structure and network complexity. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	1

#	ARTICLE	IF	CITATIONS
9874	Influence of CO ₂ /HCO ₃ ²⁻ on Microbial Communities in Two Karst Caves with High CO ₂ . <i>Journal of Earth Science (Wuhan, China)</i> , 2023, 34, 145-155.	1.1	0
9875	Impact of environmental factors on diversity of fungi in sediments from the Shenzhen River Estuary. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	2
9876	Trade-offs between fertilizer-N availability and Cd pollution potential under crop straw incorporation by ¹⁵ N stable isotopes in rice. <i>Environmental Science and Pollution Research</i> , 2023, 30, 51075-51088.	2.7	1
9877	mtR_find: A Parallel Processing Tool to Identify and Annotate RNAs Derived from the Mitochondrial Genome. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4373.	1.8	0
9878	Key Soil Physicochemical Properties Regulating Microbial Community Structure under Vegetation Restoration in a Karst Region of China. <i>Ecosystem Health and Sustainability</i> , 2023, 9, .	0.0	1
9879	Variations of arbuscular mycorrhizal fungi following succession stages in a tropical lowland rainforest ecosystem of South China. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	1
9880	Effect of tillage state of paddy soils with heavy metal pollution on the nosZ gene of N ₂ O reductase. <i>Journal of Environmental Sciences</i> , 2024, 137, 469-477.	3.2	0
9881	Small-Organella-enriched metagenomics: An improved method for environmental DNA-based identification of marine plankton. <i>Limnology and Oceanography: Methods</i> , 2023, 21, 178-191.	1.0	1
9882	Bioaugmentation of diesel-contaminated soil with <i>Pseudomonas</i> sp. DTF1. <i>International Journal of Environmental Science and Technology</i> , 0, , .	1.8	0
9883	Coexistence of Psychrophilic, Mesophilic, and Thermophilic Sulfate-Reducing Bacteria in a Deep Subsurface Aquifer Associated with Coal-Bed Methane Production. <i>Microbial Ecology</i> , 2023, 86, 1934-1946.	1.4	2
9884	Metabolic and inflammatory linkage of the chicken cecal microbiome to growth performance. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9885	The Associations between Multiple Essential Metal(loid)s and Gut Microbiota in Chinese Community-Dwelling Older Adults. <i>Nutrients</i> , 2023, 15, 1137.	1.7	1
9886	Is foliar spectrum predictive of belowground bacterial diversity? A case study in a peach orchard. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9887	Variations in gut microbiome and metabolites of dogs with acute diarrhea in poodles and Labrador retrievers. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	2
9888	Effects of altitude on the gut microbiome and metabolomics of Sanhe heifers. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9889	Microbial community dynamics and its correlation with environmental factors in the water of polyculture ponds containing <i>Penaeus japonicus</i> , <i>Portunus trituberculatus</i> and <i>Sinonovacula constricta</i> . <i>Aquatic Ecology</i> , 0, , .	0.7	0
9890	Rise and metabolic roles of <i>Vibrio</i> during the fermentation of crab paste. <i>Frontiers in Nutrition</i> , 0, 10, .	1.6	0
9891	Sample and library preparation approaches for the analysis of the virome of irrigation water. <i>Journal of the Science of Food and Agriculture</i> , 2023, 103, 4450-4457.	1.7	2

#	ARTICLE	IF	CITATIONS
9892	Patterns and drivers of anaerobic nitrogen transformations in sediments of thermokarst lakes. <i>Global Change Biology</i> , 2023, 29, 2697-2713.	4.2	3
9893	Investigation of Soil Microbial Communities Involved in N Cycling as Affected by the Long-Term Use of the N Stabilizers DMPP and NBPT. <i>Agronomy</i> , 2023, 13, 659.	1.3	1
9894	cfSNV: a software tool for the sensitive detection of somatic mutations from cell-free DNA. <i>Nature Protocols</i> , 2023, 18, 1563-1583.	5.5	3
9895	The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. <i>MSphere</i> , 2023, 8, .	1.3	4
9896	From the Sunlit to the Aphotic Zone: Assembly Mechanisms and Co-Occurrence Patterns of Protistan-Bacterial Microbiotas in the Western Pacific Ocean. <i>MSystems</i> , 2023, 8, .	1.7	5
9897	Climate warming has direct and indirect effects on microbes associated with carbon cycling in northern lakes. <i>Global Change Biology</i> , 2023, 29, 3039-3053.	4.2	3
9898	Freeze-thaw cycles alter the growth sprouting strategy of wetland plants by promoting denitrification. <i>Communications Earth & Environment</i> , 2023, 4, .	2.6	1
9899	Gene-by-environment interactions are pervasive among natural genetic variants. <i>Cell Genomics</i> , 2023, 3, 100273.	3.0	5
9901	Comparison of Fecal Microbiota Communities between Primiparous and Multiparous Cows during Non-Pregnancy and Pregnancy. <i>Animals</i> , 2023, 13, 869.	1.0	3
9902	Widespread epistasis among beneficial genetic variants revealed by high-throughput genome editing. <i>Cell Genomics</i> , 2023, 3, 100260.	3.0	7
9903	Disturbed rhythmicity of intestinal hydrogen peroxide alters gut microbial oscillations in BMAL1-deficient monkeys. <i>Cell Reports</i> , 2023, 42, 112183.	2.9	2
9904	Microbial profiles and immune responses in seahorse gut and brood pouch under chronic exposure to environmental antibiotics. <i>Ecotoxicology and Environmental Safety</i> , 2023, 253, 114711.	2.9	3
9905	Recommendations for the use of metagenomics for routine monitoring of antibiotic resistance in wastewater and impacted aquatic environments. <i>Critical Reviews in Environmental Science and Technology</i> , 2023, 53, 1731-1756.	6.6	4
9906	Shifts in soil nitrogen availability and associated microbial drivers during stand development of Mongolian pine plantations. <i>Land Degradation and Development</i> , 2023, 34, 3156-3169.	1.8	1
9907	Geographic characteristics and environmental variables determine the diversities and assembly of the algal communities in interconnected river-lake system. <i>Water Research</i> , 2023, 233, 119792.	5.3	6
9908	Inferring protein fitness landscapes from laboratory evolution experiments. <i>PLoS Computational Biology</i> , 2023, 19, e1010956.	1.5	7
9909	An integrated transcriptome and microbial community analysis reveals potential mechanisms for increased immune responses when replacing silybum marianum meal with soybean meal in growing lambs. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9910	Gene silencing dynamics are modulated by transiently active regulatory elements. <i>Molecular Cell</i> , 2023, 83, 715-730.e6.	4.5	3

#	ARTICLE	IF	CITATIONS
9911	16S rDNA-based diversity analysis of bacterial communities associated with soft corals of the Red Sea, Al Rayyis, White Head, KSA. <i>Journal of Taibah University for Science</i> , 2023, 17, .	1.1	2
9912	Astragalus-cultivated soil was a suitable bed soil for nurturing <i>Angelica sinensis</i> seedlings from the rhizosphere microbiome perspective. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
9913	Bacterial PncA improves diet-induced NAFLD in mice by enabling the transition from nicotinamide to nicotinic acid. <i>Communications Biology</i> , 2023, 6, .	2.0	2
9914	Bamboo invasion alters Collembola community composition varying with life forms. <i>Pest Management Science</i> , 0, , .	1.7	1
9915	Three decades of organic manure and chemical fertilizers co-application enhanced rice productivity through increasing the diversity and key network module of soil bacterial community. <i>Journal of Soils and Sediments</i> , 2023, 23, 2175-2188.	1.5	0
9916	Abiotic factors and endophytes co-regulate flavone and terpenoid glycoside metabolism in <i>Glycyrrhiza uralensis</i> . <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 2671-2688.	1.7	2
9917	Efficient partial nitrification performance of real printed circuit board tail wastewater by a zeolite biological fixed bed reactor. <i>Journal of Water Process Engineering</i> , 2023, 53, 103607.	2.6	2
9918	The Gut Microbiota of Young Asian Elephants with Different Milk-Containing Diets. <i>Animals</i> , 2023, 13, 916.	1.0	2
9919	Nitrogen fertilization rates mediate rhizosphere soil carbon emissions of continuous peanut monoculture by altering cellulose-specific microbes. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
9920	Cold Exposure-induced Alterations in the Brain Peptidome and Gut Microbiome Are Linked to Energy Homeostasis in Mice. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100525.	2.5	1
9921	Dry-wet cycle changes the influence of microplastics (MPs) on the antioxidant activity of lettuce and the rhizospheric bacterial community. <i>Journal of Soils and Sediments</i> , 2023, 23, 2189-2201.	1.5	3
9922	Community differentiation of rhizosphere microorganisms and their responses to environmental factors at different development stages of medicinal plant <i>Glehnia littoralis</i> . <i>PeerJ</i> , 0, 11, e14988.	0.9	4
9923	Community response of soil microorganisms to combined contamination of polycyclic aromatic hydrocarbons and potentially toxic elements in a typical coking plant. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9925	Analysis of Bacterial Diversity in Fermented Grains of Bajjiu Based on Culturomics and Amplicon Sequencing. <i>Fermentation</i> , 2023, 9, 260.	1.4	0
9926	Effects of the fungicide trifloxystrobin on the structure and function of soil bacterial community. <i>Environmental Toxicology and Pharmacology</i> , 2023, 99, 104104.	2.0	3
9927	Smoking-induced subgingival dysbiosis precedes clinical signs of periodontal disease. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
9928	pH Drives Differences in Bacterial Community β -Diversity in Hydrologically Connected Lake Sediments. <i>Microorganisms</i> , 2023, 11, 676.	1.6	2
9930	Network Analysis Indicates Microbial Assemblage Differences in Life Stages of <i>Cladophora</i> . <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	4

#	ARTICLE	IF	CITATIONS
9931	Effects of rice blast biocontrol strain <i>Pseudomonas alcaliphila</i> Ej2 on the endophytic microbiome and proteome of rice under salt stress. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
9933	Association of intestinal microbiota and its metabolite markers with excess weight in Chinese children and adolescents. <i>Pediatric Obesity</i> , 0, , .	1.4	1
9934	Effect of Different Host Plants on the Diversity of Gut Bacterial Communities of <i>Spodoptera frugiperda</i> (J. E. Smith, 1797). <i>Insects</i> , 2023, 14, 264.	1.0	0
9935	Effects of paraprobiotics on bile acid metabolism and liver health in largemouth bass (<i>Micropterus</i>) Tj ETQq1 1 0.784314 rgBT ₃ /Overlook	2.1	3
9936	Remodeling of the gut microbiome by <i>Lactobacillus johnsonii</i> alleviates the development of acute myocardial infarction. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	11
9937	Alterations in the gut microbiome and metabolome profiles of septic mice treated with Shen FuHuang formula. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
9938	Altered gut microbiota and microbial metabolism in children with hepatic glycogen storage disease: a case-control study. <i>Translational Pediatrics</i> , 2023, .	0.5	0
9939	Phosphorus mining activities alter endophytic bacterial communities and metabolic functions of surrounding vegetables and crops. <i>Plant and Soil</i> , 0, , .	1.8	11
9940	Metal-driven bacterial community variation in urban and suburban park soils of Shanghai, China. <i>European Journal of Soil Biology</i> , 2023, 115, 103475.	1.4	4
9941	Bamboo shoot dietary fiber alleviates gut microbiota dysbiosis and modulates liver fatty acid metabolism in mice with high-fat diet-induced obesity. <i>Frontiers in Nutrition</i> , 0, 10, .	1.6	4
9942	Microbiome and function alterations in the gastric mucosa of asymptomatic patients with <i>Helicobacter pylori</i> infection. <i>Helicobacter</i> , 0, , .	1.6	0
9943	Differences in Soil Microbial Communities between Healthy and Diseased <i>Lycium barbarum</i> cv. Ningqi-5 Plants with Root Rot. <i>Microorganisms</i> , 2023, 11, 694.	1.6	3
9944	Niche-mediated bacterial community composition in continental glacier alluvial valleys under cold and arid environments. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9945	Comparison of four DNA extraction kits efficiency for 16SrDNA microbiota profiling of diverse human samples. <i>Future Science OA</i> , 2023, 9, .	0.9	2
9946	Deterministic processes dominate microbial community assembly in artificially bred <i>Schizothorax wangchiachii</i> juveniles after being released into wild. <i>Integrative Zoology</i> , 0, , .	1.3	0
9947	A parasitic nematode induces dysbiosis in susceptible but not resistant gastropod hosts. <i>MicrobiologyOpen</i> , 2023, 12, .	1.2	4
9948	Orchidâ€™mycorrhizal fungi interactions reveal a duality in their network structure in two European regions differing in climate. <i>Molecular Ecology</i> , 2023, 32, 3308-3321.	2.0	2
9949	Influence of Sedimentary Environment Evolution on Fingerprint Characteristics of Methane Isotopes: A Case Study From Hangzhou Bay. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2023, 128, .	1.3	2

#	ARTICLE	IF	CITATIONS
9950	Responses of bacterial communities along vertical soil profile to the chromium-contamination stress. <i>International Biodeterioration and Biodegradation</i> , 2023, 179, 105584.	1.9	1
9951	Massively parallel characterization of CRISPR activator efficacy in human induced pluripotent stem cells and neurons. <i>Molecular Cell</i> , 2023, 83, 1125-1139.e8.	4.5	9
9952	The tropical cookbook: Termite diet and phylogeneticsâ€™Over geographical originâ€™Drive the microbiome and functional genetic structure of nests. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9953	From river to ocean: Connectivity and heterogeneity of aquatic ecosystems depicted by planktonic microeukaryotes. <i>Ecological Indicators</i> , 2023, 148, 110136.	2.6	1
9954	Microbial and Viral Genome and Proteome Nitrogen Demand Varies across Multiple Spatial Scales within a Marine Oxygen Minimum Zone. <i>MSystems</i> , 2023, 8, .	1.7	1
9955	A phytobiotic extract, in an aqueous or in a cyclodextrin encapsulated form, added in diet affects meat oxidation, cellular responses and intestinal morphometry and microbiota of broilers. <i>Frontiers in Animal Science</i> , 0, 4, .	0.8	2
9956	Evaluation of the Oral Bacterial Genome and Metabolites in Patients with Wolfram Syndrome. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5596.	1.8	1
9957	The gut microbiota diversity of five Orthoptera (Insecta, Polyneoptera) insects determined by DNA metabarcoding. <i>Biodiversity Data Journal</i> , 0, 11, .	0.4	0
9958	Diseased-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9959	Fermented cottonseed and rapeseed meals outperform soybean meal in improving performance, rumen fermentation, and bacterial composition in Hu sheep. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9960	Maternal vaginal fluids play a major role in the colonization of the neonatal intestinal microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	2
9961	Changes of intestinal microbiota in the giant salamander (<i>Andrias davidianus</i>) during growth based on high-throughput sequencing. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9963	Acupuncture improved hepatic steatosis in HFD-induced NAFLD rats by regulating intestinal microbiota. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
9964	Integrated analysis reveals important differences in the gut and oropharyngeal microbiota between children with mild and severe hand, foot, and mouth disease. <i>Emerging Microbes and Infections</i> , 2023, 12, .	3.0	1
9965	Microbe community composition differences of hand skin on similar lifestyle volunteers: a small-scale study. <i>Journal of Applied Microbiology</i> , 2023, 134, .	1.4	0
9966	Association of Fungi in the Intestine of Black Carp and Grass Carp Compared with their Cultured Water. <i>Aquaculture Research</i> , 2023, 2023, 1-10.	0.9	1
9967	Insights into the mechanisms underlying the biodegradation of phenanthrene in biochar-amended soil: from bioavailability to soil microbial communities. <i>Biochar</i> , 2023, 5, .	6.2	2
9968	High-throughput profiling of sequence recognition by tyrosine kinases and SH2 domains using bacterial peptide display. <i>ELife</i> , 0, 12, .	2.8	6

#	ARTICLE	IF	CITATIONS
9969	Assessing the potential use of environmental DNA for multifaceted genetic monitoring of cetaceans: Example of a wandering whale in a highly disturbed bay area. <i>Ecological Indicators</i> , 2023, 148, 110125.	2.6	3
9970	Using Next-Generation Sequencing to Disentangle the Diet and Incidence of Intestinal Parasites of Falkland Flightless Steamer Duck <i>Tachyeres brachypterus</i> and Patagonian Crested Duck <i>Lophonetta specularioides</i> Sharing a South Atlantic Island. <i>Genes</i> , 2023, 14, 731.	1.0	1
9971	Differences in Soil Microbiota of Continuous Cultivation of <i>Ganoderma leucocontextum</i> . <i>Agronomy</i> , 2023, 13, 888.	1.3	0
9972	Characterization of dysbiosis of the conjunctival microbiome and nasal microbiome associated with allergic rhinoconjunctivitis and allergic rhinitis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
9973	Snow Microorganisms Colonise Arctic Soils Following Snow Melt. <i>Microbial Ecology</i> , 2023, 86, 1661-1675.	1.4	0
9974	An efficient diazotrophâ€derived nitrogen transfer pathway in coral reef system. <i>Limnology and Oceanography</i> , 2023, 68, 963-981.	1.6	2
9975	<i>Brevundimonas</i> and <i>Serratia</i> as host systems for assessing associated environmental viromes and phage diversity by complementary approaches. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
9976	Histological, microecological and transcriptomic physiological responses underlying hypoxia and reoxygenation adaptation in yellowtail kingfish (<i>Seriola lalandi</i>). <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	0
9977	Metabarcoding the zooplankton species of the Saudi Arabian Gulf: A study employing mock communities and two gene markers. <i>Egyptian Journal of Aquatic Research</i> , 2023, , .	1.0	0
9978	<i>Buchnera</i> breaks the specialization of the cotton-specialized aphid (<i>Aphis gossypii</i>) by providing nutrition through zucchini. <i>Frontiers in Nutrition</i> , 0, 10, .	1.6	2
9980	Effect of natural weed and Siratro cover crop on soil fungal diversity in a banana cropping system in southwestern China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9981	Revisiting Microbial Diversity in Hypersaline Microbial Mats from Guerrero Negro for a Better Understanding of Methanogenic Archaeal Communities. <i>Microorganisms</i> , 2023, 11, 812.	1.6	2
9982	Spatial Distribution of airborne bacterial communities in caged poultry houses. <i>Journal of the Air and Waste Management Association</i> , 0, , .	0.9	0
9983	Time-restricted feedingâ€™s effect on overweight and obese patients with chronic kidney disease stages 3-4: A prospective non-randomized control pilot study. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	4
9985	Upper respiratory tract mycobionme alterations in different kinds of pulmonary disease. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
9986	Chromosome-level analysis of the <i>Colletotrichum graminicola</i> genome reveals the unique characteristics of core and minichromosomes. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
9987	The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. <i>Science</i> , 2023, 379, 1238-1242.	6.0	5
9988	Analysis of Fungal Diversity before and after Discoloration of Rubberwood in Xishuangbanna. <i>Diversity</i> , 2023, 15, 471.	0.7	1

#	ARTICLE	IF	CITATIONS
9990	Assembly processes underlying bacterial community differentiation among geographically close mangrove forests. , 2023, 2, 73-88.		3
9991	Diversity of bacterial community in the rhizosphere and bulk soil of <i>Artemisia annua</i> grown in highlands of Uganda. PLoS ONE, 2023, 18, e0269662.	1.1	1
9992	Bidirectional effects of oral anticoagulants on gut microbiota in patients with atrial fibrillation. Frontiers in Cellular and Infection Microbiology, 0, 13, .	1.8	2
9993	Exogenous and Endophytic Fungal Communities of <i>Dendrobium nobile</i> Lindl. across Different Habitats and Their Enhancement of Host Plants's Dendrobine Content and Biomass Accumulation. ACS Omega, 2023, 8, 12489-12500.	1.6	3
9995	Development and Determinants of Topsoil Bacterial and Fungal Communities of Afforestation by Aerial Sowing in Tengger Desert, China. Journal of Fungi (Basel, Switzerland), 2023, 9, 399.	1.5	1
9996	Microbial community structure in rice rhizospheres under drought stress. Journal of Plant Ecology, 2023, 16, .	1.2	3
9997	Seasonal variation of population and individual dietary niche in the avivorous bat, <i>la io</i> . Oecologia, 2023, 201, 733-747.	0.9	4
9998	The cascading effects of submerged macrophyte collapse on geese at Poyang Lake, China. Freshwater Biology, 2023, 68, 926-939.	1.2	0
9999	Effects of Mineral on Taxonomic and Functional Structures of Microbial Community in Tengchong Hot Springs via in-situ cultivation. Environmental Microbiomes, 2023, 18, .	2.2	0
10000	Correlation between the intestinal microflora and peripheral blood Th1/Th2 balance in hypothyroidism during the first half of pregnancy. Frontiers in Cellular and Infection Microbiology, 0, 13, .	1.8	1
10001	Disturbance induces similar shifts in arbuscular mycorrhizal fungal communities from grassland and arable field soils. Mycorrhiza, 0, , .	1.3	0
10002	Antibiotic-Resistant <i>Desulfovibrio</i> Produces H ₂ S from Supplements for Animal Farming. Microorganisms, 2023, 11, 838.	1.6	3
10003	Microbiota diversity, composition and drivers in waxy proso millet sourdoughs of Niandoubao, a traditional fermented cereal food in northeast China. LWT - Food Science and Technology, 2023, 180, 114699.	2.5	1
10004	Effects of dissolved oxygen on intestinal bacterial community and immunity of Atlantic salmon <i>Salmo salar</i> . Journal of Oceanology and Limnology, 2023, 41, 364-375.	0.6	0
10005	Ecological drivers of fine-scale distribution of arbuscular mycorrhizal fungi in a semiarid Mediterranean scrubland. Annals of Botany, 0, , .	1.4	1
10006	Glycoursodeoxycholic acid regulates bile acids level and alters gut microbiota and glycolipid metabolism to attenuate diabetes. Gut Microbes, 2023, 15, .	4.3	8
10007	Metal-Driven Anaerobic Oxidation of Methane as an Important Methane Sink in Methanic Cold Seep Sediments. Microbiology Spectrum, 2023, 11, .	1.2	5
10008	Isolation, identification and spoilage capability of dominant spoilage bacteria on Dezhou-braised chicken with different packaging. LWT - Food Science and Technology, 2023, 182, 114710.	2.5	0

#	ARTICLE	IF	CITATIONS
10009	<i>Klebsiella quasipneumoniae</i> in intestine damages bile acid metabolism in hematopoietic stem cell transplantation patients with bloodstream infection. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	0
10010	Niche Modification by Sulfate-Reducing Bacteria Drives Microbial Community Assembly in Anoxic Marine Sediments. <i>MBio</i> , 0, , .	1.8	1
10011	Determining chromatin architecture with Micro Capture-C. <i>Nature Protocols</i> , 2023, 18, 1687-1711.	5.5	7
10012	Gestational stress and perinatal <scp>SSRIs</scp> differentially impact the maternal and neonatal microbiomeâ€gutâ€brain axis. <i>Journal of Neuroendocrinology</i> , 2023, 35, .	1.2	2
10013	Genome-resolved analyses of oligotrophic groundwater microbial communities along phenol pollution in a continuous-flow biodegradation model system. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
10014	The Gut Microbiota of Broilers Reared with and without Antibiotic Treatment. <i>Microorganisms</i> , 2023, 11, 876.	1.6	1
10015	Biochar improves soil organic carbon stability by shaping the microbial community structures at different soil depths four years after an incorporation in a farmland soil. <i>Current Research in Environmental Sustainability</i> , 2023, 5, 100214.	1.7	4
10016	Mycobiome Study Reveals Different Pathogens of Vulvovaginal Candidiasis Shape Characteristic Vaginal Bacteriome. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
10017	Effect of <i>Limosilactobacillus reuteri</i> ZJF036 on Growth Performance and Gut Microbiota in Juvenile Beagle Dogs. <i>Current Microbiology</i> , 2023, 80, .	1.0	1
10018	Metagenomic analyses of a microbial assemblage in a subglacial lake beneath the Vatnaj�kull ice cap, Iceland. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
10019	Effects of fertilizer reduction coupled with straw returning on soil fertility, wheat root endophytic bacteria, and the occurrence of wheat crown rot. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
10020	Characterization of the oral microbiome and gut microbiome of dental caries and extrinsic black stain in preschool children. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
10021	Microbial diversity and community composition of fecal microbiota in dual-purpose and egg type ducks. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
10022	Aerosol partitioning potential of bacteria presenting antimicrobial resistance from different stages of a small decentralized septic treatment system. <i>Aerosol Science and Technology</i> , 2023, 57, 517-531.	1.5	3
10024	Species diversity of arbuscular mycorrhizal but not ectomycorrhizal plants decreases with habitat loss due to environmental filtering. <i>Plant and Soil</i> , 0, , .	1.8	0
10025	16S rRNA Gene Amplicon Sequencing of the Gut Microbiota of <i>Chimaera phantasma</i> (Silver Chimaera) Captured off Koshimoda in Suruga Bay, Japan. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	1
10026	Gut Microbiota in Children with Hand Foot and Mouth Disease on 16S rRNA Gene Sequencing. <i>Current Microbiology</i> , 2023, 80, .	1.0	0
10027	The impact of culture systems on the gut microbiota and gut metabolome of bighead carp (<i>Hypophthalmichthys nobilis</i>). <i>Animal Microbiome</i> , 2023, 5, .	1.5	1

#	ARTICLE	IF	CITATIONS
10028	Belowground microbiota analysis indicates that <i>Fusarium</i> spp. exacerbate grapevine trunk disease. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	3
10029	Effects of rhizosphere microbiome on the fruit of <i>Cinnamomum migao</i> H. W. Li: culture, amplicon sequencing, and metagenomic sequencing. <i>Horticulture Environment and Biotechnology</i> , 0, , .	0.7	0
10030	Comprehensive genomic analysis of hypocholesterolemic probiotic <i>Enterococcus faecium</i> LR13 reveals unique proteins involved in cholesterol-assimilation. <i>Frontiers in Nutrition</i> , 0, 10, .	1.6	1
10031	Response of the <i>Pardosa astrigera</i> bacterial community to Cry1B protein. <i>Ecotoxicology and Environmental Safety</i> , 2023, 256, 114855.	2.9	1
10032	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. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	3
10033	Spontaneously Produced Lysogenic Phages Are an Important Component of the Soybean <i>Bradyrhizobium</i> Mobilome. <i>MBio</i> , 2023, 14, .	1.8	2
10034	Gut microbiota from sigma-1 receptor knockout mice induces depression-like behaviors and modulates the cAMP/CREB/BDNF signaling pathway. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
10035	A longitudinal study to examine the influence of farming practices and environmental factors on pathogen prevalence using structural equation modeling. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
10036	Lung microbiome and cytokine profiles in different disease states of COPD: a cohort study. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
10037	Potential roles of the rectum keystone microbiota in modulating the microbial community and growth performance in goat model. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	2.1	5
10039	Phylotype resolved spatial variation and association patterns of planktonic Thaumarchaeota in eastern Chinese marginal seas. <i>Marine Life Science and Technology</i> , 2023, 5, 257-270.	1.8	2
10041	Probiotic Effects of <i>Bacillus subtilis</i> on Growth Performance and Intestinal Microecological Balance of Growing-to-Finishing Pigs. <i>Journal of Food Biochemistry</i> , 2023, 2023, 1-16.	1.2	1
10042	Aquafeed fermentation improves dietary nutritional quality and benefits feeding behavior, meat flavor, and intestinal microbiota of Chinese mitten crab (<i>Eriocheir sinensis</i>). <i>Animal Nutrition</i> , 2023, 14, 1-19.	2.1	3
10043	Plant pathogen resistance is mediated by recruitment of specific rhizosphere fungi. <i>ISME Journal</i> , 2023, 17, 931-942.	4.4	5
10044	RIP-PEN-seq identifies a class of kink-turn RNAs as splicing regulators. <i>Nature Biotechnology</i> , 2024, 42, 119-131.	9.4	5
10045	Dark-zone alterations expand throughout Paleolithic Lascaux Cave despite spatial heterogeneity of the cave microbiome. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	3
10046	Short-term effects of mineral and combined mineral-organic fertilization in soil microbial communities. <i>Soil Use and Management</i> , 0, , .	2.6	0
10049	Comprehensive Microbiome and Metabolome Analyses Reveal the Medicinal Components of <i>Paeonia lactiflora</i> . <i>Plants</i> , 2023, 12, 1612.	1.6	4

#	ARTICLE	IF	CITATIONS
10050	Adaptation mechanisms of the soil microbial community under stoichiometric imbalances and nutrient-limiting conditions in a subtropical nitrogen-saturated forest. <i>Plant and Soil</i> , 2023, 489, 239-258.	1.8	4
10051	Bivalves Improved Water Quality by Changing Bacterial Composition in Sediment and Water in an IMTA System. <i>Aquaculture Research</i> , 2023, 2023, 1-17.	0.9	1
10052	First Study on profiling of gut microbiome in wild and captive Sumatran orangutans (<i>Pongo abelii</i>). <i>Veterinary World</i> , 2023, , 717-727.	0.7	1
10053	Sodium butyrate supplementation impacts the gastrointestinal bacteria of dairy calves before weaning. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 3291-3304.	1.7	5
10054	<i>Fusobacterium nucleatum</i> aggravates rheumatoid arthritis through FadA-containing outer membrane vesicles. <i>Cell Host and Microbe</i> , 2023, 31, 798-810.e7.	5.1	10
10055	Dissemination of antibiotic resistance genes from the Pearl River Estuary to adjacent coastal areas. <i>Marine Environmental Research</i> , 2023, 188, 105978.	1.1	1
10056	Commensal Microbiota Regulate Renal Gene Expression in a Sex-Specific Manner. <i>American Journal of Physiology - Renal Physiology</i> , 0, , .	1.3	1
10057	Potassium-rich mining waste addition can shorten the composting period by increasing the abundance of thermophilic bacteria during high-temperature periods. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
10059	Enrichment and response of iron-metabolizing microorganisms and metabolic genes in the contaminated area of stratified stacking coal gangue dumps, Northern China. <i>Environmental Science and Pollution Research</i> , 0, , .	2.7	0
10061	The Potential Roles of Free and Attached Microbial Community in Decreasing Cadmium Level from Cadmium-Contaminated Soils by Mixotrophic Acidophiles of Different Scale-Up Cultivation Stages. <i>Minerals (Basel, Switzerland)</i> , 2023, 13, 546.	0.8	1
10062	Palmitoleic Acid on Top of HFD Ameliorates Insulin Resistance Independent of Diacylglycerols and Alters Gut Microbiota in C57BL/6J Mice. , 2023, , 1-24.		0
10063	Comparative Study of the Effects of Tartary Buckwheat Seed and Sprout Consumption on the Physiological Indices and Gut Microbiota of C57BL/6J Mice. , 2023, , 1-20.		0
10064	Yield and Rhizosphere Soil Environment of Greenhouse Zucchini in Response to Different Planting and Breeding Waste Composts. <i>Microorganisms</i> , 2023, 11, 1026.	1.6	1
10065	Short-term soil amendment by sewage sludge anaerobic digestate in a tomato monoculture suppresses <i>Fusarium</i> vascular wilt disease by changing the taxonomic characteristics of soil microbiota. <i>Applied Soil Ecology</i> , 2023, 189, 104915.	2.1	5
10066	Exploring the fungal communities and their correlation with the physicochemical properties of Zaopocu, a distinctive fermented food on Hainan island. , 0, , .		0
10067	Deep Mutational Scanning of an Oxygen-Independent Fluorescent Protein CreiLOV for Comprehensive Profiling of Mutational and Epistatic Effects. <i>ACS Synthetic Biology</i> , 2023, 12, 1461-1473.	1.9	3
10068	Diversity of endosymbionts in camellia spiny whitefly, <i>Aleurocanthus camelliae</i> (Hemiptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 T <i>Microbiology</i> , 0, 14, .	1.5	1
10070	Free-living bacteria stimulate sugarcane growth traits and edaphic factors along soil depth gradients under contrasting fertilization. <i>Scientific Reports</i> , 2023, 13, .	1.6	2

#	ARTICLE	IF	CITATIONS
10071	Indoleacrylic acid produced by <i>Parabacteroides distasonis</i> alleviates type 2 diabetes via activation of AhR to repair intestinal barrier. <i>BMC Biology</i> , 2023, 21, .	1.7	5
10072	Different grazers and grazing practices alter the growth, soil properties, and rhizosphere soil bacterial communities of <i>Medicago ruthenica</i> in the Qinghai-Tibetan Plateau grassland. <i>Agriculture, Ecosystems and Environment</i> , 2023, 352, 108522.	2.5	4
10074	Microbiomic profiles of bile in patients with benign and malignant pancreaticobiliary disease. <i>PLoS ONE</i> , 2023, 18, e0283021.	1.1	5
10075	Soil bacterial community structure at different plant maturity stages in an annual grass-legume production system. <i>Frontiers in Sustainable Food Systems</i> , 0, 7, .	1.8	1
10076	Metabarcoding of soil environmental DNA to estimate plant diversity globally. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
10077	First mitogenome phylogeny of the sun bear <i>Helarctos malayanus</i> reveals a deep split between Indochinese and Sundaic lineages. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	3
10078	Influence of Companion Planting on Microbial Compositions and Their Symbiotic Network in Pepper Continuous Cropping Soil. <i>Journal of Microbiology and Biotechnology</i> , 2023, 33, 760-770.	0.9	0
10079	State-of-the-art of data analyses in environmental DNA approaches towards its applicability to sustainable fisheries management. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	0
10080	Hydrogen peroxide treatment mitigates antibiotic resistance gene and mobile genetic element propagation in mariculture sediment. <i>Environmental Pollution</i> , 2023, 328, 121652.	3.7	18
10081	Direct correction of haemoglobin E β -thalassaemia using base editors. <i>Nature Communications</i> , 2023, 14, .	5.8	6
10082	Optimization of Electroporation and Adeno-Associated Virus-Mediated Generation of 2.7kb Knock-In Livestock Blastocysts. , 2023, 2, 120-132.		1
10083	Analytical Performance of a Highly Sensitive System to Detect Gene Variants Using Next-Generation Sequencing for Lung Cancer Companion Diagnostics. <i>Diagnostics</i> , 2023, 13, 1476.	1.3	3
10084	Closed aerobic biodegradation kinetics test with activated sludge and low concentration chemical mixtures. <i>Chemosphere</i> , 2023, , 138752.	4.2	1
10085	Effects of the synbiotic composed of mangiferin and <i>Lactobacillus reuteri</i> 12 on type 2 diabetes mellitus rats. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
10086	Alleviation of DSS-induced colitis in mice by a new-isolated <i>Lactobacillus acidophilus</i> C4. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
10089	Application of Wheat Straw Compost Mixed with Chemical Fertilizer Regulates Soil Bacterial Community Diversity in Tea (<i>Camellia sinensis</i>) Plantation. <i>Diversity</i> , 2023, 15, 580.	0.7	0
10090	The number of metabolic syndrome risk factors predicts alterations in gut microbiota in Chinese children from the Huantai study. <i>BMC Pediatrics</i> , 2023, 23, .	0.7	0
10091	Microbiota-mediated nitrogen fixation and microhabitat homeostasis in aerial root-mucilage. <i>Microbiome</i> , 2023, 11, .	4.9	7

#	ARTICLE	IF	CITATIONS
10092	Sustained anaerobic degradation of 4-chloro-2-methylphenoxyacetic acid by acclimated sludge in a continuous-flow reactor. <i>Chemosphere</i> , 2023, 330, 138749.	4.2	1
10093	Structure and Seasonal Variability of Microbial Communities of Groundwater in the City of Moscow. <i>Microbiology</i> , 2023, 92, 192-203.	0.5	0
10095	Microbial Processes of Methane Oxidation at the Kara Sea Sites of Gas Prospecting. <i>Microbiology</i> , 2023, 92, 171-182.	0.5	1
10096	Supplemental enzymes and probiotics on the gut health of broilers fed with a newly harvested corn diet. <i>Poultry Science</i> , 2023, 102, 102740.	1.5	1
10097	Assembly processes of eukaryotic plankton communities in the world's largest drinking water diversion project. <i>Science of the Total Environment</i> , 2023, 884, 163665.	3.9	0
10098	Gut Microbiome Variation Along A Lifestyle Gradient Reveals Threats Faced by Asian Elephants. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 150-163.	3.0	3
10133	A CRISPR/Cas9 Protocol for Target Gene Editing in Barley. <i>Methods in Molecular Biology</i> , 2023, , 287-296.	0.4	1
10424	Application of eDNA metabarcoding for monitoring the fish diversity of the Jiangjin to Fuling section of the upper reaches of the Yangtze River. <i>Hydrobiologia</i> , 0, , .	1.0	0
10490	Analysis of Endophytic Bacterial Diversity in Rice Seeds with Regional Characteristics in Yunnan Province, China, Based on High-Throughput Sequencing Technology. <i>Current Microbiology</i> , 2023, 80, .	1.0	1
10775	Applications of High-Throughput DNA Sequencing to Single-Domain Antibody Discovery and Engineering. <i>Methods in Molecular Biology</i> , 2023, , 489-540.	0.4	0
10795	High Efficiency of Removal of Pathogenic Microorganisms at Wastewater Treatment Plants in the City of Moscow. <i>Microbiology</i> , 2023, 92, 734-738.	0.5	1
11001	The Melody of Silent Mutations: Microbiome Adaptation Across the Subduction Zone. , 2023, , .		0
11115	Seaweed based fertilizer increases abundance of <i>Candidatus nitrosotalea</i> in paddy field soil. <i>AIP Conference Proceedings</i> , 2023, , .	0.3	0
11357	Mixed sowing improves plant and soil bacterial community restoration in the degraded alpine meadow. <i>Plant and Soil</i> , 0, , .	1.8	0
11528	Encoding Genetic Circuits with DNA Barcodes Paves the Way for High-Throughput Profiling of Dose-Response Curves of Metabolite Biosensors. <i>Methods in Molecular Biology</i> , 2024, , 309-318.	0.4	0