phyloseq: An R Package for Reproducible Interactive Ar Census Data

PLoS ONE

8, e61217

DOI: 10.1371/journal.pone.0061217

Citation Report

#	Article	IF	CITATIONS
1	High throughput sequencing methods and analysis for microbiome research. Journal of Microbiological Methods, 2013, 95, 401-414.	1.6	210
2	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	1.0	553
3	Meconium Microbiome Analysis Identifies Bacteria Correlated with Premature Birth. PLoS ONE, 2014, 9, e90784.	2.5	354
4	Biogeochemical Typing of Paddy Field by a Data-Driven Approach Revealing Sub-Systems within a Complex Environment - A Pipeline to Filtrate, Organize and Frame Massive Dataset from Multi-Omics Analyses. PLoS ONE, 2014, 9, e110723.	2.5	22
5	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. PLoS ONE, 2014, 9, e114804.	2.5	110
6	Chemical-biogeographic survey of secondary metabolism in soil. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3757-3762.	7.1	125
7	The Loss of Topography in the Microbial Communities of the Upper Respiratory Tract in the Elderly. Annals of the American Thoracic Society, 2014, 11, 513-521.	3.2	163
8	Waste Not, Want Not: Why Rarefying Microbiome Data Is Inadmissible. PLoS Computational Biology, 2014, 10, e1003531.	3.2	2,343
9	Investigations of potential microbial methanogenic and carbon monoxide utilization pathways in ultra-basic reducing springs associated with present-day continental serpentinization: the Tablelands, NL, CAN. Frontiers in Microbiology, 2014, 5, 613.	3.5	45
10	Rhizosphere heterogeneity shapes abundance and activity of sulfur-oxidizing bacteria in vegetated salt marsh sediments. Frontiers in Microbiology, 2014, 5, 309.	3.5	90
11	Pyrosequencing of supra- and subgingival biofilms from inflamed peri-implant and periodontal sites. BMC Oral Health, 2014, 14, 157.	2.3	58
12	Bacterial community composition of chronic periodontitis and novel oral sampling sites for detecting disease indicators. Microbiome, 2014, 2, 32.	11.1	77
13	Alcohol and tobacco consumption affects bacterial richness in oral cavity mucosa biofilms. BMC Microbiology, 2014, 14, 250.	3.3	71
14	Pyrosequencing reveals higher impact of silver nanoparticles than Ag+ on the microbial community structure of activated sludge. Water Research, 2014, 48, 317-325.	11.3	155
15	Sensitive, Efficient Quantitation of ¹³ C-Enriched Nucleic Acids via Ultrahigh-Performance Liquid Chromatography–Tandem Mass Spectrometry for Applications in Stable Isotope Probing. Applied and Environmental Microbiology, 2014, 80, 7206-7211.	3.1	20
16	Responsiveness of cardiometabolic-related microbiota to diet is influenced by host genetics. Mammalian Genome, 2014, 25, 583-599.	2.2	66
17	Low Temperature Partial Nitritation/Anammox in a Moving Bed Biofilm Reactor Treating Low Strength Wastewater. Environmental Science & Environmental Sc	10.0	319
18	A guide to statistical analysis in microbial ecology: a community-focused, living review of multivariate data analyses. FEMS Microbiology Ecology, 2014, 90, 543-550.	2.7	314

#	Article	IF	CITATIONS
19	Niche partitioning of bacterial communities in biological crusts and soils under grasses, shrubs and trees in the Kalahari. Biodiversity and Conservation, 2014, 23, 1709-1733.	2.6	47
20	Microbial Profiling of Combat Wound Infection through Detection Microarray and Next-Generation Sequencing. Journal of Clinical Microbiology, 2014, 52, 2583-2594.	3.9	47
21	Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. Molecular Ecology, 2014, 23, 3356-3370.	3.9	285
22	Assessing impacts of unconventional natural gas extraction on microbial communities in headwater stream ecosystems in Northwestern Pennsylvania. Frontiers in Microbiology, 2014, 5, 522.	3.5	58
23	Network construction and structure detection with metagenomic count data. BioData Mining, 2015, 8, 40.	4.0	8
24	Impact of a wastewater treatment plant on microbial community composition and function in a hyporheic zone of a eutrophic river. Scientific Reports, 2015, 5, 17284.	3.3	70
25	Habitat fragmentation is associated to gut microbiota diversity of an endangered primate: implications for conservation. Scientific Reports, 2015, 5, 14862.	3.3	170
26	Dietary silver nanoparticles can disturb the gut microbiota in mice. Particle and Fibre Toxicology, 2015, 13, 38.	6.2	133
27	Increased diversity of egg-associated bacteria on brown trout (Salmo trutta) at elevated temperatures. Scientific Reports, 2015, 5, 17084.	3.3	29
28	MICCA: a complete and accurate software for taxonomic profiling of metagenomic data. Scientific Reports, 2015, 5, 9743.	3.3	228
29	Microbial communities on flower surfaces act as signatures of pollinator visitation. Scientific Reports, 2015, 5, 8695.	3.3	80
30	Microbial Community Analysis Using High-Throughput Amplicon Sequencing. , 2015, , 2.4.2-1-2.4.2-26.		4
31	Reverse enGENEering of Regulatory Networks from Big Data: A Roadmap for Biologists. Bioinformatics and Biology Insights, 2015, 9, BBI.S12467.	2.0	38
32	Back to Basics – The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. PLoS ONE, 2015, 10, e0132783.	2.5	437
33	The effect of antibiotics on the microbiome in acute exacerbations of chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2015, 5, 884-893.	2.8	38
34	Microbial ecosystems are dominated by specialist taxa. Ecology Letters, 2015, 18, 974-982.	6.4	74
35	The Microbial Community of a Passive Biochemical Reactor Treating Arsenic, Zinc, and Sulfate-Rich Seepage. Frontiers in Bioengineering and Biotechnology, 2015, 3, 27.	4.1	88
36	The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. Frontiers in Genetics, 2015, 6, 348.	2.3	252

#	Article	IF	CITATIONS
37	Microbial community structure and function on sinking particles in the North Pacific Subtropical Gyre. Frontiers in Microbiology, 2015, 6, 469.	3.5	148
38	Bacterial diversity differences along an epigenic cave stream reveal evidence of community dynamics, succession, and stability. Frontiers in Microbiology, 2015, 6, 729.	3.5	26
39	Soil bacterial and fungal community responses to nitrogen addition across soil depth and microhabitat in an arid shrubland. Frontiers in Microbiology, 2015, 6, 891.	3.5	127
40	Metagenomic analysis of the rumen microbial community following inhibition of methane formation by a halogenated methane analog. Frontiers in Microbiology, 2015, 6, 1087.	3.5	97
41	Actinobacterial Diversity in Volcanic Caves and Associated Geomicrobiological Interactions. Frontiers in Microbiology, 2015, 6, 1342.	3.5	99
42	Bacterial Composition and Survival on Sahara Dust Particles Transported to the European Alps. Frontiers in Microbiology, 2015, 6, 1454.	3.5	77
43	Bacterial and Fungal Communities in a Degraded Ombrotrophic Peatland Undergoing Natural and Managed Re-Vegetation. PLoS ONE, 2015, 10, e0124726.	2.5	57
44	Chronic Trichuris muris Infection Decreases Diversity of the Intestinal Microbiota and Concomitantly Increases the Abundance of Lactobacilli. PLoS ONE, 2015, 10, e0125495.	2.5	190
45	Pyrosequencing Characterization of the Microbiota from Atlantic Intertidal Marine Sponges Reveals High Microbial Diversity and the Lack of Co-Occurrence Patterns. PLoS ONE, 2015, 10, e0127455.	2.5	34
46	Assessment of Zooplankton Community Composition along a Depth Profile in the Central Red Sea. PLoS ONE, 2015, 10, e0133487.	2.5	30
47	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. PLoS ONE, 2015, 10, e0142825.	2.5	84
48	Oral Microbiota and Risk for Esophageal Squamous Cell Carcinoma in a High-Risk Area of China. PLoS ONE, 2015, 10, e0143603.	2.5	146
49	Variability of Symbiodinium Communities in Waters, Sediments, and Corals of Thermally Distinct Reef Pools in American Samoa. PLoS ONE, 2015, 10, e0145099.	2.5	81
50	Navigating the labyrinth: a guide to sequenceâ€based, community ecology of arbuscular mycorrhizal fungi. New Phytologist, 2015, 207, 235-247.	7.3	106
51	Microbial biogeography of the transnational fermented milk matsoni. Food Microbiology, 2015, 50, 12-19.	4.2	47
52	Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. Bioinformatics and Biology Insights, 2015, 9, BBI.S12462.	2.0	317
53	Global biogeographic sampling of bacterial secondary metabolism. ELife, 2015, 4, e05048.	6.0	117
54	Long-term forest soil warming alters microbial communities in temperate forest soils. Frontiers in Microbiology, 2015, 6, 104.	3.5	270

#	Article	IF	CITATIONS
55	Shifts in the phylogenetic structure of arbuscular mycorrhizal fungi in response to experimental nitrogen and carbon dioxide additions. Oecologia, 2015, 179, 175-185.	2.0	26
56	Soil microbial community structure is unaltered by plant invasion, vegetation clipping, and nitrogen fertilization in experimental semi-arid grasslands. Frontiers in Microbiology, 2015, 6, 466.	3.5	73
57	Seasonal diversity and dynamics of haptophytes in the <scp>S</scp> kagerrak, <scp>N</scp> orway, explored by highâ€throughput sequencing. Molecular Ecology, 2015, 24, 3026-3042.	3.9	90
58	Increased efficiency in identifying mixed pollen samples by meta-barcoding with a dual-indexing approach. BMC Ecology, 2015, 15, 20.	3.0	167
59	Combined amendment of immobilizers and the plant growth-promoting strain Burkholderia phytofirmans PsJN favours plant growth and reduces heavy metal uptake. Soil Biology and Biochemistry, 2015, 91, 140-150.	8.8	88
60	Bayesian nonparametric inference for shared species richness in multiple populations. Journal of Statistical Planning and Inference, 2015, 166, 14-23.	0.6	2
61	Seed: a user-friendly tool for exploring and visualizing microbial community data. Bioinformatics, 2015, 31, 602-603.	4.1	7
62	Association of Shifting Populations in the Root Zone Microbiome of Millet with Enhanced Crop Productivity in the Sahel Region (Africa). Applied and Environmental Microbiology, 2015, 81, 2841-2851.	3.1	41
63	Culture and molecular-based profiles show shifts in bacterial communities of the upper respiratory tract that occur with age. ISME Journal, 2015, 9, 1246-1259.	9.8	165
64	Metagenomic Analysis of the Airborne Environment in Urban Spaces. Microbial Ecology, 2015, 69, 346-355.	2.8	76
65	Testing the coâ€invasion hypothesis: ectomycorrhizal fungal communities on ⟨i>Alnus glutinosa⟨/i> and ⟨i>Salix fragilis⟨/i> in New Zealand. Diversity and Distributions, 2015, 21, 268-278.	4.1	65
66	Respiratory microbiota: addressing clinical questions, informing clinical practice. Thorax, 2015, 70, 74-81.	5.6	75
67	Distinct composition signatures of archaeal and bacterial phylotypes in the Wanda Glacier forefield, Antarctic Peninsula. FEMS Microbiology Ecology, 2015, 91, 1-10.	2.7	55
68	Ammonia and temperature determine potential clustering in the anaerobic digestion microbiome. Water Research, 2015, 75, 312-323.	11.3	276
69	Microbiota and host determinants of behavioural phenotype in maternally separated mice. Nature Communications, 2015, 6, 7735.	12.8	372
70	Efficient anaerobic transformation of raw wheat straw by a robust cow rumen-derived microbial consortium. Bioresource Technology, 2015, 196, 241-249.	9.6	45
71	Shiny-phyloseq: Web application for interactive microbiome analysis with provenance tracking. Bioinformatics, 2015, 31, 282-283.	4.1	131
72	Biological control in the microbiome era: Challenges and opportunities. Biological Control, 2015, 89, 98-108.	3.0	145

#	Article	IF	CITATIONS
73	Inner workings of thrombolites: spatial gradients of metabolic activity as revealed by metatranscriptome profiling. Scientific Reports, 2015, 5, 12601.	3.3	48
74	Microbial community composition and diversity in Caspian Sea sediments. FEMS Microbiology Ecology, 2015, 91, 1-11.	2.7	70
75	Propane biostimulation in biologically activated carbon (BAC) selects for bacterial clades adept at degrading persistent water pollutants. Environmental Sciences: Processes and Impacts, 2015, 17, 1405-1414.	3.5	9
76	Proton Pump Inhibitors Alter Specific Taxa in the Human Gastrointestinal Microbiome: A Crossover Trial. Gastroenterology, 2015, 149, 883-885.e9.	1.3	268
77	phylogeo: an R package for geographic analysis and visualization of microbiome data. Bioinformatics, 2015, 31, 2909-2911.	4.1	20
78	Patterns and Determinants of Halophilic Archaea (Class Halobacteria) Diversity in Tunisian Endorheic Salt Lakes and Sebkhet Systems. Applied and Environmental Microbiology, 2015, 81, 4432-4441.	3.1	35
79	Deciphering chicken gut microbial dynamics based on high-throughput 16S rRNA metagenomics analyses. Gut Pathogens, 2015, 7, 4.	3.4	230
80	Perturbation and restoration of the fathead minnow gut microbiome after low-level triclosan exposure. Microbiome, 2015, 3, 6.	11.1	134
81	Multiplexed metagenome mining using short DNA sequence tags facilitates targeted discovery of epoxyketone proteasome inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4221-4226.	7.1	104
82	Two decades of warming increases diversity of a potentially lignolytic bacterial community. Frontiers in Microbiology, 2015, 6, 480.	3.5	73
83	Power and sample-size estimation for microbiome studies using pairwise distances and PERMANOVA. Bioinformatics, 2015, 31, 2461-2468.	4.1	326
84	Declining diversity of egg-associated bacteria during development of naturally spawned whitefish embryos (Coregonus spp.). Aquatic Sciences, 2015, 77, 481-497.	1.5	17
85	Fecal Microbiota Transplantation Induces Remission in Patients With Active Ulcerative Colitis in a Randomized Controlled Trial. Gastroenterology, 2015, 149, 102-109.e6.	1.3	1,161
86	The bacterial communities associated with fecal types and body weight of rex rabbits. Scientific Reports, 2015, 5, 9342.	3.3	115
87	Early infancy microbial and metabolic alterations affect risk of childhood asthma. Science Translational Medicine, 2015, 7, 307ra152.	12.4	1,277
88	Effect of Whole-Grain Barley on the Human Fecal Microbiota and Metabolome. Applied and Environmental Microbiology, 2015, 81, 7945-7956.	3.1	120
89	Antibiotics in neonatal life increase murine susceptibility to experimental psoriasis. Nature Communications, 2015, 6, 8424.	12.8	135
90	Republished: Respiratory microbiota: addressing clinical questions, informing clinical practice. Postgraduate Medical Journal, 2015, 91, 463-470.	1.8	1

#	Article	IF	CITATIONS
91	Impact of urine and the application of the nitrification inhibitor DCD on microbial communities in dairy-grazed pasture soils. Soil Biology and Biochemistry, 2015, 88, 344-353.	8.8	26
92	Earlyâ€life establishment of the swine gut microbiome and impact on host phenotypes. Environmental Microbiology Reports, 2015, 7, 554-569.	2.4	320
93	Microhabitat heterogeneity across leaves and flower organs promotes bacterial diversity. FEMS Microbiology Ecology, 2015, 91, fiv097.	2.7	97
94	Feeding on microbiomes: effects of detritivory on the taxonomic and phylogenetic bacterial composition of animal manures. FEMS Microbiology Ecology, 2015, 91, fiv117.	2.7	53
95	Limited dissemination of the wastewater treatment plant core resistome. Nature Communications, 2015, 6, 8452.	12.8	173
96	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. BMC Medical Genomics, 2015, 8, 50.	1.5	63
97	Intestinal Microbiota Modulates Gluten-Induced Immunopathology in Humanized Mice. American Journal of Pathology, 2015, 185, 2969-2982.	3.8	106
98	Temporal and spatial variation of the human microbiota during pregnancy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11060-11065.	7.1	876
99	Humanized microbiota mice as a model of recurrent Clostridium difficile disease. Microbiome, 2015, 3, 35.	11.1	68
100	Gut Microbial Dysbiosis Due toHelicobacterDrives an Increase in Marginal Zone B Cells in the Absence of IL-10 Signaling in Macrophages. Journal of Immunology, 2015, 195, 3071-3085.	0.8	21
101	Dynamics of an experimental microbial invasion. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11594-11599.	7.1	56
102	Pregnancy-related changes in the maternal gut microbiota are dependent upon the mother's periconceptional diet. Gut Microbes, 2015, 6, 310-320.	9.8	161
103	An improved method to set significance thresholds for $\langle i \rangle \hat{l}^2 \langle i \rangle$ diversity testing in microbial community comparisons. Environmental Microbiology, 2015, 17, 3154-3167.	3.8	6
104	The current provided by oxygen-reducing microbial cathodes is related to the composition of their bacterial community. Bioelectrochemistry, 2015, 102, 42-49.	4.6	40
105	Towards a better understanding of <i><scp>A</scp>pis mellifera</i> and <i><scp>V</scp>arroa destructor</i> microbiomes: introducing â€~ <scp>phyloh</scp> ' as a novel phylogenetic diversity analysis tool. Molecular Ecology Resources, 2015, 15, 697-710.	4.8	17
106	Longâ€term balanced fertilization increases the soil microbial functional diversity in a phosphorusâ€limited paddy soil. Molecular Ecology, 2015, 24, 136-150.	3.9	197
107	Species specificity of symbiosis and secondary metabolism in ascidians. ISME Journal, 2015, 9, 615-628.	9.8	85
108	Endophytic Microbiota Associated with the Root Tips and Leaves of Baccharis dracunculifolia. Brazilian Archives of Biology and Technology, 2016, 59, .	0.5	7

#	Article	IF	CITATIONS
109	Soil bacterial community and functional shifts in response to altered snowpack in moist acidic tundra of northern Alaska. Soil, 2016, 2, 459-474.	4.9	20
110	Smoking Cessation and the Microbiome in Induced Sputum Samples from Cigarette Smoking Asthma Patients. PLoS ONE, 2016, 11, e0158622.	2.5	24
111	Methanogen Diversity in Indigenous and Introduced Ruminant Species on the Tibetan Plateau. Archaea, 2016, 2016, 1-10.	2.3	43
112	Characterisation of the human uterine microbiome in non-pregnant women through deep sequencing of the V1-2 region of the 16S rRNA gene. PeerJ, 2016, 4, e1602.	2.0	217
113	Bioconductor Workflow for Microbiome Data Analysis: from raw reads to community analyses. F1000Research, 2016, 5, 1492.	1.6	664
114	16S rRNA amplicon sequencing identifies microbiota associated with oral cancer, human papilloma virus infection and surgical treatment. Oncotarget, 2016, 7, 51320-51334.	1.8	237
115	Gut Microbial Alterations Associated With Protection From Autoimmune Uveitis., 2016, 57, 3747.		156
116	Diversity and Temporal Dynamics of the Epiphytic Bacterial Communities Associated with the Canopy-Forming Seaweed Cystoseira compressa (Esper) Gerloff and Nizamuddin. Frontiers in Microbiology, 2016, 7, 476.	3.5	112
117	Does the Urinary Microbiome Play a Role in Urgency Urinary Incontinence and Its Severity?. Frontiers in Cellular and Infection Microbiology, 2016, 6, 78.	3.9	224
118	Tissue-Associated Bacterial Alterations in Rectal Carcinoma Patients Revealed by 16S rRNA Community Profiling. Frontiers in Cellular and Infection Microbiology, 2016, 6, 179.	3.9	125
119	Microbiome Analysis Across a Natural Copper Gradient at a Proposed Northern Canadian Mine Site. Frontiers in Environmental Science, 2016, 3, .	3.3	8
120	Short-Term Rhizosphere Effect on Available Carbon Sources, Phenanthrene Degradation, and Active Microbiome in an Aged-Contaminated Industrial Soil. Frontiers in Microbiology, 2016, 7, 92.	3.5	69
121	Biogeochemical and Microbial Variation across 5500 km of Antarctic Surface Sediment Implicates Organic Matter as a Driver of Benthic Community Structure. Frontiers in Microbiology, 2016, 7, 284.	3.5	57
122	Associations between Ectomycorrhizal Fungi and Bacterial Needle Endophytes in Pinus radiata: Implications for Biotic Selection of Microbial Communities. Frontiers in Microbiology, 2016, 7, 399.	3.5	21
123	Development of Ruminal and Fecal Microbiomes Are Affected by Weaning But Not Weaning Strategy in Dairy Calves. Frontiers in Microbiology, 2016, 7, 582.	3.5	148
124	Seasonal Succession Leads to Habitat-Dependent Differentiation in Ribosomal RNA:DNA Ratios among Freshwater Lake Bacteria. Frontiers in Microbiology, 2016, 7, 606.	3.5	37
125	Unearthing the Ecology of Soil Microorganisms Using a High Resolution DNA-SIP Approach to Explore Cellulose and Xylose Metabolism in Soil. Frontiers in Microbiology, 2016, 7, 703.	3.5	154
126	A Novel Treatment Protects Chlorella at Commercial Scale from the Predatory Bacterium Vampirovibrio chlorellavorus. Frontiers in Microbiology, 2016, 7, 848.	3.5	47

#	Article	IF	CITATIONS
127	Epimicrobiota Associated with the Decay and Recovery of Orbicella Corals Exhibiting Dark Spot Syndrome. Frontiers in Microbiology, 2016, 7, 893.	3.5	41
128	Microbial Community Responses to Increased Water and Organic Matter in the Arid Soils of the McMurdo Dry Valleys, Antarctica. Frontiers in Microbiology, 2016, 7, 1040.	3.5	59
129	Methane Inhibition Alters the Microbial Community, Hydrogen Flow, and Fermentation Response in the Rumen of Cattle. Frontiers in Microbiology, 2016, 7, 1122.	3.5	97
130	Age and Gender Affect the Composition of Fungal Population of the Human Gastrointestinal Tract. Frontiers in Microbiology, 2016, 7, 1227.	3.5	170
131	Chronic Polyaromatic Hydrocarbon (PAH) Contamination Is a Marginal Driver for Community Diversity and Prokaryotic Predicted Functioning in Coastal Sediments. Frontiers in Microbiology, 2016, 7, 1303.	3.5	39
132	From Mouth to Model: Combining in vivo and in vitro Oral Biofilm Growth. Frontiers in Microbiology, 2016, 7, 1448.	3.5	25
133	Niche Filtering of Bacteria in Soil and Rock Habitats of the Colorado Plateau Desert, Utah, USA. Frontiers in Microbiology, 2016, 7, 1489.	3.5	51
134	Physical Factors Correlate to Microbial Community Structure and Nitrogen Cycling Gene Abundance in a Nitrate Fed Eutrophic Lagoon. Frontiers in Microbiology, 2016, 7, 1691.	3.5	17
135	Seasonal Succession of Free-Living Bacterial Communities in Coastal Waters of the Western Antarctic Peninsula. Frontiers in Microbiology, 2016, 7, 1731.	3.5	53
136	Rapid Fermentable Substance Modulates Interactions between Ruminal Commensals and Toll-Like Receptors in Promotion of Immune Tolerance of Goat Rumen. Frontiers in Microbiology, 2016, 7, 1812.	3.5	57
137	Diazotroph Diversity in the Sea Ice, Melt Ponds, and Surface Waters of the Eurasian Basin of the Central Arctic Ocean. Frontiers in Microbiology, 2016, 7, 1884.	3.5	39
138	Microbial Communities of Lycaenid Butterflies Do Not Correlate with Larval Diet. Frontiers in Microbiology, 2016, 7, 1920.	3.5	75
139	Effect of Saccharomyces boulardii and Mode of Delivery on the Early Development of the Gut Microbial Community in Preterm Infants. PLoS ONE, 2016, 11, e0150306.	2.5	29
140	Evaluation of Lysis Methods for the Extraction of Bacterial DNA for Analysis of the Vaginal Microbiota. PLoS ONE, 2016, 11, e0163148.	2.5	67
141	Assessment of the Microbial Constituents of the Home Environment of Individuals with Cystic Fibrosis (CF) and Their Association with Lower Airways Infections. PLoS ONE, 2016, 11, e0148534.	2.5	34
142	Impact of the Chromatin Remodeling Factor CHD1 on Gut Microbiome Composition of Drosophila melanogaster. PLoS ONE, 2016, 11, e0153476.	2.5	11
143	Phenylketonuria and Gut Microbiota: A Controlled Study Based on Next-Generation Sequencing. PLoS ONE, 2016, 11, e0157513.	2.5	52
144	Microbes on a Bottle: Substrate, Season and Geography Influence Community Composition of Microbes Colonizing Marine Plastic Debris. PLoS ONE, 2016, 11, e0159289.	2.5	403

#	Article	IF	CITATIONS
145	Data Mining of Lung Microbiota in Cystic Fibrosis Patients. PLoS ONE, 2016, 11, e0164510.	2.5	20
146	Host-Microbiome Interaction and Cancer: Potential Application in Precision Medicine. Frontiers in Physiology, 2016, 7, 606.	2.8	40
147	Leaf Treatments with a Protein-Based Resistance Inducer Partially Modify Phyllosphere Microbial Communities of Grapevine. Frontiers in Plant Science, 2016, 7, 1053.	3.6	20
148	Rhizospheric Bacterial Community of Endemic Rhododendron arboreum Sm. Ssp. delavayi along Eastern Himalayan Slope in Tawang. Frontiers in Plant Science, 2016, 07, 1345.	3.6	14
149	Exploring the cockatiel (<i>Nymphicus hollandicus</i>) fecal microbiome, bacterial inhabitants of a worldwide pet. PeerJ, 2016, 4, e2837.	2.0	22
150	Characterization of the gut microbiota of migratory passerines during stopover along the northern coast of the Gulf of Mexico. Journal of Avian Biology, 2016, 47, 659-668.	1.2	66
151	Diversity analysis of sulfite―and sulfateâ€reducing microorganisms by multiplex <i>dsrA</i> and <i>dsrB</i> amplicon sequencing using new primers and mock communityâ€optimized bioinformatics. Environmental Microbiology, 2016, 18, 2994-3009.	3.8	98
152	Differential Functional Constraints Cause Strain-Level Endemism in <i>Polynucleobacter</i> Populations. MSystems, 2016, 1, .	3.8	18
153	Effects of Specimen Collection Methodologies and Storage Conditions on the Short-Term Stability of Oral Microbiome Taxonomy. Applied and Environmental Microbiology, 2016, 82, 5519-5529.	3.1	30
154	The role of tissueâ€specific microbiota in initial establishment success of <scp>P</scp> acific oysters. Environmental Microbiology, 2016, 18, 970-987.	3.8	107
155	Interaction between lithification and resource availability in the microbialites of RÃo Mesquites, Cuatro CiÃ@negas, MÃ@xico. Geobiology, 2016, 14, 176-189.	2.4	19
156	Copiotrophic marine bacteria are associated with strong ironâ€binding ligand production during phytoplankton blooms. Limnology and Oceanography Letters, 2016, 1, 36-43.	3.9	25
157	Mucosa-Associated Ileal Microbiota in New-Onset Pediatric Crohn $\hat{E}^{1}\!\!/\!\!4$ s Disease. Inflammatory Bowel Diseases, 2016, 22, 1533-1539.	1.9	43
158	Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. Scientific Reports, 2016, 6, 33430.	3.3	25
159	Roux-en-Y gastric bypass surgery of morbidly obese patients induces swift and persistent changes of the individual gut microbiota. Genome Medicine, 2016, 8, 67.	8.2	260
160	Temporal bacterial and metabolic development of the preterm gut reveals specific signatures in health and disease. Microbiome, 2016, 4, 67.	11.1	135
161	Maternal effects and <i>Symbiodinium</i> community composition drive differential patterns in juvenile survival in the coral <i>Acropora tenuis</i> . Royal Society Open Science, 2016, 3, 160471.	2.4	86
162	A randomised, controlled, crossover study of the effect of diet on angiopoietin-like protein 4 (ANGPTL4) through modification of the gut microbiome. Journal of Nutritional Science, 2016, 5, e45.	1.9	16

#	ARTICLE	IF	Citations
163	The Genetic Basis of Natural Variation in <i>Caenorhabditis elegans</i> Telomere Length. Genetics, 2016, 204, 371-383.	2.9	117
164	Calypso: a user-friendly web-server for mining and visualizing microbiome–environment interactions. Bioinformatics, 2017, 33, 782-783.	4.1	627
165	Large-scale benchmarking reveals false discoveries and count transformation sensitivity in 16S rRNA gene amplicon data analysis methods used in microbiome studies. Microbiome, 2016, 4, 62.	11.1	138
166	SSUnique: Detecting Sequence Novelty in Microbiome Surveys. MSystems, 2016, 1, .	3.8	4
167	Phylogenetic and functional potential links pH and N2O emissions in pasture soils. Scientific Reports, 2016, 6, 35990.	3.3	67
168	Redox Conditions Alter Biodegradation Rates and Microbial Community Dynamics of Hydraulic Fracturing Fluid Organic Additives in Soil–Groundwater Microcosms. Environmental Engineering Science, 2016, 33, 827-838.	1.6	28
169	Exploring the methanogen and bacterial communities of rumen environments: solid adherent, fluid and epimural. FEMS Microbiology Ecology, 2017, 93, fiw251.	2.7	83
170	The human milk oligosaccharide $2\hat{a} \in \mathbb{R}^2$ -fucosyllactose attenuates the severity of experimental necrotising enterocolitis by enhancing mesenteric perfusion in the neonatal intestine. British Journal of Nutrition, 2016, 116, 1175-1187.	2.3	145
171	Acetylcholine-producing T cells in the intestine regulate antimicrobial peptide expression and microbial diversity. American Journal of Physiology - Renal Physiology, 2016, 311, G920-G933.	3.4	40
172	Presence does not imply activity: DNA and RNA patterns differ in response to salt perturbation in anaerobic digestion. Biotechnology for Biofuels, 2016, 9, 244.	6.2	81
173	The developing hypopharyngeal microbiota in early life. Microbiome, 2016, 4, 70.	11.1	46
174	Influence of maternal breast milk ingestion on acquisition of the intestinal microbiome in preterm infants. Microbiome, 2016, 4, 68.	11.1	155
175	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. Gut, 2016, 65, 1681-1689.	12.1	312
176	A distinct and active bacterial community in cold oxygenated fluids circulating beneath the western flank of the Mid-Atlantic ridge. Scientific Reports, 2016, 6, 22541.	3.3	62
177	Skin microbiome in melanomas and melanocytic nevi. European Journal of Dermatology, 2016, 26, 49-55.	0.6	26
178	Resilient microorganisms in dust samples of the International Space Stationâ€"survival of the adaptation specialists. Microbiome, 2016, 4, 65.	11.1	69
179	Bacterial and protist community changes during a phytoplankton bloom. Limnology and Oceanography, 2016, 61, 198-213.	3.1	22
180	The Truffle Microbiome: Species and Geography Effects on Bacteria Associated with Fruiting Bodies of Hypogeous Pezizales. Microbial Ecology, 2016, 72, 4-8.	2.8	94

#	Article	IF	CITATIONS
181	Extracellular DNA amplicon sequencing reveals high levels of benthic eukaryotic diversity in the central Red Sea. Marine Genomics, 2016, 26, 29-39.	1.1	17
182	Dynamic changes in microbiota and mycobiota during spontaneous â€~ <scp>V</scp> ino <scp>S</scp> anto <scp>T</scp> rentino' fermentation. Microbial Biotechnology, 2016, 9, 195-208.	4.2	52
183	Metagenomic analysis between free-living and cultured Epinephelus fuscoguttatus under different environmental conditions in Indonesian waters. Marine Pollution Bulletin, 2016, 110, 726-734.	5.0	19
184	Microbiome profiling of drinking water in relation to incidence of inflammatory bowel disease. Canadian Journal of Microbiology, 2016, 62, 781-793.	1.7	12
185	Evolution of the nasopharyngeal microbiota of beef cattle from weaning to 40 days after arrival at a feedlot. Veterinary Microbiology, 2016, 187, 75-81.	1.9	70
186	High-rate activated sludge communities have a distinctly different structure compared to low-rate sludge communities, and are less sensitive towards environmental and operational variables. Water Research, 2016, 100, 137-145.	11.3	62
187	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. ISME Journal, 2016, 10, 2352-2364.	9.8	62
188	Biocathodes reducing oxygen at high potential select biofilms dominated by Ectothiorhodospiraceae populations harboring a specific association of genes. Bioresource Technology, 2016, 214, 55-62.	9.6	19
189	Oceanic fronts: transition zones for bacterioplankton community composition. Environmental Microbiology Reports, 2016, 8, 132-138.	2.4	65
190	Exploring soil microbial 16S <scp>rRNA</scp> sequence data to increase carbon yield and nitrogen efficiency of a bioenergy crop. GCB Bioenergy, 2016, 8, 867-879.	5.6	66
191	Selection of fungi by candidate cover crops. Applied Soil Ecology, 2016, 103, 72-82.	4.3	39
192	Unique microbial-derived volatile organic compounds in portal venous circulation in murine non-alcoholic fatty liver disease. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2016, 1862, 1337-1344.	3.8	20
193	Microbiome analysis and detection of pathogenic bacteria of Penaeus monodon from Jakarta Bay and Bali. Marine Pollution Bulletin, 2016, 110, 718-725.	5.0	22
194	Respiratory syncytial virus and rhinovirus severe bronchiolitis are associated with distinct nasopharyngeal microbiota. Journal of Allergy and Clinical Immunology, 2016, 137, 1909-1913.e4.	2.9	82
195	Microbial-Derived Metabolites Reflect an Altered Intestinal Microbiota during Catch-Up Growth in Undernourished Neonatal Mice. Journal of Nutrition, 2016, 146, 940-948.	2.9	19
196	A humanized microbiota mouse model of ovalbumin-induced lung inflammation. Gut Microbes, 2016, 7, 342-352.	9.8	35
197	A Pathogen-Selective Antibiotic Minimizes Disturbance to the Microbiome. Antimicrobial Agents and Chemotherapy, 2016, 60, 4264-4273.	3.2	42
198	Effect of long-term application of agrotechnical techniques and crops on soil microbial communities. Microbiology, 2016, 85, 231-242.	1.2	5

#	Article	IF	CITATIONS
199	Depletion of regulatory T cells leads to an exacerbation of delayed-type hypersensitivity arthritis in C57BL/6 mice that can be counteracted by IL-17 blockade. DMM Disease Models and Mechanisms, 2016, 9, 427-40.	2.4	10
200	High-throughput sequencing of 16S rRNA Gene Reveals Substantial Bacterial Diversity on the Municipal Dumpsite. BMC Microbiology, 2016, 16, 145.	3.3	34
201	Dietary fat drives whole-body insulin resistance and promotes intestinal inflammation independent of body weight gain. Metabolism: Clinical and Experimental, 2016, 65, 1706-1719.	3.4	22
202	Impacts of coal ash on methylmercury production and the methylating microbial community in anaerobic sediment slurries. Environmental Sciences: Processes and Impacts, 2016, 18, 1427-1439.	3.5	12
203	Urine Bacterial Community Convergence through Fertilizer Production: Storage, Pasteurization, and Struvite Precipitation. Environmental Science & Eamp; Technology, 2016, 50, 11619-11626.	10.0	42
204	Diet may influence the oral microbiome composition in cats. Microbiome, 2016, 4, 23.	11.1	43
205	Urban greenness influences airborne bacterial community composition. Science of the Total Environment, 2016, 571, 680-687.	8.0	137
206	A Pleiotropic Missense Variant in SLC39A8 Is Associated With Crohn's Disease and Human Gut Microbiome Composition. Gastroenterology, 2016, 151, 724-732.	1.3	109
207	Effects of host genetics and environment on eggâ€associated microbiotas in brown trout (<i>Salmo) Tj ETQq0</i>	O O ggBT /C	verlock 10 Tf
208	Effects of environmental conditions on aerobic degradation of a commercial naphthenic acid. Chemosphere, 2016, 161, 491-500.	8.2	9
208	Effects of environmental conditions on aerobic degradation of a commercial naphthenic acid. Chemosphere, 2016, 161, 491-500. SHPâ€2 Phosphatase Prevents Colonic Inflammation by Controlling Secretory Cell Differentiation and Maintaining Hostâ€Microbiota Homeostasis. Journal of Cellular Physiology, 2016, 231, 2529-2540.	8.2	9
	Chemosphere, 2016, 161, 491-500. SHPâ€2 Phosphatase Prevents Colonic Inflammation by Controlling Secretory Cell Differentiation and		
209	Chemosphere, 2016, 161, 491-500. SHPâ€2 Phosphatase Prevents Colonic Inflammation by Controlling Secretory Cell Differentiation and Maintaining Hostâ€Microbiota Homeostasis. Journal of Cellular Physiology, 2016, 231, 2529-2540. Response of diatomâ€associated bacteria to host growth state, nutrient concentrations, and viral host	4.1	21
209	Chemosphere, 2016, 161, 491-500. SHPâ€2 Phosphatase Prevents Colonic Inflammation by Controlling Secretory Cell Differentiation and Maintaining Hostâ€Microbiota Homeostasis. Journal of Cellular Physiology, 2016, 231, 2529-2540. Response of diatomâ€associated bacteria to host growth state, nutrient concentrations, and viral host infection in a model system. Environmental Microbiology Reports, 2016, 8, 917-927. Grapevine (Vitis vinifera) Crown Galls Host Distinct Microbiota. Applied and Environmental	4.1 2.4	21
209 210 211	Chemosphere, 2016, 161, 491-500. SHPâ€2 Phosphatase Prevents Colonic Inflammation by Controlling Secretory Cell Differentiation and Maintaining Hostâ€Microbiota Homeostasis. Journal of Cellular Physiology, 2016, 231, 2529-2540. Response of diatomâ€associated bacteria to host growth state, nutrient concentrations, and viral host infection in a model system. Environmental Microbiology Reports, 2016, 8, 917-927. Grapevine (Vitis vinifera) Crown Galls Host Distinct Microbiota. Applied and Environmental Microbiology, 2016, 82, 5542-5552. Sedimentary DNA Reveals Cyanobacterial Community Diversity over 200 Years in Two Perialpine Lakes.	4.1 2.4 3.1	21 15 62
209 210 211 212	Chemosphere, 2016, 161, 491-500. SHPâ€2 Phosphatase Prevents Colonic Inflammation by Controlling Secretory Cell Differentiation and Maintaining Hostâ€Microbiota Homeostasis. Journal of Cellular Physiology, 2016, 231, 2529-2540. Response of diatomâ€essociated bacteria to host growth state, nutrient concentrations, and viral host infection in a model system. Environmental Microbiology Reports, 2016, 8, 917-927. Grapevine (Vitis vinifera) Crown Galls Host Distinct Microbiota. Applied and Environmental Microbiology, 2016, 82, 5542-5552. Sedimentary DNA Reveals Cyanobacterial Community Diversity over 200 Years in Two Perialpine Lakes. Applied and Environmental Microbiology, 2016, 82, 6472-6482. Effect of Wild and Cultivated Rice Genotypes on Rhizosphere Bacterial Community Composition. Rice,	4.1 2.4 3.1 3.1	21 15 62 75
209 210 211 212 213	Chemosphere, 2016, 161, 491-500. SHPâ€2 Phosphatase Prevents Colonic Inflammation by Controlling Secretory Cell Differentiation and Maintaining Hostâ€Microbiota Homeostasis. Journal of Cellular Physiology, 2016, 231, 2529-2540. Response of diatomâ€associated bacteria to host growth state, nutrient concentrations, and viral host infection in a model system. Environmental Microbiology Reports, 2016, 8, 917-927. Grapevine (Vitis vinifera) Crown Galls Host Distinct Microbiota. Applied and Environmental Microbiology, 2016, 82, 5542-5552. Sedimentary DNA Reveals Cyanobacterial Community Diversity over 200 Years in Two Perialpine Lakes. Applied and Environmental Microbiology, 2016, 82, 6472-6482. Effect of Wild and Cultivated Rice Genotypes on Rhizosphere Bacterial Community Composition. Rice, 2016, 9, 42.	4.1 2.4 3.1 4.0	21 15 62 75

#	Article	IF	CITATIONS
217	Urban park soil microbiomes are a rich reservoir of natural product biosynthetic diversity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14811-14816.	7.1	89
218	Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. Nature Communications, 2016, 7, 12151.	12.8	754
219	Effects of exposure to bisphenol A and ethinyl estradiol on the gut microbiota of parents and their offspring in a rodent model. Gut Microbes, 2016, 7, 471-485.	9.8	121
220	Spatiotemporal distribution of bacterioplankton functional groups along a freshwater estuary to pelagic gradient in Lake Michigan. Journal of Great Lakes Research, 2016, 42, 1036-1048.	1.9	29
221	Differences in CD8 $\hat{l}\pm\hat{l}\pm$ and cecal microbiome community during proliferation and late cytolytic phases of Marek's disease virus infection are associated with genetic resistance to Marek's disease. FEMS Microbiology Ecology, 2016, 92, fiw188.	2.7	17
222	Rare Taxa Maintain Microbial Diversity and Contribute to Terrestrial Community Dynamics throughout Bark Beetle Infestation. Applied and Environmental Microbiology, 2016, 82, 6912-6919.	3.1	15
223	Bacterial community dynamics in a rumen fluid bioreactor during in-vitro cultivation. Journal of Biotechnology, 2016, 234, 43-49.	3.8	10
224	Recurrent <i>Clostridium difficile</i> infection associates with distinct bile acid and microbiome profiles. Alimentary Pharmacology and Therapeutics, 2016, 43, 1142-1153.	3.7	151
225	Effects of multiple dimensions of bacterial diversity on functioning, stability and multifunctionality. Ecology, 2016, 97, 2716-2728.	3.2	64
226	Identification of active aerobic methanotrophs in plateau wetlands using DNA stable isotope probing. FEMS Microbiology Letters, 2016, 363, fnw168.	1.8	22
227	Mango Supplementation Modulates Gut Microbial Dysbiosis and Short-Chain Fatty Acid Production Independent of Body Weight Reduction in C57BL/6 Mice Fed a High-Fat Diet. Journal of Nutrition, 2016, 146, 1483-1491.	2.9	47
228	The impact of orally administered phages on host immune response and surrounding microbial communities. Bacteriophage, 2016, 6, e1211066.	1.9	23
229	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	27.8	1,506
230	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. MSphere, 2016, 1 , .	2.9	28
231	Nitrous oxide emission related to ammonia-oxidizing bacteria and mitigation options from N fertilization in a tropical soil. Scientific Reports, 2016, 6, 30349.	3.3	99
232	Reemergence of Lower-Airway Microbiota in Lung Transplant Patients with Cystic Fibrosis. Annals of the American Thoracic Society, 2016, 13, 2132-2142.	3.2	23
233	Evaluation of a membrane bioreactor system as post-treatment in waste water treatment for better removal of micropollutants. Water Research, 2016, 107, 37-46.	11.3	44
234	Discovery of a Novel Seminal Fluid Microbiome and Influence of Estrogen Receptor Alpha Genetic Status. Scientific Reports, 2016, 6, 23027.	3.3	59

#	Article	IF	CITATIONS
235	Shifts in <i>Lachnospira</i> and <i>Clostridium sp.</i> in the 3-month stool microbiome are associated with preschool age asthma. Clinical Science, 2016, 130, 2199-2207.	4.3	100
236	The effect of DNA extraction methodology on gut microbiota research applications. BMC Research Notes, 2016, 9, 365.	1.4	66
237	Dispersal of Bacillus subtilis and its effect on strawberry phyllosphere microbiota under open field and protection conditions. Scientific Reports, 2016, 6, 22611.	3.3	74
238	Gut microbiome alterations in patients with stage 4 hepatitis C. Gut Pathogens, 2016, 8, 42.	3.4	113
239	Fungal Microbiota Profile in Newly Diagnosed Treatment-naÃ⁻ve Children with Crohn's Disease. Journal of Crohn's and Colitis, 2017, 11, 586-592.	1.3	38
240	Human Thanatomicrobiome Succession and Time Since Death. Scientific Reports, 2016, 6, 29598.	3.3	136
241	Printing-Assisted Surface Modifications of Patterned Ultrafiltration Membranes. ACS Applied Materials & Samp; Interfaces, 2016, 8, 30271-30280.	8.0	26
242	Integrative microbial community analysis reveals full-scale enhanced biological phosphorus removal under tropical conditions. Scientific Reports, 2016, 6, 25719.	3.3	61
243	Dysbiosis of small intestinal microbiota in liver cirrhosis and its association with etiology. Scientific Reports, 2016, 6, 34055.	3.3	165
244	Attached biofilms and suspended aggregates are distinct microbial lifestyles emanating from differing hydraulics. Nature Microbiology, 2016, 1, 16178.	13.3	60
245	Mineral and organic growing media have distinct community structure, stability and functionality in soilless culture systems. Scientific Reports, 2016, 6, 18837.	3.3	72
246	Association of nasopharyngeal microbiota profiles with bronchiolitis severity in infants hospitalised for bronchiolitis. European Respiratory Journal, 2016, 48, 1329-1339.	6.7	144
247	Altered gut microbiota in Rett syndrome. Microbiome, 2016, 4, 41.	11.1	120
248	Impact of Sample Type and DNA Isolation Procedure on Genomic Inference of Microbiome Composition. MSystems, 2016, 1, .	3.8	153
249	The role of the gastrointestinal microbiome in infectious complications during induction chemotherapy for acute myeloid leukemia. Cancer, 2016, 122, 2186-2196.	4.1	121
250	Gypsum amendment to rice paddy soil stimulated bacteria involved in sulfur cycling but largely preserved the phylogenetic composition of the total bacterial community. Environmental Microbiology Reports, 2016, 8, 413-423.	2.4	29
251	Colitis susceptibility in p47 phoxâ^'/â^' mice is mediated by the microbiome. Microbiome, 2016, 4, 13.	11.1	34
252	Impact of sludge retention time on the fine composition of the microbial community and extracellular polymeric substances in a membrane bioreactor. Applied Microbiology and Biotechnology, 2016, 100, 8507-8521.	3.6	18

#	Article	IF	CITATIONS
253	Restructuring of the Aquatic Bacterial Community by Hydric Dynamics Associated with Superstorm Sandy. Applied and Environmental Microbiology, 2016, 82, 3525-3536.	3.1	15
254	Site-specific environmental factors control bacterial and viral diversity in stormwater retention ponds. Aquatic Microbial Ecology, 2016, 77, 23-36.	1.8	16
255	Microbial Reconstitution Reverses Maternal Diet-Induced Social and Synaptic Deficits in Offspring. Cell, 2016, 165, 1762-1775.	28.9	840
256	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA. , 2016, , .		16
257	Effects of Walnut Consumption on Colon Carcinogenesis and Microbial Community Structure. Cancer Prevention Research, 2016, 9, 692-703.	1.5	50
258	Importance of the fat content within the cheese-matrix for blood lipid profile, faecal fat excretion, and gut microbiome in growing pigs. International Dairy Journal, 2016, 61, 67-75.	3.0	15
259	Structural modulation of gut microbiota by chondroitin sulfate and its oligosaccharide. International Journal of Biological Macromolecules, 2016, 89, 489-498.	7.5	68
260	Interpreting Prevotella and Bacteroides as biomarkers of diet and lifestyle. Microbiome, 2016, 4, 15.	11.1	348
261	Contribution of Vegetation to the Microbial Composition of Nearby Outdoor Air. Applied and Environmental Microbiology, 2016, 82, 3822-3833.	3.1	141
262	PERMANOVA-S: association test for microbial community composition that accommodates confounders and multiple distances. Bioinformatics, 2016, 32, 2618-2625.	4.1	120
263	Large differences in potential denitrification and sediment microbial communities across the Laurentian great lakes. Biogeochemistry, 2016, 128, 353-368.	3.5	34
264	Biogeochemical and 16S rRNA gene sequence evidence supports a novel mode of anaerobic methanotrophy in permanently iceâ€covered Lake Fryxell, Antarctica. Limnology and Oceanography, 2016, 61, S119.	3.1	44
265	The Fecal Microbiota Profile and Bronchiolitis in Infants. Pediatrics, 2016, 138, .	2.1	58
266	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.	1.9	114
267	Microbiome change by symbiotic invasion in lichens. Environmental Microbiology, 2016, 18, 1428-1439.	3.8	41
268	Phylogenetic conservation of freshwater lake habitat preference varies between abundant bacterioplankton phyla. Environmental Microbiology, 2016, 18, 1212-1226.	3.8	70
269	Assembly of the <i>Caenorhabditis elegans</i> gut microbiota from diverse soil microbial environments. ISME Journal, 2016, 10, 1998-2009.	9.8	296
270	Bacterial Diversity and Community Structure in Two Bornean Nepenthes Species with Differences in Nitrogen Acquisition Strategies. Microbial Ecology, 2016, 71, 938-953.	2.8	11

#	Article	IF	CITATIONS
271	Altered edaphic parameters couple to shifts in terrestrial bacterial community structure associated with insect-induced tree mortality. Soil Biology and Biochemistry, 2016, 95, 19-29.	8.8	25
272	Biodiversity patterns of plankton assemblages at the extremes of the Red Sea. FEMS Microbiology Ecology, 2016, 92, fiw002.	2.7	31
273	Aquatic nitrogen-fixing cyanobacteria associated with blooms of Didymosphenia geminata: insights from a field study. Hydrobiologia, 2016, 770, 37-52.	2.0	3
274	DNA-metabarcoding uncovers the diversity of soil-inhabiting fungi in the tropical island of Puerto Rico. Mycoscience, 2016, 57, 217-227.	0.8	22
275	Bacterial communities from Arctic seasonal sea ice are more compositionally variable than those from multi-year sea ice. ISME Journal, 2016, 10, 2543-2552.	9.8	24
276	Probiotics modulated gut microbiota suppresses hepatocellular carcinoma growth in mice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1306-15.	7.1	442
277	Diet-induced obesity, energy metabolism and gut microbiota in C57BL/6J mice fed Western diets based on lean seafood or lean meat mixtures. Journal of Nutritional Biochemistry, 2016, 31, 127-136.	4.2	32
278	Novel microbial assemblages inhabiting crustal fluids within mid-ocean ridge flank subsurface basalt. ISME Journal, 2016, 10, 2033-2047.	9.8	59
279	Ecological and evolutionary significance of novel protist lineages. European Journal of Protistology, 2016, 55, 4-11.	1.5	25
280	Effect of Advanced HIV Infection on the Respiratory Microbiome. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 226-235.	5.6	83
281	Linking Microbial Community and Catabolic Gene Structures during the Adaptation of Three Contaminated Soils under Continuous Long-Term Pollutant Stress. Applied and Environmental Microbiology, 2016, 82, 2227-2237.	3.1	30
282	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. Nature Communications, 2016, 7, 10516.	12.8	196
283	Stress and the microbiome: linking glucocorticoids to bacterial community dynamics in wild red squirrels. Biology Letters, 2016, 12, 20150875.	2.3	81
284	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. Journal of Crohn's and Colitis, 2016, 10, 735-746.	1.3	37
285	Biofilms in shower hoses – choice of pipe material influences bacterial growth and communities. Environmental Science: Water Research and Technology, 2016, 2, 670-682.	2.4	57
286	Characterizing root-associated fungal communities and soils of Douglas-fir (Pseudotsuga menziesii) stands that naturally produce Oregon white truffles (Tuber oregonense and Tuber gibbosum). Mycorrhiza, 2016, 26, 367-376.	2.8	16
287	Assessment throughout a whole fishing year of the dominant microbiota of peeled brown shrimp (Crangon crangon) stored for 7 days under modified atmosphere packaging at 4°C without preservatives. Food Microbiology, 2016, 54, 60-71.	4.2	21
288	Microbial and Functional Diversity within the Phyllosphere of Espeletia Species in an Andean High-Mountain Ecosystem. Applied and Environmental Microbiology, 2016, 82, 1807-1817.	3.1	55

#	Article	IF	Citations
289	Corticosteroid therapy and airflow obstruction influence the bronchial microbiome, which is distinct from that of bronchoalveolar lavage in asthmatic airways. Journal of Allergy and Clinical Immunology, 2016, 137, 1398-1405.e3.	2.9	128
290	<i>Lactobacillus rhamnosus</i> GG-supplemented formula expands butyrate-producing bacterial strains in food allergic infants. ISME Journal, 2016, 10, 742-750.	9.8	407
291	Characterization of the bacterial communities of casts from Eisenia andrei fed with different substrates. Applied Soil Ecology, 2016, 98, 103-111.	4.3	56
292	Microbiome shifts and the inhibition of quorum sensing by Black Band Disease cyanobacteria. ISME Journal, 2016, 10, 1204-1216.	9.8	82
293	The activated sludge ecosystem contains a core community of abundant organisms. ISME Journal, 2016, 10, 11-20.	9.8	416
294	Assembly of Active Bacterial and Fungal Communities Along a Natural Environmental Gradient. Microbial Ecology, 2016, 71, 57-67.	2.8	37
295	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. Gut, 2016, 65, 57-62.	12.1	737
296	Regulation of Glucose Uptake and Enteroendocrine Function by the Intestinal Epithelial Insulin Receptor. Diabetes, 2017, 66, 886-896.	0.6	32
297	A study of Glycine max (soybean) fungal communities under different agricultural practices. Plant Gene, 2017, 11, 8-16.	2.3	7
298	Microbial community structures in high rate algae ponds for bioconversion of agricultural wastes from livestock industry for feed production. Science of the Total Environment, 2017, 580, 1185-1196.	8.0	54
299	Comparison of sputum microbiome of legionellosis-associated patients and other pneumonia patients: indications for polybacterial infections. Scientific Reports, 2017, 7, 40114.	3.3	18
300	Influence of CuSO 4 and chelated copper algaecide exposures on biodegradation of microcystin-LR. Chemosphere, 2017, 174, 538-544.	8.2	15
301	Composition of Gut Microbiota in the Gibel Carp (Carassius auratus gibelio) Varies with Host Development. Microbial Ecology, 2017, 74, 239-249.	2.8	115
302	Primary productivity of snow algae communities on stratovolcanoes of the Pacific Northwest. Geobiology, 2017, 15, 280-295.	2.4	54
303	A primer to metabarcoding surveys of Antarctic terrestrial biodiversity. Antarctic Science, 2017, 29, 3-15.	0.9	13
304	Gut Microbiome of the Canadian Arctic Inuit. MSphere, 2017, 2, .	2.9	40
305	Epiphytic <i>Planctomycetes</i> communities associated with three main groups of macroalgae. FEMS Microbiology Ecology, 2017, 93, fiw255.	2.7	71
306	Salivary Gluten Degradation and Oral Microbial Profiles in Healthy Individuals and Celiac Disease Patients. Applied and Environmental Microbiology, 2017, 83, .	3.1	47

#	Article	IF	CITATIONS
307	Exploring the symbiont diversity of ancient western redcedars: arbuscular mycorrhizal fungi of longâ€lived hosts. Molecular Ecology, 2017, 26, 1586-1597.	3.9	4
308	Ursodeoxycholic Acid and Its Taurine- or Glycine-Conjugated Species Reduce Colitogenic Dysbiosis and Equally Suppress Experimental Colitis in Mice. Applied and Environmental Microbiology, 2017, 83, .	3.1	96
309	Arbuscular mycorrhizal fungi inoculation mediated changes in rhizosphere bacterial community structure while promoting revegetation in a semiarid ecosystem. Science of the Total Environment, 2017, 584-585, 838-848.	8.0	65
310	A family of interaction-adjusted indices of community similarity. ISME Journal, 2017, 11, 791-807.	9.8	39
311	Randomised clinical trial: faecal microbiota transplantation for recurrent ⟨i⟩Clostridum difficile⟨ i⟩ infection – fresh, or frozen, or lyophilised microbiota from a small pool of healthy donors delivered by colonoscopy. Alimentary Pharmacology and Therapeutics, 2017, 45, 899-908.	3.7	148
312	Microbial population dynamics in continuous anaerobic digester systems during start up, stable conditions and recovery after starvation. Bioresource Technology, 2017, 232, 313-320.	9.6	41
313	New evidences on the altered gut microbiota in autism spectrum disorders. Microbiome, 2017, 5, 24.	11.1	668
314	Optimization of DNA extraction for advancing coral microbiota investigations. Microbiome, 2017, 5, 18.	11.1	39
315	Organic nitrogen rearranges both structure and activity of the soil-borne microbial seedbank. Scientific Reports, 2017, 7, 42634.	3.3	44
316	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. Gut, 2017, 66, 1968-1974.	12.1	370
317	Highâ€resolution sequencing reveals unexplored archaeal diversity in freshwater wetland soils. Environmental Microbiology, 2017, 19, 2192-2209.	3.8	56
318	<i>Syntrophobacteraceae</i> àêeffiliated species are major propionateâ€degrading sulfate reducers in paddy soil. Environmental Microbiology, 2017, 19, 1669-1686.	3.8	57
319	Long chain arabinoxylans shift the mucosa-associated microbiota in the proximal colon of the simulator of the human intestinal microbial ecosystem (M-SHIME). Journal of Functional Foods, 2017, 32, 226-237.	3.4	23
320	Modelling plankton ecosystems in the meta-omics era. Are we ready?. Marine Genomics, 2017, 32, 1-17.	1.1	29
321	Temporal and spatial variations in the composition of freshwater photosynthetic picoeukaryotes revealed by MiSeq sequencing from flow cytometry sorted samples. Environmental Microbiology, 2017, 19, 2286-2300.	3.8	25
322	Legal immigrants: invasion of alien microbial communities during winter occurring desert dust storms. Microbiome, 2017, 5, 32.	11.1	69
323	Giardia duodenalis induces pathogenic dysbiosis of human intestinal microbiota biofilms. International Journal for Parasitology, 2017, 47, 311-326.	3.1	125
324	Loss of cutaneous microbial diversity during first 3Âweeks of life in very low birthweight infants. Experimental Dermatology, 2017, 26, 861-867.	2.9	21

#	Article	IF	CITATIONS
325	Changes in Microbiota in Rumen Digesta and Feces Due to a Grain-Based Subacute Ruminal Acidosis (SARA) Challenge. Microbial Ecology, 2017, 74, 485-495.	2.8	122
326	IgA-coated <i>E. coli</i> enriched in Crohn's disease spondyloarthritis promote T _H 17-dependent inflammation. Science Translational Medicine, 2017, 9, .	12.4	246
327	Wildfire impact: Natural experiment reveals differential short-term changes in soil microbial communities. Soil Biology and Biochemistry, 2017, 109, 1-13.	8.8	68
328	Maintaining stability of the rumen ecosystem is associated with changes of microbial composition and epithelial TLR signaling. MicrobiologyOpen, 2017, 6, e00436.	3.0	14
329	Comparison of Fecal Collection Methods for Microbiota Studies in Bangladesh. Applied and Environmental Microbiology, 2017, 83, .	3.1	50
330	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	11.1	1,434
331	Use of Endophytic and Rhizosphere Bacteria To Improve Phytoremediation of Arsenic-Contaminated Industrial Soils by Autochthonous Betula celtiberica. Applied and Environmental Microbiology, 2017, 83, .	3.1	105
332	Dynamics of the human gut microbiome in inflammatory bowel disease. Nature Microbiology, 2017, 2, 17004.	13.3	830
333	Deciphering composition and function of the root microbiome of a legume plant. Microbiome, 2017, 5, 2.	11.1	152
334	Host genetic variation in mucosal immunity pathways influences the upper airway microbiome. Microbiome, $2017, 5, 16$.	11.1	61
335	Fumigation with dazomet modifies soil microbiota in apple orchards affected by replant disease. Applied Soil Ecology, 2017, 113, 71-79.	4.3	62
336	Effects of nasal instillation of a nitric oxide-releasing solution or parenteral administration of tilmicosin on the nasopharyngeal microbiota of beef feedlot cattle at high-risk of developing respiratory tract disease. Research in Veterinary Science, 2017, 115, 117-124.	1.9	23
337	Age-Associated Microbial Dysbiosis Promotes Intestinal Permeability, Systemic Inflammation, and Macrophage Dysfunction. Cell Host and Microbe, 2017, 21, 455-466.e4.	11.0	799
338	Does intensified boreal forest harvesting impact soil microbial community structure and function?. Canadian Journal of Forest Research, 2017, 47, 916-925.	1.7	14
339	Smokeless tobacco products harbor diverse bacterial microbiota that differ across products and brands. Applied Microbiology and Biotechnology, 2017, 101, 5391-5403.	3.6	40
340	Codiversification of gastrointestinal microbiota and phylogeny in passerines is not explained by ecological divergence. Molecular Ecology, 2017, 26, 5292-5304.	3.9	63
341	Liver microbiome of Peromyscus leucopus, a key reservoir host species for emerging infectious diseases in North America. Infection, Genetics and Evolution, 2017, 52, 10-18.	2.3	14
342	Bayesian Nonparametric Ordination for the Analysis of Microbial Communities. Journal of the American Statistical Association, 2017, 112, 1430-1442.	3.1	30

#	Article	IF	CITATIONS
343	The effects of inhaled aztreonam on the cystic fibrosis lung microbiome. Microbiome, 2017, 5, 51.	11.1	53
344	Pilot plant demonstration of stable and efficient high rate biological nutrient removal with low dissolved oxygen conditions. Water Research, 2017, 121, 72-85.	11.3	80
345	Postmortem microbial communities in burial soil layers of skeletonized humans. Journal of Clinical Forensic and Legal Medicine, 2017, 49, 43-49.	1.0	19
346	Plastics in the North Atlantic garbage patch: A boat-microbe for hitchhikers and plastic degraders. Science of the Total Environment, 2017, 599-600, 1222-1232.	8.0	274
347	Growth of <i>Nitrosococcus</i> -Related Ammonia Oxidizing Bacteria Coincides with Extremely Low pH Values in Wastewater with High Ammonia Content. Environmental Science & Technology, 2017, 51, 6857-6866.	10.0	64
348	Oral microbiome in HIV-associated periodontitis. Medicine (United States), 2017, 96, e5821.	1.0	42
349	Analysis of soil microbial communities based on amplicon sequencing of marker genes. Biology and Fertility of Soils, 2017, 53, 485-489.	4.3	197
350	Cutting through the smoke: the diversity of microorganisms in deep-sea hydrothermal plumes. Royal Society Open Science, 2017, 4, 160829.	2.4	20
351	Nasal Airway Microbiota Profile and Severe Bronchiolitis in Infants. Pediatric Infectious Disease Journal, 2017, 36, 1044-1051.	2.0	58
352	Perinatal Bacterial Exposure Contributes to IL-13 Aeroallergen Response. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 419-427.	2.9	13
353	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. Microbiome, 2017, 5, 22.	11.1	33
354	MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. Nucleic Acids Research, 2017, 45, W180-W188.	14.5	1,359
355	Acute infection with the intestinal parasite <i>Trichuris muris</i> has longâ€term consequences on mucosal mast cell homeostasis and epithelial integrity. European Journal of Immunology, 2017, 47, 257-268.	2.9	18
356	Changes in gut microbiota of migratory passerines during stopover after crossing an ecological barrier. Auk, 2017, 134, 137-145.	1.4	45
357	Oomycete Species Associated with Soybean Seedlings in North Americaâ€"Part II: Diversity and Ecology in Relation to Environmental and Edaphic Factors. Phytopathology, 2017, 107, 293-304.	2.2	83
358	A combined meta-barcoding and shotgun metagenomic analysis of spontaneous wine fermentation. GigaScience, 2017, 6, 1-10.	6.4	67
359	Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. Applied and Environmental Microbiology, 2017, 83, .	3.1	78
360	Determination of nasal and oropharyngeal microbiomes in a multicenter population-based study – findings from Pretest 1 of the German National Cohort. Scientific Reports, 2017, 7, 1855.	3.3	13

#	Article	IF	CITATIONS
361	Uncovering the trimethylamine-producing bacteria of the human gut microbiota. Microbiome, 2017, 5, 54.	11.1	336
362	Exploring a Possible Link between the Intestinal Microbiota and Feed Efficiency in Pigs. Applied and Environmental Microbiology, 2017, 83, .	3.1	258
363	Characterising and predicting cyanobacterial blooms in an 8-year amplicon sequencing time course. ISME Journal, 2017, 11, 1746-1763.	9.8	97
364	Soil depth and crop determinants of bacterial communities under ten biofuel cropping systems. Soil Biology and Biochemistry, 2017, 112, 140-152.	8.8	61
365	Sulfide-Induced Dissimilatory Nitrate Reduction to Ammonium Supports Anaerobic Ammonium Oxidation (Anammox) in an Open-Water Unit Process Wetland. Applied and Environmental Microbiology, 2017, 83, .	3.1	49
366	Preferential suppression of Anopheles gambiae host sequences allows detection of the mosquito eukaryotic microbiome. Scientific Reports, 2017, 7, 3241.	3.3	38
367	Phylogenetic and Functional Diversity of Total (DNA) and Expressed (RNA) Bacterial Communities in Urban Green Infrastructure Bioswale Soils. Applied and Environmental Microbiology, 2017, 83, .	3.1	41
368	Transcriptomic differentiation underlying marineâ€toâ€freshwater transitions in the South American silversides <i>Odontesthes argentinensis</i> and <i>O.Âbonariensis</i> (Atheriniformes). Ecology and Evolution, 2017, 7, 5258-5268.	1.9	23
369	Carbon quantity and quality drives variation in cave microbial communitiesÂand regulates Mn(II) oxidation. Biogeochemistry, 2017, 134, 77-94.	3.5	19
370	Metformin alters the gut microbiome of individuals with treatment-naive type 2 diabetes, contributing to the therapeutic effects of the drug. Nature Medicine, 2017, 23, 850-858.	30.7	1,165
371	<i>Nitrotoga</i> is selected over <i>Nitrospira</i> in newly assembled biofilm communities from a tap water source community at increased nitrite loading. Environmental Microbiology, 2017, 19, 2785-2793.	3.8	32
372	The Evolving Cystic Fibrosis Microbiome: A Comparative Cohort Study Spanning 16 Years. Annals of the American Thoracic Society, 2017, 14, 1288-1297.	3.2	60
373	Individual and nonâ€additive effects of exotic sapâ€feeders on root functional and mycorrhizal traits of a shared conifer host. Functional Ecology, 2017, 31, 2024-2033.	3.6	4
374	Probiotic yogurt and acidified milk similarly reduce postprandial inflammation and both alter the gut microbiota of healthy, young men. British Journal of Nutrition, 2017, 117, 1312-1322.	2.3	81
375	Genetic Characterization of Periphyton Communities Associated with Selenium Bioconcentration and Trophic Transfer in a Simple Food Chain. Environmental Science & Echnology, 2017, 51, 7532-7541.	10.0	14
376	Dispersal enhances beta diversity in nectar microbes. Ecology Letters, 2017, 20, 901-910.	6.4	130
377	Sedimentary and egg-bank DNA from 3 European lakes reveal concurrent changes in the composition and diversity of cyanobacterial and Daphnia communities. Hydrobiologia, 2017, 800, 155-172.	2.0	17
378	High-throughput metataxonomic characterization of the raw milk microbiota identifies changes reflecting lactation stage and storage conditions. International Journal of Food Microbiology, 2017, 255, 1-6.	4.7	36

#	Article	IF	CITATIONS
379	Methanotrophic bacterial diversity in two diverse soils under varying land-use practices as determined by high-throughput sequencing of the pmoA gene. Applied Soil Ecology, 2017, 119, 35-45.	4.3	45
380	Enhancement of IFN \hat{I}^3 Production by Distinct Commensals Ameliorates Salmonella-Induced Disease. Cell Host and Microbe, 2017, 21, 682-694.e5.	11.0	91
381	Differential effects of nitrate, ammonium, and urea as N sources for microbial communities in the North Pacific Ocean. Limnology and Oceanography, 2017, 62, 2550-2574.	3.1	39
382	Sequential bioavailability of sedimentary organic matter to heterotrophic bacteria. Environmental Microbiology, 2017, 19, 2629-2644.	3.8	39
383	A distinct bacterial dysbiosis associated skin inflammation in ovine footrot. Scientific Reports, 2017, 7, 45220.	3.3	36
384	Weaning age influences the severity of gastrointestinal microbiome shifts in dairy calves. Scientific Reports, 2017, 7, 198.	3.3	87
385	Ecological and Transcriptional Responses of Anode-Respiring Communities to Nitrate in a Microbial Fuel Cell. Environmental Science & Echnology, 2017, 51, 5334-5342.	10.0	34
386	Autogenic succession and deterministic recovery following disturbance in soil bacterial communities. Scientific Reports, 2017, 7, 45691.	3.3	71
387	Microbial community response to hydration-desiccation cycles in desert soil. Scientific Reports, 2017, 7, 45735.	3.3	80
388	In-depth analysis of core methanogenic communities from high elevation permafrost-affected wetlands. Soil Biology and Biochemistry, 2017, 111, 66-77.	8.8	36
389	Defining the Core Citrus Leaf- and Root-Associated Microbiota: Factors Associated with Community Structure and Implications for Managing Huanglongbing (Citrus Greening) Disease. Applied and Environmental Microbiology, 2017, 83, .	3.1	78
390	Ethnic and diet-related differences in the healthy infant microbiome. Genome Medicine, 2017, 9, 32.	8.2	93
391	Bacterial diversity of the rhizosphere and nearby surface soil of rice (Oryza sativa) growing in the Camargue (France). Rhizosphere, 2017, 3, 112-122.	3.0	29
392	The role of adaptive immunity as an ecological filter on the gut microbiota in zebrafish. ISME Journal, 2017, 11, 1630-1639.	9.8	93
393	The role of inoculum and reactor configuration for microbial community composition and dynamics in mainstream partial nitritation anammox reactors. MicrobiologyOpen, 2017, 6, e00456.	3.0	32
394	Effects of Dry and Wet Sieving of Soil on Identification and Interpretation of Microbial Community Composition. Advances in Agronomy, 2017, 142, 119-142.	5.2	40
395	Characterization of oral and gut microbiome temporal variability in hospitalized cancer patients. Genome Medicine, 2017, 9, 21.	8.2	80
396	The presence of aggressive ants is associated with fewer insect visits to and altered microbe communities in coffee flowers. Basic and Applied Ecology, 2017, 20, 62-74.	2.7	12

#	Article	IF	Citations
397	Distinct ecological niches of marine symbiotic N ₂ â€fixing cyanobacterium <i>Candidatus Atelocyanobacterium thalassa</i> sublineages. Journal of Phycology, 2017, 53, 451-461.	2.3	66
398	Microbial community redundancy in anaerobic digestion drives process recovery after salinity exposure. Water Research, 2017, 111, 109-117.	11.3	111
399	Cyanobacterial harmful algal blooms are a biological disturbance to Western Lake Erie bacterial communities. Environmental Microbiology, 2017, 19, 1149-1162.	3.8	193
400	Environmental fluctuations and host skin bacteria shift survival advantage between frogs and their fungal pathogen. ISME Journal, 2017, 11, 349-361.	9.8	100
401	Seasonal induced changes in spinach rhizosphere microbial community structure with varying salinity and drought. Science of the Total Environment, 2017, 579, 1485-1495.	8.0	39
402	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. Science of the Total Environment, 2017, 579, 1804-1814.	8.0	43
403	Depth-dependent influence of different land-use systems on bacterial biogeography. FEMS Microbiology Ecology, 2017, 93, fiw239.	2.7	48
404	Eosinophilic airway inflammation in asthmatic patients is associated with an altered airway microbiome. Journal of Allergy and Clinical Immunology, 2017, 140, 407-417.e11.	2.9	89
405	Comparison of Collection Methods for Fecal Samples in Microbiome Studies. American Journal of Epidemiology, 2017, 185, 115-123.	3.4	112
406	Comparison of morphological and next generation DNA sequencing methods for assessing zooplankton assemblages. Journal of Experimental Marine Biology and Ecology, 2017, 487, 113-126.	1.5	45
407	The effect of inoculum source and fluid shear force on the development of <i>inÂvitro </i> oral multispecies biofilms. Journal of Applied Microbiology, 2017, 122, 796-808.	3.1	19
408	Imbalance of bacteriome profiles within the Finnish Diabetes Prediction and Prevention study: Parallel use of 16S profiling and virome sequencing in stool samples from children with islet autoimmunity and matched controls. Pediatric Diabetes, 2017, 18, 588-598.	2.9	44
409	Rhizosphere microbiomes of potato cultivated in the High Andes show stable and dynamic core microbiomes with different responses to plant development. FEMS Microbiology Ecology, 2017, 93, fiw242.	2.7	114
410	Biogeography of soil Thaumarchaeota in relation to soil depth and land usage. FEMS Microbiology Ecology, 2017, 93, fiw246.	2.7	42
411	Consumption of a high-fat diet alters the seminal fluid and gut microbiomes in male mice. Reproduction, Fertility and Development, 2017, 29, 1602.	0.4	38
412	Tideless estuaries in brackish seas as possible freshwaterâ€marine transition zones for bacteria: the case study of the Vistula river estuary. Environmental Microbiology Reports, 2017, 9, 129-143.	2.4	28
413	A first insight into the intestinal microbiota of snow trout (Schizothorax zarudnyi). Symbiosis, 2017, 72, 183-193.	2.3	16
414	Distinct Microbial Communities Trigger Colitis Development upon Intestinal Barrier Damage via Innate or Adaptive Immune Cells. Cell Reports, 2017, 21, 994-1008.	6.4	105

#	ARTICLE	IF	CITATIONS
415	Biologically induced formation of realgar deposits in soil. Geochimica Et Cosmochimica Acta, 2017, 218, 237-256.	3.9	23
416	Heritability of the Symbiodinium community in vertically- and horizontally-transmitting broadcast spawning corals. Scientific Reports, 2017, 7, 8219.	3.3	89
417	Strong impact of anthropogenic contamination on the coâ€occurrence patterns of a riverine microbial community. Environmental Microbiology, 2017, 19, 4993-5009.	3.8	213
418	The Wheat Microbiome Under Four Management Strategies, and Potential for Endophytes in Disease Protection. Phytobiomes Journal, 2017, 1, 158-168.	2.7	141
419	Processing and Analyzing Human Microbiome Data. Methods in Molecular Biology, 2017, 1666, 649-677.	0.9	4
420	Can intestinal microbiota be associated with non-intestinal cancers?. Scientific Reports, 2017, 7, 12722.	3.3	19
421	Rapid replacement by non-vaccine pneumococcal serotypes may mitigate the impact of the pneumococcal conjugate vaccine on nasopharyngeal bacterial ecology. Scientific Reports, 2017, 7, 8127.	3.3	49
422	Stenotrophomonas-Like Bacteria Are Widespread Symbionts in Cone Snail Venom Ducts. Applied and Environmental Microbiology, 2017, 83, .	3.1	10
423	Extensive Core Microbiome in Drone-Captured Whale Blow Supports a Framework for Health Monitoring. MSystems, 2017, 2, .	3.8	93
424	Bacterial natural product biosynthetic domain composition in soil correlates with changes in latitude on a continent-wide scale. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11615-11620.	7.1	53
425	Household triclosan and triclocarban effects on the infant and maternal microbiome. EMBO Molecular Medicine, 2017, 9, 1732-1741.	6.9	76
426	Wild Mouse Gut Microbiota Promotes Host Fitness and Improves Disease Resistance. Cell, 2017, 171, 1015-1028.e13.	28.9	603
427	Secondary compound hypothesis revisited: Selected plant secondary metabolites promote bacterial degradation of cis-1,2-dichloroethylene (cDCE). Scientific Reports, 2017, 7, 8406.	3.3	38
428	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. MBio, 2017, 8, .	4.1	219
429	The Female Genital Tract Microbiome Is Associated With Vaginal Antiretroviral Drug Concentrations in Human Immunodeficiency Virus–Infected Women on Antiretroviral Therapy. Journal of Infectious Diseases, 2017, 216, 990-999.	4.0	23
430	Seawater transfer alters the intestinal microbiota profiles of Atlantic salmon (Salmo salar L.). Scientific Reports, 2017, 7, 13877.	3.3	121
431	Metabarcoding Techniques for Assessing Biodiversity of Marine Animal Forests., 2017,, 445-473.		28
432	Microbial Landscape of the Grapevine Endosphere in the Context of Pierce's Disease. Phytobiomes Journal, 2017, 1, 138-149.	2.7	48

#	Article	IF	CITATIONS
433	Gut microbiota of a longâ€distance migrant demonstrates resistance against environmental microbe incursions. Molecular Ecology, 2017, 26, 5842-5854.	3.9	51
434	Maternal microbiomes in preterm birth: Recent progress and analytical pipelines. Seminars in Perinatology, 2017, 41, 392-400.	2.5	28
435	Recurrent Reverse Evolution Maintains Polymorphism after Strong Bottlenecks in Commensal Gut Bacteria. Molecular Biology and Evolution, 2017, 34, 2879-2892.	8.9	38
436	Land cover and forest connectivity alter the interactions among host, pathogen and skin microbiome. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170582.	2.6	50
437	Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9966-9971.	7.1	297
438	Microbial communities in placentas from term normal pregnancy exhibit spatially variable profiles. Scientific Reports, 2017, 7, 11200.	3.3	137
439	Antibiotic treatment for Tuberculosis induces a profound dysbiosis of the microbiome that persists long after therapy is completed. Scientific Reports, 2017, 7, 10767.	3.3	148
440	The impact of immigration on microbial community composition in full-scale anaerobic digesters. Scientific Reports, 2017, 7, 9343.	3.3	127
441	More than constipation – bowel symptoms in Parkinson's disease and their connection to gut microbiota. European Journal of Neurology, 2017, 24, 1375-1383.	3.3	112
442	A single early-in-life macrolide course has lasting effects on murine microbial network topology and immunity. Nature Communications, 2017, 8, 518.	12.8	119
443	Deep <i>nirS</i> amplicon sequencing of San Francisco Bay sediments enables prediction of geography and environmental conditions from denitrifying community composition. Environmental Microbiology, 2017, 19, 4897-4912.	3.8	11
444	In vitro colonisation of the distal colon by Akkermansia muciniphila is largely mucin and pH dependent. Beneficial Microbes, 2017, 8, 81-96.	2.4	80
445	Comparison of the Microbiota of Older Adults Living in Nursing Homes and the Community. MSphere, 2017, 2, .	2.9	33
446	Microbial communities with distinct denitrification potential in spruce and beech soils differing in nitrate leaching. Scientific Reports, 2017, 7, 9738.	3.3	34
447	Bacterial diversity among four healthcare-associated institutes in Taiwan. Scientific Reports, 2017, 7, 8230.	3.3	18
448	Microbial Communities Associated with Primary and Metastatic Head and Neck Squamous Cell Carcinoma – A High Fusobacterial and Low Streptococcal Signature. Scientific Reports, 2017, 7, 9934.	3.3	70
449	Drought Stress Results in a Compartment-Specific Restructuring of the Rice Root-Associated Microbiomes. MBio, 2017, 8, .	4.1	336
450	A bidirectional association between the gut microbiota and CNS disease in a biphasic murine model of multiple sclerosis. Gut Microbes, 2017, 8, 561-573.	9.8	79

#	Article	IF	CITATIONS
451	Hydrothermal vent fields discovered in the southern Gulf of California clarify role of habitat in augmenting regional diversity. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170817.	2.6	48
452	Comparative analysis of microbial diversity in two hot springs of Bakreshwar, West Bengal, India. Genomics Data, 2017, 12, 122-129.	1.3	18
453	Analysis of large 16S <scp>rRNA</scp> Illumina data sets: Impact of singleton read filtering on microbial community description. Molecular Ecology Resources, 2017, 17, e122-e132.	4.8	55
454	Biogeography and organic matter removal shape long-term effects of timber harvesting on forest soil microbial communities. ISME Journal, 2017, 11, 2552-2568.	9.8	48
455	<i>Fibrobacter</i> communities in the gastrointestinal tracts of diverse hindgutâ€fermenting herbivores are distinct from those of the rumen. Environmental Microbiology, 2017, 19, 3768-3783.	3.8	35
456	Response to nitrogen addition reveals metabolic and ecological strategies of soil bacteria. Molecular Ecology, 2017, 26, 5500-5514.	3.9	26
457	Soil classification predicts differences in prokaryotic communities across a range of geographically distant soils once pH is accounted for. Scientific Reports, 2017, 7, 45369.	3.3	19
458	Rapid Response of Eastern Mediterranean Deep Sea Microbial Communities to Oil. Scientific Reports, 2017, 7, 5762.	3.3	27
459	The salivary microbiome as an indicator of carcinogenesis in patients with oropharyngeal squamous cell carcinoma: A pilot study. Scientific Reports, 2017, 7, 5867.	3.3	70
460	Post-hypoxia Invasion of the fetal brain by multidrug resistant Staphylococcus. Scientific Reports, 2017, 7, 6458.	3.3	17
461	Microbial planktonic communities in the Red Sea: high levels of spatial and temporal variability shaped by nutrient availability and turbulence. Scientific Reports, 2017, 7, 6611.	3.3	54
462	Bacteriophages as potential new mammalian pathogens. Scientific Reports, 2017, 7, 7043.	3.3	94
463	Microbial communities in the cysts of soybean cyst nematode affected by tillage and biocide in a suppressive soil. Applied Soil Ecology, 2017, 119, 396-406.	4.3	54
464	The role of microbial diversity and composition in minimizing sludge production in the oxic-settling-anoxic process. Science of the Total Environment, 2017, 607-608, 558-567.	8.0	28
465	Early-Life Antibiotic Exposure Causes Intestinal Dysbiosis and Exacerbates Skin and Lung Pathology in Experimental Systemic Sclerosis. Journal of Investigative Dermatology, 2017, 137, 2316-2325.	0.7	35
466	Streptococcus pneumoniae Colonization Is Required To Alter the Nasal Microbiota in Cigarette Smoke-Exposed Mice. Infection and Immunity, 2017, 85, .	2.2	11
467	A clinician's guide to microbiome analysis. Nature Reviews Gastroenterology and Hepatology, 2017, 14, 585-595.	17.8	124
468	Spatiotemporal dynamics of the bacterial microbiota on lacustrine <i>Cladophora glomerata</i> (Chlorophyta). Journal of Phycology, 2017, 53, 1255-1262.	2.3	17

#	Article	IF	CITATIONS
469	Fungal microbiomes associated with green and non-green building materials. International Biodeterioration and Biodegradation, 2017, 125, 251-257.	3.9	16
470	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. Pedosphere, 2017, 27, 832-845.	4.0	8
471	Soil microbial community composition is correlated to soil carbon processing along a boreal wetland formation gradient. European Journal of Soil Biology, 2017, 82, 17-26.	3.2	19
472	Microbiota-activated PPAR- \hat{I}^3 signaling inhibits dysbiotic Enterobacteriaceae expansion. Science, 2017, 357, 570-575.	12.6	796
473	<i>Bifiguratus adelaidae</i> , gen. et sp. nov., a new member of Mucoromycotina in endophytic and soil-dwelling habitats. Mycologia, 2017, 109, 363-378.	1.9	27
474	Ecosystem Resilience and Limitations Revealed by Soil Bacterial Community Dynamics in a Bark Beetle-Impacted Forest. MBio, 2017, 8, .	4.1	9
475	Novel ITS1 Fungal Primers for Characterization of the Mycobiome. MSphere, 2017, 2, .	2.9	79
476	The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. Scientific Reports, 2017, 7, 16324.	3.3	115
477	Carbonate-rich dendrolitic cones: insights into a modern analog for incipient microbialite formation, Little Hot Creek, Long Valley Caldera, California. Npj Biofilms and Microbiomes, 2017, 3, 32.	6.4	30
478	Vertical vs. horizontal transmission of the microbiome in a key disease vector, <i>lxodes pacificus</i> . Molecular Ecology, 2017, 26, 6578-6589.	3.9	64
479	Direct PCR Offers a Fast and Reliable Alternative to Conventional DNA Isolation Methods for Gut Microbiomes. MSystems, 2017, 2 , .	3.8	26
480	First Insights into the Diverse Human Archaeome: Specific Detection of Archaea in the Gastrointestinal Tract, Lung, and Nose and on Skin. MBio, 2017, 8, .	4.1	169
481	Previous crop and rotation history effects on maize seedling health and associated rhizosphere microbiome. Scientific Reports, 2017, 7, 15709.	3.3	78
482	Host-genotype dependent gut microbiota drives zooplankton tolerance to toxic cyanobacteria. Nature Communications, 2017, 8, 1608.	12.8	113
483	Computational Methods for Human Microbiome Analysis. Current Protocols in Microbiology, 2017, 47, 1E.14.1-1E.14.17.	6.5	4
484	Mitochondrial gene polymorphism is associated with gut microbial communities in mice. Scientific Reports, 2017, 7, 15293.	3.3	49
485	Structured subcomposition selection in regression and its application to microbiome data analysis. Annals of Applied Statistics, 2017, 11, .	1.1	28
486	Quantitative microbiome profiling links gut community variation to microbial load. Nature, 2017, 551, 507-511.	27.8	791

#	Article	IF	CITATIONS
487	Microbe biogeography tracks water masses in a dynamic oceanic frontal system. Royal Society Open Science, 2017, 4, 170033.	2.4	46
488	Ecological and sanitary impacts of bacterial communities associated to biological invasions in African commensal rodent communities. Scientific Reports, 2017, 7, 14995.	3.3	18
489	Microbiome measurement: Possibilities and pitfalls. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2017, 31, 619-623.	2.4	7
490	Comparison of DNA-fingerprinting (T-RFLP) and high-throughput sequencing (HTS) to assess the diversity and composition of microbial communities in groundwater ecosystems. Limnologica, 2017, 67, 45-53.	1.5	29
491	Shifts in microbial communities in soil, rhizosphere and roots of two major crop systems under elevated CO2 and O3. Scientific Reports, 2017, 7, 15019.	3.3	75
492	Linking the development and functioning of a carnivorous pitcher plant's microbial digestive community. ISME Journal, 2017, 11, 2439-2451.	9.8	24
493	Interplay between stochastic and deterministic processes in the maintenance of alternative community states in Verrucomicrobia-dominated shallow lakes. FEMS Microbiology Ecology, 2017, 93, .	2.7	12
494	Effects of oral antibiotics and isotretinoin on the murine gut microbiota. International Journal of Antimicrobial Agents, 2017, 50, 342-351.	2.5	27
495	High Temporal and Spatial Variability of Atmospheric-Methane Oxidation in Alpine Glacier Forefield Soils. Applied and Environmental Microbiology, 2017, 83, .	3.1	21
496	Microbial survival strategies in ancient permafrost: insights from metagenomics. ISME Journal, 2017, 11, 2305-2318.	9.8	149
497	Seasonal and spatial variations of prokaryoplankton communities in a salinity-influenced watershed, China. FEMS Microbiology Ecology, 2017, 93, .	2.7	12
498	Circadian rhythm disruption impairs tissue homeostasis and exacerbates chronic inflammation in the intestine. FASEB Journal, 2017, 31, 4707-4719.	0.5	59
499	Serum LL-37 Levels Associated With Severity of Bronchiolitis and Viral Etiology. Clinical Infectious Diseases, 2017, 65, 967-975.	5.8	28
500	Hypothesis testing and statistical analysis of microbiome. Genes and Diseases, 2017, 4, 138-148.	3.4	142
501	Gut microbiota of liver transplantation recipients. Scientific Reports, 2017, 7, 3762.	3.3	40
502	Diet-induced reconstruction of mucosal microbiota associated with alterations of epithelium lectin expression and regulation in the maintenance of rumen homeostasis. Scientific Reports, 2017, 7, 3941.	3.3	5
503	Estrogen protection against EAE modulates the microbiota and mucosal-associated regulatory cells. Journal of Neuroimmunology, 2017, 310, 51-59.	2.3	47
504	Temporal variation of the microbiome is dependent on body region in a wild mammal (Tamiasciurus) Tj ETQq1 1 (0.784314 2.7	rgBT /Overloo

#	Article	IF	Citations
505	Microbiome Structural and Functional Interactions across Host Dietary Niche Space. Integrative and Comparative Biology, 2017, 57, 743-755.	2.0	30
506	The Repertoire Dissimilarity Index as a method to compare lymphocyte receptor repertoires. BMC Bioinformatics, 2017, 18, 155.	2.6	52
507	Vipie: web pipeline for parallel characterization of viral populations from multiple NGS samples. BMC Genomics, 2017, 18, 378.	2.8	20
508	Dynamics of two methanogenic microbiomes incubated in polycyclic aromatic hydrocarbons, naphthenic acids, and oil field produced water. Biotechnology for Biofuels, 2017, 10, 123.	6.2	8
509	Microbial community compositions in the gastrointestinal tract of Chinese Mongolian sheep using Illumina MiSeq sequencing revealed high microbial diversity. AMB Express, 2017, 7, 75.	3.0	54
510	Linking rhizosphere microbiome composition of wild and domesticated <i>Phaseolus vulgaris</i> to genotypic and root phenotypic traits. ISME Journal, 2017, 11, 2244-2257.	9.8	298
511	Temperature drives the assembly of endophytic communities' seasonal succession. Environmental Microbiology, 2017, 19, 3353-3364.	3.8	54
512	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. MSphere, 2017, 2, .	2.9	84
513	Gut Dysbiosis and Neurobehavioral Alterations in Rats Exposed to Silver Nanoparticles. Scientific Reports, 2017, 7, 2822.	3.3	91
514	Exploring the Impacts of Postharvest Processing on the Microbiota and Metabolite Profiles during Green Coffee Bean Production. Applied and Environmental Microbiology, 2017, 83, .	3.1	162
515	Trade-offs between microbiome diversity and productivity in a stratified microbial mat. ISME Journal, 2017, 11, 405-414.	9.8	26
516	Thirty-one years of rice-rice-green manure rotations shape the rhizosphere microbial community and enrich beneficial bacteria. Soil Biology and Biochemistry, 2017, 104, 208-217.	8.8	205
517	Human Oral Buccal Microbiomes Are Associated with Farmworker Status and Azinphos-Methyl Agricultural Pesticide Exposure. Applied and Environmental Microbiology, 2017, 83, .	3.1	33
518	Integrated multi-omics of the human gut microbiome in a case study of familial type 1 diabetes. Nature Microbiology, 2017 , 2 , 16180 .	13.3	233
519	Gut microbiome in children with enthesitis-related arthritis in a developing country and the effect of probiotic administration. Clinical and Experimental Immunology, 2017, 187, 480-489.	2.6	53
520	Enteral High Fat-Polyunsaturated Fatty Acid Blend Alters the Pathogen Composition of the Intestinal Microbiome in Premature Infants with an Enterostomy. Journal of Pediatrics, 2017, 181, 93-101.e6.	1.8	46
521	Fineâ€scale spatial distribution of orchid mycorrhizal fungi in the soil of hostâ€rich grasslands. New Phytologist, 2017, 213, 1428-1439.	7.3	57
522	Microbiome analysis shows enrichment for specific bacteria in separate anatomical regions of the deep-sea carnivorous sponge <i>Chondrocladia grandis </i> fiw214.	2.7	22

#	ARTICLE	IF	Citations
523	Seasonality of freshwater bacterioplankton diversity in two tropical shallow lakes from the Brazilian Atlantic Forest. FEMS Microbiology Ecology, 2017, 93, fiw218.	2.7	31
524	Plant–soil feedbacks and the dominance of conifers in a tropical montane forest in Borneo. Ecological Monographs, 2017, 87, 105-129.	5.4	19
525	Migrating SSU rRNA gene surveys to the metagenomics era. Environmental Microbiology Reports, 2017, 9, 23-24.	2.4	9
526	Impacts of Seasonal Housing and Teat Preparation on Raw Milk Microbiota: a High-Throughput Sequencing Study. Applied and Environmental Microbiology, 2017, 83, .	3.1	104
527	Biotechnological potential of Actinobacteria from Canadian and Azorean volcanic caves. Applied Microbiology and Biotechnology, 2017, 101, 843-857.	3.6	40
528	<scp>ggtree</scp> : an <scp>r</scp> package for visualization and annotation of phylogenetic trees with their covariates and other associated data. Methods in Ecology and Evolution, 2017, 8, 28-36.	5.2	2,998
529	Bacterial microbiota of the upper respiratory tract and childhood asthma. Journal of Allergy and Clinical Immunology, 2017, 139, 826-834.e13.	2.9	165
530	Environmental and mucosal microbiota and their role in childhood asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2017, 72, 109-119.	5.7	94
531	Differential specificity between closely related corals and abundant <i>Endozoicomonas</i> endosymbionts across global scales. ISME Journal, 2017, 11, 186-200.	9.8	259
532	Efficacy and safety of single fecal microbiota transplantation for Japanese patients with mild to moderately active ulcerative colitis. Journal of Gastroenterology, 2017, 52, 476-482.	5.1	66
533	Analysis of bacterial composition in marine sponges reveals the influence of host phylogeny and environment. FEMS Microbiology Ecology, 2017, 93, fiw204.	2.7	31
534	A critical evaluation of ecological indices for the comparative analysis of microbial communities based on molecular datasets. FEMS Microbiology Ecology, 2017, 93, fiw209.	2.7	44
535	Spatiotemporal Characterization of San Francisco Bay Denitrifying Communities: a Comparison of nirK and nirS Diversity and Abundance. Microbial Ecology, 2017, 73, 271-284.	2.8	56
536	Environmental and physiological factors shape the gut microbiota of Atlantic salmon parr (Salmo) Tj ETQq1 I	1 0.784314 rgE	3T ₃₅₄ Overlock
537	Addition of arabinoxylan and mixed linkage glucans in porcine diets affects the large intestinal bacterial populations. European Journal of Nutrition, 2017, 56, 2193-2206.	3.9	27
538	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. Nature Microbiology, 2017, 2, 16221.	13.3	138
539	Composition and diversity of mucosaâ€associated microbiota along the entire length of the pig gastrointestinal tract; dietary influences. Environmental Microbiology, 2017, 19, 1425-1438.	3.8	120
540	Mucosaâ€associated biohydrogenating microbes protect the simulated colon microbiome from stress associated with high concentrations of polyâ€unsaturated fat. Environmental Microbiology, 2017, 19, 722-739.	3.8	18

#	Article	IF	Citations
541	Shared and hostâ€specific microbiome diversity and functioning of grapevine and accompanying weed plants. Environmental Microbiology, 2017, 19, 1407-1424.	3.8	100
542	Experimental metagenomics and ribosomal profiling of the human skin microbiome. Experimental Dermatology, 2017, 26, 211-219.	2.9	34
543	Interleukin-15 promotes intestinal dysbiosis with butyrate deficiency associated with increased susceptibility to colitis. ISME Journal, 2017, 11, 15-30.	9.8	68
544	Household siblings and nasal and fecal microbiota in infants. Pediatrics International, 2017, 59, 473-481.	0.5	32
545	Fecal bacterial communities of wild-captured and stranded green turtles (Chelonia mydas) on the Great Barrier Reef. FEMS Microbiology Ecology, 2017, 93, .	2.7	44
546	Changes in vaginal community state types reflect major shifts in the microbiome. Microbial Ecology in Health and Disease, 2017, 28, 1303265.	3.5	66
547	Shaping of Intestinal Microbiota in Nlrp6- and Rag2-Deficient Mice Depends on Community Structure. Cell Reports, 2017, 21, 3914-3926.	6.4	77
548	Community structure of rare methanogenic archaea: insight from a single functional group. FEMS Microbiology Ecology, 2017, 93, .	2.7	16
549	Lake Bacterial Assemblage Composition Is Sensitive to Biological Disturbance Caused by an Invasive Filter Feeder. MSphere, 2017, 2, .	2.9	13
550	Organismal and spatial partitioning of energy and macronutrient transformations within a hypersaline mat. FEMS Microbiology Ecology, 2017, 93, .	2.7	23
551	Biodegradation of weathered polystyrene films in seawater microcosms. Scientific Reports, 2017, 7, 17991.	3.3	121
552	Preventive Trichuris suis ova (TSO) treatment protects immunocompetent rabbits from DSS colitis but may be detrimental under conditions of immunosuppression. Scientific Reports, 2017, 7, 16500.	3.3	17
553	A comprehensive evaluation of the sl1p pipeline for 16S rRNA gene sequencing analysis. Microbiome, 2017, 5, 100.	11.1	82
554	Upper and lower respiratory tract microbiota in horses: bacterial communities associated with health and mild asthma (inflammatory airway disease) and effects of dexamethasone. BMC Microbiology, 2017, 17, 184.	3.3	49
555	Whole metagenome profiles of particulates collected from the International Space Station. Microbiome, 2017, 5, 81.	11.1	54
556	Enrichment of beneficial bacteria in the skin microbiota of bats persisting with white-nose syndrome. Microbiome, 2017, 5, 115.	11.1	174
557	Tree Leaf Bacterial Community Structure and Diversity Differ along a Gradient of Urban Intensity. MSystems, 2017, 2, .	3.8	49
558	Early nasopharyngeal microbial signature associated with severe influenza in children: a retrospective pilot study. Journal of General Virology, 2017, 98, 2425-2437.	2.9	48

#	Article	IF	CITATIONS
559	The Effects of Weaning Methods on Gut Microbiota Composition and Horse Physiology. Frontiers in Physiology, 2017, 8, 535.	2.8	80
560	Root Hair Mutations Displace the Barley Rhizosphere Microbiota. Frontiers in Plant Science, 2017, 8, 1094.	3.6	85
561	Application of Mycorrhiza and Soil from a Permaculture System Improved Phosphorus Acquisition in Naranjilla. Frontiers in Plant Science, 2017, 8, 1263.	3.6	13
562	Community Profiling of Fusarium in Combination with Other Plant-Associated Fungi in Different Crop Species Using SMRT Sequencing. Frontiers in Plant Science, 2017, 8, 2019.	3.6	46
563	Rhizosphere Microbiome Recruited from a Suppressive Compost Improves Plant Fitness and Increases Protection against Vascular Wilt Pathogens of Tomato. Frontiers in Plant Science, 2017, 8, 2022.	3.6	82
564	Type 1 Diabetes: Urinary Proteomics and Protein Network Analysis Support Perturbation of Lysosomal Function. Theranostics, 2017, 7, 2704-2717.	10.0	30
565	Root and Rhizosphere Bacterial Phosphatase Activity Varies with Tree Species and Soil Phosphorus Availability in Puerto Rico Tropical Forest. Frontiers in Plant Science, 2017, 8, 1834.	3.6	54
566	The Intestinal Eukaryotic and Bacterial Biome of Spotted Hyenas: The Impact of Social Status and Age on Diversity and Composition. Frontiers in Cellular and Infection Microbiology, 2017, 7, 262.	3.9	34
567	Changes in Composition of the Gut Bacterial Microbiome after Fecal Microbiota Transplantation for Recurrent Clostridium difficile Infection in a Pediatric Heart Transplant Patient. Frontiers in Cardiovascular Medicine, 2017, 4, 17.	2.4	28
568	Hot Spring Microbial Community Composition, Morphology, and Carbon Fixation: Implications for Interpreting the Ancient Rock Record. Frontiers in Earth Science, 2017, 5, .	1.8	50
569	Lactobacillus johnsonii N6.2 Modulates the Host Immune Responses: A Double-Blind, Randomized Trial in Healthy Adults. Frontiers in Immunology, 2017, 8, 655.	4.8	73
570	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. Frontiers in Immunology, 2017, 8, 1164.	4.8	77
571	Metabarcoding Reveals Seasonal and Temperature-Dependent Succession of Zooplankton Communities in the Red Sea. Frontiers in Marine Science, 2017, 4, .	2.5	23
572	Evaluation of Filtration and DNA Extraction Methods for Environmental DNA Biodiversity Assessments across Multiple Trophic Levels. Frontiers in Marine Science, 2017, 4, .	2.5	160
573	Temperature and Water Quality-Related Patterns in Sediment-Associated Symbiodinium Communities Impact Symbiont Uptake and Fitness of Juveniles in the Genus Acropora. Frontiers in Marine Science, 2017, 4, .	2.5	51
574	Soil Microbiome Is More Heterogeneous in Organic Than in Conventional Farming System. Frontiers in Microbiology, 2016, 7, 2064.	3.5	250
575	Characterization of Gut Microbiome Dynamics in Developing Pekin Ducks and Impact of Management System. Frontiers in Microbiology, 2016, 7, 2125.	3.5	46
576	Nutritional Models of Experimentally-Induced Subacute Ruminal Acidosis (SARA) Differ in Their Impact on Rumen and Hindgut Bacterial Communities in Dairy Cows. Frontiers in Microbiology, 2016, 7, 2128.	3.5	97

#	Article	IF	Citations
577	Temporal Stability and the Effect of Transgenerational Transfer on Fecal Microbiota Structure in a Long Distance Migratory Bird. Frontiers in Microbiology, 2017, 8, 50.	3.5	70
578	Response of Deep Subsurface Microbial Community to Different Carbon Sources and Electron Acceptors during â ¹ / ₄ 2 months Incubation in Microcosms. Frontiers in Microbiology, 2017, 8, 232.	3.5	39
579	Temporal Variations in Cigarette Tobacco Bacterial Community Composition and Tobacco-Specific Nitrosamine Content Are Influenced by Brand and Storage Conditions. Frontiers in Microbiology, 2017, 08, 358.	3.5	45
580	Differences in Ureolytic Bacterial Composition between the Rumen Digesta and Rumen Wall Based on ureC Gene Classification. Frontiers in Microbiology, 2017, 8, 385.	3.5	65
581	Core Microbiota and Metabolome of Vitis vinifera L. cv. Corvina Grapes and Musts. Frontiers in Microbiology, 2017, 8, 457.	3.5	24
582	Comparative Metagenomics of the Polymicrobial Black Band Disease of Corals. Frontiers in Microbiology, 2017, 8, 618.	3.5	27
583	Toward a Metagenomic Understanding on the Bacterial Composition and Resistome in Hong Kong Banknotes. Frontiers in Microbiology, 2017, 8, 632.	3.5	21
584	Bioreactor Scalability: Laboratory-Scale Bioreactor Design Influences Performance, Ecology, and Community Physiology in Expanded Granular Sludge Bed Bioreactors. Frontiers in Microbiology, 2017, 8, 664.	3.5	36
585	A Critical Assessment of the Microorganisms Proposed to be Important to Enhanced Biological Phosphorus Removal in Full-Scale Wastewater Treatment Systems. Frontiers in Microbiology, 2017, 8, 718.	3.5	212
586	Colonization and Succession within the Human Gut Microbiome by Archaea, Bacteria, and Microeukaryotes during the First Year of Life. Frontiers in Microbiology, 2017, 8, 738.	3.5	207
587	Spatial Structure of the Mormon Cricket Gut Microbiome and its Predicted Contribution to Nutrition and Immune Function. Frontiers in Microbiology, 2017, 8, 801.	3.5	37
588	Different Types of Dietary Fibers Trigger Specific Alterations in Composition and Predicted Functions of Colonic Bacterial Communities in BALB/c Mice. Frontiers in Microbiology, 2017, 8, 966.	3.5	47
589	A Small Number of Low-abundance Bacteria Dominate Plant Species-specific Responses during Rhizosphere Colonization. Frontiers in Microbiology, 2017, 8, 975.	3.5	87
590	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. Frontiers in Microbiology, 2017, 8, 1023.	3.5	32
591	The Impact of Hydration and Temperature on Bacterial Diversity in Arid Soil Mesocosms. Frontiers in Microbiology, 2017, 8, 1078.	3.5	25
592	Characterization of the Microbiome along the Gastrointestinal Tract of Growing Turkeys. Frontiers in Microbiology, 2017, 8, 1089.	3.5	80
593	The Gut Microbiota of Healthy Chilean Subjects Reveals a High Abundance of the Phylum Verrucomicrobia. Frontiers in Microbiology, 2017, 8, 1221.	3.5	225
594	Cutaneous Microbial Community Variation across Populations of Eastern Hellbenders (Cryptobranchus alleganiensis alleganiensis). Frontiers in Microbiology, 2017, 8, 1379.	3.5	39

#	Article	IF	CITATIONS
595	Wood Ash Induced pH Changes Strongly Affect Soil Bacterial Numbers and Community Composition. Frontiers in Microbiology, 2017, 8, 1400.	3.5	74
596	Intestinal Bacterial Communities of Trypanosome-Infected and Uninfected Glossina palpalis palpalis from Three Human African Trypanomiasis Foci in Cameroon. Frontiers in Microbiology, 2017, 8, 1464.	3.5	13
597	Personalization of the Microbiota of Donor Human Milk with Mother's Own Milk. Frontiers in Microbiology, 2017, 8, 1470.	3.5	73
598	Crop Establishment Practices Are a Driver of the Plant Microbiota in Winter Oilseed Rape (Brassica) Tj $$ ETQq 1 1 $$ 0	.784314 r 3.5	gBŢ_/Overlo
599	Cyanobacterial Allelochemicals But Not Cyanobacterial Cells Markedly Reduce Microbial Community Diversity. Frontiers in Microbiology, 2017, 8, 1495.	3.5	31
600	Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. Frontiers in Microbiology, 2017, 8, 1561.	3.5	265
601	Pathobiomes Differ between Two Diseases Affecting Reef Building Coralline Algae. Frontiers in Microbiology, 2017, 8, 1686.	3.5	13
602	Bacterial, Archaeal, and Eukaryotic Diversity across Distinct Microhabitats in an Acid Mine Drainage. Frontiers in Microbiology, 2017, 8, 1756.	3.5	88
603	Legacy Effects on the Recovery of Soil Bacterial Communities from Extreme Temperature Perturbation. Frontiers in Microbiology, 2017, 8, 1832.	3.5	89
604	Phloroglucinol Degradation in the Rumen Promotes the Capture of Excess Hydrogen Generated from Methanogenesis Inhibition. Frontiers in Microbiology, 2017, 8, 1871.	3.5	41
605	Microbial Community and Biochemical Dynamics of Biological Soil Crusts across a Gradient of Surface Coverage in the Central Mojave Desert. Frontiers in Microbiology, 2017, 8, 1974.	3.5	36
606	Alternative Growth Promoters Modulate Broiler Gut Microbiome and Enhance Body Weight Gain. Frontiers in Microbiology, 2017, 8, 2088.	3. 5	88
607	Cadaver Thanatomicrobiome Signatures: The Ubiquitous Nature of Clostridium Species in Human Decomposition. Frontiers in Microbiology, 2017, 8, 2096.	3.5	61
608	Distribution of Abundant and Active Planktonic Ciliates in Coastal and Slope Waters Off New England. Frontiers in Microbiology, 2017, 8, 2178.	3.5	14
609	Microbiome Datasets Are Compositional: And This Is Not Optional. Frontiers in Microbiology, 2017, 8, 2224.	3.5	1,794
610	Low Microbial Diversity and Abnormal Microbial Succession Is Associated with Necrotizing Enterocolitis in Preterm Infants. Frontiers in Microbiology, 2017, 8, 2243.	3.5	72
611	Bacterial Succession on Sinking Particles in the Ocean's Interior. Frontiers in Microbiology, 2017, 8, 2269.	3.5	59
612	Parallelized, Aerobic, Single Carbon-Source Enrichments from Different Natural Environments Contain Divergent Microbial Communities. Frontiers in Microbiology, 2017, 8, 2321.	3.5	21

#	Article	IF	CITATIONS
613	Plant Phylogeny and Life History Shape Rhizosphere Bacterial Microbiome of Summer Annuals in an Agricultural Field. Frontiers in Microbiology, 2017, 8, 2414.	3. 5	56
614	Biological Characterization of Microenvironments in a Hypersaline Cold Spring Mars Analog. Frontiers in Microbiology, 2017, 8, 2527.	3.5	7
615	Uncovering the Potential of Termite Gut Microbiome for Lignocellulose Bioconversion in Anaerobic Batch Bioreactors. Frontiers in Microbiology, 2017, 8, 2623.	3.5	64
616	Comparison of Oropharyngeal Microbiota from Children with Asthma and Cystic Fibrosis. Mediators of Inflammation, 2017, 2017, 1-10.	3.0	32
617	Comparative Metagenomic Analysis of Electrogenic Microbial Communities in Differentially Inoculated Swine Wastewater-Fed Microbial Fuel Cells. Scientifica, 2017, 2017, 1-10.	1.7	7
618	A phylogenetic transform enhances analysis of compositional microbiota data. ELife, 2017, 6, .	6.0	247
619	Primary and heterotrophic productivity relate to multikingdom diversity in a hypersaline mat. FEMS Microbiology Ecology, 2017, 93, .	2.7	7
620	Comparison of bacterial communities from lava cave microbial mats to overlying surface soils from Lava Beds National Monument, USA. PLoS ONE, 2017, 12, e0169339.	2.5	59
621	The distinct features of microbial â€~dysbiosis' of Crohn's disease do not occur to the same extent in their unaffected, genetically-linked kindred. PLoS ONE, 2017, 12, e0172605.	2.5	33
622	Salivary inflammatory markers and microbiome in normoglycemic lean and obese children compared to obese children with type 2 diabetes. PLoS ONE, 2017, 12, e0172647.	2.5	49
623	Unraveling the environmental and anthropogenic drivers of bacterial community changes in the Estuary of Bilbao and its tributaries. PLoS ONE, 2017, 12, e0178755.	2.5	34
624	Variation between the oral and faecal microbiota in a free-living passerine bird, the great tit (Parus) Tj ETQq $1\ 1\ 0$.784314 r	rgBT_/Overloc
625	Natural and artificial feeding management before weaning promote different rumen microbial colonization but not differences in gene expression levels at the rumen epithelium of newborn goats. PLoS ONE, 2017, 12, e0182235.	2.5	39
626	Grape microbiome as a reliable and persistent signature of field origin and environmental conditions in Cannonau wine production. PLoS ONE, 2017, 12, e0184615.	2.5	90
627	Denitrification potential of the eastern oyster microbiome using a 16S rRNA gene based metabolic inference approach. PLoS ONE, 2017, 12, e0185071.	2.5	76
628	Association of high-risk sexual behaviour with diversity of the vaginal microbiota and abundance of Lactobacillus. PLoS ONE, 2017, 12, e0187612.	2.5	38
629	Bile microbiota in primary sclerosing cholangitis: Impact on disease progression and development of biliary dysplasia. PLoS ONE, 2017, 12, e0182924.	2.5	71
630	Development of tailored indigenous marine consortia for the degradation of naturally weathered polyethylene films. PLoS ONE, 2017, 12, e0183984.	2.5	82

#	Article	IF	CITATIONS
631	Quantitative Comparison of Abundance Structures of Generalized Communities: From B-Cell Receptor Repertoires to Microbiomes. PLoS Computational Biology, 2017, 13, e1005362.	3.2	17
632	DNA extraction replicates improve diversity and compositional dissimilarity in metabarcoding of eukaryotes in marine sediments. PLoS ONE, 2017, 12, e0179443.	2.5	64
633	Faecal bacterial microbiota in patients with cirrhosis and the effect of lactulose administration. BMC Gastroenterology, 2017, 17, 125.	2.0	37
634	Gut microbiota and physiologic bowel 18F-FDG uptake. EJNMMI Research, 2017, 7, 72.	2.5	17
635	Season, but not symbiont state, drives microbiome structure in the temperate coral Astrangia poculata. Microbiome, 2017, 5, 120.	11.1	105
636	Associations among dietary non-fiber carbohydrate, ruminal microbiota and epithelium G-protein-coupled receptor, and histone deacetylase regulations in goats. Microbiome, 2017, 5, 123.	11.1	74
637	Bottled aqua incognita: microbiota assembly and dissolved organic matter diversity in natural mineral waters. Microbiome, 2017, 5, 126.	11.1	26
638	Microbes and associated soluble and volatile chemicals on periodically wet household surfaces. Microbiome, 2017, 5, 128.	11.1	45
639	Laboratory colonization stabilizes the naturally dynamic microbiome composition of field collected Dermacentor andersoni ticks. Microbiome, 2017, 5, 133.	11.1	27
640	Morphological and genetic factors shape the microbiome of a seabird species (Oceanodroma) Tj ETQq1 1 0.7845	314 rgBT /	Overlock 10
641	The Inuit gut microbiome is dynamic over time and shaped by traditional foods. Microbiome, 2017, 5, 151.	11.1	53
642	Multi-level comparisons of cloacal, skin, feather and nest-associated microbiota suggest considerable influence of horizontal acquisition on the microbiota assembly of sympatric woodlarks and skylarks. Microbiome, 2017, 5, 156.	11.1	73
643	The gut mycobiome of the Human Microbiome Project healthy cohort. Microbiome, 2017, 5, 153.	11.1	609
644	Sphingolipid metabolism potential in fecal microbiome and bronchiolitis in infants: a case–control study. BMC Research Notes, 2017, 10, 325.	1.4	22
645	Evaluating the accuracy of amplicon-based microbiome computational pipelines on simulated human gut microbial communities. BMC Bioinformatics, 2017, 18, 283.	2.6	51
647	High-throughput sequencing analysis provides a comprehensive insight into the complex bacterial relationships in horticultural growing substrates. Acta Horticulturae, 2017, , 19-26.	0.2	1
648	Prokaryotic Communities at Different Depths between Soils with and without Tomato Bacterial Wilt but Pathogen-Present in a Single Greenhouse. Microbes and Environments, 2017, 32, 118-124.	1.6	11
649	Comparison of Prokaryotic and Eukaryotic Communities in Soil Samples with and without Tomato Bacterial Wilt Collected from Different Fields. Microbes and Environments, 2017, 32, 376-385.	1.6	16

#	Article	IF	CITATIONS
650	Metagenomic analysis exploring taxonomic and functional diversity of soil microbial communities in Chilean vineyards and surrounding native forests. PeerJ, 2017, 5, e3098.	2.0	115
651	Probiotic Bifidobacterium longum NCC3001 Reduces Depression Scores and Alters Brain Activity: A Pilot Study in Patients With Irritable Bowel Syndrome. Gastroenterology, 2017, 153, 448-459.e8.	1.3	542
652	Ferrihydrite-associated organic matter (OM) stimulates reduction by & amp;lt;i& amp;gt;Shewanella oneidensis& amp;lt;/i& amp;gt; MR-1 and a complex microbial consortia. Biogeosciences, 2017, 14, 5171-5188.	3.3	44
653	High-resolution microbiome profiling uncovers <i>Fusobacterium nucleatum</i> , <i>Lactobacillus gasseri/johnsonii</i> , and <i>Lactobacillus vaginalis</i> associated to oral and oropharyngeal cancer in saliva from HPV positive and HPV negative patients treated with surgery and chemo-radiation. Oncotarget, 2017, 8, 110931-110948.	1.8	79
654	Microbial communities in sediment from <i>Zostera marina</i> patches, but not the <i>Z.Âmarina</i> leaf or root microbiomes, vary in relation to distance from patch edge. PeerJ, 2017, 5, e3246.	2.0	115
655	The impact of bacteriophages on phyllosphere bacterial abundance and composition. Molecular Ecology, 2018, 27, 2025-2038.	3.9	82
656	Common Hydraulic Fracturing Fluid Additives Alter the Structure and Function of Anaerobic Microbial Communities. Applied and Environmental Microbiology, 2018, 84, .	3.1	15
657	Porcine Response to a Multidrug-Resistant <i>Salmonella enterica </i> serovar I 4,[5],12:i:- Outbreak Isolate. Foodborne Pathogens and Disease, 2018, 15, 253-261.	1.8	18
658	The immunological functions of the Appendix: An example of redundancy?. Seminars in Immunology, 2018, 36, 31-44.	5.6	68
659	Market Integration Predicts Human Gut Microbiome Attributes across a Gradient of Economic Development. MSystems, 2018, 3, .	3.8	31
660	Gut Microbiome Composition Predicts Infection Risk During Chemotherapy in Children With Acute Lymphoblastic Leukemia. Clinical Infectious Diseases, 2018, 67, 541-548.	5.8	122
661	Landscape topography structures the soil microbiome in arctic polygonal tundra. Nature Communications, 2018, 9, 777.	12.8	105
662	Grape seed proanthocyanidins influence gut microbiota and enteroendocrine secretions in female rats. Food and Function, 2018, 9, 1672-1682.	4.6	87
663	The Gills of Reef Fish Support a Distinct Microbiome Influenced by Host-Specific Factors. Applied and Environmental Microbiology, 2018, 84, .	3.1	96
664	Thermal regime and host clade, rather than geography, drive Symbiodinium and bacterial assemblages in the scleractinian coral Pocillopora damicornis sensu lato. Microbiome, 2018, 6, 39.	11.1	100
665	Prenatal androgen exposure causes hypertension and gut microbiota dysbiosis. Gut Microbes, 2018, 9, 1-22.	9.8	85
666	Alimentary microbes of winterâ€form <i>Drosophila suzukii</i> . Insect Molecular Biology, 2018, 27, 383-392.	2.0	25
667	Effect of dry-rewetting stress on response pattern of soil prokaryotic communities in alpine meadow soil. Applied Soil Ecology, 2018, 126, 98-106.	4.3	12

#	Article	IF	CITATIONS
668	Microbial Community Composition of Tap Water and Biofilms Treated with or without Copper–Silver Ionization. Environmental Science & Environmental S	10.0	22
669	Elevated seawater temperature disrupts the microbiome of an ecologically important bioeroding sponge. Molecular Ecology, 2018, 27, 2124-2137.	3.9	81
670	Large Blooms of <i>Bacillales</i> (<i>Firmicutes</i>) Underlie the Response to Wetting of Cyanobacterial Biocrusts at Various Stages of Maturity. MBio, 2018, 9, .	4.1	28
671	Evolution of a key trait greatly affects underground community assembly process through habitat adaptation in earthworms. Ecology and Evolution, 2018, 8, 1726-1735.	1.9	8
672	Yeast and Bacterial Composition in Pot-Pollen Recovered from Meliponini in Colombia: Prospects for a Promising Biological Resource., 2018,, 263-279.		4
673	Relationship between microbial community, operational factors and ammonia inhibition resilience in anaerobic digesters at low and moderate ammonia background concentrations. New Biotechnology, 2018, 44, 23-30.	4.4	31
674	Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex1. Journal of Animal Science, 2018, 96, 1405-1418.	0.5	50
675	Glucocorticoids modulate gastrointestinal microbiome in a wild bird. Royal Society Open Science, 2018, 5, 171743.	2.4	83
676	Subclinical Cytomegalovirus Infection Is Associated with Altered Host Immunity, Gut Microbiota, and Vaccine Responses. Journal of Virology, 2018, 92, .	3 . 4	33
677	Impact of Long-Term Erythromycin Therapy on the Oropharyngeal Microbiome and Resistance Gene Reservoir in Non-Cystic Fibrosis Bronchiectasis. MSphere, 2018, 3, .	2.9	58
678	Impacts of Glutaraldehyde on Microbial Community Structure and Degradation Potential in Streams Impacted by Hydraulic Fracturing. Environmental Science & Environmental Science & 2018, 52, 5989-5999.	10.0	35
679	Are oceanic fronts ecotones? Seasonal changes along the subtropical front show fronts as bacterioplankton transition zones but not diversity hotspots. Environmental Microbiology Reports, 2018, 10, 184-189.	2.4	18
680	Symbiotic N2-Fixer Community Composition, but Not Diversity, Shifts in Nodules of a Single Host Legume Across a 2-Million-Year Dune Chronosequence. Microbial Ecology, 2018, 76, 1009-1020.	2.8	9
681	Metal contaminations impact archaeal community composition, abundance and function in remote alpine lakes. Environmental Microbiology, 2018, 20, 2422-2437.	3.8	5
682	Comparative analyses of the gut microbiota among three different wild geese species in the genus <i>Anser</i> . Journal of Basic Microbiology, 2018, 58, 543-553.	3.3	10
683	Nematodeâ€associated microbial taxa do not correlate with host phylogeny, geographic region or feeding morphology in marine sediment habitats. Molecular Ecology, 2018, 27, 1930-1951.	3.9	49
684	Presence of Aedes and Anopheles mosquito larvae is correlated to bacteria found in domestic water-storage containers. FEMS Microbiology Ecology, 2018, 94, .	2.7	32
685	Microbiota Composition May Predict Anti-Tnf Alpha Response in Spondyloarthritis Patients: an Exploratory Study. Scientific Reports, 2018, 8, 5446.	3.3	56

#	Article	IF	Citations
686	Soil abiotic variables are more important than Salicaceae phylogeny or habitat specialization in determining soil microbial community structure. Molecular Ecology, 2018, 27, 2007-2024.	3.9	44
687	Cultivation and genomics of the first freshwater SAR11 (LD12) isolate. ISME Journal, 2018, 12, 1846-1860.	9.8	123
688	Feeding-Related Gut Microbial Composition Associates With Peripheral T-Cell Activation and Mucosal Gene Expression in African Infants. Clinical Infectious Diseases, 2018, 67, 1237-1246.	5.8	31
689	Discriminating activated sludge flocs from biofilm microbial communities in a novel pilot-scale reciprocation MBR using high-throughput 16S rRNA gene sequencing. Journal of Environmental Management, 2018, 217, 268-277.	7.8	23
690	Drinking water microbiome assembly induced by water stagnation. ISME Journal, 2018, 12, 1520-1531.	9.8	172
691	Response of Aquatic Bacterial Communities to Hydraulic Fracturing in Northwestern Pennsylvania: A Five-Year Study. Scientific Reports, 2018, 8, 5683.	3.3	29
692	Impact of a vegan diet on the human salivary microbiota. Scientific Reports, 2018, 8, 5847.	3.3	93
693	Carrot Juice Fermentations as Man-Made Microbial Ecosystems Dominated by Lactic Acid Bacteria. Applied and Environmental Microbiology, 2018, 84, .	3.1	62
694	Diversity and metabolic potential of the microbiota associated with a soil arthropod. Scientific Reports, 2018, 8, 2491.	3.3	39
695	Amphibian chytridiomycosis outbreak dynamics are linked with host skin bacterial community structure. Nature Communications, 2018, 9, 693.	12.8	126
696	Unexpected mixed-mode transmission and moderate genetic regulation of Symbiodinium communities in a brooding coral. Heredity, 2018, 121, 524-536.	2.6	53
697	Halotolerant microbial consortia able to degrade highly recalcitrant plant biomass substrate. Applied Microbiology and Biotechnology, 2018, 102, 2913-2927.	3.6	46
698	Rivers may constitute an overlooked avenue of dispersal for terrestrial fungi. Fungal Ecology, 2018, 32, 72-79.	1.6	18
699	Effects of land use on arbuscular mycorrhizal fungal communities in Estonia. Mycorrhiza, 2018, 28, 259-268.	2.8	24
700	Effects of oak, beech and spruce on the distribution and community structure of fungi in litter and soils across a temperate forest. Soil Biology and Biochemistry, 2018, 119, 162-173.	8.8	59
701	Community structure explains antibiotic resistance gene dynamics over a temperature gradient in soil. FEMS Microbiology Ecology, 2018, 94, .	2.7	40
702	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. Cell Host and Microbe, 2018, 23, 229-240.e5.	11.0	292
703	Systems biology of the human microbiome. Current Opinion in Biotechnology, 2018, 51, 146-153.	6.6	28

#	Article	IF	CITATIONS
704	Isotope Fractionation in Biogas Allows Direct Microbial Community Stability Monitoring in Anaerobic Digestion. Environmental Science & Environmental S	10.0	19
705	Microbiome assembly of avian eggshells and their potential as transgenerational carriers of maternal microbiota. ISME Journal, 2018, 12, 1375-1388.	9.8	53
706	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. Cell Metabolism, 2018, 27, 559-571.e5.	16.2	321
707	Initial evenness determines diversity and cell density dynamics in synthetic microbial ecosystems. Scientific Reports, 2018, 8, 340.	3.3	12
708	Vaccination Against Lawsonia intracellularis Decreases Shedding of Salmonella enterica serovar Typhimurium in Co-Infected Pigs and Alters the Gut Microbiome. Scientific Reports, 2018, 8, 2857.	3.3	24
709	Differential Susceptibility to T Cell-Induced Colitis in Mice: Role of the Intestinal Microbiota. Inflammatory Bowel Diseases, 2018, 24, 361-379.	1.9	54
710	Novel Method Reveals a Narrow Phylogenetic Distribution of Bacterial Dispersers in Environmental Communities Exposed to Low-Hydration Conditions. Applied and Environmental Microbiology, 2018, 84,	3.1	2
711	Nephele: a cloud platform for simplified, standardized and reproducible microbiome data analysis. Bioinformatics, 2018, 34, 1411-1413.	4.1	99
712	Antimicrobial and stress responses to increased temperature and bacterial pathogen challenge in the holobiont of a reefâ€building coral. Molecular Ecology, 2018, 27, 1065-1080.	3.9	53
713	Association of Disease Severity With Skin Microbiome and Filaggrin Gene Mutations in Adult Atopic Dermatitis. JAMA Dermatology, 2018, 154, 293.	4.1	108
714	Corallivory and the microbial debacle in two branching scleractinians. ISME Journal, 2018, 12, 1109-1126.	9.8	18
715	MicrobiomeDB: a systems biology platform for integrating, mining and analyzing microbiome experiments. Nucleic Acids Research, 2018, 46, D684-D691.	14.5	47
716	Oral microbiota reduce wound healing capacity of epithelial monolayers, irrespective of the presence of 5-fluorouracil. Experimental Biology and Medicine, 2018, 243, 350-360.	2.4	15
717	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. ISME Journal, 2018, 12, 1344-1359.	9.8	84
718	Microbiome Sequencing Methods for Studying Human Diseases. Methods in Molecular Biology, 2018, 1706, 77-90.	0.9	27
719	A novel approach to wildlife transcriptomics provides evidence of diseaseâ€mediated differential expression and changes to the microbiome of amphibian populations. Molecular Ecology, 2018, 27, 1413-1427.	3.9	32
720	Diversity of root-associated microbial populations of Tamarix parviflora cultivated under various conditions. Applied Soil Ecology, 2018, 125, 264-272.	4.3	16
721	Targeted gene expression panels and microbiota analysis provide insight into the effects of alternative production diet formulations on channel catfish nutritional physiology. Aquaculture, 2018, 489, 46-55.	3.5	7

#	ARTICLE	IF	CITATIONS
722	Cropping practices manipulate abundance patterns of root and soil microbiome members paving the way to smart farming. Microbiome, 2018, 6, 14.	11.1	399
723	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. Nucleic Acids Research, 2018, 46, D726-D735.	14.5	175
724	Shifts in prokaryotic communities under forest and grassland within a tropical mosaic landscape. Applied Soil Ecology, 2018, 125, 156-161.	4.3	2
725	Assembly and ecological function of the root microbiome across angiosperm plant species. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1157-E1165.	7.1	739
726	Evaluation of marine zooplankton community structure through environmental DNA metabarcoding. Limnology and Oceanography: Methods, 2018, 16, 209-221.	2.0	108
727	Illumina DNA metabarcoding of Eucalyptus plantation soil reveals the presence of mycorrhizal and pathogenic fungi. Forestry, 2018, 91, 238-245.	2.3	10
728	Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig (<i>Sus) Tj ETQq0 0 0 rgBT /0</i>	Overlock 1	0 Tf 50 502 T
729	Differences in soil fungal assemblages associated with native and non-native tree species of varying weediness. Biological Invasions, 2018, 20, 891-904.	2.4	2
730	Food Storage by the Savanna Termite Cornitermes cumulans (Syntermitinae): a Strategy to Improve Hemicellulose Digestibility?. Microbial Ecology, 2018, 76, 492-505.	2.8	12
731	Correlation between gut microbiota and personality in adults: A cross-sectional study. Brain, Behavior, and Immunity, 2018, 69, 374-385.	4.1	69
732	A year in the life of a thrombolite: comparative metatranscriptomics reveals dynamic metabolic changes over diel and seasonal cycles. Environmental Microbiology, 2018, 20, 842-861.	3.8	24
733	Structure of association networks in food bacterial communities. Food Microbiology, 2018, 73, 49-60.	4.2	22
734	Comparative Metagenomics. Methods in Molecular Biology, 2018, 1704, 243-260.	0.9	2
735	A retrospective pilot study to determine whether the reproductive tract microbiota differs between women with a history of infertility and fertile women. Australian and New Zealand Journal of Obstetrics and Gynaecology, 2018, 58, 341-348.	1.0	104
736	Associations between <i>Escherichia coli</i> O157 shedding and the faecal microbiota of dairy cows. Journal of Applied Microbiology, 2018, 124, 881-898.	3.1	15
737	Recurrent patterns of microdiversity in a temperate coastal marine environment. ISME Journal, 2018, 12, 237-252.	9.8	135
738	Changes in mouse gut bacterial community in response to different types of drinking water. Water Research, 2018, 132, 79-89.	11.3	47
739	Comammox <i>Nitrospira</i> are abundant ammonia oxidizers in diverse groundwaterâ€fed rapid sand filter communities. Environmental Microbiology, 2018, 20, 1002-1015.	3.8	211

#	Article	IF	CITATIONS
740	Condensed Tannins Affect Bacterial and Fungal Microbiomes and Mycotoxin Production during Ensiling and upon Aerobic Exposure. Applied and Environmental Microbiology, 2018, 84, .	3.1	46
741	Influenza A virus subtype H9N2 infection disrupts the composition of intestinal microbiota of chickens. FEMS Microbiology Ecology, 2018, 94, .	2.7	39
742	Specificity in Arabidopsis thaliana recruitment of root fungal communities from soil and rhizosphere. Fungal Biology, 2018, 122, 231-240.	2.5	58
743	Ambient soil cation exchange capacity inversely associates with infectious and parasitic disease risk in regional Australia. Science of the Total Environment, 2018, 626, 117-125.	8.0	25
744	The Microbial Community of Tardigrades: Environmental Influence and Species Specificity of Microbiome Structure and Composition. Microbial Ecology, 2018, 76, 467-481.	2.8	28
745	The rhizosphere microbial community response to a bio-organic fertilizer: finding the mechanisms behind the suppression of watermelon Fusarium wilt disease. Acta Physiologiae Plantarum, 2018, 40, 1.	2.1	14
746	Injectable antimicrobials in commercial feedlot cattle and their effect on the nasopharyngeal microbiota and antimicrobial resistance. Veterinary Microbiology, 2018, 214, 140-147.	1.9	47
747	FROGS: Find, Rapidly, OTUs with Galaxy Solution. Bioinformatics, 2018, 34, 1287-1294.	4.1	660
748	Maturation of the gut microbiome and risk of asthma in childhood. Nature Communications, 2018, 9, 141.	12.8	380
749	Differences in Clinical Course, Genetics, and the Microbiome Between Familial and Sporadic Inflammatory Bowel Diseases. Journal of Crohn's and Colitis, 2018, 12, 525-531.	1.3	22
750	Illumina sequencing for the identification of filamentous bulking and foaming bacteria in industrial activated sludge plants. International Journal of Environmental Science and Technology, 2018, 15, 1139-1158.	3.5	24
751	Biofouling control in reverse osmosis by nitric oxide treatment and its impact on the bacterial community. Journal of Membrane Science, 2018, 550, 313-321.	8.2	24
752	Short-chain fatty acids regulate systemic bone mass and protect from pathological bone loss. Nature Communications, 2018, 9, 55.	12.8	393
753	Nutrient dynamics and stream order influence microbial community patterns along a 2914 kilometer transect of the Mississippi River. Limnology and Oceanography, 2018, 63, 1837-1855.	3.1	48
754	Identification of Key Bacteria Involved in the Induction of Incident Bacterial Vaginosis: A Prospective Study. Journal of Infectious Diseases, 2018, 218, 966-978.	4.0	70
755	Studying microbial functionality within the gut ecosystem by systems biology. Genes and Nutrition, 2018, 13, 5.	2.5	31
756	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. Genome Biology, 2018, 19, 24.	8.8	180
757	Comparison of normalization methods for the analysis of metagenomic gene abundance data. BMC Genomics, 2018, 19, 274.	2.8	125

#	Article	IF	CITATIONS
758	Bronchiolitis obliterans syndrome susceptibility and the pulmonary microbiome. Journal of Heart and Lung Transplantation, 2018, 37, 1131-1140.	0.6	23
759	Climate-driven shifts in sediment chemistry enhance methane production in northern lakes. Nature Communications, 2018, 9, 1801.	12.8	39
760	Social networks, cooperative breeding, and the human milk microbiome. American Journal of Human Biology, 2018, 30, e23131.	1.6	55
761	Fungal diversity and enzyme activity associated with sailfin sandfish egg masses in Korea. Fungal Ecology, 2018, 34, 1-9.	1.6	14
762	Initial pH influences microbial communities composition in dark fermentation of scotta permeate. International Journal of Hydrogen Energy, 2018, 43, 8707-8717.	7.1	20
763	Diversity, structure and sources of bacterial communities in earthworm cocoons. Scientific Reports, 2018, 8, 6632.	3.3	20
764	Long-term spatial and temporal microbial community dynamics in a large-scale drinking water distribution system with multiple disinfectant regimes. Water Research, 2018, 139, 406-419.	11.3	106
765	Kenaf addition has mixed effects on process performance of sequencing batch reactors treating municipal wastewater. Environmental Science: Water Research and Technology, 2018, 4, 711-720.	2.4	1
766	Investigating Colonization of the Healthy Adult Gastrointestinal Tract by Fungi. MSphere, 2018, 3 , .	2.9	173
767	Temporal response of soil prokaryotic communities to acidification and alkalization under laboratory conditions. European Journal of Soil Biology, 2018, 86, 63-71.	3.2	3
768	Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats. Environmental Science and Pollution Research, 2018, 25, 14743-14751.	5.3	3
769	Host range of antibiotic resistance genes in wastewater treatment plant influent and effluent. FEMS Microbiology Ecology, 2018, 94, .	2.7	148
770	Data and Statistical Methods To Analyze the Human Microbiome. MSystems, 2018, 3, .	3.8	29
771	Oral Antibiotic Treatment of Mice Exacerbates the Disease Severity of Multiple Flavivirus Infections. Cell Reports, 2018, 22, 3440-3453.e6.	6.4	97
772	Earthworm-induced shifts in microbial diversity in soils with rare versus established invasive earthworm populations. FEMS Microbiology Ecology, 2018, 94, .	2.7	19
773	Fecal Microbiome Among Nursing Home Residents with Advanced Dementia and Clostridium difficile. Digestive Diseases and Sciences, 2018, 63, 1525-1531.	2.3	26
774	Changes in Larval Mosquito Microbiota Reveal Non-target Effects of Insecticide Treatments in Hurricane-Created Habitats. Microbial Ecology, 2018, 76, 719-728.	2.8	13
775	Change of the pathway of methane production with progressing anoxic incubation of paddy soil. Soil Biology and Biochemistry, 2018, 121, 177-184.	8.8	39

#	Article	IF	CITATIONS
776	Oral supplementation of <i>Bifidobacterium longum </i> strain BR-108 alters cecal microbiota by stimulating gut immune system in mice irrespectively of viability. Bioscience, Biotechnology and Biochemistry, 2018, 82, 1180-1187.	1.3	19
777	Differential immune responses and microbiota profiles in children with autism spectrum disorders and co-morbid gastrointestinal symptoms. Brain, Behavior, and Immunity, 2018, 70, 354-368.	4.1	163
778	Using mock communities of arbuscular mycorrhizal fungi to evaluate fidelity associated with Illumina sequencing. Fungal Ecology, 2018, 33, 52-64.	1.6	33
779	Nutrient-Dependent Impact of Microbes on <i>Drosophila suzukii</i> Development. MBio, 2018, 9, .	4.1	109
780	Microbial communities in seawater from an Arctic and a temperate Norwegian fjord and their potentials for biodegradation of chemically dispersed oil at low seawater temperatures. Marine Pollution Bulletin, 2018, 129, 308-317.	5.0	35
781	Assessment of Passive Traps Combined with High-Throughput Sequencing To Study Airborne Fungal Communities. Applied and Environmental Microbiology, 2018, 84, .	3.1	39
782	Independent of Birth Mode or Gestational Age, Very-Low-Birth-Weight Infants Fed Their Mothers' Milk Rapidly Develop Personalized Microbiotas Low in Bifidobacterium. Journal of Nutrition, 2018, 148, 326-335.	2.9	22
783	Sulfide inhibition of nitrite oxidation in activated sludge depends on microbial community composition. Water Research, 2018, 138, 241-249.	11.3	69
784	Oyster microbial communities and implications for chalky deposit formation. Hydrobiologia, 2018, 816, 121-135.	2.0	22
785	Influence of fecal collection conditions and 16S rRNA gene sequencing at two centers on human gut microbiota analysis. Scientific Reports, 2018, 8, 4386.	3.3	46
786	Inflammatory phenotypes in patients with severe asthma are associated with distinct airway microbiology. Journal of Allergy and Clinical Immunology, 2018, 141, 94-103.e15.	2.9	233
787	The seed endosphere of Anadenanthera colubrina is inhabited by a complex microbiota, including Methylobacteriumspp. and Staphylococcus spp. with potential plant-growth promoting activities. Plant and Soil, 2018, 422, 81-99.	3.7	44
788	The active bacterial assemblages of the upper GI tract in individuals with and without <i>Helicobacter</i> infection. Gut, 2018, 67, 216-225.	12.1	151
789	Metagenomic analysis reveals changes of the <i>Drosophila suzukii</i> microbiota in the newly colonized regions. Insect Science, 2018, 25, 833-846.	3.0	25
790	Leveraging sequence-based faecal microbial community survey data to identify a composite biomarker for colorectal cancer. Gut, 2018, 67, 882-891.	12.1	159
791	A randomized trial to determine the impact of a digestion resistant starch composition on the gut microbiome in older and mid-age adults. Clinical Nutrition, 2018, 37, 797-807.	5.0	110
792	A prospective microbiomeâ€wide association study of food sensitization and food allergy in early childhood. Allergy: European Journal of Allergy and Clinical Immunology, 2018, 73, 145-152.	5 . 7	163
793	Isotretinoin and lymecycline treatments modify the skin microbiota in acne. Experimental Dermatology, 2018, 27, 30-36.	2.9	48

#	Article	IF	CITATIONS
794	The microbiota of diapause: How host–microbe associations are formed after dormancy in an aquatic crustacean. Journal of Animal Ecology, 2018, 87, 400-413.	2.8	40
795	Intestinal microbiota in patients with chronic hepatitis C with and without cirrhosis compared with healthy controls. Liver International, 2018, 38, 50-58.	3.9	72
796	Seasonal Stability in the Microbiomes of Temperate Gorgonians and the Red Coral Corallium rubrum Across the Mediterranean Sea. Microbial Ecology, 2018, 75, 274-288.	2.8	69
797	Burying beetles regulate the microbiome of carcasses and use it to transmit a core microbiota to their offspring. Molecular Ecology, 2018, 27, 1980-1991.	3.9	71
798	Influence of Host Plant on Thaumetopoea pityocampa Gut Bacterial Community. Microbial Ecology, 2018, 75, 487-494.	2.8	45
799	Microbial Community Structure and Function Decoupling Across a Phosphorus Gradient in Streams. Microbial Ecology, 2018, 75, 64-73.	2.8	33
800	Effects of host species and environment on the skin microbiome of Plethodontid salamanders. Journal of Animal Ecology, 2018, 87, 341-353.	2.8	120
801	Interactive Visualization of Hierarchically Structured Data. Journal of Computational and Graphical Statistics, 2018, 27, 553-563.	1.7	11
802	Microbial Composition Predicts Genital Tract Inflammation and Persistent Bacterial Vaginosis in South African Adolescent Females. Infection and Immunity, 2018, 86, .	2.2	136
803	Impact of Age-Related Mitochondrial Dysfunction and Exercise on Intestinal Microbiota Composition. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 571-578.	3.6	28
804	Bacterial communities in soil become sensitive to drought under intensive grazing. Science of the Total Environment, 2018, 618, 1638-1646.	8.0	33
805	Antibiotic pretreatment minimizes dietary effects on reconstructure of rumen fluid and mucosal microbiota in goats. MicrobiologyOpen, 2018, 7, e00537.	3.0	6
806	Microbiome-driven allergic lung inflammation is ameliorated by short-chain fatty acids. Mucosal Immunology, 2018, 11, 785-795.	6.0	247
807	Gut microbiome in gestational diabetes: a crossâ€sectional study of mothers and offspring 5Âyears postpartum. Acta Obstetricia Et Gynecologica Scandinavica, 2018, 97, 38-46.	2.8	51
808	Quantitative losses vs. qualitative stability of ectomycorrhizal community responses to 3Âyears of experimental summer drought in a beech–spruce forest. Global Change Biology, 2018, 24, e560-e576.	9.5	39
809	Biodegradation of dispersed oil in seawater is not inhibited by a commercial oil spill dispersant. Marine Pollution Bulletin, 2018, 129, 555-561.	5.0	59
810	Dynamic assessment of microbial ecology (DAME): a web app for interactive analysis and visualization of microbial sequencing data. Bioinformatics, 2018, 34, 1050-1052.	4.1	16
811	Excess labile carbon promotes the expression of virulence factors in coral reef bacterioplankton. ISME Journal, 2018, 12, 59-76.	9.8	58

#	Article	IF	CITATIONS
812	Microbial megacities fueled by methane oxidation in a mineral spring cave. ISME Journal, 2018, 12, 87-100.	9.8	34
813	Assembly of seed-associated microbial communities within and across successive plant generations. Plant and Soil, 2018, 422, 67-79.	3.7	91
814	Lipoâ€Protein Emulsion Structure in the Diet Affects Protein Digestion Kinetics, Intestinal Mucosa Parameters and Microbiota Composition. Molecular Nutrition and Food Research, 2018, 62, 1700570.	3.3	16
815	Effect of hydraulic retention time on microbial community in biochemical passive reactors during treatment of acid mine drainage. Bioresource Technology, 2018, 247, 624-632.	9.6	46
816	Diversity and the environmental drivers of spatial variation in Bacteria and micro-Eukarya communities from the Hawaiian anchialine ecosystem. Hydrobiologia, 2018, 806, 265-282.	2.0	14
817	High intake of dairy during energy restriction does not affect energy balance or the intestinal microflora compared with low dairy intake in overweight individuals in a randomized controlled trial. Applied Physiology, Nutrition and Metabolism, 2018, 43, 1-10.	1.9	23
818	Influence of essential oils in diet and life-stage on gut microbiota and fillet quality of rainbow trout (<i>Oncorhynchus mykiss</i>). International Journal of Food Sciences and Nutrition, 2018, 69, 318-333.	2.8	19
819	The nasal and gut microbiome in Parkinson's disease and idiopathic rapid eye movement sleep behavior disorder. Movement Disorders, 2018, 33, 88-98.	3.9	428
820	Contact with turf algae alters the coral microbiome: contact versus systemic impacts. Coral Reefs, 2018, 37, 1-13.	2.2	47
821	Examination of the Bacterial Biodiversity of Coastal Eroded Surface Soils from the Padza de Dapani (Mayotte Island). Geomicrobiology Journal, 2018, 35, 355-365.	2.0	6
822	Soil Microbiomes Associated with Verticillium Wilt-Suppressive Broccoli and Chitin Amendments are Enriched with Potential Biocontrol Agents. Phytopathology, 2018, 108, 31-43.	2.2	71
823	DNA Methylation and Transcription Patterns in Intestinal Epithelial Cells From Pediatric Patients With Inflammatory BowelÂDiseases Differentiate Disease Subtypes and Associate With Outcome. Gastroenterology, 2018, 154, 585-598.	1.3	226
824	VMG II transport medium stabilises oral microbiome samples for Next-Generation Sequencing. Journal of Microbiological Methods, 2018, 144, 91-98.	1.6	5
825	Comparative analysis of gut bacterial communities of green turtles (Chelonia mydas) pre-hospitalization and post-rehabilitation by high-throughput sequencing of bacterial 16S rRNA gene. Microbiological Research, 2018, 207, 91-99.	5.3	45
826	Organic Amendments in a Long-term Field Trialâ€"Consequences for the Bulk Soil Bacterial Community as Revealed by Network Analysis. Microbial Ecology, 2018, 76, 226-239.	2.8	51
827	Diversity and Cyclical Seasonal Transitions in the Bacterial Community in a Large and Deep Perialpine Lake. Microbial Ecology, 2018, 76, 125-143.	2.8	81
828	Bacterial and fungal composition profiling of microbial based cleaning products. Food and Chemical Toxicology, 2018, 116, 25-31.	3.6	6
829	Homogenization of lake cyanobacterial communities over a century of climate change and eutrophication. Nature Ecology and Evolution, 2018, 2, 317-324.	7.8	133

#	Article	IF	CITATIONS
830	Removal of the cecum affects intestinal fermentation, enteric bacterial community structure, and acute colitis in mice. Gut Microbes, 2018, 9, 218-235.	9.8	63
831	Biofilms in shower hoses. Water Research, 2018, 131, 274-286.	11.3	69
832	The microbiome in PTEN hamartoma tumor syndrome. Endocrine-Related Cancer, 2018, 25, 233-243.	3.1	5
833	Associations between infant fungal and bacterial dysbiosis and childhood atopic wheeze in a nonindustrialized setting. Journal of Allergy and Clinical Immunology, 2018, 142, 424-434.e10.	2.9	181
834	Ecological selection of siderophoreâ€producing microbial taxa in response to heavy metal contamination. Ecology Letters, 2018, 21, 117-127.	6.4	97
835	Functional and phylogenetic response of soil prokaryotic community under an artificial moisture gradient. Applied Soil Ecology, 2018, 124, 372-378.	4.3	16
836	Social behaviour and gut microbiota in redâ€bellied lemurs (<i><scp>E</scp>ulemur rubriventer</i>): In search of the role of immunity in the evolution of sociality. Journal of Animal Ecology, 2018, 87, 388-399.	2.8	57
837	Measuring the gut microbiome in birds: Comparison of faecal and cloacal sampling. Molecular Ecology Resources, 2018, 18, 424-434.	4.8	125
838	Gut microbiota composition is associated with environmental landscape in honey bees. Ecology and Evolution, 2018, 8, 441-451.	1.9	106
839	A rare temperate terrestrial orchid selects similar Tulasnella taxa in ex situ and in situ environments. Plant Ecology, 2018, 219, 45-55.	1.6	8
840	Active migration is associated with specific and consistent changes to gut microbiota in <i>Calidris</i> shorebirds. Journal of Animal Ecology, 2018, 87, 428-437.	2.8	73
841	Distinct responses of bacterial communities to agricultural and urban impacts in temperate southern African estuaries. Estuarine, Coastal and Shelf Science, 2018, 200, 224-233.	2.1	4
842	Identification of <i>Syntrophobacteraceae</i> as major acetateâ€degrading sulfate reducing bacteria in Italian paddy soil. Environmental Microbiology, 2018, 20, 337-354.	3.8	45
843	<i>Wolbachia</i> infection alters the relative abundance of resident bacteria in adult <i>Aedes aegypti</i> mosquitoes, but not larvae. Molecular Ecology, 2018, 27, 297-309.	3.9	85
844	Impact of breed on the rumen microbial community composition and methane emission of Holstein Friesian and Belgian Blue heifers. Livestock Science, 2018, 207, 38-44.	1.6	23
845	Metagenomic analysis of the bacterial communities and their functional profiles in water and sediments of the Apies River, South Africa, as a function of land use. Science of the Total Environment, 2018, 616-617, 326-334.	8.0	86
846	Changes in the lung bacteriome in relation to antipseudomonal therapy in children with cystic fibrosis. Folia Microbiologica, 2018, 63, 237-248.	2.3	5
847	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. Gut Microbes, 2018, 9, 38-54.	9.8	66

#	Article	IF	Citations
848	Efficacy of Anaerobic Soil Disinfestation for Control of Prunus Replant Disease. Plant Disease, 2018, 102, 209-219.	1.4	28
849	Microbial Communities in the East and West Fram Strait During Sea Ice Melting Season. Frontiers in Marine Science, 2018, 5, .	2.5	53
850	High-throughput sequencing of fungal communities across the perennial ice block of ScÄ∫riÈ™oara Ice Cave. Annals of Glaciology, 2018, 59, 134-146.	1.4	10
851	Microbiomes of the Arctic carnivorous sponges <i>Chondrocladia grandis</i> and <i>Cladorhiza oxeata</i> suggest a specific, but differential involvement of bacterial associates. Arctic Science, 2018, 4, 186-204.	2.3	14
852	Pneumococcal Colonization and the Nasopharyngeal Microbiota of Children in Botswana. Pediatric Infectious Disease Journal, 2018, 37, 1176-1183.	2.0	11
853	Probiotics Strains Modulate Gut Microbiota and Lipid Metabolism in Mule Ducks. Open Microbiology Journal, 2018, 12, 71-93.	0.7	7
854	Plant Litter Type Dictates Microbial Communities Responsible for Greenhouse Gas Production in Amended Lake Sediments. Frontiers in Microbiology, 2018, 9, 2662.	3.5	14
855	An Integrative Framework for Functional Analysis of Cattle Rumen Microbiomes. , 2018, , .		4
856	Minimal Influence of Extracellular DNA on Molecular Surveys of Marine Sedimentary Communities. Frontiers in Microbiology, 2018, 9, 2969.	3.5	57
857	Rapid increases in soil pH solubilise organic matter, dramatically increase denitrification potential and strongly stimulate microorganisms from the <i>Firmicutes </i> Phylum. PeerJ, 2018, 6, e6090.	2.0	42
858	Candidate Causal Organisms for Apple Replant Disease in the United Kingdom. Phytobiomes Journal, 2018, 2, 261-274.	2.7	43
859	Sample storage conditions induce post-collection biases in microbiome profiles. BMC Microbiology, 2018, 18, 227.	3.3	23
860	Drinking water bacterial communities exhibit specific and selective necrotrophic growth. Npj Clean Water, 2018, 1 , .	8.0	17
861	Fungal Community as a Bioindicator to Reflect Anthropogenic Activities in a River Ecosystem. Frontiers in Microbiology, 2018, 9, 3152.	3.5	34
862	Heterogeneity of Microbial Communities on Deep-Sea Ferromanganese Crusts in the Takuyo-Daigo Seamount. Microbes and Environments, 2018, 33, 366-377.	1.6	18
863	Linkages between geochemistry and microbiology in a proglacial terrain in the High Arctic. Annals of Glaciology, 2018, 59, 95-110.	1.4	11
864	Temporal Dynamics of Bacterial Communities in Soil and Leachate Water After Swine Manure Application. Frontiers in Microbiology, 2018, 9, 3197.	3.5	30
865	Assessing the impact of plant genetic diversity in shaping the microbial community structure of <i>Vitis vinifera</i> phyllosphere in the Mediterranean. Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences, 2018, 11, 35-46.	1.1	21

#	Article	IF	Citations
866	An adaptive microbiome α-diversity-based association analysis method. Scientific Reports, 2018, 8, 18026.	3.3	34
868	Rare Biosphere Archaea Assimilate Acetate in Precambrian Terrestrial Subsurface at 2.2 km Depth. Geosciences (Switzerland), 2018, 8, 418.	2.2	14
869	Microbiome shifts with onset and progression of Sea Star Wasting Disease revealed through time course sampling. Scientific Reports, 2018, 8, 16476.	3.3	34
870	The effect of drinking water pH on the human gut microbiota and glucose regulation: results of a randomized controlled cross-over intervention. Scientific Reports, 2018, 8, 16626.	3.3	26
871	Butyrate Producers as Potential Next-Generation Probiotics: Safety Assessment of the Administration of $\langle i \rangle$ Butyricicoccus pullicaecorum $\langle i \rangle$ to Healthy Volunteers. MSystems, 2018, 3, .	3.8	99
872	Quantitative Approach in Clinical Microbiology: A Paradigm Shift Toward Culture-Free Methods. , 2018, , 599-615.		1
873	Re-purposing 16S rRNA gene sequence data from within case paired tumor biopsy and tumor-adjacent biopsy or fecal samples to identify microbial markers for colorectal cancer. PLoS ONE, 2018, 13, e0207002.	2.5	25
874	Chronic Physical Disturbance Substantially Alters the Response of Biological Soil Crusts to a Wetting Pulse, as Characterized by Metatranscriptomic Sequencing. Frontiers in Microbiology, 2018, 9, 2382.	3.5	40
875	Taxa: An R package implementing data standards and methods for taxonomic data. F1000Research, 2018, 7, 272.	1.6	12
876	Gut microbiome transition across a lifestyle gradient in Himalaya. PLoS Biology, 2018, 16, e2005396.	5.6	128
877	Effect of gastric fluid aspiration on the lung microbiota of laboratory rats. Experimental Lung Research, 2018, 44, 201-210.	1.2	4
878	High Microbial Diversity Despite Extremely Low Biomass in a Deep Karst Aquifer. Frontiers in Microbiology, 2018, 9, 2823.	3.5	34
879	The prevalence and transcriptional activity of the mucosal microbiota of ulcerative colitis patients. Scientific Reports, 2018, 8, 17278.	3.3	17
880	Gut microbiome composition is associated with spatial structuring and social interactions in semi-feral Welsh Mountain ponies. Microbiome, 2018, 6, 207.	11.1	72
881	Coral-associated bacteria demonstrate phylosymbiosis and cophylogeny. Nature Communications, 2018, 9, 4921.	12.8	264
882	Impacts of Diet and Exercise on Maternal Gut Microbiota Are Transferred to Offspring. Frontiers in Endocrinology, 2018, 9, 716.	3.5	47
883	Roots and Panicles of the C4 Model Grasses Setaria viridis (L). and S. pumila Host Distinct Bacterial Assemblages With Core Taxa Conserved Across Host Genotypes and Sampling Sites. Frontiers in Microbiology, 2018, 9, 2708.	3.5	15
884	Decreased microbial co-occurrence network stability and SCFA receptor level correlates with obesity in African-origin women. Scientific Reports, 2018, 8, 17135.	3.3	42

#	Article	IF	CITATIONS
885	Combining morpho-taxonomy and metabarcoding enhances the detection of non-indigenous marine pests in biofouling communities. Scientific Reports, 2018, 8, 16290.	3.3	46
886	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. MSystems, 2018, 3, .	3.8	56
887	Reevaluating the Salty Divide: Phylogenetic Specificity of Transitions between Marine and Freshwater Systems. MSystems, 2018, 3, .	3.8	37
888	Characterization of the Microbiome at the World's Largest Potable Water Reuse Facility. Frontiers in Microbiology, 2018, 9, 2435.	3.5	43
889	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. Science Translational Medicine, $2018,10,10$	12.4	121
890	Terminal restriction fragment length polymorphism is an "old school―reliable technique for swift microbial community screening in anaerobic digestion. Scientific Reports, 2018, 8, 16818.	3.3	48
891	Fecal microbiota associated with phytohaemagglutininâ€induced immune response in nestlings of a passerine bird. Ecology and Evolution, 2018, 8, 9793-9802.	1.9	10
892	Functional and taxonomic classification of a greenhouse water drain metagenome. Standards in Genomic Sciences, 2018, 13, 20.	1.5	2
893	Bacterial Diversity and the Geochemical Landscape in the Southwestern Gulf of Mexico. Frontiers in Microbiology, 2018, 9, 2528.	3.5	39
894	Specific Effect of Trace Metals on Marine Heterotrophic Microbial Activity and Diversity: Key Role of Iron and Zinc and Hydrocarbon-Degrading Bacteria. Frontiers in Microbiology, 2018, 9, 3190.	3.5	15
895	Bacterial Associates of a Gregarious Riparian Beetle With Explosive Defensive Chemistry. Frontiers in Microbiology, 2018, 9, 2361.	3.5	19
896	Rhizosphere Microbial Communities of Spartina alterniflora and Juncus roemerianus From Restored and Natural Tidal Marshes on Deer Island, Mississippi. Frontiers in Microbiology, 2018, 9, 3049.	3.5	20
897	Microbiome analysis of Pacific white shrimp gut and rearing water from Malaysia and Vietnam: implications for aquaculture research and management. PeerJ, 2018, 6, e5826.	2.0	71
898	Carbon Source and Soil Origin Shape Soil Microbiomes and Tomato Soilborne Pathogen Populations During Anaerobic Soil Disinfestation. Phytobiomes Journal, 2018, 2, 138-150.	2.7	29
899	Stability and resilience of the intestinal microbiota in children in daycare – a 12 month cohort study. BMC Microbiology, 2018, 18, 223.	3.3	15
900	Commensals Suppress Intestinal Epithelial Cell Retinoic Acid Synthesis to Regulate Interleukin-22 Activity and Prevent Microbial Dysbiosis. Immunity, 2018, 49, 1103-1115.e6.	14.3	139
901	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. Microbiome, 2018, 6, 226.	11.1	1,729
902	Profiling mycobacterial communities in pulmonary nontuberculous mycobacterial disease. PLoS ONE, 2018, 13, e0208018.	2.5	13

#	Article	IF	CITATIONS
903	Metabolomics and 16S rRNA sequencing of human colorectal cancers and adjacent mucosa. PLoS ONE, 2018, 13, e0208584.	2.5	39
904	Cow responses and evolution of the rumen bacterial and methanogen community following a complete rumen content transfer. Journal of Agricultural Science, 2018, 156, 1047-1058.	1.3	5
905	Comparison of Bacterial Diversity in Air and Water of a Major Urban Center. Frontiers in Microbiology, 2018, 9, 2868.	3.5	24
906	Both the intratumoral immune and microbial microenvironment are linked to recurrence in human colon cancer: results from a prospective, multicenter nodal ultrastaging trial. Oncotarget, 2018, 9, 23564-23576.	1.8	7
907	Transcriptome-Stable Isotope Probing Provides Targeted Functional and Taxonomic Insights Into Microaerobic Pollutant-Degrading Aquifer Microbiota. Frontiers in Microbiology, 2018, 9, 2696.	3.5	20
908	Assessment of Microbial Community Dynamics in River Bank Filtrate Using High-Throughput Sequencing and Flow Cytometry. Frontiers in Microbiology, 2018, 9, 2887.	3.5	26
909	Design and application of a novel two-amplicon approach for defining eukaryotic microbiota. Microbiome, 2018, 6, 228.	11.1	18
910	A 12-wk whole-grain wheat intervention protects against hepatic fat: the Graandioos study, a randomized trial in overweight subjects. American Journal of Clinical Nutrition, 2018, 108, 1264-1274.	4.7	50
911	Long-term colonisation with donor bacteriophages following successful faecal microbial transplantation. Microbiome, 2018, 6, 220.	11,1	116
912	Ascitic Bacterial Composition Is Associated With Clinical Outcomes in Cirrhotic Patients With Culture-Negative and Non-neutrocytic Ascites. Frontiers in Cellular and Infection Microbiology, 2018, 8, 420.	3.9	13
913	Impact of Individual Traits, Saturated Fat, and Protein Source on the Gut Microbiome. MBio, 2018, 9, .	4.1	70
914	Developing reproducible bioinformatics analysis workflows for heterogeneous computing environments to support African genomics. BMC Bioinformatics, 2018, 19, 457.	2.6	33
915	Environmental DNA: A New Low-Cost Monitoring Tool for Pathogens in Salmonid Aquaculture. Frontiers in Microbiology, 2018, 9, 3009.	3.5	47
916	A comparative study of the gut microbiota in immune-mediated inflammatory diseases—does a common dysbiosis exist?. Microbiome, 2018, 6, 221.	11.1	303
917	Impact of CFTR modulation with Ivacaftor on Gut Microbiota and Intestinal Inflammation. Scientific Reports, 2018, 8, 17834.	3.3	99
918	Performance Evaluation of Normalization Approaches for Metagenomic Compositional Data on Differential Abundance Analysis. ICSA Book Series in Statistics, 2018, , 329-344.	0.2	5
919	Microbial dysbiosis and mortality during mechanical ventilation: a prospective observational study. Respiratory Research, 2018, 19, 245.	3.6	64
920	Citizen science charts two major "stomatotypes―in the oral microbiome of adolescents and reveals links with habits and drinking water composition. Microbiome, 2018, 6, 218.	11.1	86

#	Article	IF	CITATIONS
921	Gut microbial features can predict host phenotype response to protein deficiency. Physiological Reports, 2018, 6, e13932.	1.7	17
922	Host-targeted niclosamide inhibits C. difficile virulence and prevents disease in mice without disrupting the gut microbiota. Nature Communications, 2018, 9, 5233.	12.8	40
923	Members of the Uncultured Taxon OP1 ("Acetothermiaâ€) Predominate in the Microbial Community of an Alkaline Hot Spring at East-Tuvinian Upland. Microbiology, 2018, 87, 783-795.	1.2	6
924	Microbiota profile in new-onset pediatric Crohn's disease: data from a non-Western population. Gut Pathogens, 2018, 10, 49.	3.4	35
925	Reproductive and Behavior Dysfunction Induced by Maternal Androgen Exposure and Obesity Is Likely Not Gut Microbiome-Mediated. Journal of the Endocrine Society, 2018, 2, 1363-1380.	0.2	8
926	Impact of Dinophysis acuminata Feeding Mesodinium rubrum on Nutrient Dynamics and Bacterial Composition in a Microcosm. Toxins, 2018, 10, 443.	3.4	24
927	Land-Use Intensity Rather Than Plant Functional Identity Shapes Bacterial and Fungal Rhizosphere Communities. Frontiers in Microbiology, 2018, 9, 2711.	3.5	62
928	Responses of the Endophytic Bacterial Communities of Juncus acutus to Pollution With Metals, Emerging Organic Pollutants and to Bioaugmentation With Indigenous Strains. Frontiers in Plant Science, 2018, 9, 1526.	3.6	35
929	Birth mode is associated with earliest strain-conferred gut microbiome functions and immunostimulatory potential. Nature Communications, 2018, 9, 5091.	12.8	190
930	Short- and long-term impacts of azithromycin treatment on the gut microbiota in children: A double-blind, randomized, placebo-controlled trial. EBioMedicine, 2018, 38, 265-272.	6.1	58
931	Bacterial Diversity Associated With the Rhizosphere and Endosphere of Two Halophytes: Glaux maritima and Salicornia europaea. Frontiers in Microbiology, 2018, 9, 2878.	3.5	73
932	Depth and Dissolved Organic Carbon Shape Microbial Communities in Surface Influenced but Not Ancient Saline Terrestrial Aquifers. Frontiers in Microbiology, 2018, 9, 2880.	3.5	20
933	Effects of Gut Bacteria Depletion and Highâ€Na+and Lowâ€K+Intake on Circulating Levels of Biogenic Amines. Molecular Nutrition and Food Research, 2018, 63, 1801184.	3.3	12
934	Skin and gut microbiomes of a wild mammal respond to different environmental cues. Microbiome, 2018, 6, 209.	11.1	47
935	Gut microbiota diversity across ethnicities in the United States. PLoS Biology, 2018, 16, e2006842.	5.6	216
936	Opportunistic Bacteria Dominate the Soil Microbiome Response to Phenanthrene in a Microcosm-Based Study. Frontiers in Microbiology, 2018, 9, 2815.	3.5	19
937	A Method for Collecting Atmospheric Microbial Samples From Set Altitudes for Use With Next-Generation Sequencing Techniques to Characterize Communities. Air, Soil and Water Research, 2018, 11, 117862211878887.	2.5	8
938	Accounting for Bacterial Overlap Between Raw Water Communities and Contaminating Sources Improves the Accuracy of Signature-Based Microbial Source Tracking. Frontiers in Microbiology, 2018, 9, 2364.	3.5	16

#	Article	IF	Citations
939	Deciphering intra-species bacterial diversity of meat and seafood spoilage microbiota using gyrB amplicon sequencing: A comparative analysis with 16S rDNA V3-V4 amplicon sequencing. PLoS ONE, 2018, 13, e0204629.	2.5	84
940	Airborne Bacteria in Earth's Lower Stratosphere Resemble Taxa Detected in the Troposphere: Results From a New NASA Aircraft Bioaerosol Collector (ABC). Frontiers in Microbiology, 2018, 9, 1752.	3.5	64
941	Comparative assessment of autochthonous bacterial and fungal communities and microbial biomarkers of polluted agricultural soils of the Terra dei Fuochi. Scientific Reports, 2018, 8, 14281.	3.3	45
942	Titanium as a modifier of the periâ€implant microbiome structure. Clinical Implant Dentistry and Related Research, 2018, 20, 945-953.	3.7	58
943	Host diet mediates a negative relationship between abundance and diversity of <i>Drosophila</i> gut microbiota. Ecology and Evolution, 2018, 8, 9491-9502.	1.9	29
944	Antibiotic Effects on Microbial Communities Responsible for Denitrification and N2O Production in Grassland Soils. Frontiers in Microbiology, 2018, 9, 2121.	3.5	55
945	Expansion of commensal fungus Wallemia mellicola in the gastrointestinal mycobiota enhances the severity of allergic airway disease in mice. PLoS Pathogens, 2018, 14, e1007260.	4.7	76
946	Evolution of the nasopharyngeal bacterial microbiota of beef calves from spring processing to 40 days after feedlot arrival. Veterinary Microbiology, 2018, 225, 139-148.	1.9	30
947	Intestinal microbiota profiling and predicted metabolic dysregulation in psoriasis patients. Experimental Dermatology, 2018, 27, 1336-1343.	2.9	79
948	The gut of the finch: uniqueness of the gut microbiome of the Gal \tilde{A}_i pagos vampire finch. Microbiome, 2018, 6, 167.	11.1	63
949	Temporal dynamics and compartment specific rice straw degradation in bulk soil and the rhizosphere of maize. Soil Biology and Biochemistry, 2018, 127, 200-212.	8.8	34
950	The effects of amine-modified single-walled carbon nanotubes on the mouse microbiota. International Journal of Nanomedicine, 2018, Volume 13, 5275-5286.	6.7	2
951	Integrating coalescent species delimitation with analysis of host specificity reveals extensive cryptic diversity despite minimal mitochondrial divergence in the malaria parasite genus Leucocytozoon. BMC Evolutionary Biology, 2018, 18, 128.	3.2	49
952	The time response of anaerobic digestion microbiome during an organic loading rate shock. Applied Microbiology and Biotechnology, 2018, 102, 10285-10297.	3.6	29
953	Rabbit Microbiota Changes Throughout the Intestinal Tract. Frontiers in Microbiology, 2018, 9, 2144.	3.5	50
954	Microbiota disruption leads to reduced cold tolerance in Drosophila flies. Die Naturwissenschaften, 2018, 105, 59.	1.6	27
955	Air and waterborne microbiome of a pharmaceutical plant provide insights on spatiotemporal variations and community resilience after disturbance. BMC Microbiology, 2018, 18, 124.	3.3	5
956	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. Nature Communications, 2018, 9, 3891.	12.8	313

#	Article	IF	CITATIONS
957	Systematic Comparison of Bacterial Colonization of Endometrial Tissue and Fluid Samples in Recurrent Miscarriage Patients: Implications for Future Endometrial Microbiome Studies. Clinical Chemistry, 2018, 64, 1743-1752.	3.2	45
958	Comprehensive Longitudinal Microbiome Analysis of the Chicken Cecum Reveals a Shift From Competitive to Environmental Drivers and a Window of Opportunity for Campylobacter. Frontiers in Microbiology, 2018, 9, 2452.	3.5	60
959	Microbial responses to combined oxidation and catalysis treatment of 1,4-dioxane and co-contaminants in groundwater and soil. Frontiers of Environmental Science and Engineering, 2018, 12, 1.	6.0	12
960	Neonatally imprinted stromal cell subsets induce tolerogenic dendritic cells in mesenteric lymph nodes. Nature Communications, 2018, 9, 3903.	12.8	69
961	Unlocking preservation bias in the amber insect fossil record through experimental decay. PLoS ONE, 2018, 13, e0195482.	2.5	12
962	Autoprobiotics as an Approach for Restoration of Personalised Microbiota. Frontiers in Microbiology, 2018, 9, 1869.	3.5	28
963	Normalization of Microbiome Profiling Data. Methods in Molecular Biology, 2018, 1849, 143-168.	0.9	10
964	Characterization of Eukaryotic Microbiome Using 18S Amplicon Sequencing. Methods in Molecular Biology, 2018, 1849, 29-48.	0.9	10
965	Culture and Molecular Profiling of the Respiratory Tract Microbiota. Methods in Molecular Biology, 2018, 1849, 49-61.	0.9	2
966	Introductory Overview of Statistical Analysis of Microbiome Data. ICSA Book Series in Statistics, 2018, , 43-75.	0.2	7
967	Effect of a butyrate-fortified milk replacer on gastrointestinal microbiota and products of fermentation in artificially reared dairy calves at weaning. Scientific Reports, 2018, 8, 14901.	3.3	37
968	Tomato Seeds Preferably Transmit Plant Beneficial Endophytes. Phytobiomes Journal, 2018, 2, 183-193.	2.7	124
969	Exploratory Analysis of Microbiome Data and Beyond. ICSA Book Series in Statistics, 2018, , 191-249.	0.2	3
970	Understanding the Mechanisms Behind the Response to Environmental Perturbation in Microbial Mats: A Metagenomic-Network Based Approach. Frontiers in Microbiology, 2018, 9, 2606.	3.5	41
971	Diversity of foliar endophytic ascomycetes in the endemic Corsican pine forests. Fungal Ecology, 2018, 36, 128-140.	1.6	14
972	Microbiome composition within a sympatric species complex of intertidal isopods (Jaera albifrons). PLoS ONE, 2018, 13, e0202212.	2.5	12
973	Stability of Ferrihydrite–Humic Acid Coprecipitates under Iron-Reducing Conditions. Environmental Science & Conditions and Science & Conditions	10.0	31
974	Gut microbiota and plasma metabolites associated with diabetes in women with, or at high risk for, HIV infection. EBioMedicine, 2018, 37, 392-400.	6.1	61

#	ARTICLE	IF	CITATIONS
975	Host blood meal source has a strong impact on gut microbiota of Aedes aegypti. FEMS Microbiology Ecology, $2019, 95, .$	2.7	80
976	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. Genome Medicine, 2018, 10, 78.	8.2	107
977	Reduced diversity of gut microbiota in two Aedes mosquitoes species in areas of recent invasion. Scientific Reports, 2018, 8, 16091.	3.3	41
978	The endangered northern bettong, <i>Bettongia tropica</i> , performs a unique and potentially irreplaceable dispersal function for ectomycorrhizal truffle fungi. Molecular Ecology, 2018, 27, 4960-4971.	3.9	13
979	Spatial Structuring of Cellulase Gene Abundance and Activity in Soil. Frontiers in Environmental Science, 2018, 6, .	3.3	4
980	Intra-host Symbiont Diversity and Extended Symbiont Maintenance in Photosymbiotic Acantharea (Clade F). Frontiers in Microbiology, 2018, 9, 1998.	3.5	14
981	Plant Nutrient Resource Use Strategies Shape Active Rhizosphere Microbiota Through Root Exudation. Frontiers in Plant Science, 2018, 9, 1662.	3.6	67
982	Legitimate visitors and nectar robbers of <i>Aquilegia formosa</i> have different effects on nectar bacterial communities. Ecosphere, 2018, 9, e02459.	2.2	16
983	Assessing Pathogen Presence in an Intensively Tile Drained, Agricultural Watershed. Journal of Environmental Quality, 2018, 47, 1033-1042.	2.0	14
984	Bacterial Communities in Tissues and Surficial Mucus of the Cold-Water Coral Paragorgia arborea. Frontiers in Marine Science, 2018, 5, .	2.5	35
985	Association with a sea anemone alters the skin microbiome of clownfish. Coral Reefs, 2018, 37, 1119-1125.	2.2	17
986	Genotype-Environment Interaction Shapes the Microbial Assemblage in Grapevine's Phyllosphere and Carposphere: An NGS Approach. Microorganisms, 2018, 6, 96.	3.6	54
987	Cetobacterium Is a Major Component of the Microbiome of Giant Amazonian Fish (Arapaima gigas) in Ecuador. Animals, 2018, 8, 189.	2.3	74
988	Soil microbial response following wildfires in thermic oak-pine forests. Biology and Fertility of Soils, 2018, 54, 985-997.	4.3	17
989	Untangling the knots: Coâ€infection and diversity of <i>Bartonella</i> from wild gerbils and their associated fleas. Molecular Ecology, 2018, 27, 4787-4807.	3.9	37
990	Biodiversity–function relationships in methanogenic communities. Molecular Ecology, 2018, 27, 4641-4651.	3.9	30
991	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dysbiosis and alteration of community structure. Microbiome, 2018, 6, 180.	11.1	23
992	Effects of Chloramine and Coupon Material on Biofilm Abundance and Community Composition in Bench-Scale Simulated Water Distribution Systems and Comparison with Full-Scale Water Mains. Environmental Science & Environmental	10.0	42

#	Article	IF	CITATIONS
993	Immune-suppression by OsHV-1 viral infection causes fatal bacteraemia in Pacific oysters. Nature Communications, 2018, 9, 4215.	12.8	217
994	Liver Injury, Endotoxemia, and Their Relationship to Intestinal Microbiota Composition in Alcoholâ€Preferring Rats. Alcoholism: Clinical and Experimental Research, 2018, 42, 2313-2325.	2.4	29
995	Protists Within Corals: The Hidden Diversity. Frontiers in Microbiology, 2018, 9, 2043.	3.5	39
996	Anaerobic lignocellulolytic microbial consortium derived from termite gut: enrichment, lignocellulose degradation and community dynamics. Biotechnology for Biofuels, 2018, 11, 284.	6.2	32
997	Reindeer grazing alter soil fungal community structure and litter decomposition related enzyme activities in boreal coniferous forests in Finnish Lapland. Applied Soil Ecology, 2018, 132, 74-82.	4.3	20
998	Striped UniFrac: enabling microbiome analysis at unprecedented scale. Nature Methods, 2018, 15, 847-848.	19.0	71
999	Species-level bacterial community profiling of the healthy sinonasal microbiome using Pacific Biosciences sequencing of full-length 16S rRNA genes. Microbiome, 2018, 6, 190.	11.1	117
1000	The impact of exercise training and resveratrol supplementation on gut microbiota composition in high-fat diet fed mice. Physiological Reports, 2018, 6, e13881.	1.7	24
1001	A Nematode of the Mid-Atlantic Ridge Hydrothermal Vents Harbors a Possible Symbiotic Relationship. Frontiers in Microbiology, 2018, 9, 2246.	3.5	38
1002	Virus–virus interactions and host ecology are associated with <scp>RNA</scp> virome structure in wild birds. Molecular Ecology, 2018, 27, 5263-5278.	3.9	77
1003	The Cloacal Microbiome of Five Wild Duck Species Varies by Species and Influenza A Virus Infection Status. MSphere, 2018, 3, .	2.9	28
1004	Comparing the bacterial communities of wild and captive golden mantella frogs: Implications for amphibian conservation. PLoS ONE, 2018, 13, e0205652.	2.5	12
1005	Bleaching-Associated Changes in the Microbiome of Large Benthic Foraminifera of the Great Barrier Reef, Australia. Frontiers in Microbiology, 2018, 9, 2404.	3.5	12
1006	Impact of DNA Sequencing and Analysis Methods on 16S rRNA Gene Bacterial Community Analysis of Dairy Products. MSphere, 2018, 3, .	2.9	49
1007	Uncovering vector, parasite, blood meal and microbiome patterns from mixed-DNA specimens of the Chagas disease vector Triatoma dimidiata. PLoS Neglected Tropical Diseases, 2018, 12, e0006730.	3.0	38
1008	Experimental Evidence of Functional Group-Dependent Effects of Tree Diversity on Soil Fungi in Subtropical Forests. Frontiers in Microbiology, 2018, 9, 2312.	3.5	28
1009	Biogeographic and anthropogenic correlates of Aleutian Islands plant diversity: A machineâ€learning approach. Journal of Systematics and Evolution, 2018, 56, 476-497.	3.1	9
1010	Poisoning with Soman, an Organophosphorus Nerve Agent, Alters Fecal Bacterial Biota and Urine Metabolites: a Case for Novel Signatures for Asymptomatic Nerve Agent Exposure. Applied and Environmental Microbiology, 2018, 84, .	3.1	6

#	Article	IF	CITATIONS
1011	The relationship of cervical microbiota diversity with race and disparities in preterm birth. Journal of Neonatal-Perinatal Medicine, 2018, 11, 305-310.	0.8	12
1012	Dietary Cows' Milk Protein A1 Beta-Casein Increases the Incidence of T1D in NOD Mice. Nutrients, 2018, 10, 1291.	4.1	30
1013	Biodegradability of polar compounds formed from weathered diesel. Biodegradation, 2018, 29, 443-461.	3.0	10
1014	Oral administration of viable Bifidobacterium pseudolongum strain Patronus modified colonic microbiota and increased mucus layer thickness in rat. FEMS Microbiology Ecology, 2018, 94, .	2.7	22
1015	A Single Vibrionales 16S rRNA Oligotype Dominates the Intestinal Microbiome in Two Geographically Separated Atlantic cod Populations. Frontiers in Microbiology, 2018, 9, 1561.	3.5	18
1016	Comparisons of gut microbiota profiles in wild-type and gelatinase B/matrix metalloproteinase-9-deficient mice in acute DSS-induced colitis. Npj Biofilms and Microbiomes, 2018, 4, 18.	6.4	10
1017	Oil type and temperature dependent biodegradation dynamics - Combining chemical and microbial community data through multivariate analysis. BMC Microbiology, 2018, 18, 83.	3.3	59
1018	High-resolution ISR amplicon sequencing reveals personalized oral microbiome. Microbiome, 2018, 6, 153.	11.1	32
1019	Assessment of Bacterial Communities Associated With the Skin of Costa Rican Amphibians at La Selva Biological Station. Frontiers in Microbiology, 2018, 9, 2001.	3. 5	21
1020	Plankton community assessment in anthropogenic-impacted oligotrophic coastal regions. Environmental Science and Pollution Research, 2018, 25, 31017-31030.	5.3	9
1021	Root-Associated Microbiome of Maize Genotypes with Contrasting Phosphorus Use Efficiency. Phytobiomes Journal, 2018, 2, 129-137.	2.7	59
1022	Lignocellulose degradation at the holobiont level: teamwork in a keystone soil invertebrate. Microbiome, 2018, 6, 162.	11.1	70
1023	Comparison of initial oral microbiomes of young adults with and without cavitated dentin caries lesions using an in situ biofilm model. Scientific Reports, 2018, 8, 14010.	3.3	12
1024	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. Genome Research, 2018, 28, 1467-1480.	5.5	117
1025	Exposures Related to House Dust Microbiota in a U.S. Farming Population. Environmental Health Perspectives, 2018, 126, 067001.	6.0	23
1026	Aquatic Bacterial Communities Associated With Land Use and Environmental Factors in Agricultural Landscapes Using a Metabarcoding Approach. Frontiers in Microbiology, 2018, 9, 2301.	3.5	44
1027	Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. Cell, 2018, 175, 277-291.e31.	28.9	137
1028	Antibiotic multidrug resistance in the cystic fibrosis airway microbiome is associated with decreased diversity. Heliyon, 2018, 4, e00795.	3.2	31

#	Article	IF	CITATIONS
1029	Direct-fed microbial supplementation influences the bacteria community composition of the gastrointestinal tract of pre- and post-weaned calves. Scientific Reports, 2018, 8, 14147.	3.3	50
1030	Bacterial community response to a preindustrialâ€toâ€future CO ₂ gradient is limited and soil specific in Texas Prairie grassland. Global Change Biology, 2018, 24, 5815-5827.	9.5	8
1031	Cloacal and Ocular Microbiota of the Endangered Australian Northern Quoll. Microorganisms, 2018, 6, 68.	3.6	5
1032	Effects of extruded aquafeed on growth performance and gut microbiome of juvenile Totoaba macdonaldi. Animal Feed Science and Technology, 2018, 245, 91-103.	2.2	34
1033	Comparison of microbial community dynamics induced by distinct crude oil dispersions reveals compositional differences. Journal of Sea Research, 2018, 141, 112-118.	1.6	5
1034	Quantification of variation and the impact of biomass in targeted 16S rRNA gene sequencing studies. Microbiome, 2018, 6, 155.	11.1	44
1035	Field-collected Triatoma sordida from central Brazil display high microbiota diversity that varies with regard to developmental stage and intestinal segmentation. PLoS Neglected Tropical Diseases, 2018, 12, e0006709.	3.0	38
1036	Genetic and Functional Diversity of Bacterial Microbiome in Soils With Long Term Impacts of Petroleum Hydrocarbons. Frontiers in Microbiology, 2018, 9, 1923.	3.5	73
1037	Root exudates drive the soil-borne legacy of aboveground pathogen infection. Microbiome, 2018, 6, 156.	11.1	354
1038	Microbial Transplantation With Human Gut Commensals Containing CutC Is Sufficient to Transmit Enhanced Platelet Reactivity and Thrombosis Potential. Circulation Research, 2018, 123, 1164-1176.	4.5	122
1039	A Preliminary Checklist of Fungi at the Boston Harbor Islands. Northeastern Naturalist, 2018, 25, 45.	0.3	32
1040	Humic acid inhibition of hydrolysis and methanogenesis with different anaerobic inocula. Waste Management, 2018, 80, 130-136.	7.4	49
1041	Nitrogen cycling players and processes in green roof ecosystems. Applied Soil Ecology, 2018, 132, 114-125.	4.3	17
1042	In Situ Diazotroph Population Dynamics Under Different Resource Ratios in the North Pacific Subtropical Gyre. Frontiers in Microbiology, 2018, 9, 1616.	3.5	23
1043	Exposure to Yeast Shapes the Intestinal Bacterial Community Assembly in Zebrafish Larvae. Frontiers in Microbiology, 2018, 9, 1868.	3.5	35
1044	Using †Omic Approaches to Compare Temporal Bacterial Colonization of Lolium perenne, Lotus corniculatus, and Trifolium pratense in the Rumen. Frontiers in Microbiology, 2018, 9, 2184.	3.5	19
1045	Analysis of the Rumen Microbiome and Metabolome to Study the Effect of an Antimethanogenic Treatment Applied in Early Life of Kid Goats. Frontiers in Microbiology, 2018, 9, 2227.	3.5	31
1046	Next Generation Sequencing of Ancient Fungal Specimens: The Case of the Saccardo Mycological Herbarium. Frontiers in Ecology and Evolution, 2018, 6, .	2.2	29

#	Article	IF	CITATIONS
1047	The microbiota of hematophagous ectoparasites collected from migratory birds. PLoS ONE, 2018, 13, e0202270.	2.5	20
1048	The Use of a Mini-Bioreactor Fermentation System as a Reproducible, High-Throughput ex vivo Batch Model of the Distal Colon. Frontiers in Microbiology, 2018, 9, 1844.	3.5	36
1049	Biodegradation of dispersed oil in natural seawaters from Western Greenland and a Norwegian fjord. Polar Biology, 2018, 41, 2435-2450.	1.2	23
1050	A potential central role of Thaumarchaeota in N-Cycling in a semi-arid environment, Fort Stanton Cave, Snowy River passage, New Mexico, USA. FEMS Microbiology Ecology, 2018, 94, .	2.7	25
1051	Changes in the Gut Microbiota of Urban Subjects during an Immersion in the Traditional Diet and Lifestyle of a Rainforest Village. MSphere, 2018, 3, .	2.9	34
1052	Enrichment of syngas-converting mixed microbial consortia for ethanol production and thermodynamics-based design of enrichment strategies. Biotechnology for Biofuels, 2018, 11, 198.	6.2	32
1053	Effects of limestone inclusion on growth performance, intestinal microbiota, and the jejunal transcriptomic profile when fed to weaning pigs. Animal Feed Science and Technology, 2018, 242, 8-20.	2.2	5
1054	Dynamics of soil microbial recovery from cropland to orchard along a 20-year chronosequence in a degraded karst ecosystem. Science of the Total Environment, 2018, 639, 1051-1059.	8.0	22
1055	Extrathymically Generated Regulatory T Cells Establish a Niche for Intestinal Border-Dwelling Bacteria and Affect Physiologic Metabolite Balance. Immunity, 2018, 48, 1245-1257.e9.	14.3	100
1056	Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water. Science of the Total Environment, 2018, 639, 1126-1137.	8.0	43
1057	Deterministic mechanisms define the long-term anaerobic digestion microbiome and its functionality regardless of the initial microbial community. Water Research, 2018, 141, 366-376.	11.3	82
1058	Nature-derived microbiota exposure as a novel immunomodulatory approach. Future Microbiology, 2018, 13, 737-744.	2.0	50
1059	Interactive effects of multiple stressors revealed by sequencing total (DNA) and active (RNA) components of experimental sediment microbial communities. Science of the Total Environment, 2018, 637-638, 1383-1394.	8.0	27
1060	Helicobacter pylori-infected C57BL/6 mice with different gastrointestinal microbiota have contrasting gastric pathology, microbial and host immune responses. Scientific Reports, 2018, 8, 8014.	3.3	31
1061	Chronic rhinosinusitis with nasal polyps is characterized by dysbacteriosis of the nasal microbiota. Scientific Reports, 2018, 8, 7926.	3.3	67
1062	Variation in electrode redox potential selects for different microorganisms under cathodic current flow from electrodes in marine sediments. Environmental Microbiology, 2018, 20, 2270-2287.	3.8	17
1064	Early Salmonella Typhimurium infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa. Scientific Reports, 2018, 8, 7788.	3.3	61
1065	Iron Sequestration in Microbiota Biofilms As A Novel Strategy for Treating Inflammatory Bowel Diseases. Inflammatory Bowel Diseases, 2018, 24, 1493-1502.	1.9	30

#	ARTICLE	IF	CITATIONS
1066	Enrichment of Clinically Relevant Organisms in Spontaneous Preterm-Delivered Placentas and Reagent Contamination across All Clinical Groups in a Large Pregnancy Cohort in the United Kingdom. Applied and Environmental Microbiology, 2018, 84, .	3.1	63
1067	The gut microbiome is associated with behavioural task in honey bees. Insectes Sociaux, 2018, 65, 419-429.	1.2	90
1068	Fecal <i>Enterobacteriales</i> enrichment is associated with increased inÂvivo intestinal permeability in humans. Physiological Reports, 2018, 6, e13649.	1.7	37
1069	Molecular profiling of mucosal tissue associated microbiota in patients manifesting acute exacerbations and remission stage of ulcerative colitis. World Journal of Microbiology and Biotechnology, 2018, 34, 76.	3.6	53
1070	Microbial anodic consortia fed with fermentable substrates in microbial electrolysis cells: Significance of microbial structures. Bioelectrochemistry, 2018, 123, 219-226.	4.6	30
1071	Cross-shelf investigation of coral reef cryptic benthic organisms reveals diversity patterns of the hidden majority. Scientific Reports, 2018, 8, 8090.	3.3	58
1072	Cold adaptation and replicable microbial community development during long-term low-temperature anaerobic digestion treatment of synthetic sewage. FEMS Microbiology Ecology, 2018, 94, .	2.7	34
1073	Smokeless tobacco impacts oral microbiota in a Syrian Golden hamster cheek pouch carcinogenesis model. Anaerobe, 2018, 52, 29-42.	2.1	18
1074	Consistent patterns of high alpha and low beta diversity in tropical parasitic and freeâ€living protists. Molecular Ecology, 2018, 27, 2846-2857.	3.9	43
1075	Variation in faecal microbiota in a group of horses managed at pasture over a 12-month period. Scientific Reports, 2018, 8, 8510.	3.3	69
1076	High turnover of faecal microbiome from algal feedstock experimental manipulations in the Pacific oyster (<i>Crassostrea gigas</i>). Microbial Biotechnology, 2018, 11, 848-858.	4.2	22
1077	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. GigaScience, 2018, 7, .	6.4	95
1078	Bacterial endophyte communities in Pinus flexilis are structured by host age, tissue type, and environmental factors. Plant and Soil, 2018, 428, 335-352.	3.7	32
1079	Gut microflora may facilitate adaptation to anthropic habitat: A comparative study in <i>Rattus</i> Ecology and Evolution, 2018, 8, 6463-6472.	1.9	4
1080	Carbon and nitrogen in the topsoils of Inceptisols and Mollisols under native sage scrub and non-native grasslands in southern California. Geoderma Regional, 2018, 14, e00172.	2.1	8
1081	Intestinal microbial-derived sphingolipids are inversely associated with childhood food allergy. Journal of Allergy and Clinical Immunology, 2018, 142, 335-338.e9.	2.9	37
1082	Effect of spatial origin and hydrocarbon composition on bacterial consortia community structure and hydrocarbon biodegradation rates. FEMS Microbiology Ecology, 2018, 94, .	2.7	25
1083	Carbon amendment stimulates benthic nitrogen cycling during the bioremediation of particulate aquaculture waste. Biogeosciences, 2018, 15, 1863-1878.	3.3	11

#	Article	IF	CITATIONS
1084	Microbial distribution and turnover in Antarctic microbial mats highlight the relevance of heterotrophic bacteria in low-nutrient environments. FEMS Microbiology Ecology, 2018, 94, .	2.7	19
1085	Asymptomatic Intestinal Colonization with Protist <i>Blastocystis</i> li>Is Strongly Associated with Distinct Microbiome Ecological Patterns. MSystems, 2018, 3, .	3.8	99
1086	Spatial structuring of soil microbial communities in commercial apple orchards. Applied Soil Ecology, 2018, 130, 1-12.	4.3	60
1087	Indigenous microorganisms residing in oil sands tailings biodegrade residual bitumen. Chemosphere, 2018, 209, 551-559.	8.2	17
1088	Temperature effects on structure and function of the methanogenic microbial communities in two paddy soils and one desert soil. Soil Biology and Biochemistry, 2018, 124, 236-244.	8.8	47
1089	Distinct bacterial metacommunities inhabit the upper and lower respiratory tracts of healthy feedlot cattle and those diagnosed with bronchopneumonia. Veterinary Microbiology, 2018, 221, 105-113.	1.9	65
1090	Intracellular nitrate in sediments of an oxygen-deficient marine basin is linked to pelagic diatoms. FEMS Microbiology Ecology, 2018, 94, .	2.7	3
1091	Pathogen colonization of the gastrointestinal microbiome at intensive care unit admission and risk for subsequent death or infection. Intensive Care Medicine, 2018, 44, 1203-1211.	8.2	121
1092	Microbial community adaptability to altered temperature conditions determines the potential for process optimisation in biogas production. Applied Energy, 2018, 226, 838-848.	10.1	96
1093	Genetic variability and ontogeny predict microbiome structure in a disease-challenged montane amphibian. ISME Journal, 2018, 12, 2506-2517.	9.8	49
1094	Effects of Substance Use and Sex Practices on the Intestinal Microbiome During HIV-1 Infection. Journal of Infectious Diseases, 2018, 218, 1560-1570.	4.0	41
1095	Vertically distinct microbial communities in the Mariana and Kermadec trenches. PLoS ONE, 2018, 13, e0195102.	2.5	62
1096	Native bacteria promote plant growth under drought stress condition without impacting the rhizomicrobiome. FEMS Microbiology Ecology, 2018, 94, .	2.7	54
1097	Linking patterns of net community production and marine microbial community structure in the western North Atlantic. ISME Journal, 2018, 12, 2582-2595.	9.8	15
1098	Exploring the diversity-stability paradigm using sponge microbial communities. Scientific Reports, 2018, 8, 8425.	3.3	66
1099	Investigation of viable taxa in the deep terrestrial biosphere suggests high rates of nutrient recycling. FEMS Microbiology Ecology, 2018, 94, .	2.7	29
1100	Resilience of small intestinal beneficial bacteria to the toxicity of soybean oil fatty acids. ELife, 2018, 7,	6.0	14
1101	Astrovirus infections induce age-dependent dysbiosis in gut microbiomes of bats. ISME Journal, 2018, 12, 2883-2893.	9.8	38

#	Article	IF	CITATIONS
1102	Types of tobacco consumption and the oral microbiome in the United Arab Emirates Healthy Future (UAEHFS) Pilot Study. Scientific Reports, 2018, 8, 11327.	3.3	51
1103	Community dynamics and functional characteristics of naphthaleneâ€degrading populations in contaminated surface sediments and hypoxic/anoxic groundwater. Environmental Microbiology, 2018, 20, 3543-3559.	3.8	22
1104	Tucumã Oil Shifted Ruminal Fermentation, Reducing Methane Production and Altering the Microbiome but Decreased Substrate Digestibility Within a RUSITEC Fed a Mixed Hay – Concentrate Diet. Frontiers in Microbiology, 2018, 9, 1647.	3.5	37
1105	The Environmental Exposures and Inner- and Intercity Traffic Flows of the Metro System May Contribute to the Skin Microbiome and Resistome. Cell Reports, 2018, 24, 1190-1202.e5.	6.4	56
1106	Alternate life history phases of a common seaweed have distinct microbial surface communities. Molecular Ecology, 2018, 27, 3555-3568.	3.9	41
1107	High sequence variation in the exon 10 of TSHR gene is associated with flightless-domestic geese. 3 Biotech, 2018, 8, 353.	2.2	1
1108	Spatiotemporal trends in PM2.5 levels from 2013 to 2017 and regional demarcations for joint prevention and control of atmospheric pollution in China. Chemosphere, 2018, 210, 1176-1184.	8.2	82
1109	Bacterial communities related to 3-nitro-1-propionic acid degradation in the rumen of grazing ruminants in the Qinghai-Tibetan Plateau. Anaerobe, 2018, 54, 42-54.	2.1	8
1110	Selection of Appropriate Metagenome Taxonomic Classifiers for Ancient Microbiome Research. MSystems, 2018, 3, .	3.8	35
1111	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. PLoS Biology, 2018, 16, e2006352.	5.6	236
1112	Long-Term Irrigation Affects the Dynamics and Activity of the Wheat Rhizosphere Microbiome. Frontiers in Plant Science, 2018, 9, 345.	3.6	73
1113	Functional Microbial Features Driving Community Assembly During Seed Germination and Emergence. Frontiers in Plant Science, 2018, 9, 902.	3.6	92
1114	Microbial community assembly differs across minerals in a rhizosphere microcosm. Environmental Microbiology, 2018, 20, 4444-4460.	3.8	77
1115	Diarrhea-Associated Intestinal Microbiota in Captive Sichuan Golden Snub-Nosed Monkeys (<i>Rhinopithecus roxellana</i>). Microbes and Environments, 2018, 33, 249-256.	1.6	14
1116	Lithocholic Acid Improves the Survival of <i>Drosophila Melanogaster</i> . Molecular Nutrition and Food Research, 2018, 62, e1800424.	3.3	11
1117	Prokaryotic footprints in urban water ecosystems: A case study of urban landscape ponds in a coastal city, China. Environmental Pollution, 2018, 242, 1729-1739.	7.5	35
1118	Bacterial interactions during sequential degradation of cyanobacterial necromass in a sulfidic arctic marine sediment. Environmental Microbiology, 2018, 20, 2927-2940.	3.8	50
1119	Structure and function of high Arctic pelagic, particleâ€associated and benthic bacterial communities. Environmental Microbiology, 2018, 20, 2941-2954.	3.8	31

#	Article	IF	CITATIONS
1120	Jellyfish Life Stages Shape Associated Microbial Communities, While a Core Microbiome Is Maintained Across All. Frontiers in Microbiology, 2018, 9, 1534.	3. 5	28
1121	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. Frontiers in Microbiology, 2018, 9, 1492.	3.5	41
1122	Gut microbiota components are associated with fixed airway obstruction in asthmatic patients living in the tropics. Scientific Reports, 2018, 8, 9582.	3.3	16
1123	<i>Papio</i> spp. Colon microbiome and its link to obesity in pregnancy. Journal of Medical Primatology, 2018, 47, 393-401.	0.6	3
1124	Do we treat our patients or rather periodontal microbes with adjunctive antibiotics in periodontal therapy? A 16S rDNA microbial community analysis. PLoS ONE, 2018, 13, e0195534.	2.5	37
1125	Humic Substances Alter Ammonia Production and the Microbial Populations Within a RUSITEC Fed a Mixed Hay – Concentrate Diet. Frontiers in Microbiology, 2018, 9, 1410.	3.5	30
1126	Microbiota Reconstitution Does Not Cause Bone Loss in Germ-Free Mice. MSphere, 2018, 3, .	2.9	36
1127	Coreopsis Tinctoria Modulates Lipid Metabolism by Decreasing Low-Density Lipoprotein and Improving Gut Microbiota. Cellular Physiology and Biochemistry, 2018, 48, 1060-1074.	1.6	9
1128	Effect of administration of a probiotic preparation on gut microbiota and immune response in healthy women in India: anÂopen-label, single-arm pilot study. BMC Gastroenterology, 2018, 18, 85.	2.0	21
1129	Elevated Levels of Pathogenic Indicator Bacteria and Antibiotic Resistance Genes after Hurricane Harvey's Flooding in Houston. Environmental Science and Technology Letters, 2018, 5, 481-486.	8.7	65
1130	Microbial biogeography of 925 geothermal springs in New Zealand. Nature Communications, 2018, 9, 2876.	12.8	163
1131	Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. Scientific Reports, 2018, 8, 11159.	3.3	60
1132	Endocervical and vaginal microbiota in South African adolescents with asymptomatic Chlamydia trachomatis infection. Scientific Reports, 2018, 8, 11109.	3.3	37
1133	Gut microbes contribute to variation in solid organ transplant outcomes in mice. Microbiome, 2018, 6, 96.	11.1	49
1134	The murine female intestinal microbiota does not shift throughout the estrous cycle. PLoS ONE, 2018, 13, e0200729.	2.5	22
1135	The Microbial Landscape of Sea Stars and the Anatomical and Interspecies Variability of Their Microbiome. Frontiers in Microbiology, 2018, 9, 1829.	3.5	35
1136	Guild Patterns of Basidiomycetes Community Associated With Quercus mongolica in Mt. Jeombong, Republic of Korea. Mycobiology, 2018, 46, 13-23.	1.7	6
1137	Metabolomic signatures distinguish the impact of formula carbohydrates on disease outcome in a preterm piglet model of NEC. Microbiome, 2018, 6, 111.	11.1	28

#	Article	IF	CITATIONS
1138	Chronic Rhinosinusitis: Potential Role of Microbial Dysbiosis and Recommendations for Sampling Sites. Frontiers in Cellular and Infection Microbiology, 2018, 8, 57.	3.9	75
1139	Clay Flocculation Effect on Microbial Community Composition in Water and Sediment. Frontiers in Environmental Science, 2018, 6, .	3.3	8
1140	Feeding Immunity: Physiological and Behavioral Responses to Infection and Resource Limitation. Frontiers in Immunology, 2017, 8, 1914.	4.8	29
1141	Respiratory Disease following Viral Lung Infection Alters the Murine Gut Microbiota. Frontiers in Immunology, 2018, 9, 182.	4.8	178
1142	Analyzing Immunoglobulin Repertoires. Frontiers in Immunology, 2018, 9, 462.	4.8	89
1143	Corals and Their Microbiomes Are Differentially Affected by Exposure to Elevated Nutrients and a Natural Thermal Anomaly. Frontiers in Marine Science, 0, 5, .	2.5	68
1144	Bacterial Community Response in Deep Faroe-Shetland Channel Sediments Following Hydrocarbon Entrainment With and Without Dispersant Addition. Frontiers in Marine Science, 2018, 5, .	2.5	12
1145	Characterization of the Skin Microbiota of the Cane Toad Rhinella cf. marina in Puerto Rico and Costa Rica. Frontiers in Microbiology, 2017, 8, 2624.	3.5	20
1146	Low Light Availability Alters Root Exudation and Reduces Putative Beneficial Microorganisms in Seagrass Roots. Frontiers in Microbiology, 2017, 8, 2667.	3.5	88
1147	Composition and Activity of Microbial Communities along the Redox Gradient of an Alkaline, Hypersaline, Lake. Frontiers in Microbiology, 2018, 9, 14.	3 . 5	35
1148	Distribution of Archaeal Communities along the Coast of the Gulf of Finland and Their Response to Oil Contamination. Frontiers in Microbiology, 2018, 9, 15.	3.5	34
1149	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. Frontiers in Microbiology, 2018, 9, 31.	3. 5	45
1150	â€~TIME': A Web Application for Obtaining Insights into Microbial Ecology Using Longitudinal Microbiome Data. Frontiers in Microbiology, 2018, 9, 36.	3.5	47
1151	Spatial Heterogeneity and Co-occurrence of Mucosal and Luminal Microbiome across Swine Intestinal Tract. Frontiers in Microbiology, 2018, 9, 48.	3 . 5	172
1152	Diversity of Rare and Abundant Prokaryotic Phylotypes in the Prony Hydrothermal Field and Comparison with Other Serpentinite-Hosted Ecosystems. Frontiers in Microbiology, 2018, 9, 102.	3.5	23
1153	Competitive Traits Are More Important than Stress-Tolerance Traits in a Cadmium-Contaminated Rhizosphere: A Role for Trait Theory in Microbial Ecology. Frontiers in Microbiology, 2018, 9, 121.	3.5	60
1154	Linking Associations of Rare Low-Abundance Species to Their Environments by Association Networks. Frontiers in Microbiology, 2018, 9, 297.	3.5	19
1155	Assessing the Influence of Vegan, Vegetarian and Omnivore Oriented Westernized Dietary Styles on Human Gut Microbiota: A Cross Sectional Study. Frontiers in Microbiology, 2018, 9, 317.	3.5	78

#	Article	IF	CITATIONS
1156	The Response of a 16S Ribosomal RNA Gene Fragment Amplified Community to Lead, Zinc, and Copper Pollution in a Shanghai Field Trial. Frontiers in Microbiology, 2018, 9, 366.	3.5	73
1157	Mycobiome of Cysts of the Soybean Cyst Nematode Under Long Term Crop Rotation. Frontiers in Microbiology, 2018, 9, 386.	3.5	45
1158	The Intestinal Mycobiota in Wild Zebrafish Comprises Mainly Dothideomycetes While Saccharomycetes Predominate in Their Laboratory-Reared Counterparts. Frontiers in Microbiology, 2018, 9, 387.	3.5	26
1159	Distributions and Abundances of Sublineages of the N2-Fixing Cyanobacterium Candidatus Atelocyanobacterium thalassa (UCYN-A) in the New Caledonian Coral Lagoon. Frontiers in Microbiology, 2018, 9, 554.	3.5	23
1160	Nitrosospira sp. Govern Nitrous Oxide Emissions in a Tropical Soil Amended With Residues of Bioenergy Crop. Frontiers in Microbiology, 2018, 9, 674.	3.5	41
1161	Gut Microbiota Profiling and Gut–Brain Crosstalk in Children Affected by Pediatric Acute-Onset Neuropsychiatric Syndrome and Pediatric Autoimmune Neuropsychiatric Disorders Associated With Streptococcal Infections. Frontiers in Microbiology, 2018, 9, 675.	3.5	88
1162	Circadian Disruption Changes Gut Microbiome Taxa and Functional Gene Composition. Frontiers in Microbiology, 2018, 9, 737.	3.5	148
1163	Agricultural Freshwater Pond Supports Diverse and Dynamic Bacterial and Viral Populations. Frontiers in Microbiology, 2018, 9, 792.	3.5	27
1164	Comparing Microbiome Sampling Methods in a Wild Mammal: Fecal and Intestinal Samples Record Different Signals of Host Ecology, Evolution. Frontiers in Microbiology, 2018, 9, 803.	3.5	395
1165	Conditionally Rare Taxa Contribute but Do Not Account for Changes in Soil Prokaryotic Community Structure. Frontiers in Microbiology, 2018, 9, 809.	3.5	12
1166	Pig Farmers' Homes Harbor More Diverse Airborne Bacterial Communities Than Pig Stables or Suburban Homes. Frontiers in Microbiology, 2018, 9, 870.	3.5	33
1167	Enrichment of Bacteria From Eastern Mediterranean Sea Involved in Lignin Degradation via the Phenylacetyl-CoA Pathway. Frontiers in Microbiology, 2018, 9, 922.	3.5	22
1168	Benchmark Evaluation of True Single Molecular Sequencing to Determine Cystic Fibrosis Airway Microbiome Diversity. Frontiers in Microbiology, 2018, 9, 1069.	3.5	7
1169	Comparison of Channel Catfish and Blue Catfish Gut Microbiota Assemblages Shows Minimal Effects of Host Genetics on Microbial Structure and Inferred Function. Frontiers in Microbiology, 2018, 9, 1073.	3.5	36
1170	Physicochemical Drivers of Microbial Community Structure in Sediments of Lake Hazen, Nunavut, Canada. Frontiers in Microbiology, 2018, 9, 1138.	3.5	46
1171	Sediment Microbial Communities Influenced by Cool Hydrothermal Fluid Migration. Frontiers in Microbiology, 2018, 9, 1249.	3.5	14
1172	Crop Rotation and Straw Application Impact Microbial Communities in Italian and Philippine Soils and the Rhizosphere of Zea mays. Frontiers in Microbiology, 2018, 9, 1295.	3.5	74
1173	Exposure to Arsenic Alters the Microbiome of Larval Zebrafish. Frontiers in Microbiology, 2018, 9, 1323.	3.5	42

#	Article	IF	CITATIONS
1174	Persistence of Cellulolytic Bacteria Fibrobacter and Treponema After Short-Term Corn Stover-Based Dietary Intervention Reveals the Potential to Improve Rumen Fibrolytic Function. Frontiers in Microbiology, 2018, 9, 1363.	3.5	92
1175	Microplastic bacterial communities in the Bay of Brest: Influence of polymer type and size. Environmental Pollution, 2018, 242, 614-625.	7.5	280
1176	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. Microbiome, 2018, 6, 112.	11.1	65
1177	Evidence of Ash Tree (Fraxinus spp.) Specific Associations with Soil Bacterial Community Structure and Functional Capacity. Forests, 2018, 9, 187.	2.1	10
1178	Acetogen Communities in the Gut of Herbivores and Their Potential Role in Syngas Fermentation. Fermentation, 2018, 4, 40.	3.0	20
1179	Survey of Soil Fungal Communities in Strawberry Fields by Illumina Amplicon Sequencing. Eurasian Soil Science, 2018, 51, 682-691.	1.6	13
1180	Sjögren-Like Lacrimal Keratoconjunctivitis in Germ-Free Mice. International Journal of Molecular Sciences, 2018, 19, 565.	4.1	57
1181	Altered Bacterial Communities in Long-Term No-Till Soils Associated with Stratification of Soluble Aluminum and Soil pH. Soil Systems, 2018, 2, 7.	2.6	29
1182	Microbial Diversity and Toxin Risk in Tropical Freshwater Reservoirs of Cape Verde. Toxins, 2018, 10, 186.	3.4	8
1183	Fumonisin-Exposure Impairs Age-Related Ecological Succession of Bacterial Species in Weaned Pig Gut Microbiota. Toxins, 2018, 10, 230.	3.4	32
1184	Early-life skin microbiota in hospitalized preterm and full-term infants. Microbiome, 2018, 6, 98.	11.1	63
1185	Disruption of maternal gut microbiota during gestation alters offspring microbiota and immunity. Microbiome, 2018, 6, 124.	11.1	109
1186	Altered gut microbiota profile in patients with generalized anxiety disorder. Journal of Psychiatric Research, 2018, 104, 130-136.	3.1	229
1187	Profiling of bacterial and fungal communities of Mexican cheeses by high throughput DNA sequencing. Food Research International, 2018, 113, 371-381.	6.2	38
1188	Parkinson's disease and bacteriophages as its overlooked contributors. Scientific Reports, 2018, 8, 10812.	3.3	93
1189	The cecal microbiome of commercial broiler chickens varies significantly by season. Poultry Science, 2018, 97, 3635-3644.	3.4	26
1190	Aerodigestive dysbiosis in children with chronic cough. Pediatric Pulmonology, 2018, 53, 1288-1298.	2.0	6
1191	16S rRNA sequencing reveals likely beneficial core microbes within faecal samples of the EU protected slug Geomalacus maculosus. Scientific Reports, 2018, 8, 10402.	3.3	10

#	Article	IF	Citations
1192	Robust Microbial Markers for Non-Invasive Inflammatory Bowel Disease Identification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 16, 1-1.	3.0	7
1193	Functional exploration of natural networks and ecological communities. Methods in Ecology and Evolution, 2018, 9, 2028-2033.	5.2	5
1194	Methane-oxidizing seawater microbial communities from an Arctic shelf. Biogeosciences, 2018, 15, 3311-3329.	3.3	13
1195	Stool Microbiota Composition Differs in Patients with Stomach, Colon, and Rectal Neoplasms. Digestive Diseases and Sciences, 2018, 63, 2950-2958.	2.3	65
1196	Stochastic processes govern invasion success in microbial communities when the invader is phylogenetically close to resident bacteria. ISME Journal, 2018, 12, 2748-2756.	9.8	41
1197	Eighty years of maize breeding alters plant nitrogen acquisition but not rhizosphere bacterial community composition. Plant and Soil, 2018, 431, 53-69.	3.7	29
1198	Gut microbial and metabolomic profiles after fecal microbiota transplantation in pediatric ulcerative colitis patients. FEMS Microbiology Ecology, 2018, 94, .	2.7	73
1199	Microbial community response to growing season and plant nutrient optimisation in a boreal Norway spruce forest. Soil Biology and Biochemistry, 2018, 125, 197-209.	8.8	64
1200	Electron donorâ€driven bacterial and archaeal community patterns along forest ring edges in Ontario, Canada. Environmental Microbiology Reports, 2018, 10, 663-672.	2.4	4
1201	Effect of the Synthetic Bile Salt Analog CamSA on the Hamster Model of Clostridium difficile Infection. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	23
1202	Attachment between heterotrophic bacteria and microalgae influences symbiotic microscale interactions. Environmental Microbiology, 2018, 20, 4385-4400.	3.8	55
1203	Fecal Aliquot Straw Technique (FAST) allows for easy and reproducible subsampling: assessing interpersonal variation in trimethylamine-N-oxide (TMAO) accumulation. Microbiome, 2018, 6, 91.	11.1	20
1204	White and infrared light continuous photobioreactors for resource recovery from poultry processing wastewater – A comparison. Water Research, 2018, 144, 665-676.	11.3	64
1205	Removal of antibiotic resistance genes in an anaerobic membrane bioreactor treating primary clarifier effluent at 20 ŰC. Environmental Science: Water Research and Technology, 2018, 4, 1783-1793.	2.4	35
1206	Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. Biotechnology for Biofuels, 2018, 11, 200.	6.2	99
1207	Gastrointestinal microbial community changes in Atlantic cod (Gadus morhua) exposed to crude oil. BMC Microbiology, 2018, 18, 25.	3.3	36
1208	Defoliation intensity and elevated precipitation effects on microbiome and interactome depend on site type in northern mixed-grass prairie. Soil Biology and Biochemistry, 2018, 122, 163-172.	8.8	23
1209	Thermophilic endospores associated with migrated thermogenic hydrocarbons in deep Gulf of Mexico marine sediments. ISME Journal, 2018, 12, 1895-1906.	9.8	38

#	Article	IF	CITATIONS
1210	Predator size divergence depends on community context. Ecology Letters, 2018, 21, 1097-1107.	6.4	9
1211	The influence of oxygen and methane on nitrogen fixation in subarctic Sphagnum mosses. AMB Express, 2018, 8, 76.	3.0	16
1212	Microbiota inoculum composition affects holobiont assembly and host growth in Daphnia. Microbiome, 2018, 6, 56.	11.1	74
1213	Mind the gut: genomic insights to population divergence and gut microbial composition of two marine keystone species. Microbiome, 2018, 6, 82.	11.1	28
1214	The active microbial community more accurately reflects the anaerobic digestion process: 16S rRNA (gene) sequencing as a predictive tool. Microbiome, 2018, 6, 63.	11.1	138
1215	Use of dietary indices to control for diet in human gut microbiota studies. Microbiome, 2018, 6, 77.	11.1	85
1216	Comparative study on the gut microbiotas of four economically important Asian carp species. Science China Life Sciences, 2018, 61, 696-705.	4.9	52
1217	Sexâ€related differences in the thanatomicrobiome in postmortem heart samples using bacterial gene regions V1â€2 and V4. Letters in Applied Microbiology, 2018, 67, 144-153.	2.2	25
1218	Exposure to toxic metals triggers unique responses from the rat gut microbiota. Scientific Reports, 2018, 8, 6578.	3.3	95
1219	Community composition and diversity of Neotropical rootâ€associated fungi in common and rare trees. Biotropica, 2018, 50, 694-703.	1.6	6
1220	Impact of long-term salinity exposure in anaerobic membrane bioreactors treating phenolic wastewater: Performance robustness and endured microbial community. Water Research, 2018, 141, 172-184.	11.3	88
1221	Fungal communities in organic and mineral soil horizons in an industrially polluted boreal forest. Biodiversity, 2018, 19, 161-171.	1.1	2
1222	Taxon-Driven Functional Shifts Associated with Storm Flow in an Urban Stream Microbial Community. MSphere, 2018, 3, .	2.9	20
1223	Enteric virome of Ethiopian children participating in a clean water intervention trial. PLoS ONE, 2018, 13, e0202054.	2.5	29
1224	Bacterial and archaeal profiling of hypersaline microbial mats and endoevaporites, under natural conditions and methanogenic microcosm experiments. Extremophiles, 2018, 22, 903-916.	2.3	16
1225	Mosquito microbiota cluster by host sampling location. Parasites and Vectors, 2018, 11, 468.	2.5	61
1226	3-NOP vs. Halogenated Compound: Methane Production, Ruminal Fermentation and Microbial Community Response in Forage Fed Cattle. Frontiers in Microbiology, 2018, 9, 1582.	3.5	62
1227	Chronic d-serine supplementation impairs insulin secretion. Molecular Metabolism, 2018, 16, 191-202.	6.5	29

#	Article	IF	CITATIONS
1228	Litter species richness and composition effects on fungal richness and community structure in decomposing foliar and root litter. Soil Biology and Biochemistry, 2018, 125, 328-339.	8.8	58
1229	Effects of transportation to and co-mingling at an auction market on nasopharyngeal and tracheal bacterial communities of recently weaned beef cattle. Veterinary Microbiology, 2018, 223, 126-133.	1.9	31
1230	Impact of chlorine dioxide disinfection of irrigation water on the epiphytic bacterial community of baby spinach and underlying soil. PLoS ONE, 2018, 13, e0199291.	2.5	38
1231	Ultra-Violet Radiation Has a Limited Impact on Seasonal Differences in the Acropora Muricata Holobiont. Frontiers in Marine Science, $2018, 5, \ldots$	2.5	6
1232	Differential effects of selective and non-selective cyclooxygenase inhibitors on fecal microbiota in adult horses. PLoS ONE, 2018, 13, e0202527.	2.5	20
1233	Marchantia liverworts as a proxy to plants' basal microbiomes. Scientific Reports, 2018, 8, 12712.	3.3	46
1234	Characterization of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions. Scientific Reports, 2018, 8, 12727.	3.3	141
1235	Ammonia oxidizers in the sea-surface microlayer of a coastal marine inlet. PLoS ONE, 2018, 13, e0202636.	2.5	7
1236	Depicting the composition of gut microbiota in a population with varied ethnic origins but shared geography. Nature Medicine, 2018, 24, 1526-1531.	30.7	436
1237	Differences in foliar endophyte communities of red alder (<i>Alnus rubra</i>) exposed to varying air pollutant levels. Botany, 2018, 96, 825-835.	1.0	8
1238	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. Cell Reports, 2018, 24, 1842-1851.	6.4	72
1239	Following the terrestrial tracks of <i>Caulobacter</i> - redefining the ecology of a reputed aquatic oligotroph. ISME Journal, 2018, 12, 3025-3037.	9.8	56
1240	Climate warming leads to divergent succession of grassland microbial communities. Nature Climate Change, 2018, 8, 813-818.	18.8	208
1241	<i>In situ</i> substrate-formed biofilms using IDODS mimic supragingival tooth-formed biofilms. Journal of Oral Microbiology, 2018, 10, 1495975.	2.7	4
1242	The Role of Pulmonary and Systemic Immunosenescence in Acute Lung Injury., 2018, 9, 553.		34
1243	Influence of commercial DNA extraction kit choice on prokaryotic community metrics in marine sediment. Limnology and Oceanography: Methods, 2018, 16, 525-536.	2.0	13
1244	Distributing regionally, distinguishing locally: examining the underlying effects of local land use on airborne bacterial biodiversity. Environmental Microbiology, 2018, 20, 3529-3542.	3.8	26
1245	Snake fungal disease alters skin bacterial and fungal diversity in an endangered rattlesnake. Scientific Reports, 2018, 8, 12147.	3.3	35

#	Article	IF	CITATIONS
1246	Comparison of Fecal Collection Methods for Microbiome and Metabolomics Studies. Frontiers in Cellular and Infection Microbiology, 2018, 8, 301.	3.9	114
1247	Microbial Biogeography Along the Gastrointestinal Tract of a Red Panda. Frontiers in Microbiology, 2018, 9, 1411.	3.5	26
1248	Bacteria and Competing Herbivores Weaken Top–Down and Bottom–Up Aphid Suppression. Frontiers in Plant Science, 2018, 9, 1239.	3.6	16
1249	D-lactic Acidosis: Successful Suppression of D-lactate–Producing <i>Lactobacillus</i> by Probiotics. Pediatrics, 2018, 142, .	2.1	26
1250	Effect of Antibiotic-Mediated Microbiome Modulation on Rotavirus Vaccine Immunogenicity: A Human, Randomized-Control Proof-of-Concept Trial. Cell Host and Microbe, 2018, 24, 197-207.e4.	11.0	92
1251	Petroleum hydrocarbon and microbial community structure successions in marine oil-related aggregates associated with diatoms relevant for Arctic conditions. Marine Pollution Bulletin, 2018, 135, 759-768.	5.0	13
1252	Phylogeny-corrected identification of microbial gene families relevant to human gut colonization. PLoS Computational Biology, 2018, 14, e1006242.	3.2	39
1253	An anaerobic hybrid bioreactor for biologically enhanced primary treatment of domestic wastewater under low temperatures. Environmental Science: Water Research and Technology, 2018, 4, 1851-1866.	2.4	14
1254	The bacteriome at the onset of type 1 diabetes: A study from four geographically distant African and Asian countries. Diabetes Research and Clinical Practice, 2018, 144, 51-62.	2.8	35
1255	Stunted childhood growth is associated with decompartmentalization of the gastrointestinal tract and overgrowth of oropharyngeal taxa. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8489-E8498.	7.1	119
1256	Metabolic Capability and Phylogenetic Diversity of Mono Lake during a Bloom of the Eukaryotic Phototroph Picocystis sp. Strain ML. Applied and Environmental Microbiology, 2018, 84, .	3.1	18
1257	Chloroplast sequence variation and the efficacy of peptide nucleic acids for blocking host amplification in plant microbiome studies. Microbiome, 2018, 6, 144.	11.1	74
1258	PARP1 Is Up-Regulated in Non-small Cell Lung Cancer Tissues in the Presence of the Cyanobacterial Toxin Microcystin. Frontiers in Microbiology, 2018, 9, 1757.	3.5	76
1259	Sample size effects on the assessment of eukaryotic diversity and community structure in aquatic sediments using high-throughput sequencing. Scientific Reports, 2018, 8, 11737.	3.3	55
1260	Unraveling the Composition of the Root-Associated Bacterial Microbiota of Phragmites australis and Typha latifolia. Frontiers in Microbiology, 2018, 9, 1650.	3.5	46
1261	Temporal dynamics of microbiota before and after host death. ISME Journal, 2018, 12, 2076-2085.	9.8	21
1262	Water soluble fraction from ethanolic extract of Clausena lansium seeds alleviates obesity and insulin resistance, and changes the composition of gut microbiota in high-fat diet-fed mice. Journal of Functional Foods, 2018, 47, 192-199.	3.4	17
1263	Does universal 16S rRNA gene amplicon sequencing of environmental communities provide an accurate description of nitrifying guilds?. Journal of Microbiological Methods, 2018, 151, 28-34.	1.6	11

#	Article	IF	CITATIONS
1264	Methane and nitrous oxide cycling microbial communities in soils above septic leach fields: Abundances with depth and correlations with net surface emissions. Science of the Total Environment, 2018, 640-641, 429-441.	8.0	20
1265	Assessing Cat Flea Microbiomes in Northern and Southern California by 16S rRNA Next-Generation Sequencing. Vector-Borne and Zoonotic Diseases, 2018, 18, 491-499.	1.5	19
1266	Computational and Statistical Considerations in the Analysis of Metagenomic Data. , 2018, , 81-102.		10
1267	Seed bank and seasonal patterns of the eukaryotic SAR (Stramenopila, Alveolata and Rhizaria) clade in a New England vernal pool. Journal of Plankton Research, 2018, 40, 376-390.	1.8	15
1268	Spatial and Environmental Variation of the Human Hair Microbiota. Scientific Reports, 2018, 8, 9017.	3.3	29
1269	HTSSIP: An R package for analysis of high throughput sequencing data from nucleic acid stable isotope probing (SIP) experiments. PLoS ONE, 2018, 13, e0189616.	2.5	37
1270	Instar- and host-associated differentiation of bacterial communities in the Mediterranean fruit fly Ceratitis capitata. PLoS ONE, 2018, 13, e0194131.	2.5	91
1271	Verrucomicrobia are prevalent in north-temperate freshwater lakes and display class-level preferences between lake habitats. PLoS ONE, 2018, 13, e0195112.	2.5	56
1272	Host: Microbiome co-metabolic processing of dietary polyphenols – An acute, single blinded, cross-over study with different doses of apple polyphenols in healthy subjects. Food Research International, 2018, 112, 108-128.	6.2	67
1273	High soil microbial activity in the winter season enhances nitrogen cycling in a cool-temperate deciduous forest. Soil Biology and Biochemistry, 2018, 124, 90-100.	8.8	83
1274	Ecotype-Dependent Response of Bacterial Communities Associated with <i>Arabidopsis</i> to Cold Acclimation. Phytobiomes Journal, 2018, 2, 3-13.	2.7	8
1275	Insights into the skin microbiome dynamics of leprosy patients during multi-drug therapy and in healthy individuals from Brazil. Scientific Reports, 2018, 8, 8783.	3.3	19
1276	Response of fermenting bacterial and methanogenic archaeal communities in paddy soil to progressing rice straw degradation. Soil Biology and Biochemistry, 2018, 124, 70-80.	8.8	85
1277	Camellia Oil (<i>Camellia oleifera</i> Abel.) Modifies the Composition of Gut Microbiota and Alleviates Acetic Acid-Induced Colitis in Rats. Journal of Agricultural and Food Chemistry, 2018, 66, 7384-7392.	5.2	52
1278	Rapid environmental effects on gut nematode susceptibility in rewilded mice. PLoS Biology, 2018, 16, e2004108.	5.6	97
1279	Characterization of the fecal and mucosa-associated microbiota in dogs with colorectal epithelial tumors. PLoS ONE, 2018, 13, e0198342.	2.5	27
1280	â€~Concord' grapevine nutritional status and chlorosis rank associated with fungal and bacterial root zone microbiomes. Plant Physiology and Biochemistry, 2018, 129, 429-436.	5.8	4
1281	Applying predictive models to decipher rhizobacterial modifications in common reed die-back affected populations. Science of the Total Environment, 2018, 642, 708-722.	8.0	14

#	Article	IF	Citations
1282	The benign helminth <i>Hymenolepis diminuta </i> ameliorates chemically induced colitis in a rat model system. Parasitology, 2018, 145, 1324-1335.	1.5	13
1283	A novel mouse model of Campylobacter jejuni enteropathy and diarrhea. PLoS Pathogens, 2018, 14, e1007083.	4.7	55
1284	A strong link between marine microbial community composition and function challenges the idea of functional redundancy. ISME Journal, 2018, 12, 2470-2478.	9.8	180
1285	Co-occurrence Networks Among Bacteria and Microbial Eukaryotes of Lake Baikal During a Spring Phytoplankton Bloom. Microbial Ecology, 2019, 77, 96-109.	2.8	97
1286	A brief history of bioinformatics. Briefings in Bioinformatics, 2019, 20, 1981-1996.	6.5	147
1287	Long-term farming systems modulate multi-trophic responses. Science of the Total Environment, 2019, 646, 480-490.	8.0	18
1288	Gut microbiome analysis as a tool towards targeted non-invasive biomarkers for early hepatocellular carcinoma. Gut, 2019, 68, 1014-1023.	12.1	498
1289	Finding flies in the mushroom soup: Host specificity of fungusâ€essociated communities revisited with a novel molecular method. Molecular Ecology, 2019, 28, 190-202.	3.9	18
1290	Microbial Community Composition and Putative Biogeochemical Functions in the Sediment and Water of Tropical Granite Quarry Lakes. Microbial Ecology, 2019, 77, 1-11.	2.8	51
1291	Histological improvement of non-alcoholic steatohepatitis with a prebiotic: a pilot clinical trial. European Journal of Nutrition, 2019, 58, 1735-1745.	3.9	88
1292	Rapid Microbial Community Changes During Initial Stages of Pine Litter Decomposition. Microbial Ecology, 2019, 77, 56-75.	2.8	40
1293	Bifidobacterium bifidum TMC3115 Can Characteristically Influence Glucose and Lipid Profile and Intestinal Microbiota in the Middle-Aged and Elderly. Probiotics and Antimicrobial Proteins, 2019, 11, 1182-1194.	3.9	33
1294	Computation Cluster Validation in the Big Data Era. , 2019, , 449-455.		0
1295	Seasonality of the gut microbiota of free-ranging white-faced capuchins in a tropical dry forest. ISME Journal, 2019, 13, 183-196.	9.8	83
1296	Co-occurrence of Anaerobes in Human Chronic Wounds. Microbial Ecology, 2019, 77, 808-820.	2.8	40
1297	Assessment of urinary 3-indoxyl sulfate as a marker for gut microbiota diversity and abundance of <i>Clostridiales</i> . Gut Microbes, 2019, 10, 133-141.	9.8	15
1298	The biology of fog: results from coastal Maine and Namib Desert reveal common drivers of fog microbial composition. Science of the Total Environment, 2019, 647, 1547-1556.	8.0	40
1299	Feather mites play a role in cleaning host feathers: New insights from <scp>DNA</scp> metabarcoding and microscopy. Molecular Ecology, 2019, 28, 203-218.	3.9	49

#	Article	IF	CITATIONS
1300	Do composition and diversity of bacterial communities and abiotic conditions of spring water reflect characteristics of groundwater ecosystems exposed to different agricultural activities?. MicrobiologyOpen, 2019, 8, e00681.	3.0	5
1301	Terrestriality and bacterial transfer: a comparative study of gut microbiomes in sympatric Malagasy mammals. ISME Journal, 2019, 13, 50-63.	9.8	59
1302	Human Milk Fortification with Bovine Colostrum Is Superior to Formulaâ€Based Fortifiers to Prevent Gut Dysfunction, Necrotizing Enterocolitis, and Systemic Infection in Preterm Pigs. Journal of Parenteral and Enteral Nutrition, 2019, 43, 252-262.	2.6	39
1303	The salivary microbiome of diabetic and nonâ€diabetic adults with periodontal disease. Journal of Periodontology, 2019, 90, 26-34.	3.4	54
1304	Longitudinal Comparison of Bacterial Diversity and Antibiotic Resistance Genes in New York City Sewage. MSystems, 2019, 4, .	3.8	19
1305	Agroforestry alters the rhizosphere soil bacterial and fungal communities of moso bamboo plantations in subtropical China. Applied Soil Ecology, 2019, 143, 192-200.	4.3	65
1306	Understanding soil biodiversity using two orthogonal 1000km transects across New South Wales, Australia. Geoderma, 2019, 354, 113860.	5.1	10
1307	Reduced genetic potential for butyrate fermentation in the gut microbiome of infants who develop allergic sensitization. Journal of Allergy and Clinical Immunology, 2019, 144, 1638-1647.e3.	2.9	95
1308	Vancomycin relieves mycophenolate mofetil–induced gastrointestinal toxicity by eliminating gut bacterial β-glucuronidase activity. Science Advances, 2019, 5, eaax2358.	10.3	73
1309	Finding a common core microbiota in two Brazilian dairies through culture and DNA metabarcoding studies. Journal of Food Science and Technology, 2019, 56, 5326-5335.	2.8	5
1310	Identification of Fungal Communities Within the Tar Spot Complex of Corn in Michigan via Next-Generation Sequencing. Phytobiomes Journal, 2019, 3, 235-243.	2.7	28
1311	rpoB, a promising marker for analyzing the diversity of bacterial communities by amplicon sequencing. BMC Microbiology, 2019, 19, 171.	3.3	71
1312	Gut Microbiome Biomarkers and Functional Diversity Within an Amazonian Semi-Nomadic Hunter–Gatherer Group. Frontiers in Microbiology, 2019, 10, 1743.	3.5	32
1313	Environmental pollution effects on plant microbiota: the case study of poplar bacterial-fungal response to silver nanoparticles. Applied Microbiology and Biotechnology, 2019, 103, 8215-8227.	3.6	21
1314	Genetic risk for autoimmunity is associated with distinct changes in the human gut microbiome. Nature Communications, 2019, 10, 3621.	12.8	132
1315	Abnormal vaginal microbiome associated with vaginal mesh complications. Neurourology and Urodynamics, 2019, 38, 2255-2263.	1.5	11
1316	A first insight into the structure and function of rhizosphere microbiota in Antarctic plants using shotgun metagenomic. Polar Biology, 2019, 42, 1825-1835.	1.2	18
1317	Data Analysis for DNA Stable Isotope Probing Experiments Using Multiple Window High-Resolution SIP. Methods in Molecular Biology, 2019, 2046, 109-128.	0.9	8

#	Article	IF	CITATIONS
1318	Oral vancomycin treatment does not alter markers of postprandial inflammation in lean and obese subjects. Physiological Reports, 2019, 7, e14199.	1.7	10
1319	Depth and location influence prokaryotic and eukaryotic microbial community structure in New Zealand fjords. Science of the Total Environment, 2019, 693, 133507.	8.0	13
1320	Evolutionary lability of host associations promotes phylogenetic overdispersion of coâ€infecting blood parasites. Journal of Animal Ecology, 2019, 88, 1936-1949.	2.8	17
1321	Deciphering rhizosphere microbiome assembly of wild and modern common bean (Phaseolus vulgaris) in native and agricultural soils from Colombia. Microbiome, 2019, 7, 114.	11.1	140
1322	Gut Microbiota Analysis in Postoperative Lynch Syndrome Patients. Frontiers in Microbiology, 2019, 10, 1746.	3 . 5	23
1323	Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes. Cell, 2019, 178, 795-806.e12.	28.9	830
1324	Biogeographical patterns in soil bacterial communities across the Arctic region. FEMS Microbiology Ecology, 2019, 95, .	2.7	53
1325	Restriction of plant roots in boreal forest organic soils affects the microbial community but does not change the dominance from ectomycorrhizal to saprotrophic fungi. FEMS Microbiology Ecology, 2019, 95, .	2.7	11
1326	Biochar-induced changes in metal mobility and uptake by perennial plants in a ferralsol of Brazil's Atlantic forest. Biochar, 2019, 1, 309-324.	12.6	9
1327	Impact of hydraulic retention time and organic matter concentration on side-stream aerobic granular membrane bioreactor. Science of the Total Environment, 2019, 693, 133525.	8.0	15
1328	Microbiomes of Velloziaceae from phosphorus-impoverished soils of the campos rupestres, a biodiversity hotspot. Scientific Data, 2019, 6, 140.	5. 3	10
1329	Laboratory mice born to wild mice have natural microbiota and model human immune responses. Science, 2019, 365, .	12.6	360
1330	Productivity and Community Composition of Low Biomass/High Silica Precipitation Hot Springs: A Possible Window to Earth's Early Biosphere?. Life, 2019, 9, 64.	2.4	18
1331	Plantâ€driven changes in soil microbial communities influence seed germination through negative feedbacks. Ecology and Evolution, 2019, 9, 9298-9311.	1.9	21
1332	Antibiotic resistance gene distribution in agricultural fields and crops. A soil-to-food analysis. Environmental Research, 2019, 177, 108608.	7.5	84
1333	Global change-driven use of onshore habitat impacts polar bear faecal microbiota. ISME Journal, 2019, 13, 2916-2926.	9.8	33
1334	Impact of microwave disinfestation treatments on the bacterial communities of noâ€till agricultural soils. European Journal of Soil Science, 2020, 71, 1006-1017.	3.9	15
1335	Characterization of fungal biodiversity and communities associated with the reef macroalga Sargassum ilicifolium reveals fungal community differentiation according to geographic locality and algal structure. Marine Biodiversity, 2019, 49, 2601-2608.	1.0	19

#	Article	IF	CITATIONS
1336	The microbiome reflects diagnosis and predicts disease severity in paediatric onset inflammatory bowel disease. Scandinavian Journal of Gastroenterology, 2019, 54, 969-975.	1.5	20
1337	Baseline microbiota composition modulates antibiotic-mediated effects on the gut microbiota and host. Microbiome, $2019, 7, 111$.	11.1	50
1338	Analysis of the Stomal Microbiota of a Percutaneous Osseointegrated Prosthesis: A Longitudinal Prospective Cohort Study. Journal of Orthopaedic Research, 2019, 37, 2645-2654.	2.3	13
1339	Influence of rate of salinity increase on nitrifying biofilms. Journal of Cleaner Production, 2019, 238, 117835.	9.3	36
1340	Nitrogen Fertilizers Shape the Composition and Predicted Functions of the Microbiota of Field-Grown Tomato Plants. Phytobiomes Journal, 2019, 3, 315-325.	2.7	26
1341	VOLARE: visual analysis of disease-associated microbiome-immune system interplay. BMC Bioinformatics, 2019, 20, 432.	2.6	6
1342	Characterizing the soil microbiome and quantifying antibiotic resistance gene dynamics in agricultural soil following swine CAFO manure application. PLoS ONE, 2019, 14, e0220770.	2.5	42
1343	The occurrence of Listeria monocytogenes is associated with built environment microbiota in three tree fruit processing facilities. Microbiome, 2019, 7, 115.	11.1	61
1344	Soil bacterial and fungal response to wildfires in the Canadian boreal forest across a burn severity gradient. Soil Biology and Biochemistry, 2019, 138, 107571.	8.8	139
1345	Experimental Inoculation of Coral Recruits With Marine Bacteria Indicates Scope for Microbiome Manipulation in Acropora tenuis and Platygyra daedalea. Frontiers in Microbiology, 2019, 10, 1702.	3.5	55
1346	Salinity, microbe and carbonate mineral relationships in brackish and hypersaline lake sediments: A case study from the tropical Pacific coral atoll of Kiritimati. Depositional Record, 2019, 5, 212-229.	1.7	14
1347	Meta-Analysis Reveals Reproducible Gut Microbiome Alterations in Response to a High-Fat Diet. Cell Host and Microbe, 2019, 26, 265-272.e4.	11.0	194
1348	Next-generation sequencing reveals predominant bacterial communities during fermentation of Thai fish sauce in large manufacturing plants. LWT - Food Science and Technology, 2019, 114, 108375.	5.2	30
1349	A method of processing nasopharyngeal swabs to enable multiple testing. Pediatric Research, 2019, 86, 651-654.	2.3	12
1350	Continuous Monoculture Shapes Root and Rhizosphere Fungal Communities of Corn and Soybean in Soybean Cyst Nematode-Infested Soil. Phytobiomes Journal, 2019, 3, 300-314.	2.7	10
1351	Diversity and Characterization of Oomycetes Associated with Corn Seedlings in Michigan. Phytobiomes Journal, 2019, 3, 224-234.	2.7	26
1352	Geological gasâ€storage shapes deep life. Environmental Microbiology, 2019, 21, 3953-3964.	3.8	15
1353	Anthropogenic N deposition alters soil organic matter biochemistry and microbial communities on decaying fine roots. Global Change Biology, 2019, 25, 4369-4382.	9.5	40

#	Article	IF	Citations
1354	Characterization of the Wood Mycobiome of Vitis vinifera in a Vineyard Affected by Esca. Spatial Distribution of Fungal Communities and Their Putative Relation With Leaf Symptoms. Frontiers in Plant Science, 2019, 10, 910.	3.6	66
1355	Microbial Profile of the Leachate from Mexico City's Bordo Poniente Composting Plant: An Inoculum to Digest Organic Waste. Energies, 2019, 12, 2343.	3.1	5
1356	Population Genetic Divergence and Environment Influence the Gut Microbiome in Oregon Threespine Stickleback. Genes, 2019, 10, 484.	2.4	27
1357	Storage and handling of human faecal samples affect the gut microbiome composition: A feasibility study. Journal of Microbiological Methods, 2019, 164, 105668.	1.6	14
1358	Insights into the Microbiome of Breast Implants and Periprosthetic Tissue in Breast Implant-Associated Anaplastic Large Cell Lymphoma. Scientific Reports, 2019, 9, 10393.	3.3	76
1359	Molecular Diagnosis of Vaginitis: Comparing Quantitative PCR and Microbiome Profiling Approaches to Current Microscopy Scoring. Journal of Clinical Microbiology, 2019, 57, .	3.9	19
1360	Fecal microbiota of different reproductive stages of the central population of the lesser-long nosed bat, Leptonycteris yerbabuenae. PLoS ONE, 2019, 14, e0219982.	2.5	15
1361	Functional analysis of gut microbiota and immunoinflammation in children with autism spectrum disorders. Digestive and Liver Disease, 2019, 51, 1366-1374.	0.9	38
1362	The effect of levofloxacin on the lung microbiota of laboratory rats. Experimental Lung Research, 2019, 45, 200-208.	1.2	4
1363	Host genetics and geography influence microbiome composition in the sponge <i>lrcinia campana</i> Journal of Animal Ecology, 2019, 88, 1684-1695.	2.8	57
1364	Patterns of protist diversity associated with raw sewage in New York City. ISME Journal, 2019, 13, 2750-2763.	9.8	33
1365	Spatial Variations of Bacterial Communities of an Anaerobic Lagoon-Type Biodigester Fed with Dairy Manure. Processes, 2019, 7, 408.	2.8	11
1366	Interkingdom interactions on the denture surface: Implications for oral hygiene. Biofilm, 2019, 1, 100002.	3.8	15
1367	$31 \hat{A}^\circ$ South: The physiology of adaptation to arid conditions in a passerine bird. Molecular Ecology, 2019, 28, 3709-3721.	3.9	11
1368	Biodegradation of metformin and its transformation product, guanylurea, by natural and exposed microbial communities. Ecotoxicology and Environmental Safety, 2019, 182, 109414.	6.0	46
1369	Changes in the composition and function of bacterial communities during vermicomposting may explain beneficial properties of vermicompost. Scientific Reports, 2019, 9, 9657.	3.3	69
1370	Incense Burning is Associated with Human Oral Microbiota Composition. Scientific Reports, 2019, 9, 10039.	3.3	12
1371	A pollution gradient contributes to the taxonomic, functional, and resistome diversity of microbial communities in marine sediments. Microbiome, 2019, 7, 104.	11.1	100

#	Article	IF	CITATIONS
1372	Composted biosolids for golf course turfgrass management: Impacts on the soil microbiome and nutrient cycling. Applied Soil Ecology, 2019, 144, 31-41.	4.3	16
1373	Petunia- and Arabidopsis-Specific Root Microbiota Responses to Phosphate Supplementation. Phytobiomes Journal, 2019, 3, 112-124.	2.7	37
1374	Multiple Data Analyses and Statistical Approaches for Analyzing Data from Metagenomic Studies and Clinical Trials. Methods in Molecular Biology, 2019, 1910, 605-634.	0.9	8
1375	Vertical transmission of sponge microbiota is inconsistent and unfaithful. Nature Ecology and Evolution, 2019, 3, 1172-1183.	7.8	82
1376	Increased Fecal Lactobacillus Is Associated With a Positive Glucose Hydrogen Breath Test in Bangladeshi Children. Open Forum Infectious Diseases, 2019, 6, ofz266.	0.9	4
1377	Microbial Succession of Anaerobic Chitin Degradation in Freshwater Sediments. Applied and Environmental Microbiology, 2019, 85, .	3.1	12
1378	Biogeography of soil bacterial populations in the Jutulsessen and Ahlmannryggen of Western Dronning Maud Land, Antarctica. Polar Biology, 2019, 42, 1445-1458.	1.2	6
1379	Are bacteria responsible for aroma deterioration upon storage of the black truffle Tuber aestivum: A microbiome and volatilome study. Food Microbiology, 2019, 84, 103251.	4.2	32
1380	Combining KMnO4 pre-oxidation and bioaugmented sand filtration to simultaneously treat cyanobacterial bloom lake water and released Mn(II). Separation and Purification Technology, 2019, 228, 115765.	7.9	11
1381	Type 1 Diabetes: an Association Between Autoimmunity, the Dynamics of Gut Amyloid-producing E. coli and Their Phages. Scientific Reports, 2019, 9, 9685.	3.3	53
1382	Characterization of the gastrointestinal bacterial microbiome of farmed juvenile and adult white Cachama (Piaractus brachypomus). Aquaculture, 2019, 512, 734325.	3.5	19
1383	Gut microbiome and serum metabolome analyses identify molecular biomarkers and altered glutamate metabolism in fibromyalgia. EBioMedicine, 2019, 46, 499-511.	6.1	128
1384	Diversity decoupled from sulfur isotope fractionation in a sulfateâ€reducing microbial community. Geobiology, 2019, 17, 660-675.	2.4	7
1385	Influence of introduced arbuscular mycorrhizal fungi and phosphorus sources on plant traits, soil properties, and rhizosphere microbial communities in organic legume-flax rotation. Plant and Soil, 2019, 443, 87-106.	3.7	13
1386	Feline gut microbiota composition in association with feline coronavirus infection: A pilot study. Research in Veterinary Science, 2019, 125, 272-278.	1.9	9
1387	Exploiting the unwanted: Sulphate reduction enables phosphate recovery from energy-rich sludge during anaerobic digestion. Water Research, 2019, 163, 114859.	11.3	28
1388	Treatment-Specific Composition of the Gut Microbiota Is Associated With Disease Remission in a Pediatric Crohn's Disease Cohort. Inflammatory Bowel Diseases, 2019, 25, 1927-1938.	1.9	20
1389	Targeted ITS1 sequencing unravels the mycodiversity of deepâ€sea sediments from the Gulf of Mexico. Environmental Microbiology, 2019, 21, 4046-4061.	3.8	19

#	Article	IF	CITATIONS
1390	Salinity drives meiofaunal community structure dynamics across the Baltic ecosystem. Molecular Ecology, 2019, 28, 3813-3829.	3.9	31
1391	The roles of age, parentage and environment on bacterial and algal endosymbiont communities in <i>Acropora</i> corals. Molecular Ecology, 2019, 28, 3830-3843.	3.9	17
1392	Combining stable isotope analysis with DNA metabarcoding improves inferences of trophic ecology. PLoS ONE, 2019, 14, e0219070.	2.5	15
1393	Effect of live yeast Saccharomyces cerevisiae supplementation on the performance and cecum microbial profile of suckling piglets. PLoS ONE, 2019, 14, e0219557.	2.5	43
1394	Orchard Conditions and Fruiting Body Characteristics Drive the Microbiome of the Black Truffle Tuber aestivum. Frontiers in Microbiology, 2019, 10, 1437.	3. 5	31
1395	Temporal Variation in the Microbiome of Acropora Coral Species Does Not Reflect Seasonality. Frontiers in Microbiology, 2019, 10, 1775.	3.5	29
1396	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
1397	The Phytoplankton Taxon-Dependent Oil Response and Its Microbiome: Correlation but Not Causation. Frontiers in Microbiology, 2019, 10, 385.	3.5	12
1398	Associations between fungal and bacterial microbiota of airways and asthma endotypes. Journal of Allergy and Clinical Immunology, 2019, 144, 1214-1227.e7.	2.9	96
1399	Response of gastrointestinal fermentative activity and colonic microbiota to protected sodium butyrate and protected sodium heptanoate in weaned piglets challenged with ETEC F4 ⁺ . Archives of Animal Nutrition, 2019, 73, 339-359.	1.8	9
1400	The human microbiota is associated with cardiometabolic risk across the epidemiologic transition. PLoS ONE, 2019, 14, e0215262.	2.5	29
1401	MODIMA, a Method for Multivariate Omnibus Distance Mediation Analysis, Allows for Integration of Multivariate Exposure–Mediator–Response Relationships. Genes, 2019, 10, 524.	2.4	12
1402	Drivers and patterns of microbial community assembly in a Lyme disease vector. Ecology and Evolution, 2019, 9, 7768-7779.	1.9	30
1403	Co-cultivation of the marine sponge Halichondria panicea and its associated microorganisms. Scientific Reports, 2019, 9, 10403.	3.3	19
1404	Diversity of tryptophan halogenases in sponges of the genus Aplysina. FEMS Microbiology Ecology, 2019, 95, .	2.7	11
1405	Algae and Clay Water Additives Differentially Impact Survival and Microbial Community Structure in Sablefish (Anoplopoma fimbria) Rearing Tanks. Frontiers in Marine Science, 2019, 6, .	2.5	4
1406	Non-sterile heterotrophic cultivation of native wastewater yeast and microalgae for integrated municipal wastewater treatment and bioethanol production. Biochemical Engineering Journal, 2019, 151, 107319.	3.6	58
1407	Temporal association of the development of oropharyngeal microbiota with early life wheeze in a population-based birth cohort. EBioMedicine, 2019, 46, 486-498.	6.1	18

#	Article	IF	Citations
1408	Significant alterations in soil fungal communities along a chronosequence of Spartina alterniflora invasion in a Chinese Yellow Sea coastal wetland. Science of the Total Environment, 2019, 693, 133548.	8.0	58
1409	Effects of Hardwood Biochar on Methane Production, Fermentation Characteristics, and the Rumen Microbiota Using Rumen Simulation. Frontiers in Microbiology, 2019, 10, 1534.	3.5	40
1410	Highly Diverse Aquatic Microbial Communities Separated by Permafrost in Greenland Show Distinct Features According to Environmental Niches. Frontiers in Microbiology, 2019, 10, 1583.	3.5	12
1411	Analysis of Soil Properties, Bacterial Community Composition, and Metabolic Diversity in Fluvisols of a Floodplain Area. Sustainability, 2019, 11, 3929.	3.2	20
1412	Visualization of microbes by 16S in situ hybridization in term and preterm placentas without intraamniotic infection. American Journal of Obstetrics and Gynecology, 2019, 221, 146.e1-146.e23.	1.3	96
1413	Short communication: Surface charring from prescribed burning has minimal effects on soil bacterial community composition two weeks post-fire in jack pine barrens. Applied Soil Ecology, 2019, 144, 134-138.	4.3	12
1414	Microbiome composition and implications for ballast water classification using machine learning. Science of the Total Environment, 2019, 691, 810-818.	8.0	12
1415	Shifts in bentonite bacterial community and mineralogy in response to uranium and glycerol-2-phosphate exposure. Science of the Total Environment, 2019, 692, 219-232.	8.0	21
1416	Microbial Similarity between Students in a Common Dormitory Environment Reveals the Forensic Potential of Individual Microbial Signatures. MBio, 2019, 10, .	4.1	31
1417	Total and Potentially Active Bacterial Communities Entrapped in a Late Glacial Through Holocene Ice Core From Scarisoara Ice Cave, Romania. Frontiers in Microbiology, 2019, 10, 1193.	3.5	23
1418	Captivity and Infection by the Fungal Pathogen Batrachochytrium salamandrivorans Perturb the Amphibian Skin Microbiome. Frontiers in Microbiology, 2019, 10, 1834.	3.5	39
1419	Sebacinoids within rhizospheric fungal communities associated with subsistence farming in the Congo Basin: a needle in each haystack. FEMS Microbiology Ecology, 2019, 95, .	2.7	10
1420	Longitudinal microbiome profiling reveals impermanence of probiotic bacteria in domestic pigeons. PLoS ONE, 2019, 14, e0217804.	2.5	12
1421	Mixed Spices at Culinary Doses Have Prebiotic Effects in Healthy Adults: A Pilot Study. Nutrients, 2019, 11, 1425.	4.1	25
1422	Assessment of the impact of different fecal storage protocols on the microbiota diversity and composition: a pilot study. BMC Microbiology, 2019, 19, 145.	3.3	19
1423	Soil fungal communities vary with invasion by the exotic Spartina alternifolia Loisel. in coastal salt marshes of eastern China. Plant and Soil, 2019, 442, 215-232.	3.7	20
1424	Effects of thermal hydrolytic pre-treatment on biogas process efficiency and microbial community structure in industrial- and laboratory-scale digesters. Waste Management, 2019, 95, 150-160.	7.4	33
1425	Microbial Diversity Exploration of Marine Hosts at Serrana Bank, a Coral Atoll of the Seaflower Biosphere Reserve. Frontiers in Marine Science, 2019, 6, .	2.5	18

#	Article	IF	CITATIONS
1426	Monitored Indoor Environmental Quality of a Mass Timber Office Building: A Case Study. Buildings, 2019, 9, 142.	3.1	11
1427	Spatial ecology of a wastewater network defines the antibiotic resistance genes in downstream receiving waters. Water Research, 2019, 162, 347-357.	11.3	108
1428	DNA extraction and amplicon production strategies deeply inf luence the outcome of gut mycobiome studies. Scientific Reports, 2019, 9, 9328.	3.3	51
1429	Enrichment of intestinal Lactobacillus by enhanced secretory IgA coating alters glucose homeostasis in P2rx7â^'/â^' mice. Scientific Reports, 2019, 9, 9315.	3.3	18
1431	Gut microbiota density influences host physiology and is shaped by host and microbial factors. ELife, 2019, 8, .	6.0	118
1432	Association between the pig genome and its gut microbiota composition. Scientific Reports, 2019, 9, 8791.	3.3	64
1433	Microbial communities in top- and subsoil of repacked soil columns respond differently to amendments but their diversity is negatively correlated with plant productivity. Scientific Reports, 2019, 9, 8890.	3.3	27
1434	Interannual comparison of core taxa and community composition of the blow microbiota from East Australian humpback whales. FEMS Microbiology Ecology, 2019, 95, .	2.7	10
1435	Comparison of boreal acid sulfate soil microbial communities in oxidative and reductive environments. Research in Microbiology, 2019, 170, 288-295.	2.1	8
1436	Phylogenetic Techniques in Geomicrobiology. , 2019, , 360-404.		0
1437	Altered Stool Microbiota of Infants with Cystic Fibrosis Shows a Reduction in Genera Associated with Immune Programming from Birth. Journal of Bacteriology, 2019, 201, .	2.2	60
1438	Biogeochemical Behavior of Metals Along Two Permeable Reactive Barriers in a Miningâ€Affected Wetland. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 3536-3554.	3.0	4
1439	Organic Soils Control Beetle Survival While Competitors Limit Aphid Population Growth. Environmental Entomology, 2019, 48, 1323-1330.	1.4	14
1440	Distinctive microbial communities in subzero hypersaline brines from Arctic coastal sea ice and rarely sampled cryopegs. FEMS Microbiology Ecology, 2019, 95, .	2.7	20
1441	Above-below surface interactions mediate effects of seagrass disturbance on meiobenthic diversity, nematode and polychaete trophic structure. Communications Biology, 2019, 2, 362.	4.4	6
1442	Microbial composition in seasonal time series of free tropospheric air and precipitation reveals community separation. Aerobiologia, 2019, 35, 671-701.	1.7	41
1443	Analysis of Gut Microbiota and Their Metabolic Potential in Patients with Schizophrenia Treated with Olanzapine: Results from a Six-Week Observational Prospective Cohort Study. Journal of Clinical Medicine, 2019, 8, 1605.	2.4	37
1444	Changes in the Bacterioplankton Community Structure from Southern Gulf of Mexico During a Simulated Crude Oil Spill at Mesocosm Scale. Microorganisms, 2019, 7, 441.	3.6	18

#	Article	IF	CITATIONS
1445	An artificial neural network and Random Forest identify glyphosate-impacted brackish communities based on 16S rRNA amplicon MiSeq read counts. Marine Pollution Bulletin, 2019, 149, 110530.	5.0	22
1446	Fungicides and the Grapevine Wood Mycobiome: A Case Study on Tracheomycotic Ascomycete Phaeomoniella chlamydospora Reveals Potential for Two Novel Control Strategies. Frontiers in Plant Science, 2019, 10, 1405.	3.6	18
1447	Gastro-intestinal and oral microbiome signatures associated with healthy aging. GeroScience, 2019, 41, 907-921.	4.6	89
1448	Saccharomyces cerevisiae Induces Immune Enhancing and Shapes Gut Microbiota in Social Wasps. Frontiers in Microbiology, 2019, 10, 2320.	3.5	22
1449	Colonizing multidrug-resistant bacteria and the longitudinal evolution of the intestinal microbiome after liver transplantation. Nature Communications, 2019, 10, 4715.	12.8	70
1450	Alterations to the Gastrointestinal Microbiome Associated with Methamphetamine Use among Young Men who have Sex with Men. Scientific Reports, 2019, 9, 14840.	3.3	38
1451	Changes in motor behavior, neuropathology, and gut microbiota of a Batten disease mouse model following administration of acidified drinking water. Scientific Reports, 2019, 9, 14962.	3.3	21
1452	Viral respiratory infections and the oropharyngeal bacterial microbiota in acutely wheezing children. PLoS ONE, 2019, 14, e0223990.	2.5	14
1453	Yeasts of Burden: Exploring the Mycobiome–Bacteriome of the Piglet GI Tract. Frontiers in Microbiology, 2019, 10, 2286.	3.5	37
1454	An assessment of Oxford Nanopore sequencing for human gut metagenome profiling: A pilot study of head and neck cancer patients. Journal of Microbiological Methods, 2019, 166, 105739.	1.6	13
1455	Looking at the Origin: Some Insights into the General and Fermentative Microbiota of Vineyard Soils. Fermentation, 2019, 5, 78.	3.0	11
1456	Elemental diet induces alterations of the gut microbial community in mice. Journal of Clinical Biochemistry and Nutrition, 2019, 65, 118-124.	1.4	10
1457	Electrochemical and Microbiological Characterization of Bioanode Communities Exhibiting Variable Levels of Startup Activity. Frontiers in Energy Research, 2019, 7, .	2.3	5
1458	A Bioinformatics Guide to Plant Microbiome Analysis. Frontiers in Plant Science, 2019, 10, 1313.	3.6	54
1459	The vaginal microbial communities of healthy expectant Brazilian mothers and its correlation with the newborn's gut colonization. World Journal of Microbiology and Biotechnology, 2019, 35, 159.	3.6	18
1460	Genetic, epigenetic and microbiome characterisation of an earthworm species (Octolasion lacteum) along a radiation exposure gradient at Chernobyl. Environmental Pollution, 2019, 255, 113238.	7.5	19
1461	How should we store avian faecal samples for microbiota analyses? Comparing efficacy and cost-effectiveness. Journal of Microbiological Methods, 2019, 165, 105689.	1.6	5
1462	Fungal and bacterial community dynamics in substrates during the cultivation of morels (<i>Morchella rufobrunnea</i>) indoors. FEMS Microbiology Letters, 2019, 366, .	1.8	31

#	Article	IF	CITATIONS
1463	Temporal patterns of variability for prokaryotic and eukaryotic diversity in the urban air of Madrid (Spain). Atmospheric Environment, 2019, 217, 116972.	4.1	26
1464	Copper-Induced Stimulation of Nitrification in Biological Rapid Sand Filters for Drinking Water Production by Proliferation of <i>Nitrosomonas</i> spp Environmental Science & Environmental Science	10.0	13
1465	Beneficial effects of Lactobacillus reuteri 6475 on bone density in male mice is dependent on lymphocytes. Scientific Reports, 2019, 9, 14708.	3.3	28
1466	Bacterial Communities from Extreme Environments: Vulcano Island. Diversity, 2019, 11, 140.	1.7	9
1467	Seagrassâ€associated fungal communities show distance decay of similarity that has implications for seagrass management and restoration. Ecology and Evolution, 2019, 9, 11288-11297.	1.9	32
1468	Assessing different components of diversity across a river network using eDNA. Environmental DNA, 2019, 1, 290-301.	5.8	64
1469	Community structure and distribution of benthic Bacteria and Archaea in a stratified coastal lagoon in the Southern Gulf of Mexico. Estuarine, Coastal and Shelf Science, 2019, 230, 106433.	2.1	7
1470	The biodiversity benefit of native forests and mixedâ€species plantations over monoculture plantations. Diversity and Distributions, 2019, 25, 1721-1735.	4.1	50
1471	Glucorticoidâ€induced obesity individuals have distinct signatures of the gut microbiome. BioFactors, 2019, 45, 892-901.	5.4	30
1472	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. Genome Biology, 2019, 20, 219.	8.8	94
1473	Caecal Microbiota of Experimentally Campylobacter jejuni-Infected Chickens at Different Ages. Frontiers in Microbiology, 2019, 10, 2303.	3.5	19
1474	Rapid Bacterial Community Changes during Vermicomposting of Grape Marc Derived from Red Winemaking. Microorganisms, 2019, 7, 473.	3.6	19
1475	Impacts of Maize Domestication and Breeding on Rhizosphere Microbial Community Recruitment from a Nutrient Depleted Agricultural Soil. Scientific Reports, 2019, 9, 15611.	3.3	91
1476	Agricultural management and plant selection interactively affect rhizosphere microbial community structure and nitrogen cycling. Microbiome, 2019, 7, 146.	11.1	202
1477	Prokaryotic and eukaryotic microbiomes associated with blooms of the ichthyotoxic dinoflagellate Cochlodinium (Margalefidinium) polykrikoides in New York, USA, estuaries. PLoS ONE, 2019, 14, e0223067.	2.5	16
1478	Microbial communities of the house fly Musca domestica vary with geographical location and habitat. Microbiome, 2019, 7, 147.	11.1	70
1479	Microbiome of vineyard soils is shaped by geography and management. Microbiome, 2019, 7, 140.	11.1	94
1480	The bacterial community in potato is recruited from soil and partly inherited across generations. PLoS ONE, 2019, 14, e0223691.	2.5	39

#	Article	IF	CITATIONS
1481	Honey bee microbiome associated with different hive and sample types over a honey production season. PLoS ONE, 2019, 14, e0223834.	2.5	25
1482	Tissue-Specific Microbiomes of the Red Sea Giant Clam Tridacna maxima Highlight Differential Abundance of Endozoicomonadaceae. Frontiers in Microbiology, 2019, 10, 2661.	3.5	13
1483	Site-Specific Microbial Decomposer Communities Do Not Imply Faster Decomposition: Results from a Litter Transplantation Experiment. Microorganisms, 2019, 7, 349.	3.6	17
1484	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. Science, 2019, 366, 606-612.	12.6	621
1485	Regional biogeography of microbiota composition in the Chagas disease vector Rhodnius pallescens. Parasites and Vectors, 2019, 12, 504.	2.5	17
1486	The Regulation of Ruminal Short-Chain Fatty Acids on the Functions of Rumen Barriers. Frontiers in Physiology, 2019, 10, 1305.	2.8	33
1487	Infant airway microbiota and topical immune perturbations in the origins of childhood asthma. Nature Communications, 2019, 10, 5001.	12.8	92
1488	<i>Serratia marcescens</i> shapes cutaneous bacterial communities and influences survival of an amphibian host. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191833.	2.6	9
1489	Helicobacter pylori Infection Aggravates Dysbiosis of Gut Microbiome in Children With Gastritis. Frontiers in Cellular and Infection Microbiology, 2019, 9, 375.	3.9	45
1490	Differences in Applied Redox Potential on Cathodes Enrich for Diverse Electrochemically Active Microbial Isolates From a Marine Sediment. Frontiers in Microbiology, 2019, 10, 1979.	3.5	24
1491	The Bacterial Communities of Little Cigars and Cigarillos Are Dynamic Over Time and Varying Storage Conditions. Frontiers in Microbiology, 2019, 10, 2371.	3.5	12
1492	Changes in human gut microbiota composition are linked to the energy metabolic switch during 10 d of Buchinger fasting. Journal of Nutritional Science, 2019, 8, e36.	1.9	50
1493	Gut microbiota and their putative metabolic functions in fragmented Bengal tiger population of Nepal. PLoS ONE, 2019, 14, e0221868.	2.5	13
1494	Primer and Database Choice Affect Fungal Functional but Not Biological Diversity Findings in a National Soil Survey. Frontiers in Environmental Science, 2019, 7, .	3.3	26
1495	Habitat filters mediate successional trajectories in bacterial communities associated with the striped shore crab. Oecologia, 2019, 191, 957-970.	2.0	3
1496	The Human Milk Microbiota is Modulated by Maternal Diet. Microorganisms, 2019, 7, 502.	3.6	59
1497	Intermediate-Salinity Systems at High Altitudes in the Peruvian Andes Unveil a High Diversity and Abundance of Bacteria and Viruses. Genes, 2019, 10, 891.	2.4	12
1498	Profiling population-level diversity and dynamics of Accumulibacter via high throughput sequencing of ppk1. Applied Microbiology and Biotechnology, 2019, 103, 9711-9722.	3.6	13

#	Article	IF	CITATIONS
1499	Impact of quality trimming on the efficiency of reads joining and diversity analysis of Illumina paired-end reads in the context of QIIME1 and QIIME2 microbiome analysis frameworks. BMC Bioinformatics, 2019, 20, 581.	2.6	52
1500	Assessing the potential of culture-independent 16S rRNA microbiome analysis in disease diagnostics: the example of Dianthus gratianopolitanus and Robbsia andropogonis. European Journal of Plant Pathology, 2019, 155, 1211-1223.	1.7	4
1501	Microbiota Analysis Using Two-step PCR and Next-generation 16S rRNA Gene Sequencing. Journal of Visualized Experiments, 2019, , .	0.3	24
1502	Deterministic and stochastic processes driving the shift in the prokaryotic community composition in wastewater treatment plants of a coastal Chinese city. Applied Microbiology and Biotechnology, 2019, 103, 9155-9168.	3.6	15
1503	Microbial Community Shifts Associated With the Ongoing Stony Coral Tissue Loss Disease Outbreak on the Florida Reef Tract. Frontiers in Microbiology, 2019, 10, 2244.	3.5	143
1504	Reduced Gut Microbiome Diversity and Metabolome Differences in Rhinoceros Species at Risk for Iron Overload Disorder. Frontiers in Microbiology, 2019, 10, 2291.	3.5	26
1505	Chinese Black Truffle-Associated Bacterial Communities of Tuber indicum From Different Geographical Regions With Nitrogen Fixing Bioactivity. Frontiers in Microbiology, 2019, 10, 2515.	3.5	29
1506	Storage media and not extraction method has the biggest impact on recovery of bacteria from the oral microbiome. Scientific Reports, 2019, 9, 14968.	3.3	20
1507	Soil domestication by rice cultivation results in plant-soil feedback through shifts in soil microbiota. Genome Biology, 2019, 20, 221.	8.8	54
1508	Dietary fibre enrichment of supplemental feed modulates the development of the intestinal tract in suckling piglets. Journal of Animal Science and Biotechnology, 2019, 10, 83.	5.3	25
1509	Assessment of Artificial and Natural Transport Mechanisms of Ice Nucleating Particles in an Alpine Ski Resort in Obergurgl, Austria. Frontiers in Microbiology, 2019, 10, 2278.	3.5	6
1510	Metagenomics Reveals Bacterial and Archaeal Adaptation to Urban Land-Use: N Catabolism, Methanogenesis, and Nutrient Acquisition. Frontiers in Microbiology, 2019, 10, 2330.	3.5	12
1511	Linking pollen foraging of megachilid bees to their nest bacterial microbiota. Ecology and Evolution, 2019, 9, 10788-10800.	1.9	36
1512	Characterization of Microbial Communities in a Dairy Farm Matrix in Ningxia, China, by 16S rDNA Analysis. International Journal of Genomics, 2019, 2019, 1-13.	1.6	3
1513	Is It First the Egg or the Shrimp? – Diversity and Variation in Microbial Communities Colonizing Broods of the Vent Shrimp Rimicaris exoculata During Embryonic Development. Frontiers in Microbiology, 2019, 10, 808.	3.5	22
1514	Defining the Distinct Skin and Gut Microbiomes of the Northern Pike (Esox lucius). Frontiers in Microbiology, 2019, 10, 2118.	3.5	25
1515	Comparison of Different Invasive and Non-Invasive Methods to Characterize Intestinal Microbiota throughout a Production Cycle of Broiler Chickens. Microorganisms, 2019, 7, 431.	3.6	14
1516	Weekly dynamics of abundance and size structure of specific nanophytoplankton lineages in coastal waters (Baltic Sea). Limnology and Oceanography, 2019, 64, 2172-2186.	3.1	11

#	Article	IF	CITATIONS
1517	iVikodakâ€"A Platform and Standard Workflow for Inferring, Analyzing, Comparing, and Visualizing the Functional Potential of Microbial Communities. Frontiers in Microbiology, 2018, 9, 3336.	3.5	70
1518	Enhanced Immobilization of Arsenic from Acid Mine Drainage by Detrital Clay Minerals. ACS Earth and Space Chemistry, 2019, 3, 2525-2538.	2.7	7
1520	It's what's on the inside that counts: stress physiology and the bacterial microbiome of a wild urban mammal. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20192111.	2.6	45
1521	Largeâ€scale biogeography and environmental regulation of methanotrophic bacteria across boreal inland waters. Molecular Ecology, 2019, 28, 4181-4196.	3.9	23
1522	A Metagenomic-Based Approach for the Characterization of Bacterial Diversity Associated with Spontaneous Malolactic Fermentations in Wine. International Journal of Molecular Sciences, 2019, 20, 3980.	4.1	39
1523	Differential Impact of Subtherapeutic Antibiotics and Ionophores on Intestinal Microbiota of Broilers. Microorganisms, 2019, 7, 282.	3.6	35
1524	Analysis of Transcriptionally Active Bacteria Throughout the Gastrointestinal Tract of Healthy Individuals. Gastroenterology, 2019, 157, 1081-1092.e3.	1.3	103
1525	Association of dietary patterns with the gut microbiota in older, community-dwelling men. American Journal of Clinical Nutrition, 2019, 110, 1003-1014.	4.7	55
1526	Successional Dynamics in the Gut Microbiome Determine the Success of Clostridium difficile Infection in Adult Pig Models. Frontiers in Cellular and Infection Microbiology, 2019, 9, 271.	3.9	5
1527	Effect of the vaginal microbiome on the pregnancy rate in women receiving assisted reproductive treatment. Journal of Assisted Reproduction and Genetics, 2019, 36, 2111-2119.	2.5	48
1528	Exploring interactions between Blastocystis sp., Strongyloides spp. and the gut microbiomes of wild chimpanzees in Senegal. Infection, Genetics and Evolution, 2019, 74, 104010.	2.3	16
1529	Cholestasis induced by bile duct ligation promotes changes in the intestinal microbiome in mice. Scientific Reports, 2019, 9, 12324.	3.3	34
1530	Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. MSphere, 2019, 4, .	2.9	40
1531	Antibiotic-Induced Perturbations Are Manifested in the Dominant Intestinal Bacterial Phyla of Atlantic Salmon. Microorganisms, 2019, 7, 233.	3.6	41
1532	Enrichment of intracellular sulphur cycle –associated bacteria in intertidal benthic foraminifera revealed by 16S and aprA gene analysis. Scientific Reports, 2019, 9, 11692.	3.3	13
1533	Surface Water Microbial Community Response to the Biocide 2,2-Dibromo-3-Nitrilopropionamide, Used in Unconventional Oil and Gas Extraction. Applied and Environmental Microbiology, 2019, 85, .	3.1	12
1534	Tomato Seed-Associated Bacteria Confer Protection of Seedlings Against Foliar Disease Caused by <i>Pseudomonas syringae</i>). Phytobiomes Journal, 2019, 3, 177-190.	2.7	36
1535	Batch effect exerts a bigger influence on the rat urinary metabolome and gut microbiota than uraemia: a cautionary tale. Microbiome, 2019, 7, 127.	11.1	17

#	Article	IF	CITATIONS
1536	Take care of the environment: housing conditions affect the interplay of nutritional interventions and intestinal microbiota in broiler chickens. Animal Microbiome, 2019, 1, 10.	3.8	35
1537	Gut microbiota features associated with Clostridioides difficile colonization in puppies. PLoS ONE, 2019, 14, e0215497.	2.5	15
1538	Vaginal Microbiome Signature Is Associated With Spontaneous Preterm Delivery. Frontiers in Medicine, 2019, 6, 201.	2.6	71
1539	Genetic determinants of gut microbiota composition and bile acid profiles in mice. PLoS Genetics, 2019, 15, e1008073.	3.5	75
1540	Culturing Simpler and Bacterial Wilt Suppressive Microbial Communities from Tomato Rhizosphere. Plant Pathology Journal, 2019, 35, 362-371.	1.7	20
1541	The human gut chemical landscape predicts microbe-mediated biotransformation of foods and drugs. ELife, 2019, 8, .	6.0	39
1542	Responses of Bacterial and Fungal Community Structure to Different Rates of 1,3-Dichloropropene Fumigation. Phytobiomes Journal, 2019, 3, 212-223.	2.7	10
1543	Leaf-Associated Shifts in Bacterial and Fungal Communities in Response to Chicken Rearing Under Moso Bamboo Forests in Subtropical China. Forests, 2019, 10, 216.	2.1	9
1544	Profiling of lung microbiota discloses differences in adenocarcinoma and squamous cell carcinoma. Scientific Reports, 2019, 9, 12838.	3.3	64
1545	Improved single-swab sample preparation for recovering bacterial and phage DNA from human skin and wound microbiomes. BMC Microbiology, 2019, 19, 214.	3.3	14
1546	Intraspecific variation on epiphytic bacterial community from Laguncularia racemosa phylloplane. Brazilian Journal of Microbiology, 2019, 50, 1041-1050.	2.0	3
1547	Differential dynamics of microbial community networks help identify microorganisms interacting with residue-borne pathogens: the case of Zymoseptoria tritici in wheat. Microbiome, 2019, 7, 125.	11.1	41
1548	Diet-induced remission in chronic enteropathy is associated with altered microbial community structure and synthesis of secondary bile acids. Microbiome, 2019, 7, 126.	11.1	108
1549	Transcription and microbial profiling of body fluids using a massively parallel sequencing approach. Forensic Science International: Genetics, 2019, 43, 102149.	3.1	23
1550	Microbiome Signatures Associated With Steatohepatitis and Moderate to Severe Fibrosis in Children With Nonalcoholic Fatty Liver Disease. Gastroenterology, 2019, 157, 1109-1122.	1.3	184
1551	Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. Microbiome, 2019, 7, 121.	11.1	109
1552	The association of gut microbiota characteristics in Malawian infants with growth and inflammation. Scientific Reports, 2019, 9, 12893.	3.3	25
1553	Macroalga-Derived Alginate Oligosaccharide Alters Intestinal Bacteria of Atlantic Salmon. Frontiers in Microbiology, 2019, 10, 2037.	3.5	49

#	Article	IF	CITATIONS
1554	Effects of Dietary-SCFA on Microbial Protein Synthesis and Urinal Urea-N Excretion Are Related to Microbiota Diversity in Rumen. Frontiers in Physiology, 2019, 10, 1079.	2.8	12
1555	Analysis of Microbial Community Dynamics during the Acclimatization Period of a Membrane Bioreactor Treating Table Olive Processing Wastewater. Applied Sciences (Switzerland), 2019, 9, 3647.	2.5	4
1556	Dynamics and diversity of bacteria associated with the disease vectors Aedes aegypti and Aedes albopictus. Scientific Reports, 2019, 9, 12160.	3.3	39
1557	Plumage iridescence is associated with distinct feather microbiota in a tropical passerine. Scientific Reports, 2019, 9, 12921.	3.3	6
1558	Statistical Analysis of Metagenomics Data. Genomics and Informatics, 2019, 17, e6.	0.8	166
1559	Impact of cleaning and disinfection procedures on microbial ecology and Salmonella antimicrobial resistance in a pig slaughterhouse. Scientific Reports, 2019, 9, 12947.	3.3	23
1560	Changes in the Substrate Source Reveal Novel Interactions in the Sediment-Derived Methanogenic Microbial Community. International Journal of Molecular Sciences, 2019, 20, 4415.	4.1	7
1561	Seasonal bacterial community dynamics in a crude oil refinery wastewater treatment plant. Applied Microbiology and Biotechnology, 2019, 103, 9131-9141.	3.6	11
1562	Microbial Metabolism Modulates Antibiotic Susceptibility within the Murine Gut Microbiome. Cell Metabolism, 2019, 30, 800-823.e7.	16.2	70
1563	Successful strategies for human microbiome data generation, storage and analyses. Journal of Biosciences, 2019, 44, 1.	1.1	1
1564	Unveiling resistome profiles in the sediments of an Antarctic volcanic island. Environmental Pollution, 2019, 255, 113240.	7.5	15
1565	Metagenomic deep sequencing reveals association of microbiome signature with functional biases in bovine mastitis. Scientific Reports, 2019, 9, 13536.	3.3	97
1566	Gut microbiome comparability of fresh-frozen versus stabilized-frozen samples from hospitalized patients using 16S rRNA gene and shotgun metagenomic sequencing. Scientific Reports, 2019, 9, 13351.	3.3	16
1567	Visual exploration of microbiome data. Journal of Biosciences, 2019, 44, 1.	1.1	2
1568	Temporal Dynamics of the Sap Microbiome of Grapevine Under High Pierce's Disease Pressure. Frontiers in Plant Science, 2019, 10, 1246.	3.6	48
1569	Adenovirus infection is associated with altered gut microbial communities in a non-human primate. Scientific Reports, 2019, 9, 13410.	3.3	32
1570	Bacillus sp. probiotic supplementation diminish the Escherichia coli F4ac infection in susceptible weaned pigs by influencing the intestinal immune response, intestinal microbiota and blood metabolomics. Journal of Animal Science and Biotechnology, 2019, 10, 74.	5.3	56
1571	Microbiome data science. Journal of Biosciences, 2019, 44, 1.	1.1	35

#	Article	IF	Citations
1572	Microbiome and imputed metagenome study of crude and refined petroleum-oil-contaminated soils: Potential for hydrocarbon degradation and plant-growth promotion. Journal of Biosciences, 2019, 44, 1.	1.1	34
1573	Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of prakriti. Journal of Biosciences, 2019, 44, 1.	1.1	11
1574	Differences in the bacterial profiles of infant gut by birth process, milk diet, and choice of 16S rRNA gene target region. Human Microbiome Journal, 2019, 13, 100062.	3.8	4
1575	Remission in Crohn's disease is accompanied by alterations in the gut microbiota and mucins production. Scientific Reports, 2019, 9, 13263.	3.3	30
1576	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. Microbiome, 2019, 7, 131.	11.1	65
1577	Microbial characterization and fermentative characteristics of crop maize ensiled with unsalable vegetables. Scientific Reports, 2019, 9, 13183.	3.3	7
1578	Characterization of the microbiome and bioluminescent symbionts across life stages of Ceratioid Anglerfishes of the Gulf of Mexico. FEMS Microbiology Ecology, 2019, 95, .	2.7	14
1579	Nod2 deficiency functionally impairs adaptation to short bowel syndrome via alterations of the epithelial barrier function. American Journal of Physiology - Renal Physiology, 2019, 317, G727-G738.	3.4	9
1580	Comparison of the plant growth-promotion performance of a consortium of Bacilli inoculated as endospores or as vegetative cells. FEMS Microbiology Ecology, 2019, 95, .	2.7	15
1581	Fecal Transplant in Children With Clostridioides difficile Gives Sustained Reduction in Antimicrobial Resistance and Potential Pathogen Burden. Open Forum Infectious Diseases, 2019, 6, ofz379.	0.9	32
1582	Analysis of Sinonasal Microbiota in Exacerbations of Chronic Rhinosinusitis Subgroups. OTO Open, 2019, 3, 2473974X1987510.	1.4	10
1583	Preliminary study on microeukaryotic community analysis using NGS technology to determine postmortem submersion interval (PMSI) in the drowned pig. Journal of Microbiology, 2019, 57, 1003-1011.	2.8	6
1584	Trophic networks improve the performance of microbial anodes treating wastewater. Npj Biofilms and Microbiomes, 2019, 5, 27.	6.4	23
1585	Transgenerational inheritance of shuffled symbiont communities in the coral Montipora digitata. Scientific Reports, 2019, 9, 13328.	3.3	42
1586	Letrozole treatment of pubertal female mice results in activational effects on reproduction, metabolism and the gut microbiome. PLoS ONE, 2019, 14, e0223274.	2.5	37
1587	Characteristics and Evolution of sill-driven off-axis hydrothermalism in Guaymas Basin – the Ringvent site. Scientific Reports, 2019, 9, 13847.	3.3	33
1588	Moving Beyond the Host: Unraveling the Skin Microbiome of Endangered Costa Rican Amphibians. Frontiers in Microbiology, 2019, 10, 2060.	3 . 5	23
1589	Microbiota Composition and Functional Profiling Throughout the Gastrointestinal Tract of Commercial Weaning Piglets. Microorganisms, 2019, 7, 343.	3.6	61

#	Article	IF	CITATIONS
1590	Sugar Beet Pectin Supplementation Did Not Alter Profiles of Fecal Microbiota and Exhaled Breath in Healthy Young Adults and Healthy Elderly. Nutrients, 2019, 11, 2193.	4.1	35
1591	Environmental DNA Metabarcoding: A Promising Tool for Ballast Water Monitoring. Environmental Science & Environmental Science	10.0	25
1592	A mutation in mouse KrÃ $\frac{1}{4}$ ppel-like factor 15 alters the gut microbiome and response to obesogenic diet. PLoS ONE, 2019, 14, e0222536.	2.5	3
1593	Geographical location influences the composition of the gut microbiota in wild house mice (Mus) Tj ETQq1 1 0.78	4314 rgB1 2.5	T <u>JO</u> verlock
1594	Evaluation of the Nasopharyngeal Microbiota in Beef Cattle Transported to a Feedlot, With a Focus on Lactic Acid-Producing Bacteria. Frontiers in Microbiology, 2019, 10, 1988.	3.5	22
1595	N2 fixation, and the relative contribution of fixed N, in corals from Curaçao and Hawaii. Coral Reefs, 2019, 38, 1145-1158.	2.2	8
1596	Highly diverse anaerobe-predominant vaginal microbiota among HIV-infected pregnant women in Zambia. PLoS ONE, 2019, 14, e0223128.	2.5	28
1597	High specificity of a rare terrestrial orchid toward a rare fungus within the North American tallgrass prairie. Fungal Biology, 2019, 123, 895-904.	2.5	17
1598	Specific Wheat Fractions Influence Hepatic Fat Metabolism in Diet-Induced Obese Mice. Nutrients, 2019, 11, 2348.	4.1	9
1599	Altered Middle Ear Microbiome in Children With Chronic Otitis Media With Effusion and Respiratory Illnesses. Frontiers in Cellular and Infection Microbiology, 2019, 9, 339.	3.9	19
1600	Understanding the phyllosphere microbiome assemblage in grape species (Vitaceae) with amplicon sequence data structures. Scientific Reports, 2019, 9, 14294.	3.3	40
1601	Short communication: Gut microbial colonization of the mouse colon using faecal transfer was equally effective when comparing rectal inoculation and oral inoculation based on 16S rRNA sequencing. Research in Veterinary Science, 2019, 126, 227-232.	1.9	4
1602	The diversity and ecological roles of Penicillium in intertidal zones. Scientific Reports, 2019, 9, 13540.	3.3	29
1603	Limited changes in the fecal microbiome composition of laying hens after oral inoculation with wild duck feces. Poultry Science, 2019, 98, 6542-6551.	3.4	7
1604	Disease Specific Bacterial Communities in a Coralline Algae of the Northwestern Mediterranean Sea: A Combined Culture Dependent and Independent Approach. Frontiers in Microbiology, 2019, 10, 1850.	3.5	20
1605	Investigating the dispersal of antibiotic resistance associated genes from manure application to soil and drainage waters in simulated agricultural farmland systems. PLoS ONE, 2019, 14, e0222470.	2.5	20
1606	Effects of Habitat Partitioning on the Distribution of Bacterioplankton in Deep Lakes. Frontiers in Microbiology, 2019, 10, 2257.	3.5	26
1607	Linking Environmental DNA and RNA for Improved Detection of the Marine Invasive Fanworm Sabella spallanzanii. Frontiers in Marine Science, 2019, 6, .	2.5	51

#	Article	IF	CITATIONS
1608	Fecal Microbiome Characteristics and the Resistome Associated With Acquisition of Multidrug-Resistant Organisms Among Elderly Subjects. Frontiers in Microbiology, 2019, 10, 2260.	3 . 5	11
1609	Bark and Grape Microbiome of Vitis vinifera: Influence of Geographic Patterns and Agronomic Management on Bacterial Diversity. Frontiers in Microbiology, 2018, 9, 3203.	3.5	69
1610	Changes in arbuscular mycorrhizal fungi between young and old Vitis roots. Symbiosis, 2019, 78, 33-42.	2.3	8
1611	Microbial network disturbances in relapsing refractory Crohn's disease. Nature Medicine, 2019, 25, 323-336.	30.7	277
1612	The impact of <i>in utero </i> HIV exposure on gut microbiota, inflammation, and microbial translocation. Gut Microbes, 2019, 10, 599-614.	9.8	34
1613	Venus flytrap microbiotas withstand harsh conditions during prey digestion. FEMS Microbiology Ecology, 2019, 95, .	2.7	3
1614	Environmental biofilm communities associated with earlyâ€stage common dentex (<i>Dentex dentex</i>) culture. Journal of Applied Microbiology, 2019, 126, 1032-1043.	3.1	5
1615	Urogenital schistosomiasis is associated with signatures of microbiome dysbiosis in Nigerian adolescents. Scientific Reports, 2019, 9, 829.	3.3	41
1616	Tongue coating microbiome data distinguish patients with pancreatic head cancer from healthy controls. Journal of Oral Microbiology, 2019, 11, 1563409.	2.7	93
1617	Assessing eukaryotic biodiversity in the Florida Keys National Marine Sanctuary through environmental DNA metabarcoding. Ecology and Evolution, 2019, 9, 1029-1040.	1.9	69
1618	Analysis of the Pulmonary Microbiome Composition of Legionella pneumophila-Infected Patients. Methods in Molecular Biology, 2019, 1921, 429-443.	0.9	8
1619	Changes in the Active, Dead, and Dormant Microbial Community Structure across a Pleistocene Permafrost Chronosequence. Applied and Environmental Microbiology, 2019, 85, .	3.1	63
1620	Archaea dominate the microbial community in an ecosystem with low-to-moderate temperature and extreme acidity. Microbiome, 2019, 7, 11.	11.1	58
1621	Probiotic <i>Lactobacillus reuteri</i> Prevents Postantibiotic Bone Loss by Reducing Intestinal Dysbiosis and Preventing Barrier Disruption. Journal of Bone and Mineral Research, 2019, 34, 681-698.	2.8	119
1622	A Pilot-Scale Field Study: In Situ Treatment of PCB-Impacted Sediments with Bioamended Activated Carbon. Environmental Science & Environmental Science	10.0	52
1623	Transcriptomics analysis of host liver and meta-transcriptome analysis of rumen epimural microbial community in young calves treated with artificial dosing of rumen content from adult donor cow. Scientific Reports, 2019, 9, 790.	3.3	16
1624	Effect of temperature on the microbial community responsible for methane production in alkaline NamCo wetland soil. Soil Biology and Biochemistry, 2019, 132, 69-79.	8.8	32
1625	Lactobacillus Dominate in the Intestine of Atlantic Salmon Fed Dietary Probiotics. Frontiers in Microbiology, 2018, 9, 3247.	3.5	50

#	Article	IF	CITATIONS
1626	Short-term consumption of a high-fat diet increases host susceptibility to Listeria monocytogenes infection. Microbiome, 2019, 7, 7.	11.1	60
1627	Dynamics of bacterial communities and interaction networks in thawed fish fillets during chilled storage in air. International Journal of Food Microbiology, 2019, 293, 102-113.	4.7	55
1628	The Transcriptional Cycle Is Suited to Daytime N ₂ Fixation in the Unicellular Cyanobacterium " <i>Candidatus</i> Atelocyanobacterium thalassa―(UCYN-A). MBio, 2019, 10, .	4.1	31
1629	Traceability of different brands of bottled mineral water during shelf life, using PCR-DGGE and next generation sequencing techniques. Food Microbiology, 2019, 82, 1-10.	4.2	12
1630	Bacterial communities in an optional lichen symbiosis are determined by substrate, not algal photobionts. FEMS Microbiology Ecology, 2019, 95, .	2.7	13
1631	Oral neonatal antibiotic treatment perturbs gut microbiota and aggravates central nervous system autoimmunity in Dark Agouti rats. Scientific Reports, 2019, 9, 918.	3.3	29
1632	Key colonist pools and habitat filters mediate the composition of fiddler crab–associated bacterial communities. Ecology, 2019, 100, e02628.	3.2	12
1633	Metabarcoding and machine learning analysis of environmental DNA in ballast water arriving to hub ports. Environment International, 2019, 124, 312-319.	10.0	45
1634	Analysis of Cdcs1 colitogenic effects in the hematopoietic compartment reveals distinct microbiome interaction and a new subcongenic interval active in T cells. Mucosal Immunology, 2019, 12, 691-702.	6.0	5
1635	The Association between Objectively Measured Physical Activity and the Gut Microbiome among Older Community Dwelling Men. Journal of Nutrition, Health and Aging, 2019, 23, 538-546.	3.3	27
1636	Hydrocarbon-Degrading Microbial Communities Are Site Specific, and Their Activity Is Limited by Synergies in Temperature and Nutrient Availability in Surface Ocean Waters. Applied and Environmental Microbiology, 2019, 85, .	3.1	23
1637	Microbial community drivers of PK/NRP gene diversity in selected global soils. Microbiome, 2019, 7, 78.	11.1	30
1638	Can bacterial indicators of a grassy woodland restoration inform ecosystem assessment and microbiota-mediated human health?. Environment International, 2019, 129, 105-117.	10.0	50
1639	High dispersal levels and lake warming are emergent drivers of cyanobacterial community assembly in peri-Alpine lakes. Scientific Reports, 2019, 9, 7366.	3.3	18
1640	Comparison of Bacterial Populations in the Ceca of Swine at Two Different Stages and Their Functional Annotations. Genes, 2019, 10, 382.	2.4	13
1641	The fate of pathogens in treated wastewater-soil-crops continuum and the effect of physical barriers. Science of the Total Environment, 2019, 681, 339-349.	8.0	11
1642	Influence of own mother's milk and different proportions of formula on intestinal microbiota of very preterm newborns. PLoS ONE, 2019, 14, e0217296.	2.5	21
1643	Soil fungal responses to experimental warming and drying in a Mediterranean shrubland. Science of the Total Environment, 2019, 683, 524-536.	8.0	16

#	Article	IF	CITATIONS
1644	Advancing integration of data on food microbiome studies: FoodMicrobionet 3.1, a major upgrade of the FoodMicrobionet database. International Journal of Food Microbiology, 2019, 305, 108249.	4.7	32
1645	Controlling for Contaminants in Low-Biomass 16S rRNA Gene Sequencing Experiments. MSystems, 2019, 4, .	3.8	166
1646	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. Nature Microbiology, 2019, 4, 1826-1831.	13.3	149
1647	Changes in stool frequency following chicory inulin consumption, and effects on stool consistency, quality of life and composition of gut microbiota. Food Hydrocolloids, 2019, 96, 688-698.	10.7	33
1648	Variability of the Ability of Complex Microbial Communities to Exclude Microbes Carrying Antibiotic Resistance Genes in Rabbits. Frontiers in Microbiology, 2019, 10, 1503.	3.5	4
1649	Bacterial alkylquinolone signaling contributes to structuring microbial communities in the ocean. Microbiome, 2019, 7, 93.	11.1	25
1650	Diversity and temporal dynamics of primate milk microbiomes. American Journal of Primatology, 2019, 81, e22994.	1.7	17
1651	IL-33 drives group 2 innate lymphoid cell-mediated protection during Clostridium difficile infection. Nature Communications, 2019, 10, 2712.	12.8	93
1652	Differentiating spatial from environmental effects on foliar fungal communities of <i>Populus trichocarpa</i> . Journal of Biogeography, 2019, 46, 2001-2011.	3.0	41
1653	Microbial indicators of environmental perturbations in coral reef ecosystems. Microbiome, 2019, 7, 94.	11.1	126
1654	Actinobacteria and Cyanobacteria Diversity in Terrestrial Antarctic Microenvironments Evaluated by Culture-Dependent and Independent Methods. Frontiers in Microbiology, 2019, 10, 1018.	3.5	50
1655	Vegetation type impacts microbial interaction with antimony contaminants in a mining-contaminated soil environment. Environmental Pollution, 2019, 252, 1872-1881.	7.5	27
1656	Outbreaks of an Emerging Viral Disease Covary With Differences in the Composition of the Skin Microbiome of a Wild United Kingdom Amphibian. Frontiers in Microbiology, 2019, 10, 1245.	3.5	29
1657	Characterisation of coral-associated bacterial communities in an urbanised marine environment shows strong divergence over small geographic scales. Coral Reefs, 2019, 38, 1097-1106.	2.2	38
1658	Gut microbiota in Parkinson's disease: Temporal stability and relations to disease progression. EBioMedicine, 2019, 44, 691-707.	6.1	236
1659	Microbial Dynamics of Biosand Filters and Contributions of the Microbial Food Web to Effective Treatment of Wastewater-Impacted Water Sources. Applied and Environmental Microbiology, 2019, 85, .	3.1	5
1660	Microbiota therapy acts via a regulatory T cell MyD88/ROR \hat{I}^3 t pathway to suppress food allergy. Nature Medicine, 2019, 25, 1164-1174.	30.7	259
1661	Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. Nature Medicine, 2019, 25, 1104-1109.	30.7	477

#	Article	IF	Citations
1662	Fecal Microbiome Data Distinguish Liver Recipients With Normal and Abnormal Liver Function From Healthy Controls. Frontiers in Microbiology, 2019, 10, 1518.	3.5	19
1663	Virome heterogeneity and connectivity in waterfowl and shorebird communities. ISME Journal, 2019, 13, 2603-2616.	9.8	53
1664	Bacterial communities differ between plant species and soil type, and differentially influence seedling establishment on serpentine soils. Plant and Soil, 2019, 441, 423-437.	3.7	24
1665	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. Microbiome, 2019, 7, 84.	11.1	42
1666	Pelleted-hay alfalfa feed increases sheep wether weight gain and rumen bacterial richness over loose-hay alfalfa feed. PLoS ONE, 2019, 14, e0215797.	2.5	19
1667	Comprehensive characterization of an aspen (<i>Populus tremuloides</i>) leaf litter sample that maintained ice nucleation activity for 48 years. Biogeosciences, 2019, 16, 1675-1683.	3.3	10
1668	Phylogenetic conservation of bacterial responses to soil nitrogen addition across continents. Nature Communications, 2019, 10, 2499.	12.8	48
1669	Unveiled feather microcosm: feather microbiota of passerine birds is closely associated with host species identity and bacteriocin-producing bacteria. ISME Journal, 2019, 13, 2363-2376.	9.8	38
1670	Pyrethroid exposure alters internal and cuticle surface bacterial communities in <i>Anopheles albimanus</i> . ISME Journal, 2019, 13, 2447-2464.	9.8	38
1671	Global Structuring of Phylogenetic and Functional Diversity of Pelagic Fungi by Depth and Temperature. Frontiers in Marine Science, 2019, 6, .	2.5	39
1672	Biochar Amendment Stimulates Utilization of Plant-Derived Carbon by Soil Bacteria in an Intercropping System. Frontiers in Microbiology, 2019, 10, 1361.	3.5	40
1673	Relationship between faecal microbiota and plasma metabolome in rats fed NK603 and MON810 GM maize from the GMO90+ study. Food and Chemical Toxicology, 2019, 131, 110547.	3.6	7
1674	Microbial Diversity in Bulk and Rhizosphere Soil of Ranunculus glacialis Along a High-Alpine Altitudinal Gradient. Frontiers in Microbiology, 2019, 10, 1429.	3.5	101
1675	Host selection and stochastic effects influence bacterial community assembly on the microalgal phycosphere. Algal Research, 2019, 40, 101489.	4.6	58
1676	Climatic impacts on the bacterial community profiles of cork oak soils. Applied Soil Ecology, 2019, 143, 89-97.	4.3	15
1677	Modulation of the Caecal Gut Microbiota of Mice by Dietary Supplement Containing Resistant Starch: Impact Is Donor-Dependent. Frontiers in Microbiology, 2019, 10, 1234.	3.5	18
1678	Gut microbiota composition is associated with temperament traits in infants. Brain, Behavior, and Immunity, 2019, 80, 849-858.	4.1	91
1679	Metagenomic survey of the bacterial communities in the rhizosphere of three Andean tuber crops. Symbiosis, 2019, 79, 141-150.	2.3	7

#	Article	IF	CITATIONS
1680	Characterization of ocular and nasopharyngeal microbiome in allergic rhinoconjunctivitis. Pediatric Allergy and Immunology, 2019, 30, 624-631.	2.6	34
1681	Evaluation of Methods for the Extraction of Microbial DNA From Vaginal Swabs Used for Microbiome Studies. Frontiers in Cellular and Infection Microbiology, 2019, 9, 197.	3.9	27
1682	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. Cell, 2019, 177, 1600-1618.e17.	28.9	701
1683	Examining Inputs of Biogenic and Oil-Derived Hydrocarbons in Surface Waters Following the Deepwater Horizon Oil Spill. ACS Earth and Space Chemistry, 2019, 3, 1329-1337.	2.7	12
1684	The piglet mycobiome during the weaning transition: a pilot study1. Journal of Animal Science, 2019, 97, 2889-2900.	0.5	44
1685	Infection-Induced Intestinal Dysbiosis Is Mediated by Macrophage Activation and Nitrate Production. MBio, 2019, 10, .	4.1	49
1686	Faecal microbiota shift during weaning transition in piglets and evaluation of AO blood types as shaping factor for the bacterial community profile. PLoS ONE, 2019, 14, e0217001.	2.5	30
1687	Gut microbiome differences between wild and captive black rhinoceros – implications for rhino health. Scientific Reports, 2019, 9, 7570.	3.3	97
1688	World Workshop on Oral Medicine VII: Targeting the microbiome for oral medicine specialistsâ€"Part 1. A methodological guide. Oral Diseases, 2019, 25, 12-27.	3.0	12
1689	Soil Microbial Assemblages Are Linked to Plant Community Composition and Contribute to Ecosystem Services on Urban Green Roofs. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	36
1690	Fecal Microbiota Transplantation Controls Murine Chronic Intestinal Inflammation by Modulating Immune Cell Functions and Gut Microbiota Composition. Cells, 2019, 8, 517.	4.1	50
1691	Concurrent measurement of microbiome and allergens in the air of bedrooms of allergy disease patients in the Chicago area. Microbiome, 2019, 7, 82.	11.1	31
1692	Sample Processing Methods Impacts on Rumen Microbiome. Frontiers in Microbiology, 2019, 10, 861.	3.5	12
1693	Diversity and Co-occurrence Pattern Analysis of Cecal Microbiota Establishment at the Onset of Solid Feeding in Young Rabbits. Frontiers in Microbiology, 2019, 10, 973.	3.5	16
1694	Disrupted Maturation of the Microbiota and Metabolome among Extremely Preterm Infants with Postnatal Growth Failure. Scientific Reports, 2019, 9, 8167.	3.3	64
1695	Understanding microbial community dynamics to improve optimal microbiome selection. Microbiome, 2019, 7, 85.	11.1	233
1696	Influence of Light on Particulate Organic Matter Utilization by Attached and Free-Living Marine Bacteria. Frontiers in Microbiology, 2019, 10, 1204.	3.5	24
1697	Wheat Germ Supplementation Increases Lactobacillaceae and Promotes an Anti-inflammatory Gut Milieu in C57BL/6 Mice Fed a High-Fat, High-Sucrose Diet. Journal of Nutrition, 2019, 149, 1107-1115.	2.9	24

#	Article	IF	CITATIONS
1698	Antibiotic treatment in feedlot cattle: a longitudinal study of the effect of oxytetracycline and tulathromycin on the fecal and nasopharyngeal microbiota. Microbiome, 2019, 7, 86.	11.1	69
1699	Fecal Microbial Communities in a Large Representative Cohort of California Dairy Cows. Frontiers in Microbiology, 2019, 10, 1093.	3.5	60
1700	Low-Dose Stevia (Rebaudioside A) Consumption Perturbs Gut Microbiota and the Mesolimbic Dopamine Reward System. Nutrients, 2019, 11, 1248.	4.1	49
1701	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. MSystems, 2019, 4, .	3.8	56
1702	Physiological traits and relative abundance of species as explanatory variables of co-occurrence pattern of cultivable bacteria associated with chia seeds. Canadian Journal of Microbiology, 2019, 65, 668-680.	1.7	0
1703	Dynamic construction of gut microbiota may influence allergic diseases of infants in Southwest China. BMC Microbiology, 2019, 19, 123.	3.3	35
1704	Host species and site of collection shape the microbiota of Rift Valley fever vectors in Kenya. PLoS Neglected Tropical Diseases, 2019, 13, e0007361.	3.0	4
1705	Identification of Salivary Microbiota and Its Association With Host Inflammatory Mediators in Periodontitis. Frontiers in Cellular and Infection Microbiology, 2019, 9, 216.	3.9	88
1706	The Influence of Microfungi on the Mycelial Growth of Ectomycorrhizal Fungus Tricholoma matsutake. Microorganisms, 2019, 7, 169.	3.6	8
1707	Microbial communities in a former pilot-scale uranium mine in Eastern Finland – Association with radium immobilization. Science of the Total Environment, 2019, 686, 619-640.	8.0	12
1708	Microbial utilization of simple carbon substrates in boreal peat soils at low temperatures. Soil Biology and Biochemistry, 2019, 135, 438-448.	8.8	14
1709	Microbiota of human precolostrum and its potential role as a source of bacteria to the infant mouth. Scientific Reports, 2019, 9, 8435.	3.3	51
1710	Position-Specific Metabolic Probing and Metagenomics of Microbial Communities Reveal Conserved Central Carbon Metabolic Network Activities at High Temperatures. Frontiers in Microbiology, 2019, 10, 1427.	3.5	12
1711	Effects of rumen-protected glucose on ileal microbiota and genes involved in ileal epithelial metabolism and immune homeostasis in transition dairy cows. Animal Feed Science and Technology, 2019, 254, 114199.	2.2	14
1712	Microbial communities across a hillslopeâ€riparian transect shaped by proximity to the stream, groundwater table, and weathered bedrock. Ecology and Evolution, 2019, 9, 6869-6900.	1.9	24
1713	Metabarcoding Insights Into the Trophic Behavior and Identity of Intertidal Benthic Foraminifera. Frontiers in Microbiology, 2019, 10, 1169.	3.5	36
1714	Mediterranean grassland soil C–N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. Nature Microbiology, 2019, 4, 1356-1367.	13.3	170
1715	Alterations in the relative abundance of <i>Faecalibacterium prausnitzii</i> correlate with changes in fecal calprotectin in patients with ileal Crohn's disease: a longitudinal study. Scandinavian Journal of Gastroenterology, 2019, 54, 577-585.	1.5	15

#	Article	IF	CITATIONS
1716	Tobacco exposure associated with oral microbiota oxygen utilization in the New York City Health and Nutrition Examination Study. Annals of Epidemiology, 2019, 34, 18-25.e3.	1.9	27
1717	Analysis of oral microbiota in Japanese oral cancer patients using 16S rRNA sequencing. Journal of Oral Biosciences, 2019, 61, 120-128.	2.2	29
1718	Propionate-Producing Consortium Restores Antibiotic-Induced Dysbiosis in a Dynamic in vitro Model of the Human Intestinal Microbial Ecosystem. Frontiers in Microbiology, 2019, 10, 1206.	3.5	84
1719	A meta-analysis of the bovine gastrointestinal tract microbiota. FEMS Microbiology Ecology, 2019, 95, .	2.7	91
1720	Long-read sequencing reveals intra-species tolerance of substantial structural variations and new subtelomere formation in $\langle i \rangle$ C. elegans $\langle i \rangle$. Genome Research, 2019, 29, 1023-1035.	5.5	67
1721	Incubation and grazing effects on spirotrich ciliate diversity inferred from molecular analyses of microcosm experiments. PLoS ONE, 2019, 14, e0215872.	2.5	9
1722	The development and ecology of the Japanese macaque gut microbiome from weaning to early adolescence in association with diet. American Journal of Primatology, 2019, 81, e22980.	1.7	14
1723	Bacterial Insights into the Formation of Opaline Stromatolites from the Chimalacatepec Lava Tube System, Mexico. Geomicrobiology Journal, 2019, 36, 694-704.	2.0	3
1724	Longitudinal homogenization of the microbiome between both occupants and the built environment in a cohort of United States Air Force Cadets. Microbiome, 2019, 7, 70.	11.1	33
1725	Gut feelings: A randomised, triple-blind, placebo-controlled trial of probiotics for depressive symptoms. Journal of Affective Disorders, 2019, 253, 317-326.	4.1	142
1726	Predicting Clinical Outcomes of Cirrhosis Patients With Hepatic Encephalopathy From the Fecal Microbiome. Cellular and Molecular Gastroenterology and Hepatology, 2019, 8, 301-318.e2.	4.5	76
1727	Fecal Microbiome, Metabolites, and Stem Cell Transplant Outcomes: A Single-Center Pilot Study. Open Forum Infectious Diseases, 2019, 6, ofz173.	0.9	32
1728	Habitat fragmentation is associated with dietary shifts and microbiota variability in common vampire bats. Ecology and Evolution, 2019, 9, 6508-6523.	1.9	61
1729	The Microbiome of Temporal Arteries. Pathogens and Immunity, 2019, 4, 21.	3.1	19
1730	Influence of operation mode and wastewater strength on aerobic granulation at pilot scale: Startup period, granular sludge characteristics, and effluent quality. Water Research, 2019, 160, 81-96.	11.3	63
1731	Spatial Gradients of Fungal Abundance and Ecology throughout a Damp Building. Environmental Science and Technology Letters, 2019, 6, 329-333.	8.7	16
1732	Bacterial succession and functional diversity during vermicomposting of the white grape marc Vitis vinifera ν . Albari \tilde{A} ±0. Scientific Reports, 2019, 9, 7472.	3.3	32
1733	A Link Between Plasma Microbial Translocation, Microbiome, and Autoantibody Development in Firstâ€Degree Relatives of Systemic Lupus Erythematosus Patients. Arthritis and Rheumatology, 2019, 71, 1858-1868.	5.6	71

#	Article	IF	Citations
1734	Bioturbation of blood clam Tegillarca granosa on benthic nutrient fluxes and microbial community in an aquaculture wastewater treatment system. International Biodeterioration and Biodegradation, 2019, 142, 73-82.	3.9	27
1735	Bacterial Community Dynamics in an Oyster Hatchery in Response to Probiotic Treatment. Frontiers in Microbiology, 2019, 10, 1060.	3.5	35
1736	Tollâ€like receptorâ€2 and â€4 responses regulate neutrophil infiltration into the junctional epithelium and significantly contribute to the composition of the oral microbiota. Journal of Periodontology, 2019, 90, 1202-1212.	3.4	21
1737	Composition and stability of the vervet monkey milk microbiome. American Journal of Primatology, 2019, 81, e22982.	1.7	6
1738	Changes in the rumen and colon microbiota and effects of live yeast dietary supplementation during the transition from the dry period to lactation of dairy cows. Journal of Dairy Science, 2019, 102, 6180-6198.	3.4	70
1739	Use of a filter cartridge combined with intraâ€cartridge beadâ€beating improves detection of microbial DNA from water samples. Methods in Ecology and Evolution, 2019, 10, 1142-1156.	5.2	34
1740	Heat-shock treatment applied to inocula for H2 production decreases microbial diversities, interspecific interactions and performance using cellulose as substrate. International Journal of Hydrogen Energy, 2019, 44, 13126-13134.	7.1	22
1741	Variations of the intestinal gut microbiota of farmed rainbow trout, <i>Oncorhynchus mykiss</i> (Walbaum), depending on the infection status of the fish. Journal of Applied Microbiology, 2019, 127, 379-395.	3.1	53
1742	Selection, Succession, and Stabilization of Soil Microbial Consortia. MSystems, 2019, 4, .	3.8	64
1743	Fecal microbiota dysbiosis in macaques and humans within a shared environment. PLoS ONE, 2019, 14, e0210679.	2.5	9
1744	Pressure-Retaining Sampler and High-Pressure Systems to Study Deep-Sea Microbes Under in situ Conditions. Frontiers in Microbiology, 2019, 10, 453.	3.5	64
1745	Gut Microbiota Changes in Patients with Bipolar Depression. Advanced Science, 2019, 6, 1900752.	11.2	98
1746	Evaluating the effects of canine urine on urban soil microbial communities. Urban Ecosystems, 2019, 22, 721-732.	2.4	7
1747	Beyond the visual: using metabarcoding to characterize the hidden reef cryptobiome. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182697.	2.6	44
1748	A Natural mtDNA Polymorphism in Complex III Is a Modifier of Healthspan in Mice. International Journal of Molecular Sciences, 2019, 20, 2359.	4.1	12
1749	Source Environments of the Microbiome in Perennially Ice-Covered Lake Untersee, Antarctica. Frontiers in Microbiology, 2019, 10, 1019.	3.5	26
1750	Comparative genomics of Bifidobacterium species isolated from marmosets and humans. American Journal of Primatology, 2019, 81, e983.	1.7	12
1751	A Distinct Gut Microbiota Exists Within Crohn's Disease–Related Perianal Fistulae. Journal of Surgical Research, 2019, 242, 118-128.	1.6	18

#	ARTICLE	IF	CITATIONS
1752	Skin Microbiome Compositional Changes in Atopic Dermatitis Accompany Dead Sea Climatotherapy. Photochemistry and Photobiology, 2019, 95, 1446-1453.	2.5	15
1753	Statistical evaluation of diet-microbe associations. BMC Microbiology, 2019, 19, 90.	3.3	12
1754	Differences in resource use lead to coexistence of seed-transmitted microbial populations. Scientific Reports, 2019, 9, 6648.	3.3	17
1755	Bacterial succession and coâ€occurrence patterns of an enriched marine microbial community during light crude oil degradation in a batch reactor. Journal of Applied Microbiology, 2019, 127, 495-507.	3.1	20
1756	Complex Microbial Communities Drive Iron and Sulfur Cycling in Arctic Fjord Sediments. Applied and Environmental Microbiology, 2019, 85, .	3.1	58
1757	Early nasal microbiota and acute respiratory infections during the first years of life. Thorax, 2019, 74, 592-599.	5.6	43
1758	The Water Microbiome Through a Pilot Scale Advanced Treatment Facility for Direct Potable Reuse. Frontiers in Microbiology, 2019, 10, 993.	3. 5	36
1759	Small to modest impact of social group on the gut microbiome of wild Costa Rican capuchins in a seasonal forest. American Journal of Primatology, 2019, 81, e22985.	1.7	16
1760	A complex human gut microbiome cultured in an anaerobic intestine-on-a-chip. Nature Biomedical Engineering, 2019, 3, 520-531.	22.5	487
1761	Gut microbiome dysbiosis and increased intestinal permeability in children with islet autoimmunity and type 1 diabetes: A prospective cohort study. Pediatric Diabetes, 2019, 20, 574-583.	2.9	86
1762	Short-term effect of simulated salt marsh restoration by sand-amendment on sediment bacterial communities. PLoS ONE, 2019, 14, e0215767.	2.5	11
1763	Periodontal Health and Oral Microbiota in Patients with Rheumatoid Arthritis. Journal of Clinical Medicine, 2019, 8, 630.	2.4	63
1764	Metatranscriptomic Analysis of Sub-Acute Ruminal Acidosis in Beef Cattle. Animals, 2019, 9, 232.	2.3	21
1765	Beyond the planetary boundary layer: Bacterial and fungal vertical biogeography at Mount Sonnblick, Austria. Geo: Geography and Environment, 2019, 6, e00069.	0.8	10
1766	Gut microbial diversity increases with social rank in the African cichlid fish, Astatotilapia burtoni. Animal Behaviour, 2019, 152, 79-91.	1.9	7
1767	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. Nature Communications, 2019, 10, 2200.	12.8	317
1768	A longitudinal characterization of the Non-Cystic Fibrosis Bronchiectasis airway microbiome. Scientific Reports, 2019, 9, 6871.	3.3	36
1769	Chemosynthetic ectosymbionts associated with a shallow-water marine nematode. Scientific Reports, 2019, 9, 7019.	3.3	24

#	Article	IF	Citations
1770	Effects of H2:CO2 ratio and H2 supply fluctuation on methane content and microbial community composition during in-situ biological biogas upgrading. Biotechnology for Biofuels, 2019, 12, 104.	6.2	82
1771	High-Amylose Maize, Potato, and Butyrylated Starch Modulate Large Intestinal Fermentation, Microbial Composition, and Oncogenic miRNA Expression in Rats Fed A High-Protein Meat Diet. International Journal of Molecular Sciences, 2019, 20, 2137.	4.1	34
1772	Skin Microbiome Differences in Atopic Dermatitis and Healthy Controls in Egyptian Children and Adults, and Association with Serum Immunoglobulin E. OMICS A Journal of Integrative Biology, 2019, 23, 247-260.	2.0	16
1773	Household composition and the infant fecal microbiome: The INSPIRE study. American Journal of Physical Anthropology, 2019, 169, 526-539.	2.1	27
1774	Characterizing Structure and Potential Function of Bacterial and Fungal Root Microbiota in Hulless Barley Cultivars. Journal of Soil Science and Plant Nutrition, 2019, 19, 420-429.	3.4	5
1775	Bacterial communities protect the alga Microchloropsis salina from grazing by the rotifer Brachionus plicatilis. Algal Research, 2019, 40, 101500.	4.6	18
1776	Biodegradation of mixture of plastic films by tailored marine consortia. Journal of Hazardous Materials, 2019, 375, 33-42.	12.4	91
1777	The cooling tower water microbiota: Seasonal dynamics and co-occurrence of bacterial and protist phylotypes. Water Research, 2019, 159, 464-479.	11.3	51
1778	Deciphering the Assembly Processes of the Key Ecological Assemblages of Microbial Communities in Thirteen Full-Scale Wastewater Treatment Plants. Microbes and Environments, 2019, 34, 169-179.	1.6	13
1779	Comparison of the microbiome, metabolome, and lipidome of obese and non-obese horses. PLoS ONE, 2019, 14, e0215918.	2.5	21
1780	Data of metal and microbial analyses from anaerobic co-digestion of organic and mineral wastes. Data in Brief, 2019, 24, 103934.	1.0	5
1781	Diesel uptake by an indigenous microbial consortium isolated from sediments of the Southern Gulf of Mexico: Emulsion characterisation. Environmental Pollution, 2019, 250, 849-855.	7.5	17
1782	Bacterial community structure and function distinguish gut sites in captive redâ€shanked doucs (Pygathrix nemaeus). American Journal of Primatology, 2019, 81, e22977.	1.7	9
1783	Impact of the Food Additive Titanium Dioxide (E171) on Gut Microbiota-Host Interaction. Frontiers in Nutrition, 2019, 6, 57.	3.7	90
1784	Gut Microbiota and Phytoestrogen-Associated Infertility in Southern White Rhinoceros. MBio, 2019, 10, .	4.1	37
1785	Methane yield and lag correlate with bacterial community shift following bioplastic anaerobic co-digestion. Bioresource Technology Reports, 2019, 7, 100198.	2.7	14
1786	Farm-to-fork profiling of bacterial communities associated with an artisan cheese production facility. Food Microbiology, 2019, 83, 48-58.	4.2	49
1787	Extracellular DNA in Monochloraminated Drinking Water and Its Influence on DNA-Based Profiling of a Microbial Community. Environmental Science and Technology Letters, 2019, 6, 306-312.	8.7	28

#	Article	IF	CITATIONS
1788	Variations in microbiome composition of sewer biofilms due to ferrous and ferric iron dosing. Cogent Environmental Science, 2019, 5, 1595293.	1.6	4
1789	Neonatal Vitamin A Supplementation and Vitamin A Status Are Associated with Gut Microbiome Composition in Bangladeshi Infants in Early Infancy and at 2 Years of Age. Journal of Nutrition, 2019, 149, 1075-1088.	2.9	42
1790	A novel sequencing-based vaginal health assay combining self-sampling, HPV detection and genotyping, STI detection, and vaginal microbiome analysis. PLoS ONE, 2019, 14, e0215945.	2.5	22
1791	The Soil Microbiome of GLORIA Mountain Summits in the Swiss Alps. Frontiers in Microbiology, 2019, 10, 1080.	3.5	78
1792	Metagenomes of a Freshwater Charavirus from British Columbia Provide a Window into Ancient Lineages of Viruses. Viruses, 2019, 11, 299.	3.3	21
1793	Leaf mineral content govern microbial community structure in the phyllosphere of spinach (Spinacia) Tj ETQq1 1	0.784314	rggT/Over
1794	Marine Deep Biosphere Microbial Communities Assemble in Near-Surface Sediments in Aarhus Bay. Frontiers in Microbiology, 2019, 10, 758.	3.5	54
1795	Multiple stressors interact primarily through antagonism to drive changes in the coral microbiome. Scientific Reports, 2019, 9, 6834.	3.3	64
1796	Diversity and distribution of thermophilic hydrogenogenic carboxydotrophs revealed by microbial community analysis in sediments from multiple hydrothermal environments in Japan. Archives of Microbiology, 2019, 201, 969-982.	2.2	17
1797	Gut microbiome composition of wild western lowland gorillas is associated with individual age and sex factors. American Journal of Physical Anthropology, 2019, 169, 575-585.	2.1	15
1798	Integrative analysis of the intestinal metabolome of childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 144, 442-454.	2.9	64
1799	Bacterial community composition and diversity of two different forms of an organic residue of bioenergy crop. PeerJ, 2019, 7, e6768.	2.0	5
1800	Influence of the Intestinal Microbiota on Colonization Resistance to <i>Salmonella</i> and the Shedding Pattern of Naturally Exposed Pigs. MSystems, 2019, 4, .	3.8	40
1801	Microbiota of the Gut-Lymph Node Axis: Depletion of Mucosa-Associated Segmented Filamentous Bacteria and Enrichment of Methanobrevibacter by Colistin Sulfate and Linco-Spectin in Pigs. Frontiers in Microbiology, 2019, 10, 599.	3.5	11
1802	Taxonomic and Functional Characterization of the Microbial Community During Spontaneous in vitro Fermentation of Riesling Must. Frontiers in Microbiology, 2019, 10, 697.	3.5	30
1803	Gut bacteria are critical for optimal muscle function: a potential link with glucose homeostasis. American Journal of Physiology - Endocrinology and Metabolism, 2019, 317, E158-E171.	3.5	126
1804	The impact of probiotics and lactoferrin supplementation on piglet gastrointestinal microbial communities. BioMetals, 2019, 32, 533-543.	4.1	18
1805	Impact of Warming on Greenhouse Gas Production and Microbial Diversity in Anoxic Peat From a Sphagnum-Dominated Bog (Grand Rapids, Minnesota, United States). Frontiers in Microbiology, 2019, 10, 870.	3.5	43

#	Article	IF	Citations
1806	Controlling intestinal colonization of high-risk haematology patients with ESBL-producing Enterobacteriaceae: a randomized, placebo-controlled, multicentre, Phase II trial (CLEAR). Journal of Antimicrobial Chemotherapy, 2019, 74, 2065-2074.	3.0	8
1807	Removal of adult cyathostomins alters faecal microbiota and promotes an inflammatory phenotype in horses. International Journal for Parasitology, 2019, 49, 489-500.	3.1	35
1808	Growth Characteristics and Thermodynamics of Syntrophic Acetate Oxidizers. Environmental Science & Env	10.0	56
1809	Temporal Changes in Microbial Community Composition and Geochemistry in Flowback and Produced Water from the Duvernay Formation. ACS Earth and Space Chemistry, 2019, 3, 1047-1057.	2.7	31
1810	ANCHOR: a 16S rRNA gene amplicon pipeline for microbial analysis of multiple environmental samples. Environmental Microbiology, 2019, 21, 2440-2468.	3.8	30
1811	Encrustations on ureteral stents from patients without urinary tract infection reveal distinct urotypes and a low bacterial load. Microbiome, 2019, 7, 60.	11.1	19
1812	Usability of rectal swabs for microbiome sampling in a cohort study of hematological and oncological patients. PLoS ONE, 2019, 14, e0215428.	2.5	26
1813	Dynamics of Bacterial and Viral Communities in Paddy Soil with Irrigation and Urea Application. Viruses, 2019, 11, 347.	3.3	19
1814	Characterization of Bacterial Communities in Breeding Waters of Anopheles darlingi in Manaus in the Amazon Basin Malaria-Endemic Area. Microbial Ecology, 2019, 78, 781-791.	2.8	21
1815	Microbiota-Produced <i>N</i> -Formyl Peptide fMLF Promotes Obesity-Induced Glucose Intolerance. Diabetes, 2019, 68, 1415-1426.	0.6	23
1816	Oral probiotics reduce halitosis in patients wearing orthodontic braces: a randomized, triple-blind, placebo-controlled trial. Journal of Breath Research, 2019, 13, 036010.	3.0	40
1817	Diversity and composition of the gut microbiota of Atlantic salmon (<i>Salmo salar</i>) farmed in Irish waters. Journal of Applied Microbiology, 2019, 127, 648-657.	3.1	36
1818	Microbiota in non-flooded and flooded rice culms. FEMS Microbiology Ecology, 2019, 95, .	2.7	12
1819	Linking soil's volatilome to microbes and plant roots highlights the importance of microbes as emitters of belowground volatile signals. Environmental Microbiology, 2019, 21, 3313-3327.	3.8	17
1820	A different suite: The assemblage of distinct fungal communities in water-damaged units of a poorly-maintained public housing building. PLoS ONE, 2019, 14, e0213355.	2.5	20
1821	Procyanidinâ€"Cell Wall Interactions within Apple Matrices Decrease the Metabolization of Procyanidins by the Human Gut Microbiota and the Anti-Inflammatory Effect of the Resulting Microbial Metabolome In Vitro. Nutrients, 2019, 11, 664.	4.1	42
1822	Different Degrees of Niche Differentiation for Bacteria, Fungi, and Myxomycetes Within an Elevational Transect in the German Alps. Microbial Ecology, 2019, 78, 764-780.	2.8	16
1823	Gut microbiota profile in children affected by atopic dermatitis and evaluation of intestinal persistence of a probiotic mixture. Scientific Reports, 2019, 9, 4996.	3.3	107

#	Article	IF	Citations
1824	Have the cake and eat it: Optimizing nondestructive DNA metabarcoding of macroinvertebrate samples for freshwater biomonitoring. Molecular Ecology Resources, 2019, 19, 863-876.	4.8	44
1825	The Cloacal Microbiome Changes with the Breeding Season in a Wild Bird. Integrative Organismal Biology, 2019, 1, oby009.	1.8	40
1826	Recruit symbiosis establishment and Symbiodiniaceae composition influenced by adult corals and reef sediment. Coral Reefs, 2019, 38, 405-415.	2.2	25
1827	Akkermansia muciniphila ameliorates the age-related decline in colonic mucus thickness and attenuates immune activation in accelerated aging Ercc1â~ʃi"7 mice. Immunity and Ageing, 2019, 16, 6.	4.2	130
1828	Quenching by sodium thiosulfate does not influence 16S rRNA gene sequencing profiles of reclaimed water from three sites in the Mid-Atlantic, United States. Environmental Research, 2019, 172, 296-300.	7.5	2
1829	Geophysical Monitoring of Hydrocarbon Biodegradation in Highly Conductive Environments. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 353-366.	3.0	19
1830	Molecular dialogue between arbuscular mycorrhizal fungi and the nonhost plant <i>Arabidopsis thaliana</i> switches from initial detection to antagonism. New Phytologist, 2019, 223, 867-881.	7.3	49
1831	Immunosuppression-induced alterations in fish gut microbiota may increase the susceptibility to pathogens. Fish and Shellfish Immunology, 2019, 88, 540-545.	3.6	31
1832	Forfeiting the priority effect: turnover defines biofilm community succession. ISME Journal, 2019, 13, 1865-1877.	9.8	83
1833	Fate of CMY-2-Encoding Plasmids Introduced into the Human Fecal Microbiota by Exogenous <i>Escherichia coli</i> Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	21
1834	Environmental filtering determines family-level structure of sulfate-reducing microbial communities in subsurface marine sediments. ISME Journal, 2019, 13, 1920-1932.	9.8	40
1835	Temperature-Dependent Network Modules of Soil Methanogenic Bacterial and Archaeal Communities. Frontiers in Microbiology, 2019, 10, 496.	3.5	9
1836	Heavy metal exposure causes changes in the metabolic health-associated gut microbiome and metabolites. Environment International, 2019, 126, 454-467.	10.0	125
1837	Dietary $\langle i \rangle \hat{l} \pm \langle i \rangle$ -lactalbumin alters energy balance, gut microbiota composition and intestinal nutrient transporter expression in high-fat diet-fed mice. British Journal of Nutrition, 2019, 121, 1097-1107.	2.3	21
1838	Microbial communities in hummingbird feeders are distinct from floral nectar and influenced by bird visitation. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182295.	2.6	18
1839	Diversity and composition of intertidal gastropod microbiomes across a major marine biogeographic boundary. Environmental Microbiology Reports, 2019, 11, 434-447.	2.4	16
1840	No evidence that gut microbiota impose a net cost on their butterfly host. Molecular Ecology, 2019, 28, 2100-2117.	3.9	15
1841	A Developing Symbiosis: Enabling Cross-Talk Between Ecologists and Microbiome Scientists. Frontiers in Microbiology, 2019, 10, 292.	3.5	50

#	Article	IF	CITATIONS
1842	Insight into the Bacterial Endophytic Communities of Peach Cultivars Related to Crown Gall Disease Resistance. Applied and Environmental Microbiology, 2019, 85, .	3.1	42
1843	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. Frontiers in Immunology, 2019, 10, 69.	4.8	40
1844	Host genetics and diet composition interact to modulate gut microbiota and predisposition to metabolic syndrome in spontaneously hypertensive strokeâ€prone rats. FASEB Journal, 2019, 33, 6748-6766.	0.5	16
1845	Fungal-Bacterial Networks in the Populus Rhizobiome Are Impacted by Soil Properties and Host Genotype. Frontiers in Microbiology, 2019, 10, 481.	3. 5	71
1846	Relative stability of the Pocillopora acuta microbiome throughout a thermal stress event. Coral Reefs, 2019, 38, 373-386.	2.2	42
1847	Airborne microbial transport limitation to isolated Antarctic soil habitats. Nature Microbiology, 2019, 4, 925-932.	13.3	114
1848	Spatial Variability of Antarctic Surface Snow Bacterial Communities. Frontiers in Microbiology, 2019, 10, 461.	3.5	20
1849	Crop Residues in Wheat-Oilseed Rape Rotation System: a Pivotal, Shifting Platform for Microbial Meetings. Microbial Ecology, 2019, 77, 931-945.	2.8	36
1850	Highly connected taxa located in the microbial network are prevalent in the rhizosphere soil of healthy plant. Biology and Fertility of Soils, 2019, 55, 299-312.	4.3	57
1851	Research Techniques Made Simple: Profiling the Skin Microbiota. Journal of Investigative Dermatology, 2019, 139, 747-752.e1.	0.7	49
1852	Long-term seasonal and interannual variability of marine aerobic anoxygenic photoheterotrophic bacteria. ISME Journal, 2019, 13, 1975-1987.	9.8	32
1853	Major shifts in gut microbiota during development and its relationship to growth in ostriches. Molecular Ecology, 2019, 28, 2653-2667.	3.9	53
1854	Disentangling the Influence of Environment, Host Specificity and Thallus Differentiation on Bacterial Communities in Siphonous Green Seaweeds. Frontiers in Microbiology, 2019, 10, 717.	3.5	34
1855	Evaluation of Black Soldier Fly (Hermetia illucens) Larvae and Pre-Pupae Raised on Household Organic Waste, as Potential Ingredients for Poultry Feed. Animals, 2019, 9, 98.	2.3	82
1856	Characterisation of microbial communities of drill cuttings piles from offshore oil and gas installations. Marine Pollution Bulletin, 2019, 142, 169-177.	5.0	21
1857	A Risky Business? Habitat and Social Behavior Impact Skin and Gut Microbiomes in Caribbean Cleaning Gobies. Frontiers in Microbiology, 2019, 10, 716.	3.5	22
1858	Divergent national-scale trends of microbial and animal biodiversity revealed across diverse temperate soil ecosystems. Nature Communications, 2019, 10, 1107.	12.8	104
1859	A Low-Diversity Microbiota Inhabits Extreme Terrestrial Basaltic Terrains and Their Fumaroles: Implications for the Exploration of Mars. Astrobiology, 2019, 19, 284-299.	3.0	19

#	Article	IF	CITATIONS
1860	Fur seal microbiota are shaped by the social and physical environment, show mother–offspring similarities and are associated with host genetic quality. Molecular Ecology, 2019, 28, 2406-2422.	3.9	27
1861	Shifts in Soil Bacterial Communities as a Function of Carbon Source Used During Anaerobic Soil Disinfestation. Frontiers in Environmental Science, 2019, 6, .	3.3	33
1862	Agricultural intensification reduces microbial network complexity and the abundance of keystone taxa in roots. ISME Journal, 2019, 13, 1722-1736.	9.8	716
1863	Temporal variability of diazotroph community composition in the upwelling region off NW Iberia. Scientific Reports, 2019, 9, 3737.	3.3	18
1864	No differences in microbiome changes between antiâ€adhesive and antibacterial ingredients in toothpastes during periodontal therapy. Journal of Periodontal Research, 2019, 54, 435-443.	2.7	25
1865	Patterns of community assembly in the developing chicken microbiome reveal rapid primary succession. MicrobiologyOpen, 2019, 8, e00821.	3.0	82
1866	The dynamics of the antibiotic resistome in the feces of freshly weaned pigs following therapeutic administration of oxytetracycline. Scientific Reports, 2019, 9, 4062.	3.3	45
1867	Dietary raisin intake has limited effect on gut microbiota composition in adult volunteers. Nutrition Journal, 2019, 18, 14.	3.4	20
1868	The Active Sulfate-Reducing Microbial Community in Littoral Sediment of Oligotrophic Lake Constance. Frontiers in Microbiology, 2019, 10, 247.	3. 5	21
1869	Rhizobacterial Community Assembly Patterns Vary Between Crop Species. Frontiers in Microbiology, 2019, 10, 581.	3.5	42
1870	The effects of cycled inhaled aztreonam on the cystic fibrosis (CF) lung microbiome. Journal of Cystic Fibrosis, 2019, 18, 829-837.	0.7	21
1871	Microbial community structure and microbial networks correspond to nutrient gradients within coastal wetlands of the Laurentian Great Lakes. FEMS Microbiology Ecology, 2019, 95, .	2.7	47
1872	A unified framework for unconstrained and constrained ordination of microbiome read count data. PLoS ONE, 2019, 14, e0205474.	2.5	14
1873	The nasal and oropharyngeal microbiomes of healthy livestock workers. PLoS ONE, 2019, 14, e0212949.	2.5	18
1874	Fungal Biodiversity of the Most Common Types of Polish Soil in a Long-Term Microplot Experiment. Frontiers in Microbiology, 2019, 10, 6.	3.5	46
1875	Urbanization Altered Bacterial and Archaeal Composition in Tidal Freshwater Wetlands Near Washington DC, USA, and Buenos Aires, Argentina. Microorganisms, 2019, 7, 72.	3 . 6	3
1876	Birch pollen allergen immunotherapy reprograms nasal epithelial transcriptome and recovers microbial diversity. Journal of Allergy and Clinical Immunology, 2019, 143, 2293-2296.e11.	2.9	11
1877	Nutrient-based diet modifications impact on the gut microbiome of the Javan slow loris (Nycticebus) Tj ETQq $1\ 1\ 0$).784314 r	ggŢ /Overloo

#	Article	IF	Citations
1878	Species identity dominates over environment in shaping the microbiota of small mammals. Ecology Letters, 2019, 22, 826-837.	6.4	94
1879	Effect of Dietary Carbohydrate-to-Protein Ratio on Gut Microbiota in Atlantic Salmon (Salmo salar). Animals, 2019, 9, 89.	2.3	31
1880	Variable interaction outcomes of local disturbance and El Ni $\tilde{A}\pm 0$ -induced heat stress on coral microbiome alpha and beta diversity. Coral Reefs, 2019, 38, 331-345.	2.2	24
1881	A New Method to Correct for Habitat Filtering in Microbial Correlation Networks. Frontiers in Microbiology, 2019, 10, 585.	3.5	20
1882	Ectomycorrhizal fungal communities are dominated by mammalian dispersed truffle-like taxa in north-east Australian woodlands. Mycorrhiza, 2019, 29, 181-193.	2.8	17
1883	Microbial iron metabolism as revealed by gene expression profiles in contrasted Southern Ocean regimes. Environmental Microbiology, 2019, 21, 2360-2374.	3.8	27
1884	Impact of the Timing of Antibiotic Administration on Digestive Colonization with Carbapenemase-Producing Enterobacteriaceae in a Murine Model. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	5
1885	Comprehensive analysis of different adhesives in aerobiological sampling using optical microscopy and high-throughput DNA sequencing. Journal of Environmental Management, 2019, 240, 441-450.	7.8	9
1886	Metagenomic assessment of body surface bacterial communities of the sea urchin, Tripneustes gratilla. Marine Genomics, 2019, 47, 100675.	1.1	8
1887	Plant selection initiates alternative successional trajectories in the soil microbial community after disturbance. Ecological Monographs, 2019, 89, e01367.	5.4	31
1888	Maize synthesized benzoxazinoids affect the host associated microbiome. Microbiome, 2019, 7, 59.	11.1	185
1889	Effects of a gut microbiota transfer on emotional reactivity in Japanese quails (<i>Coturnix) Tj ETQq1 1 0.784314</i>	rgBT /Ove	erlock 10 Tf
1890	Increased mucosal neutrophil survival is associated with altered microbiota in HIV infection. PLoS Pathogens, 2019, 15, e1007672.	4.7	36
1891	Early life stress induces type 2 diabetes-like features in ageing mice. Brain, Behavior, and Immunity, 2019, 80, 452-463.	4.1	16
1892	Spatial patterns of fungal endophytes in a subtropical montane rainforest of northern Taiwan. Fungal Ecology, 2019, 39, 316-327.	1.6	13
1893	Soil carbonyl sulfide exchange in relation to microbial community composition: Insights from a managed grassland soil amendment experiment. Soil Biology and Biochemistry, 2019, 135, 28-37.	8.8	9
1894	Screening of single or combined administration of 9 probiotics to reduce ammonia emissions from laying hens. Poultry Science, 2019, 98, 3977-3988.	3.4	18
1895	Green tea polyphenol (epigallocatechin-3-gallate) improves gut dysbiosis and serum bile acids dysregulation in high-fat diet-fed mice. Journal of Clinical Biochemistry and Nutrition, 2019, 65, 34-46.	1.4	96

#	Article	IF	CITATIONS
1896	Bacterial communities within Phengaris (Maculinea) alcon caterpillars are shifted following transition from solitary living to social parasitism of Myrmica ant colonies. Ecology and Evolution, 2019, 9, 4452-4464.	1.9	10
1897	Bioremediation of chlorophenol-contaminated sawmill soil using pilot-scale bioreactors under consecutive anaerobic-aerobic conditions. Chemosphere, 2019, 227, 670-680.	8.2	25
1898	Linking shifts in bacterial community with changes in dissolved organic matter pool in a tropical lake. Science of the Total Environment, 2019, 672, 990-1003.	8.0	31
1899	Assessing Microbial Community Patterns During Incipient Soil Formation From Basalt. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 941-958.	3.0	16
1900	Thickness determines microbial community structure and function in nitrifying biofilms via deterministic assembly. Scientific Reports, 2019, 9, 5110.	3.3	74
1901	The origin and role of biological rock crusts in rocky desert weathering. Biogeosciences, 2019, 16, 1133-1145.	3.3	23
1902	Submerged aerobic granular sludge membrane bioreactor (AGMBR): Organics and nutrients (nitrogen) Tj ETQq0	0 0 rgBT /0 2.7	Overlock 10
1903	What's Normal? Microbiomes in Human Milk and Infant Feces Are Related to Each Other but Vary Geographically: The INSPIRE Study. Frontiers in Nutrition, 2019, 6, 45.	3.7	148
1904	Microbiome dynamics during cast ageing in the earthworm Aporrectodea caliginosa. Applied Soil Ecology, 2019, 139, 56-63.	4.3	33
1905	Combining microfluidics and RNA-sequencing to assess the inducible defensome of a mushroom against nematodes. BMC Genomics, 2019, 20, 243.	2.8	19
1906	The influence of an antiâ€inflammatory diet on gingivitis. A randomized controlled trial. Journal of Clinical Periodontology, 2019, 46, 481-490.	4.9	85
1907	Hepatic glycogen storage diseases are associated to microbial dysbiosis. PLoS ONE, 2019, 14, e0214582.	2.5	17
1908	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. Frontiers in Microbiology, 2019, 10, 347.	3. 5	59
1909	Seasonal dynamics of DNA and RNA viral bioaerosol communities in a daycare center. Microbiome, 2019, 7, 53.	11.1	30
1910	Divergence in gut microbial communities mirrors a social group fission event in a blackâ€andâ€white colobus monkey (<i>Colobus vellerosus</i>). American Journal of Primatology, 2019, 81, e22966.	1.7	13
1911	Enrichment of periodontal pathogens from the biofilms of healthy adults. Scientific Reports, 2019, 9, 5491.	3.3	56
1912	Sediment microbial assemblage structure is modified by marine polychaete gut passage. FEMS Microbiology Ecology, 2019, 95, .	2.7	11
1913	Bamboo lignocellulose degradation by gut symbiotic microbiota of the bamboo snout beetle Cyrtotrachelus buqueti. Biotechnology for Biofuels, 2019, 12, 70.	6.2	48

#	ARTICLE	IF	CITATIONS
1914	$16S\ rRNA/rRNA$ Gene Ratios and Cell Activity Staining Reveal Consistent Patterns of Microbial Activity in Plant-Associated Soil. MSystems, 2019, 4, .	3.8	44
1915	Defining characteristics of genital health in South African adolescent girls and young women at high risk for HIV infection. PLoS ONE, 2019, 14, e0213975.	2.5	39
1916	A single application of fertiliser or manure to a cropping field has limited long-term effects on soil microbial communities. Soil Research, 2019, 57, 228.	1,1	7
1917	Creek to Table: Tracking fecal indicator bacteria, bacterial pathogens, and total bacterial communities from irrigation water to kale and radish crops. Science of the Total Environment, 2019, 666, 461-471.	8.0	28
1918	Microcapillary sampling of Baltic Sea copepod gut microbiomes indicates high variability among individuals and the potential for methane production. FEMS Microbiology Ecology, 2019, 95, .	2.7	10
1919	The mucosal–luminal interface: an ideal sample to study the mucosa-associated microbiota and the intestinal microbial biogeography. Pediatric Research, 2019, 85, 895-903.	2.3	32
1920	16S rRNA amplicon sequencing characterization of caecal microbiome composition of broilers and free-range slow-growing chickens throughout their productive lifespan. Scientific Reports, 2019, 9, 2506.	3.3	105
1921	Nasal microbial composition and chronic otitis media with effusion: A case-control study. PLoS ONE, 2019, 14, e0212473.	2.5	20
1922	High Prevalence of Cefotaxime Resistant Bacteria in Grazing Beef Cattle: A Cross Sectional Study. Frontiers in Microbiology, 2019, 10, 176.	3.5	30
1923	Succession of embryonic and the intestinal bacterial communities of Atlantic salmon (<i>Salmo) Tj ETQq1 1</i>	0.784314 rgBT	/Qyerlock I
1924	Bacterial release from pipe biofilm in a full-scale drinking water distribution system. Npj Biofilms and Microbiomes, 2019, 5, 9.	6.4	88
1925	Changes in microbiome diversity following beta-lactam antibiotic treatment are associated with therapeutic versus subtherapeutic antibiotic exposure in cystic fibrosis. Scientific Reports, 2019, 9, 2534.	3.3	17
1926	In-feed resin acids reduce matrix metalloproteinase activity in the ileal mucosa of healthy broilers without inducing major effects on the gut microbiota. Veterinary Research, 2019, 50, 15.	3.0	24
1927	Deciphering the effects of nitrogen, phosphorus, and temperature on cyanobacterial bloom intensification, diversity, and toxicity in western Lake Erie. Limnology and Oceanography, 2019, 64, 1347-1370.	3.1	135
1928	Impacts of Arsenic and Antimony Co-Contamination on Sedimentary Microbial Communities in Rivers with Different Pollution Gradients. Microbial Ecology, 2019, 78, 589-602.	2.8	45
1929	Comparison of Small Gut and Whole Gut Microbiota of First-Degree Relatives With Adult Celiac Disease Patients and Controls. Frontiers in Microbiology, 2019, 10, 164.	3.5	68
1930	Evaluation of Oral Cavity DNA Extraction Methods on Bacterial and Fungal Microbiota. Scientific Reports, 2019, 9, 1531.	3.3	31
1931	Plant hosts control microbial denitrification activity. FEMS Microbiology Ecology, 2019, 95, .	2.7	30

#	Article	IF	CITATIONS
1932	Pea polyphenolics and hydrolysis processing alter microbial community structure and early pathogen colonization in mice. Journal of Nutritional Biochemistry, 2019, 67, 101-110.	4.2	17
1933	Bacterial community structure and effects of picornavirus infection on the anterior nares microbiome in early childhood. BMC Microbiology, 2019, 19, 1.	3.3	217
1934	Offspring Microbiomes Differ Across Breeding Sites in a Panmictic Species. Frontiers in Microbiology, 2019, 10, 35.	3. 5	32
1935	Denitrification performance and microbial versatility in response to different selection pressures. Bioresource Technology, 2019, 281, 72-83.	9.6	187
1936	Serotonin Transporter Deficiency is Associated with Dysbiosis and Changes in Metabolic Function of the Mouse Intestinal Microbiome. Scientific Reports, 2019, 9, 2138.	3.3	46
1937	Compositional changes to the ileal microbiome precede the onset of spontaneous ileitis in SHIP deficient mice. Gut Microbes, 2019, 10, 578-598.	9.8	46
1938	Potential biomarkers to predict outcome of faecal microbiota transfer for recurrent Clostridioides difficile infection. Digestive and Liver Disease, 2019, 51, 944-951.	0.9	13
1939	Microbial species and biodiversity in settling dust within and between pig farms. Environmental Research, 2019, 171, 558-567.	7.5	49
1940	Rare gut microbiota associated with breeding success, hormone metabolites and ovarian cycle phase in the critically endangered eastern black rhino. Microbiome, 2019, 7, 27.	11.1	75
1941	Microbiome-based body fluid identification of samples exposed to indoor conditions. Forensic Science International: Genetics, 2019, 40, 105-113.	3.1	52
1942	Nasal and skin microbiomes are associated with disease severity in paediatric atopic dermatitis. British Journal of Dermatology, 2019, 181, 796-804.	1.5	30
1943	A culture-dependent and metagenomic approach of household drinking water from the source to point of use in a developing country. Water Research X, 2019, 2, 100026.	6.1	32
1944	Defining the role of <i>Parasutterella</i> , a previously uncharacterized member of the core gut microbiota. ISME Journal, 2019, 13, 1520-1534.	9.8	267
1945	Metabarcoding reveals that rhizospheric microbiota of Quercus pyrenaica is composed by a relatively small number of bacterial taxa highly abundant. Scientific Reports, 2019, 9, 1695.	3.3	23
1946	Spatial distribution of prokaryotic communities in hypersaline soils. Scientific Reports, 2019, 9, 1769.	3.3	33
1947	The bacterial community associated with adult vine weevil (<i>Otiorhynchus sulcatus</i>) in <scp>UK</scp> populations growing on strawberry is dominated by <i>Candidatus</i> Nardonella. Entomologia Experimentalis Et Applicata, 2019, 167, 186-196.	1.4	8
1948	Fecal Microbiota Analysis in Patients Going through a Depressive Episode during Treatment in a Psychiatric Hospital Setting. Journal of Clinical Medicine, 2019, 8, 164.	2.4	29
1949	Little cigars and cigarillos harbor diverse bacterial communities that differ between the tobacco and the wrapper. PLoS ONE, 2019, 14, e0211705.	2.5	12

#	Article	IF	CITATIONS
1950	Estimating the biodiversity of terrestrial invertebrates on a forested island using DNA barcodes and metabarcoding data. Ecological Applications, 2019, 29, e01877.	3.8	37
1951	No difference in 4â€nitroquinoline induced tumorigenesis between germâ€free and colonized mice. Molecular Carcinogenesis, 2019, 58, 627-632.	2.7	2
1952	Comparison of the nasopharyngeal bacterial microbiota of beef calves raised without the use of antimicrobials between healthy calves and those diagnosed with bovine respiratory disease. Veterinary Microbiology, 2019, 231, 56-62.	1.9	33
1953	Gut microbiota of the European Brown Hare (Lepus europaeus). Scientific Reports, 2019, 9, 2738.	3.3	14
1954	Loading ceftriaxone, vancomycin, and Bifidobacteria bifidum TMC3115 to neonatal mice could differently and consequently affect intestinal microbiota and immunity in adulthood. Scientific Reports, 2019, 9, 3254.	3.3	27
1955	c-Maf-dependent Treg cell control of intestinal TH17 cells and IgA establishes host–microbiota homeostasis. Nature Immunology, 2019, 20, 471-481.	14.5	138
1956	Antagonistic effects of (i>Streptococcus (i>and (i>Lactobacillus (i>probiotics in pharyngeal biofilms. Letters in Applied Microbiology, 2019, 68, 303-312.	2.2	26
1957	A prospective cohort for the investigation of alteration in temporal transcriptional and microbiome trajectories preceding preterm birth: a study protocol. BMJ Open, 2019, 9, e023417.	1.9	15
1958	The NLRP3 inflammasome mediates DSS-induced intestinal inflammation in <i>Nod2</i> knockout mice. Innate Immunity, 2019, 25, 132-143.	2.4	27
1959	Successional Dynamics and Seascape-Level Patterns of Microbial Communities on the Canopy-Forming Kelps Nereocystis luetkeana and Macrocystis pyrifera. Frontiers in Microbiology, 2019, 10, 346.	3.5	77
1960	Modulation of Gut Microbiota Composition by Serotonin Signaling Influences Intestinal Immune Response and Susceptibility to Colitis. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 709-728.	4.5	132
1961	Microbial residence time is a controlling parameter of the taxonomic composition and functional profile of microbial communities. ISME Journal, 2019, 13, 1589-1601.	9.8	24
1962	Fitness Cost of Aflatoxin Production in Aspergillus flavus When Competing with Soil Microbes Could Maintain Balancing Selection. MBio, 2019, 10, .	4.1	21
1963	Composition and Variation of the Human Milk Microbiota Are Influenced by Maternal and Early-Life Factors. Cell Host and Microbe, 2019, 25, 324-335.e4.	11.0	343
1964	Comparative metagenomics and functional profiling of crude oil-polluted soils in Bodo West Community, Ogoni, with other sites of varying pollution history. Annals of Microbiology, 2019, 69, 495-513.	2.6	33
1965	Co-digestion of organic and mineral wastes for enhanced biogas production: Reactor performance and evolution of microbial community and function. Waste Management, 2019, 87, 313-325.	7.4	20
1966	Trace element supplementation is associated with increases in fermenting bacteria in biogas mono-digestion of grass silage. Renewable Energy, 2019, 138, 980-986.	8.9	56
1967	The neuroactive potential of the human gut microbiota in quality of life and depression. Nature Microbiology, 2019, 4, 623-632.	13.3	1,206

#	Article	IF	CITATIONS
1968	Changes in the Composition of the Gut Microbiota and the Blood Transcriptome in Preterm Infants at Less than 29 Weeks Gestation Diagnosed with Bronchopulmonary Dysplasia. MSystems, 2019, 4, .	3.8	23
1969	Impaired glucose metabolism and altered gut microbiome despite calorie restriction of ob/ob mice. Animal Microbiome, 2019, $1,11.$	3.8	15
1970	Microbial Diversity of the Red Sea Urchin Loxechinus albus during Controlled Farming in Puerto Montt, Chile, Using 16S rRNA Gene Amplicon Sequencing. Microbiology Resource Announcements, 2019, 8, .	0.6	2
1971	Phyllosphere microbial communities of leafy vegetables affected by irrigation water sanitation. Acta Horticulturae, 2019, , 393-398.	0.2	1
1972	Impact of Sample Preservation and Manipulation on Insect Gut Microbiome Profiling. A Test Case With Fruit Flies (Diptera, Tephritidae). Frontiers in Microbiology, 2019, 10, 2833.	3.5	38
1973	Global Comparison of the Bacterial Communities of Bilge Water, Boat Surfaces, and External Port Water. Applied and Environmental Microbiology, 2019, 85, .	3.1	5
1974	Minimal residual disease negativity in multiple myeloma is associated with intestinal microbiota composition. Blood Advances, 2019, 3, 2040-2044.	5.2	50
1975	The Introduced Fanworm, Sabella spallanzanii, Alters Soft Sediment Macrofauna and Bacterial Communities. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	11
1976	Succession of microbial populations and nitrogen-fixation associated with the biodegradation of sediment-oil-agglomerates buried in a Florida sandy beach. Scientific Reports, 2019, 9, 19401.	3.3	27
1977	Sea anemone and clownfish microbiota diversity and variation during the initial steps of symbiosis. Scientific Reports, 2019, 9, 19491.	3.3	8
1978	Picoplankton accumulate and recycle polyphosphate to support high primary productivity in coastal Lake Ontario. Scientific Reports, 2019, 9, 19563.	3.3	16
1979	Uncovering the Diversity and Activity of Methylotrophic Methanogens in Freshwater Wetland Soils. MSystems, 2019, 4, .	3.8	32
1980	The Spatial Distribution of the Microbial Community in a Contaminated Aquitard below an Industrial Zone. Water (Switzerland), 2019, 11, 2128.	2.7	10
1981	Comparative analysis of microbiota along the length of the gastrointestinal tract of two tree squirrel species (<i>Sciurus aberti</i> and <i>S. niger</i>) living in sympatry. Ecology and Evolution, 2019, 9, 13344-13358.	1.9	5
1982	Linking Soil Fungal Generality to Tree Richness in Young Subtropical Chinese Forests. Microorganisms, 2019, 7, 547.	3.6	10
1983	Mixed-Cropping Between Field Pea Varieties Alters Root Bacterial and Fungal Communities. Scientific Reports, 2019, 9, 16953.	3.3	31
1984	Age, gut location and diet impact the gut microbiome of a tropical herbivorous surgeonfish. FEMS Microbiology Ecology, 2020, 96, .	2.7	18
1985	Testing sustained soil-to-soil contact as an approach for limiting the abiotic influence of source soils during experimental microbiome transfer. FEMS Microbiology Letters, 2019, 366, .	1.8	15

#	Article	IF	CITATIONS
1986	Enzymatically Digested Food Waste Altered Fecal Microbiota But Not Meat Quality and Carcass Characteristics of Growing-Finishing Pigs. Animals, 2019, 9, 970.	2.3	2
1987	Geography, seasonality, and hostâ€associated population structure influence the fecal microbiome of a genetically depauparate Arctic mammal. Ecology and Evolution, 2019, 9, 13202-13217.	1.9	21
1988	Temporal evolution of the microbiome, immune system, and epigenome with disease progression in ALS mice. DMM Disease Models and Mechanisms, 2019, 13, .	2.4	50
1989	Efficacy of medium-chain fatty acid salts distilled from coconut oil against two enteric pathogen challenges in weanling piglets. Journal of Animal Science and Biotechnology, 2019, 10, 89.	5.3	23
1990	Diversity of endocervical microbiota associated with genital Chlamydia trachomatis infection and infertility among women visiting obstetrics and gynecology clinics in Malaysia. PLoS ONE, 2019, 14, e0224658.	2.5	17
1991	Microbial Communities in Bioswale Soils and Their Relationships to Soil Properties, Plant Species, and Plant Physiology. Frontiers in Microbiology, 2019, 10, 2368.	3.5	10
1992	Determinants of the lung microbiome in intubated premature infants at risk for bronchopulmonary dysplasia. Journal of Maternal-Fetal and Neonatal Medicine, 2021, 34, 3220-3226.	1.5	6
1993	Reproducibility, stability, and accuracy of microbial profiles by fecal sample collection method in three distinct populations. PLoS ONE, 2019, 14, e0224757.	2.5	19
1994	Interactions of Microhabitat and Time Control Grassland Bacterial and Fungal Composition. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	12
1995	Sex, Age, and Bacteria: How the Intestinal Microbiota Is Modulated in a Protandrous Hermaphrodite Fish. Frontiers in Microbiology, 2019, 10, 2512.	3 . 5	52
1996	Microbiome differences in disease-resistant vs. susceptible Acropora corals subjected to disease challenge assays. Scientific Reports, 2019, 9, 18279.	3.3	54
1997	Effects of disease, antibiotic treatment and recovery trajectory on the microbiome of farmed seabass (Dicentrarchus labrax). Scientific Reports, 2019, 9, 18946.	3.3	54
1998	Tailings microbial community profile and prediction of its functionality in basins of tungsten mine. Scientific Reports, 2019, 9, 19596.	3.3	31
1999	Allergic inflammation alters the lung microbiome and hinders synergistic co-infection with H1N1 influenza virus and Streptococcus pneumoniae in C57BL/6 mice. Scientific Reports, 2019, 9, 19360.	3.3	23
2000	Temporal development of the oral microbiome and prediction of early childhood caries. Scientific Reports, 2019, 9, 19732.	3.3	65
2001	Airâ€side ammonia stripping coupled to anaerobic digestion indirectly impacts anaerobic microbiome. Microbial Biotechnology, 2019, 12, 1403-1416.	4.2	19
2002	Bayesian hierarchical negative binomial models for multivariable analyses with applications to human microbiome count data. PLoS ONE, 2019, 14, e0220961.	2.5	5
2003	Grapevine Phyllosphere Community Analysis in Response to Elicitor Application against Powdery Mildew. Microorganisms, 2019, 7, 662.	3.6	21

#	Article	IF	CITATIONS
2004	Agricultural Management Affects Root-Associated Microbiome Recruitment Over Maize Development. Phytobiomes Journal, 2019, 3, 260-272.	2.7	28
2005	Obesity during pregnancy results in maternal intestinal inflammation, placental hypoxia, and alters fetal glucose metabolism at mid-gestation. Scientific Reports, 2019, 9, 17621.	3.3	54
2006	Dietary Saccharomyces cerevisiae boulardii CNCM I-1079 Positively Affects Performance and Intestinal Ecosystem in Broilers during a Campylobacter jejuni Infection. Microorganisms, 2019, 7, 596.	3.6	21
2007	Environmental Filtering Drives the Assembly of Habitat Generalists and Specialists in the Coastal Sand Microbial Communities of Southern China. Microorganisms, 2019, 7, 598.	3.6	27
2008	Gut microbiota composition of Japanese macaques associates with extent of human encroachment. American Journal of Primatology, 2019, 81, e23072.	1.7	22
2009	Human Endometrial Microbiota at Term of Normal Pregnancies. Genes, 2019, 10, 971.	2.4	38
2010	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. Frontiers in Genetics, 2019, 10, 957.	2.3	8
2011	Mangrove-Associated Fungal Communities Are Differentiated by Geographic Location and Host Structure. Frontiers in Microbiology, 2019, 10, 2456.	3.5	32
2012	Wild specimens of sand fly phlebotomine Lutzomyia evansi, vector of leishmaniasis, show high abundance of Methylobacterium and natural carriage of Wolbachia and Cardinium types in the midgut microbiome. Scientific Reports, 2019, 9, 17746.	3.3	20
2013	Cultivar-Dependent Variation of the Cotton Rhizosphere and Endosphere Microbiome Under Field Conditions. Frontiers in Plant Science, 2019, 10, 1659.	3.6	49
2014	Early exposure to antibiotics in the neonatal intensive care unit alters the taxonomic and functional infant gut microbiome. Journal of Maternal-Fetal and Neonatal Medicine, 2021, 34, 3335-3343.	1.5	10
2015	Characterization of the Mycobiome of the Seagrass, Zostera marina, Reveals Putative Associations With Marine Chytrids. Frontiers in Microbiology, 2019, 10, 2476.	3.5	34
2016	Seasonal Variation and Crop Sequences Shape the Structure of Bacterial Communities in Cysts of Soybean Cyst Nematode. Frontiers in Microbiology, 2019, 10, 2671.	3.5	26
2017	Influence of Colostrum and Vitamins A, D3, and E on Early Intestinal Colonization of Neonatal Holstein Calves Infected with Mycobacterium avium subsp. paratuberculosis. Veterinary Sciences, 2019, 6, 93.	1.7	3
2018	Effect of Parkinson's disease and related medications on the composition of the fecal bacterial microbiota. Npj Parkinson's Disease, 2019, 5, 28.	5.3	86
2019	Crop Sorghum Ensiled With Unsalable Vegetables Increases Silage Microbial Diversity. Frontiers in Microbiology, 2019, 10, 2599.	3.5	12
2020	A Glyphosate Pulse to Brackish Long-Term Microcosms Has a Greater Impact on the Microbial Diversity and Abundance of Planktonic Than of Biofilm Assemblages. Frontiers in Marine Science, 2019, 6, .	2.5	8
2021	Diversity-Stability Dynamics of the Amphibian Skin Microbiome and Susceptibility to a Lethal Viral Pathogen. Frontiers in Microbiology, 2019, 10, 2883.	3.5	49

#	Article	IF	CITATIONS
2022	Microbial and Phenyl Acid Dynamics during the Start-up Phase of Anaerobic Straw Degradation in Meso- and Thermophilic Batch Reactors. Microorganisms, 2019, 7, 657.	3.6	15
2023	Acute changes in the colonic microbiota are associated with large intestinal forms of surgical colic. BMC Veterinary Research, 2019, 15, 468.	1.9	11
2024	The subway microbiome: seasonal dynamics and direct comparison of air and surface bacterial communities. Microbiome, 2019, 7, 160.	11.1	40
2025	Colonic bacterial composition is sex-specific in aged CD-1 mice fed diets varying in fat quality. PLoS ONE, 2019, 14, e0226635.	2.5	9
2026	Mucosa-Associated Microbiota in Ileoanal Pouches May Contribute to Clinical Symptoms, Particularly Stool Frequency, Independent of Endoscopic Disease Activity. Clinical and Translational Gastroenterology, 2019, 10, e00038.	2.5	9
2027	Host phylogeny, diet, and habitat differentiate the gut microbiomes of Darwin's finchesÂon Santa Cruz Island. Scientific Reports, 2019, 9, 18781.	3.3	35
2028	An inter-island comparison of Darwin's finches reveals the impact of habitat, host phylogeny, and island on the gut microbiome. PLoS ONE, 2019, 14, e0226432.	2.5	14
2029	The Effect of Increasing Inclusion Levels of a Fucoidan-Rich Extract Derived from Ascophyllum nodosum on Growth Performance and Aspects of Intestinal Health of Pigs Post-Weaning. Marine Drugs, 2019, 17, 680.	4.6	10
2030	Microbiota composition of the dorsal patch of reproductive male Leptonycteris yerbabuenae. PLoS ONE, 2019, 14, e0226239.	2.5	13
2031	Glacial Runoff Promotes Deep Burial of Sulfur Cycling-Associated Microorganisms in Marine Sediments. Frontiers in Microbiology, 2019, 10, 2558.	3. 5	16
2032	Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. Nature, 2019, 574, 117-121.	27.8	617
2033	The microbiota regulate neuronal function and fear extinction learning. Nature, 2019, 574, 543-548.	27.8	302
2034	Altered microbiome composition in individuals with fibromyalgia. Pain, 2019, 160, 2589-2602.	4.2	130
2035	Longitudinal Analysis of the Microbiota Composition and Enterotypes of Pigs from Post-Weaning to Finishing. Microorganisms, 2019, 7, 622.	3.6	20
2036	From Genes to Nitrogen Removal: Determining the Impacts of Poultry Industry Wastewater on Tidal Creek Denitrification. Environmental Science & Environ	10.0	17
2037	A Prospective Study on Child Morbidity and Gut Microbiota in Rural Malawi. Journal of Pediatric Gastroenterology and Nutrition, 2019, 69, 431-437.	1.8	8
2038	Hair eruption initiates and commensal skin microbiota aggravate adverse events of anti-EGFR therapy. Science Translational Medicine, 2019, 11 , .	12.4	23
2039	Impact of oral probiotic Lactobacillus acidophilus vaccine strains on the immune response and gut microbiome of mice. PLoS ONE, 2019, 14, e0225842.	2.5	15

#	ARTICLE	IF	CITATIONS
2040	Discordant transmission of bacteria and viruses from mothers to babies at birth. Microbiome, 2019, 7, 156.	11.1	71
2041	A Plant Growth-Promoting Microbial Soil Amendment Dynamically Alters the Strawberry Root Bacterial Microbiome. Scientific Reports, 2019, 9, 17677.	3.3	50
2042	The Role of Housing Environment and Dietary Protein Source on the Gut Microbiota of Chicken. Animals, 2019, 9, 1085.	2.3	32
2043	Defining the root endosphere and rhizosphere microbiomes from the World Olive Germplasm Collection. Scientific Reports, 2019, 9, 20423.	3.3	65
2044	Using recirculating flumes and a response surface model to investigate the role of hyporheic exchange and bacterial diversity on micropollutant half-lives. Environmental Sciences: Processes and Impacts, 2019, 21, 2093-2108.	3.5	27
2045	Rapid and Concomitant Gut Microbiota and Endocannabinoidome Response to Diet-Induced Obesity in Mice. MSystems, 2019, 4, .	3.8	52
2046	Characterizing Chemoautotrophy and Heterotrophy in Marine Archaea and Bacteria With Single-Cell Multi-isotope NanoSIP. Frontiers in Microbiology, 2019, 10, 2682.	3.5	37
2047	Differently Pre-treated Alfalfa Silages Affect the in vitro Ruminal Microbiota Composition. Frontiers in Microbiology, 2019, 10, 2761.	3. 5	8
2048	Soil Bacterial and Fungal Communities Exhibit Distinct Long-Term Responses to Disturbance in Temperate Forests. Frontiers in Microbiology, 2019, 10, 2872.	3.5	37
2049	Comparative metatranscriptomic analysis of anaerobic digesters treating anionic surfactant contaminated wastewater. Science of the Total Environment, 2019, 649, 482-494.	8.0	33
2050	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. Gut, 2019, 68, 1180-1189.	12.1	149
2051	The Human Mesenteric Lymph Node Microbiome Differentiates Between Crohn's Disease and Ulcerative Colitis. Journal of Crohn's and Colitis, 2019, 13, 58-66.	1.3	46
2052	Evaluation of the bacterial diversity of Spanish-type chorizo during the ripening process using high-throughput sequencing and physicochemical characterization. Meat Science, 2019, 150, 7-13.	5 . 5	46
2053	Impacts of DNA extraction and PCR on DNA metabarcoding estimates of soil biodiversity. Methods in Ecology and Evolution, 2019, 10, 120-133.	5. 2	62
2054	Cellulaseâ^'Hemicellulase Activities and Bacterial Community Composition of Different Soils from Algerian Ecosystems. Microbial Ecology, 2019, 77, 713-725.	2.8	21
2055	Lactococci dominate the bacterial communities of fermented maize, sorghum and millet slurries in Zimbabwe. International Journal of Food Microbiology, 2019, 289, 77-87.	4.7	15
2056	Impact of Introduction of Arbuscular Mycorrhizal Fungi on the Root Microbial Community in Agricultural Fields. Microbes and Environments, 2019, 34, 23-32.	1.6	35
2057	Diet-Independent Correlations between Bacteria and Dysfunction of Gut, Adipose Tissue, and Liver: A Comprehensive Microbiota Analysis in Feces and Mucosa of the Ileum and Colon in Obese Mice with NAFLD. International Journal of Molecular Sciences, 2019, 20, 1.	4.1	929

#	ARTICLE	IF	CITATIONS
2058	The effect of rhizosphere microbes outweighs host plant genetics in reducing insect herbivory. Molecular Ecology, 2019, 28, 1801-1811.	3.9	55
2059	Rapid profiling of tropical marine cyanobacterial communities. Regional Studies in Marine Science, 2019, 25, 100485.	0.7	7
2060	Snow algae drive productivity and weathering at volcanic rock-hosted glaciers. Geochimica Et Cosmochimica Acta, 2019, 247, 220-242.	3.9	26
2061	Inhibiting antibiotic-resistant Enterobacteriaceae by microbiota-mediated intracellular acidification. Journal of Experimental Medicine, 2019, 216, 84-98.	8.5	135
2062	Assessing the Influence of Dietary History on Gut Microbiota. Current Microbiology, 2019, 76, 237-247.	2.2	10
2063	Assessing fungal contributions to cellulose degradation in soil by using high-throughput stable isotope probing. Soil Biology and Biochemistry, 2019, 130, 150-158.	8.8	67
2064	Distribution of antibiotic resistance genes in soils and crops. A field study in legume plants (Vicia faba) Tj ETQq0	0 0 rgBT /0 7.g	Overlock 10
2065	Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. Nature Microbiology, 2019, 4, 447-458.	13.3	68
2066	Moisture Is More Important than Temperature for Assembly of Both Potentially Active and Whole Prokaryotic Communities in Subtropical Grassland. Microbial Ecology, 2019, 77, 460-470.	2.8	28
2067	Local fungi, willow and municipal compost effectively remediate petroleum-contaminated soil in the Canadian North. Chemosphere, 2019, 220, 47-55.	8.2	23
2068	Microtopographic differences in soil properties and microbial community composition at the field scale. Soil Biology and Biochemistry, 2019, 131, 71-80.	8.8	32
2069	Culturomics-Based Taxonomic Diversity of Bacterial Communities in the Hot Springs of Saudi Arabia. OMICS A Journal of Integrative Biology, 2019, 23, 17-27.	2.0	13
2070	The Vaginal Microbiome of Transgender Men. Clinical Chemistry, 2019, 65, 199-207.	3.2	29
2071	Differential co-occurrence relationships shaping ecotype diversification within <i>Thaumarchaeota</i> populations in the coastal ocean water column. ISME Journal, 2019, 13, 1144-1158.	9.8	80
2072	Alterations in gut microbiota composition and metabolic parameters after dietary intervention with barley beta glucans in patients with high risk for metabolic syndrome development. Anaerobe, 2019, 55, 67-77.	2.1	78
2073	Organic and inorganic amendments did not affect microbial community composition in the bulk soil differently but did change the relative abundance of selected taxa. European Journal of Soil Science, 2019, 70, 796-806.	3.9	7
2074	Microbial life beyond the grave: 16S rRNA gene-based metagenomic analysis of bacteria diversity and their functional profiles in cemetery environments. Science of the Total Environment, 2019, 655, 831-841.	8.0	39
2075	Characterization of fungal dysbiosis in Japanese patients with inflammatory bowel disease. Journal of Gastroenterology, 2019, 54, 149-159.	5.1	43

#	Article	IF	CITATIONS
2076	Exploring the Human Microbiome: The Potential Future Role of Next-Generation Sequencing in Disease Diagnosis and Treatment. Frontiers in Immunology, 2018, 9, 2868.	4.8	207
2077	Microbial communities in local and transplanted soils along a latitudinal gradient. Catena, 2019, 173, 456-464.	5. 0	11
2078	Variations in Microbial Diversity and Metabolite Profiles of the Tropical Marine Sponge Xestospongia muta with Season and Depth. Microbial Ecology, 2019, 78, 243-256.	2.8	25
2079	Extensive studies on the treatment of pulp mill wastewater using aerobic granular sludge (AGS) technology. Chemical Engineering Journal, 2019, 359, 1175-1194.	12.7	39
2080	Importance of soil texture to the fate of pathogens introduced by irrigation with treated wastewater. Science of the Total Environment, 2019, 653, 886-896.	8.0	21
2081	Microbiome of drinking water: A full-scale spatio-temporal study to monitor water quality in the Paris distribution system. Water Research, 2019, 149, 375-385.	11.3	81
2082	Rootstocks Shape the Rhizobiome: Rhizosphere and Endosphere Bacterial Communities in the Grafted Tomato System. Applied and Environmental Microbiology, 2019, 85, .	3.1	77
2083	Core and Dynamic Microbial Communities of Two Invasive Ascidians: Can Host–Symbiont Dynamics Plasticity Affect Invasion Capacity?. Microbial Ecology, 2019, 78, 170-184.	2.8	29
2084	Response of microbial communities and enzyme activities to amendments in saline-alkaline soils. Applied Soil Ecology, 2019, 135, 16-24.	4.3	97
2085	Bacterial diversity in the marine sponge <i>Halichondria panicea</i> from Icelandic waters and host-specificity of its dominant symbiont " <i>Candidatus</i> Halichondribacter symbioticus― FEMS Microbiology Ecology, 2019, 95, .	2.7	46
2086	Community structural differences shape microbial responses to high molecular weight organic matter. Environmental Microbiology, 2019, 21, 557-571.	3.8	40
2087	Response and recovery of microbial communities subjected to oxidative and biological treatments of 1,4-dioxane and co-contaminants. Water Research, 2019, 149, 74-85.	11.3	41
2088	Host selectively contributes to shaping intestinal microbiota of carnivorous and omnivorous fish. Journal of General and Applied Microbiology, 2019, 65, 129-136.	0.7	11
2089	Pressure and temperature effects on deepâ€sea hydrocarbonâ€degrading microbial communities in subarctic sediments. MicrobiologyOpen, 2019, 8, e00768.	3.0	20
2090	Diazotrophic community and associated dinitrogen fixation within the temperate coral <i>Oculina patagonica</i> . Environmental Microbiology, 2019, 21, 480-495.	3.8	27
2091	Metabarcoding successfully tracks temporal changes in eukaryotic communities in coastal sediments. FEMS Microbiology Ecology, 2019, 95, .	2.7	19
2092	Decreased Snow Cover Stimulates Under-Ice Primary Producers but Impairs Methanotrophic Capacity. MSphere, 2019, 4, .	2.9	18
2093	Socioeconomic Status and the Gut Microbiome: A TwinsUK Cohort Study. Microorganisms, 2019, 7, 17.	3.6	93

#	Article	IF	CITATIONS
2094	Effects of diet on the childhood gut microbiome and its implications for atopic dermatitis. Journal of Allergy and Clinical Immunology, 2019, 143, 1636-1637.e5.	2.9	35
2095	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. American Journal of Epidemiology, 2019, 188, 1023-1026.	3.4	30
2096	Increased methane concentration alters soil prokaryotic community structure along an artificial pH gradient. Annals of Microbiology, 2019, 69, 329-339.	2.6	6
2097	Investigation of effects of omeprazole on the fecal and gastric microbiota of healthy adult horses. American Journal of Veterinary Research, 2019, 80, 79-86.	0.6	12
2098	Microbial Biomarker Transition in High-Altitude Sinter Mounds From El Tatio (Chile) Through Different Stages of Hydrothermal Activity. Frontiers in Microbiology, 2019, 9, 3350.	3.5	25
2099	Bioreactivity and Microbiome of Biodeposits from Filter-Feeding Bivalves. Microbial Ecology, 2019, 77, 343-357.	2.8	23
2100	IL-22 Preserves Gut Epithelial Integrity and Promotes Disease Remission during Chronic <i>Salmonella</i> Infection. Journal of Immunology, 2019, 202, 956-965.	0.8	49
2101	Metabarcoding to investigate changes in soil microbial communities within forensic burial contexts. Forensic Science International: Genetics, 2019, 39, 73-85.	3.1	40
2102	Earthworms and cadmium – Heavy metal resistant gut bacteria as indicators for heavy metal pollution in soils?. Ecotoxicology and Environmental Safety, 2019, 171, 843-853.	6.0	75
2103	Bacterial Dispersers along Preferential Flow Paths of a Clay Till Depth Profile. Applied and Environmental Microbiology, 2019, 85, .	3.1	6
2104	Diversity and Composition of Pelagic Prokaryotic and Protist Communities in a Thin Arctic Sea-Ice Regime. Microbial Ecology, 2019, 78, 388-408.	2.8	26
2105	Microbiomes of the polychaete Hydroides elegans (Polychaeta: Serpulidae) across its life-history stages. Marine Biology, 2019, 166, 1.	1.5	27
2106	Bacillus velezensis AP193 exerts probiotic effects in channel catfish (Ictalurus punctatus) and reduces aquaculture pond eutrophication. Aquaculture, 2019, 503, 347-356.	3.5	79
2107	Potential role of host-derived quorum quenching in modulating bacterial colonization in the moon jellyfish Aurelia aurita. Scientific Reports, 2019, 9, 34.	3.3	30
2108	OTUX: V-region specific OTU database for improved 16S rRNA OTU picking and efficient cross-study taxonomic comparison of microbiomes. DNA Research, 2019, 26, 147-156.	3.4	18
2109	Preferential flow paths shape the structure of bacterial communities in a clayey till depth profile. FEMS Microbiology Ecology, 2019, 95, .	2.7	13
2110	Longitudinal changes during pregnancy in gut microbiota and methylmercury biomarkers, and reversal of microbe-exposure correlations. Environmental Research, 2019, 172, 700-712.	7.5	20
2111	Microbiotas from Humans with Inflammatory Bowel Disease Alter the Balance of Gut Th17 and $ROR\hat{I}^3t+Regulatory T$ Cells and Exacerbate Colitis in Mice. Immunity, 2019, 50, 212-224.e4.	14.3	345

#	Article	IF	CITATIONS
2112	Transitions in microbial communities along a 1600†km freshwater trophic gradient. Journal of Great Lakes Research, 2019, 45, 263-276.	1.9	10
2113	Daily Consumption of Orange Juice from <i>Citrus sinensis</i> L. Osbeck cv. Cara Cara and cv. Bahia Differently Affects Gut Microbiota Profiling as Unveiled by an Integrated Meta-Omics Approach. Journal of Agricultural and Food Chemistry, 2019, 67, 1381-1391.	5 . 2	39
2114	Invited Commentary: Improving the Accessibility of Human Microbiome Project Data Through Integration With R/Bioconductor. American Journal of Epidemiology, 2019, 188, 1027-1030.	3.4	3
2115	Murine Methyl Donor Deficiency Impairs Early Growth in Association with Dysmorphic Small Intestinal Crypts and Reduced Gut Microbial Community Diversity. Current Developments in Nutrition, 2019, 3, nzy070.	0.3	12
2116	Metabarcoding targeting the EF1 alpha region to assess Fusarium diversity on cereals. PLoS ONE, 2019, 14, e0207988.	2.5	31
2117	Pilot study of probiotic/colostrum supplementation on gut function in children with autism and gastrointestinal symptoms. PLoS ONE, 2019, 14, e0210064.	2.5	126
2118	Antarctic Relic Microbial Mat Community Revealed by Metagenomics and Metatranscriptomics. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	36
2119	Long Term Diversity and Distribution of Non-photosynthetic Cyanobacteria in Peri-Alpine Lakes. Frontiers in Microbiology, 2018, 9, 3344.	3.5	55
2120	Variation of bacterial biodiversity from saline soils and estuary sediments present near the Mediterranean Sea coast of Camargue (France). Antonie Van Leeuwenhoek, 2019, 112, 351-365.	1.7	12
2121	Comamonadaceae OTU as a Remnant of an Ancient Microbial Community in Sulfidic Waters. Microbial Ecology, 2019, 78, 85-101.	2.8	21
2122	Optimization of organics to nutrients (COD:N:P) ratio for aerobic granular sludge treating high-strength organic wastewater. Science of the Total Environment, 2019, 650, 3168-3179.	8.0	53
2123	Oxygen loss from seagrass roots coincides with colonisation of sulphide-oxidising cable bacteria and reduces sulphide stress. ISME Journal, 2019, 13, 707-719.	9.8	89
2124	Plant-plant interactions and N fertilization shape soil bacterial and fungal communities. Soil Biology and Biochemistry, 2019, 128, 127-138.	8.8	94
2125	Effects of temperature on <i>Paramoeba perurans</i> growth in culture and the associated microbial community. Parasitology, 2019, 146, 533-542.	1.5	10
2126	Antibiotic resistance genes distribution in microbiomes from the soil-plant-fruit continuum in commercial Lycopersicon esculentum fields under different agricultural practices. Science of the Total Environment, 2019, 652, 660-670.	8.0	65
2127	Bacterial community structure and succession in nests of two megachilid bee genera. FEMS Microbiology Ecology, 2019, 95, .	2.7	40
2128	Methods for normalizing microbiome data: An ecological perspective. Methods in Ecology and Evolution, 2019, 10, 389-400.	5.2	225
2129	Combined Consumption of Beefâ€Based Cooked Mince and Sucrose Stimulates Oxidative Stress, Cardiac Hypertrophy, and Colonic Outgrowth of Desulfovibrionaceae in Rats. Molecular Nutrition and Food Research, 2019, 63, e1800962.	3.3	25

#	Article	IF	Citations
2130	Balance of saccharolysis and proteolysis underpins improvements in stool quality induced by adding a fiber bundle containing bound polyphenols to either hydrolyzed meat or grain-rich foods. Gut Microbes, 2019, 10, 298-320.	9.8	56
2131	Sputum Microbiome Is Associated with 1-Year Mortality after Chronic Obstructive Pulmonary Disease Hospitalizations. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 1205-1213.	5. 6	95
2132	Acid mine drainage affects the diversity and metal resistance gene profile of sediment bacterial community along a river. Chemosphere, 2019, 217, 790-799.	8.2	83
2133	Comprehensive insights into the key components of bacterial assemblages in pharmaceutical wastewater treatment plants. Science of the Total Environment, 2019, 651, 2148-2157.	8.0	25
2134	Gut microbiota dynamics in travelers returning from India colonized with extended-spectrum cephalosporin-resistant Enterobacteriaceae: A longitudinal study. Travel Medicine and Infectious Disease, 2019, 27, 72-80.	3.0	26
2135	The role of gut microbiome and its interaction with arsenic exposure in carotid intima-media thickness in a Bangladesh population. Environment International, 2019, 123, 104-113.	10.0	30
2136	Biogeography of thermophiles and predominance of Thermus scotoductus in domestic water heaters. Extremophiles, 2019, 23, 119-132.	2.3	4
2137	Chlortetracycline Enhances Tonsil Colonization and Fecal Shedding of Multidrug-Resistant <i>Salmonella enterica </i> Serovar Typhimurium DT104 without Major Alterations to the Porcine Tonsillar and Intestinal Microbiota. Applied and Environmental Microbiology, 2019, 85, .	3.1	14
2138	Marine probiotics: increasing coral resistance to bleaching through microbiome manipulation. ISME Journal, 2019, 13, 921-936.	9.8	269
2139	Factors governing extracellular DNA degradation dynamics in soil. Environmental Microbiology Reports, 2019, 11, 173-184.	2.4	57
2140	Fermenters in the earthworm gut: do transients matter?. FEMS Microbiology Ecology, 2019, 95, .	2.7	18
2141	Structure and function of the bacterial and fungal gut microbiota of Neotropical butterflies. Ecological Monographs, 2019, 89, e01346.	5.4	56
2142	TheSuhomycesclade: from single isolate to multiple species to disintegrating sex loci. FEMS Yeast Research, 2019, 19, .	2.3	10
2143	Bacterial diversity in the waterholes of the Kruger National Park: an eDNA metabarcoding approach. Genome, 2019, 62, 229-242.	2.0	11
2144	Dietary ursolic acid improves health span and life span in male <i>Drosophila melanogaster</i> BioFactors, 2019, 45, 169-186.	5.4	39
2145	Analysis of the gut and gill microbiome of resistant and susceptible lines of rainbow trout (Oncorhynchus mykiss). Fish and Shellfish Immunology, 2019, 86, 497-506.	3.6	109
2146	Mechanisms Underlying Microbial-Mediated Changes in Social Behavior in Mouse Models of Autism Spectrum Disorder. Neuron, 2019, 101, 246-259.e6.	8.1	477
2147	Impact of Cross-Contamination Concentrations of Doxycycline Hyclate on the Microbial Ecosystem in an <i>Ex Vivo</i> Model of the Pig's Cecum. Microbial Drug Resistance, 2019, 25, 304-315.	2.0	2

#	Article	IF	CITATIONS
2148	Evolution of intestinal microbiota and body compartments during spontaneous hyperphagia in the Greylag goose. Poultry Science, 2019, 98, 1390-1402.	3.4	6
2149	Microbial community composition of nest-carton and adjoining soil of the ant Lasius fuliginosus and the role of host secretions in structuring microbial communities. Fungal Ecology, 2019, 38, 44-53.	1.6	18
2150	Dynamics of geosmin-producing bacteria in a full-scale saltwater recirculated aquaculture system. Aquaculture, 2019, 500, 170-177.	3.5	11
2151	Glucomannan Hydrolysate Promotes Gut Proliferative Homeostasis and Extends Life Span in Drosophila melanogaster. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 1549-1556.	3.6	5
2152	Effects of nutrient enrichment on surface microbial community gene expression in the oligotrophic North Pacific Subtropical Gyre. ISME Journal, 2019, 13, 374-387.	9.8	17
2153	Bacterial contributions to delignification and lignocellulose degradation in forest soils with metagenomic and quantitative stable isotope probing. ISME Journal, 2019, 13, 413-429.	9.8	246
2154	Comparison of Oral Collection Methods for Studies of Microbiota. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 137-143.	2.5	28
2155	Novel Cardinium strains in non-marine ostracod (Crustacea) hosts from natural populations. Molecular Phylogenetics and Evolution, 2019, 130, 406-415.	2.7	14
2156	Fungal, Bacterial, and Archaeal Diversity in Soils Beneath Native and Introduced Plants in Fiji, South Pacific. Microbial Ecology, 2019, 78, 136-146.	2.8	8
2157	Characterization of the skin and gill microbiomes of the farmed seabass (Dicentrarchus labrax) and seabream (Sparus aurata). Aquaculture, 2019, 500, 57-64.	3.5	69
2158	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. ISME Journal, 2019, 13, 468-481.	9.8	63
2159	A review of methods and databases for metagenomic classification and assembly. Briefings in Bioinformatics, 2019, 20, 1125-1136.	6.5	368
2160	A broken promise: microbiome differential abundance methods do not control the false discovery rate. Briefings in Bioinformatics, 2019, 20, 210-221.	6.5	132
2161	Computational profiling of the gut–brain axis: microflora dysbiosis insights to neurological disorders. Briefings in Bioinformatics, 2019, 20, 825-841.	6.5	27
2162	OBSOLETE: Bioinformatic Platforms for Metagenomics. , 2020, , .		0
2163	Does birth mode modify associations of maternal pre-pregnancy BMI and gestational weight gain with the infant gut microbiome?. International Journal of Obesity, 2020, 44, 23-32.	3.4	37
2164	Supplementation with dairy matrices impacts on homocysteine levels and gut microbiota composition of hyperhomocysteinemic mice. European Journal of Nutrition, 2020, 59, 345-358.	3.9	14
2165	Influence of moderate beer consumption on human gut microbiota and its impact on fasting glucose and \hat{l}^2 -cell function. Alcohol, 2020, 85, 77-94.	1.7	37

#	Article	IF	CITATIONS
2166	Dynamic immunoglobulin responses to gut bacteria during inflammatory bowel disease. Gut Microbes, 2020, 11, 405-420.	9.8	44
2167	Belowground microbial communities respond to water deficit and are shaped by decades of maize hybrid breeding. Environmental Microbiology, 2020, 22, 889-904.	3.8	15
2168	Dispersal alters soil microbial community response to drought. Environmental Microbiology, 2020, 22, 905-916.	3.8	38
2169	The association between gut microbiome and anthropometric measurements in Bangladesh. Gut Microbes, 2020, 11, 63-76.	9.8	31
2170	Mind and gut: Associations between mood and gastrointestinal distress in children exposed to adversity. Development and Psychopathology, 2020, 32, 309-328.	2.3	48
2171	Specific class of intrapartum antibiotics relates to maturation of the infant gut microbiota: a prospective cohort study. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 217-227.	2.3	82
2172	Changes induced by heavy metals in the plant-associated microbiome of Miscanthus x giganteus. Science of the Total Environment, 2020, 711, 134433.	8.0	56
2173	Diverse respiratory capacity among Thermus strains from US Great Basin hot springs. Extremophiles, 2020, 24, 71-80.	2.3	13
2174	Heritability and Functional Importance of the <i>Setaria viridis</i> Bacterial Seed Microbiome. Phytobiomes Journal, 2020, 4, 40-52.	2.7	71
2175	Interactive Effects of Microbes and Nitrogen on <i>Panicum virgatum</i> Root Functional Traits and Patterns of Phenotypic Selection. International Journal of Plant Sciences, 2020, 181, 20-32.	1.3	10
2176	Seaweed natural products modify the host inflammatory response via Nrf2 signaling and alter colon microbiota composition and gene expression. Free Radical Biology and Medicine, 2020, 146, 306-323.	2.9	13
2177	Assessment of graphene oxide ecotoxicity at several trophic levels using aquatic microcosms. Carbon, 2020, 156, 261-271.	10.3	32
2178	Niche partitioning of methane-oxidizing bacteria along the oxygen–methane counter gradient of stratified lakes. ISME Journal, 2020, 14, 274-287.	9.8	63
2179	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. Journal of Agricultural and Food Chemistry, 2020, 68, 10299-10309.	5.2	25
2180	Plant growth rate and nitrogen uptake shape rhizosphere bacterial community composition and activity in an agricultural field. New Phytologist, 2020, 225, 960-973.	7.3	69
2181	Corn and Soybean Host Root Endophytic Fungi with Toxicity Toward the Soybean Cyst Nematode. Phytopathology, 2020, 110, 603-614.	2.2	10
2182	Mycobiont contribution to tundra plant acquisition of permafrostâ€derived nitrogen. New Phytologist, 2020, 226, 126-141.	7.3	34
2183	Starving the Gut: A Deficit of Butyrate in the Intestinal Ecosystem of Children With Intestinal Failure. Journal of Parenteral and Enteral Nutrition, 2020, 44, 1112-1123.	2.6	12

#	Article	IF	CITATIONS
2184	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments. Limnology and Oceanography, 2020, 65, S233.	3.1	20
2185	Bacterial communities associated with the midgut microbiota of wild Anopheles gambiae complex in Burkina Faso. Molecular Biology Reports, 2020, 47, 211-224.	2.3	12
2186	Biotransformation of hexachlorocyclohexanes contaminated biomass for energetic utilization demonstrated in continuous anaerobic digestion system. Journal of Hazardous Materials, 2020, 384, 121448.	12.4	8
2187	Culture-independent analysis of an endophytic core microbiome in two species of wheat: Triticum aestivum L. (cv. †Hondiaâ€) and the first report of microbiota in Triticum spelta L. (cv. †Rokoszâ€). Systematic and Applied Microbiology, 2020, 43, 126025.	2.8	65
2188	Consecutive lactate formation and chain elongation to reduce exogenous chemicals input in repeated-batch food waste fermentation. Water Research, 2020, 169, 115215.	11.3	132
2189	Early Life Stages of a Common Broadcast Spawning Coral Associate with Specific Bacterial Communities Despite Lack of Internalized Bacteria. Microbial Ecology, 2020, 79, 706-719.	2.8	30
2190	Unique and specific Proteobacteria diversity in urinary microbiota of tolerant kidney transplanted recipients. American Journal of Transplantation, 2020, 20, 145-158.	4.7	19
2191	Nonâ€cyanobacterial diazotrophs dominate nitrogenâ€fixing communities in permafrost thaw ponds. Limnology and Oceanography, 2020, 65, S180.	3.1	19
2192	Variation in the Microbiota Associated with Daphnia magna Across Genotypes, Populations, and Temperature. Microbial Ecology, 2020, 79, 731-742.	2.8	33
2193	What Goes Up Might Come Down: the Spectacular Spread of an Endosymbiont is Followed by Its Decline a Decade Later. Microbial Ecology, 2020, 79, 482-494.	2.8	18
2194	Trimethylamine But Not Trimethylamine Oxide Increases With Age in Rat Plasma and Affects Smooth Muscle Cells Viability. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 1276-1283.	3.6	37
2195	Sharp contrasts between freshwater and marine microbial enzymatic capabilities, community composition, and DOM pools in a NE Greenland fjord. Limnology and Oceanography, 2020, 65, 77-95.	3.1	17
2196	Bacterial colonization of minerals in grassland soils is selective and highly dynamic. Environmental Microbiology, 2020, 22, 917-933.	3.8	23
2198	Role of trees and herbaceous vegetation beneath trees in maintaining arbuscular mycorrhizal communities in temperate alley cropping systems. Plant and Soil, 2020, 453, 153-171.	3.7	34
2199	Defining microbial biomarkers for risk of preterm labor. Brazilian Journal of Microbiology, 2020, 51, 151-159.	2.0	12
2200	Ammonia removal during leach-bed acidification leads to optimized organic acid production from chicken manure. Renewable Energy, 2020, 146, 1021-1030.	8.9	12
2201	Viral metagenomic analysis of the cheese surface: A comparative study of rapid procedures for extracting viral particles. Food Microbiology, 2020, 85, 103278.	4.2	31
2202	Metagenomic and chemical characterization of soil cobalamin production. ISME Journal, 2020, 14, 53-66.	9.8	59

#	Article	IF	CITATIONS
2203	IL-13 mRNA Tissue Content Identifies Two Subsets of Adult Ulcerative Colitis Patients With Different Clinical and Mucosa-Associated Microbiota Profiles. Journal of Crohn's and Colitis, 2020, 14, 369-380.	1.3	25
2204	Gut Microbiome Signatures Are Predictive of Infectious Risk Following Induction Therapy for Acute Myeloid Leukemia. Clinical Infectious Diseases, 2020, 71, 63-71.	5.8	61
2205	Fusarium Head Blight Modifies Fungal Endophytic Communities During Infection of Wheat Spikes. Microbial Ecology, 2020, 79, 397-408.	2.8	56
2206	Structured exercise alters the gut microbiota in humans with overweight and obesity—A randomized controlled trial. International Journal of Obesity, 2020, 44, 125-135.	3.4	76
2207	Cultureâ€independent and dependent evaluation of the equine paranasal sinus microbiota in health and disease. Equine Veterinary Journal, 2020, 52, 455-463.	1.7	11
2208	Diversity and phylogenetic composition of bacterial communities and their association with anthropogenic pollutants in sewage sludge. Chemosphere, 2020, 238, 124629.	8.2	21
2209	Early Colonization of Weathered Polyethylene by Distinct Bacteria in Marine Coastal Seawater. Microbial Ecology, 2020, 79, 517-526.	2.8	96
2210	No evidence for phylosymbiosis in western chipmunk species. FEMS Microbiology Ecology, 2020, 96, .	2.7	22
2211	Soil bacterial community differences along a coastal restoration chronosequence. Plant Ecology, 2020, 221, 795-811.	1.6	12
2212	Accumulation of polybrominated diphenyl ethers and microbiome response in the great pond snail Lymnaea stagnalis with exposure to nylon (polyamide) microplastics. Ecotoxicology and Environmental Safety, 2020, 188, 109882.	6.0	40
2213	<scp>pime</scp> : A package for discovery of novel differences among microbial communities. Molecular Ecology Resources, 2020, 20, 415-428.	4.8	38
2214	Effect of recycled manure solids as bedding on bulk tank milk and implications for cheese microbiological quality. Journal of Dairy Science, 2020, 103, 128-140.	3.4	16
2215	Interactions between soil properties, fungal communities, the soybean cyst nematode, and crop yield under continuous corn and soybean monoculture. Applied Soil Ecology, 2020, 147, 103388.	4.3	41
2216	Spatial and temporal axes impact ecology of the gut microbiome in juvenile European lobster (<i>Homarus gammarus</i>). ISME Journal, 2020, 14, 531-543.	9.8	35
2217	Coâ€dynamics of Symbiodiniaceae and bacterial populations during the first year of symbiosis with <i>Acropora tenuis</i> juveniles. MicrobiologyOpen, 2020, 9, e959.	3.0	30
2218	Dynamics of microbial contaminants is driven by selection during ethanol production. Brazilian Journal of Microbiology, 2020, 51, 303-312.	2.0	2
2219	Synergistic effect of Pseudomonas putida II-2 and Achromobacter sp. QC36 for the effective biodegradation of the herbicide quinclorac. Ecotoxicology and Environmental Safety, 2020, 188, 109826.	6.0	46
2220	Bacterial succession in oil-contaminated soil under phytoremediation with poplars. Chemosphere, 2020, 243, 125242.	8.2	30

#	Article	IF	CITATIONS
2221	Emergence and fate of volatile iodinated organic compounds during biological treatment of oil and gas produced water. Science of the Total Environment, 2020, 699, 134202.	8.0	24
2222	Phylogenetic signature of fungal response to long-term chemical pollution. Soil Biology and Biochemistry, 2020, 140, 107644.	8.8	18
2223	Red Wine Consumption Associated With Increased Gut Microbiota α-Diversity in 3 Independent Cohorts. Gastroenterology, 2020, 158, 270-272.e2.	1.3	58
2224	Composition of the microbial communities in the gastrointestinal tract of perch (<i>Perca) Tj ETQq1 1 0.784314 to 2020, 43, 23-38.</i>	gBT /Ovei 1.9	rlock 10 Tf 5 17
2225	The Role of Ames Dwarfism and Calorie Restriction on Gut Microbiota. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, e1-e8.	3.6	16
2226	Mixedâ€mode bacterial transmission in the common brooding coral <i>Pocillopora acuta</i> Environmental Microbiology, 2020, 22, 397-412.	3.8	31
2227	Stream Algal Biofilm Community Diversity Along An Acid Mine Drainage Recovery Gradient Using Multimarker Metabarcoding. Journal of Phycology, 2020, 56, 11-22.	2.3	8
2228	Symbiodiniaceae probiotics for use in bleaching recovery. Restoration Ecology, 2020, 28, 282-288.	2.9	36
2229	Complex associations between crossâ€kingdom microbial endophytes and host genotype in ash dieback disease dynamics. Journal of Ecology, 2020, 108, 291-309.	4.0	37
2230	Bacterial communities of the reproductive organs of virgin and mated common bedbugs, <i>Cimex lectularius</i> . Ecological Entomology, 2020, 45, 142-154.	2.2	21
2231	Host genotype and amoxicillin administration affect the incidence of diarrhoea and faecal microbiota of weaned piglets during a natural multiresistant ETEC infection. Journal of Animal Breeding and Genetics, 2020, 137, 60-72.	2.0	12
2232	The effect of peracetic acid on microbial community, water quality, nitrification and rainbow trout (Oncorhynchus mykiss) performance in recirculating aquaculture systems. Aquaculture, 2020, 516, 734534.	3.5	25
2233	Analysis of bacterial microbiome associated with nylon and copper nets in an aquaculture context. Aquaculture, 2020, 516, 734540.	3.5	10
2234	Comparative metagenomics of microbial mats from hypersaline lakes at Rottnest Island (WA,) Tj ETQq1 1 0.7843 microbialite accretion. Limnology and Oceanography, 2020, 65, S293.	14 rgBT /C 3.1	Overlock 10 6
2235	Metagenomics coupled with biogeochemical rates measurements provide evidence that nitrate addition stimulates respiration in salt marsh sediments. Limnology and Oceanography, 2020, 65, S321.	3.1	25
2236	Insect-associated bacterial communities in an alpine stream. Hydrobiologia, 2020, 847, 331-344.	2.0	10
2237	Association of Alterations in Intestinal Microbiota With Impaired Psychological Function in Patients With Inflammatory Bowel Diseases in Remission. Clinical Gastroenterology and Hepatology, 2020, 18, 2019-2029.e11.	4.4	64
2238	Long-term exposure of activated sludge in chemostats leads to changes in microbial communities composition and enhanced biodegradation of 4-chloroaniline and N-methylpiperazine. Chemosphere, 2020, 242, 125102.	8.2	12

#	Article	IF	CITATIONS
2239	Fire history and plant community composition outweigh decadal multiâ€factor global change as drivers of microbial composition in an annual grassland. Journal of Ecology, 2020, 108, 611-625.	4.0	19
2240	A single <i>Thaumarchaeon</i> drives nitrification in deep oligotrophic Lake Constance. Environmental Microbiology, 2020, 22, 212-228.	3.8	33
2241	Evaluating Bioinformatic Pipeline Performance for Forensic Microbiome Analysis ^{*,â€,‡} . Journal of Forensic Sciences, 2020, 65, 513-525.	1.6	10
2242	Analysis of leaf microbiome composition of nearâ€isogenic maize lines differing in broadâ€spectrum disease resistance. New Phytologist, 2020, 225, 2152-2165.	7.3	42
2243	Transient exposure to novel high temperatures reshapes coastal phytoplankton communities. ISME Journal, 2020, 14, 413-424.	9.8	29
2244	Increased loading stress leads to convergence of microbial communities and high methane yields in adapted anaerobic co-digesters. Water Research, 2020, 169, 115155.	11.3	13
2245	The Composition and Phosphorus Cycling Potential of Bacterial Communities Associated With Hyphae of Penicillium in Soil Are Strongly Affected by Soil Origin. Frontiers in Microbiology, 2019, 10, 2951.	3.5	19
2246	Inoculum Source Determines Acetate and Lactate Production during Anaerobic Digestion of Sewage Sludge and Food Waste. Bioengineering, 2020, 7, 3.	3.5	28
2247	BCdatabaser: on-the-fly reference database creation for (meta-)barcoding. Bioinformatics, 2020, 36, 2630-2631.	4.1	30
2248	Investigating temporal microbial dynamics in the rumen of beef calves raised on two farms during early life. FEMS Microbiology Ecology, 2020, 96, .	2.7	30
2249	Exercise improves metabolic function and alters the microbiome in rats with gestational diabetes. FASEB Journal, 2020, 34, 1728-1744.	0.5	19
2250	Disparate effects of antibiotic-induced microbiome change and enhanced fitness inÂDaphnia magna. PLoS ONE, 2020, 15, e0214833.	2.5	26
2251	Microbial abundance, composition, and function in nectar are shaped by flower visitor identity. FEMS Microbiology Ecology, 2020, 96, .	2.7	46
2252	What human sperm RNA-Seq tells us about the microbiome. Journal of Assisted Reproduction and Genetics, 2020, 37, 359-368.	2.5	20
2253	Panel 3: Genomics, precision medicine and targeted therapies. International Journal of Pediatric Otorhinolaryngology, 2020, 130, 109835.	1.0	5
2254	Expression of Free Fatty Acid Receptor 2 by Dendritic Cells Prevents Their Expression of Interleukin 27 and Is Required for Maintenance of Mucosal Barrier and Immune Response Against Colorectal Tumors in Mice. Gastroenterology, 2020, 158, 1359-1372.e9.	1.3	54
2255	Colon Cancer Prevention with Walnuts: A Longitudinal Study in Mice from the Perspective of a Gut Enterotype–like Cluster. Cancer Prevention Research, 2020, 13, 15-24.	1.5	3
2256	Postâ€natal coâ€development of the microbiota and gut barrier function follows different paths in the small and large intestine in piglets. FASEB Journal, 2020, 34, 1430-1446.	0.5	26

#	ARTICLE	IF	Citations
2257	Provision of Lipid-Based Nutrient Supplements to Mothers During Pregnancy and 6 Months Postpartum and to Their Infants from 6 to 18 Months Promotes Infant Gut Microbiota Diversity at 18 Months of Age but Not Microbiota Maturation in a Rural Malawian Setting: Secondary Outcomes of a Randomized Trial. Journal of Nutrition, 2020, 150, 918-928.	2.9	23
2258	Unique bacterial assembly, composition, and interactions in a parasitic plant and its host. Journal of Experimental Botany, 2020, 71, 2198-2209.	4.8	22
2259	The olfactory G protein-coupled receptor (Olfr-78/OR51E2) modulates the intestinal response to colitis. American Journal of Physiology - Cell Physiology, 2020, 318, C502-C513.	4.6	26
2260	Microbial imbalance in inflammatory bowel disease patients at different taxonomic levels. Gut Pathogens, 2020, 12, 1.	3.4	230
2261	Involvement of the Gut Microbiota and Barrier Function in Glucocorticoidâ€Induced Osteoporosis. Journal of Bone and Mineral Research, 2020, 35, 801-820.	2.8	101
2262	The impact of food additives, artificial sweeteners and domestic hygiene products on the human gut microbiome and its fibre fermentation capacity. European Journal of Nutrition, 2020, 59, 3213-3230.	3.9	77
2263	Carbon and nitrogen recycling during cyanoHABs in dreissenid-invaded and non-invaded US midwestern lakes and reservoirs. Hydrobiologia, 2020, 847, 939-965.	2.0	8
2264	Development of microbial communities in organochlorine pesticide contaminated soil: A post-reclamation perspective. Applied Soil Ecology, 2020, 150, 103467.	4.3	20
2265	Effect of a bioactive cement on the microbial community in carious dentin after selective caries removal $\hat{a}\in$ An in-vivo study. Journal of Dentistry, 2020, 92, 103264.	4.1	9
2266	Effect of dimethyl disulfide on the sulfur formation and microbial community composition during the biological H2S removal from sour gas streams. Journal of Hazardous Materials, 2020, 386, 121916.	12.4	24
2267	Effects of a Companion Plant on the Formation of Mycorrhizal Propagules in Artemisia tridentata Seedlings. Rangeland Ecology and Management, 2020, 73, 138-146.	2.3	2
2268	Rapid PCR identification of Prevotella copri in an Australian cohort of pregnant women. Journal of Developmental Origins of Health and Disease, 2020, 11, 228-234.	1.4	2
2269	A diverse uncultivated microbial community is responsible for organic matter degradation in the Black Sea sulphidic zone. Environmental Microbiology, 2021, 23, 2709-2728.	3.8	47
2270	Variation in soybean rhizosphere oomycete communities from Michigan fields with contrasting disease pressures. Applied Soil Ecology, 2020, 150, 103435.	4.3	14
2271	Root microbiomes as indicators of seagrass health. FEMS Microbiology Ecology, 2020, 96, .	2.7	38
2272	Microbial Community Composition in Deepâ€Subsurface Reservoir Fluids Reveals Natural Interwell Connectivity. Water Resources Research, 2020, 56, e2019WR025916.	4.2	19
2273	Water quality and associated microbial ecology in selected Alaska Native communities: Challenges in off-the-grid water supplies. Science of the Total Environment, 2020, 711, 134450.	8.0	6
2274	Manganese/ironâ€supported sulfateâ€dependent anaerobic oxidation of methane by archaea in lake sediments. Limnology and Oceanography, 2020, 65, 863-875.	3.1	54

#	Article	IF	CITATIONS
2275	Microbial biomass, marine invertebrate meals and feed restriction influence the biological and gut microbiota response of shrimp Penaeus monodon. Aquaculture, 2020, 520, 734679.	3.5	30
2276	Tillage practices with different soil disturbance shape the rhizosphere bacterial community throughout crop growth. Soil and Tillage Research, 2020, 197, 104501.	5.6	46
2277	Microbial communities of the Laurentian Great Lakes reflect connectivity and local biogeochemistry. Environmental Microbiology, 2020, 22, 433-446.	3.8	34
2278	Microbial signatures of protected and impacted Northern Caribbean reefs: changes from Cuba to the Florida Keys. Environmental Microbiology, 2020, 22, 499-519.	3.8	25
2279	Microbial Signatures and Innate Immune Gene Expression in Lamina Propria Phagocytes of Inflammatory Bowel Disease Patients. Cellular and Molecular Gastroenterology and Hepatology, 2020, 9, 387-402.	4.5	14
2280	Comparing Approaches for Capturing Bacterial Assemblages Associated with Symptomatic (Bacterial) Tj ETQq1 1 90-99.	0.784314 2.7	1 rgBT /Over 7
2281	Genome analysis of sponge symbiont â€~ <i>Candidatus</i> Halichondribacter symbioticus' shows genomic adaptation to a hostâ€dependent lifestyle. Environmental Microbiology, 2020, 22, 483-498.	3.8	20
2282	Fungal endophytic communities of two wild Rosa varieties and the role of an endophytic Seimatosporium sp. in enhancing host plant powdery mildew resistance. Plant and Soil, 2020, 447, 553-564.	3.7	7
2283	Gut microbiome composition and diversity are related to human personality traits. Human Microbiome Journal, 2020, 15, 100069.	3.8	119
2284	Gut microbiota structure differs between honeybees in winter and summer. ISME Journal, 2020, 14, 801-814.	9.8	175
2285	Soil characteristics and land-use drive bacterial community assembly patterns. FEMS Microbiology Ecology, 2020, 96, .	2.7	58
2286	Characterization of gastrointestinal pathologies in the dystonia musculorum mouse model for hereditary sensory and autonomic neuropathy type VI. Neurogastroenterology and Motility, 2020, 32, e13773.	3.0	O
2287	Swift evolutionary response of microbes to a rise in anthropogenic mercury in the Northern Hemisphere. ISME Journal, 2020, 14, 788-800.	9.8	18
2288	<tt>MDiNE</tt> : a model to estimate differential co-occurrence networks in microbiome studies. Bioinformatics, 2020, 36, 1840-1847.	4.1	30
2289	Factors determining microbial colonization of liquid nitrogen storage tanks used for archiving biological samples. Applied Microbiology and Biotechnology, 2020, 104, 131-144.	3.6	11
2290	Immune Dysregulation in the Tonsillar Microenvironment of Periodic Fever, Aphthous Stomatitis, Pharyngitis, Adenitis (PFAPA) Syndrome. Journal of Clinical Immunology, 2020, 40, 179-190.	3.8	19
2291	Influence of terminal electron-accepting conditions on the soil microbial community and degradation of organic contaminants of emerging concern. Science of the Total Environment, 2020, 706, 135327.	8.0	19
2292	Response of prokaryotic communities to extreme precipitation events in an urban coastal lagoon: A case study of Yundang lagoon, China. Science of the Total Environment, 2020, 706, 135937.	8.0	14

#	Article	IF	CITATIONS
2293	The Association Between Smoking and Gut Microbiome in Bangladesh. Nicotine and Tobacco Research, 2020, 22, 1339-1346.	2.6	39
2294	Analysis of the microbial communities in soils of different ages following volcanic eruptions. Pedosphere, 2020, 30, 126-134.	4.0	17
2295	Biowaste-source-dependent synthetic pathways of redox functional groups within humic acids favoring pentachlorophenol dechlorination in composting process. Environment International, 2020, 135, 105380.	10.0	77
2296	Protist Interactions and Community Structure During Early Autumn in the Kerguelen Region (Southern Ocean). Protist, 2020, 171, 125709.	1.5	25
2297	Response of Rhizobacterial Community to Biochar Amendment in Coal Mining Soils with <i>Brachiaria Decumbens</i> as Pioneer Plant. Soil and Sediment Contamination, 2020, 29, 26-42.	1.9	2
2298	Walnuts and Vegetable Oils Containing Oleic Acid Differentially Affect the Gut Microbiota and Associations with Cardiovascular Risk Factors: Follow-up of a Randomized, Controlled, Feeding Trial in Adults at Risk for Cardiovascular Disease. Journal of Nutrition, 2020, 150, 806-817.	2.9	51
2299	Photoperiod Manipulation Affects Transcriptional Profile of Genes Related to Lipid Metabolism and Apoptosis in Zebrafish (Danio rerio) Larvae: Potential Roles of Gut Microbiota. Microbial Ecology, 2020, 79, 933-946.	2.8	16
2300	Soil exposed to silver nanoparticles reveals significant changes in community structure and altered microbial transcriptional profiles. Environmental Pollution, 2020, 258, 113816.	7.5	30
2301	Microbial community shifts in streams receiving treated wastewater effluent. Science of the Total Environment, 2020, 709, 135727.	8.0	52
2302	Age-Related Changes in the Gut Microbiota Modify Brain Lipid Composition. Frontiers in Cellular and Infection Microbiology, 2019, 9, 444.	3.9	50
2303	Depthâ€dependent detritus production in the sponge, <i>Halisarca caerulea</i> Limnology and Oceanography, 2020, 65, 1200-1216.	3.1	24
2304	Variation in the Slimy Salamander (Plethodon spp.) Skin and Gut-Microbial Assemblages Is Explained by Geographic Distance and Host Affinity. Microbial Ecology, 2020, 79, 985-997.	2.8	10
2305	Ecological impact of a rare sugar on grapevine phyllosphere microbial communities. Microbiological Research, 2020, 232, 126387.	5.3	20
2306	Biodiversity of protists and nematodes in the wild nonhuman primate gut. ISME Journal, 2020, 14, 609-622.	9.8	32
2307	Successive passaging of a plant-associated microbiome reveals robust habitat and host genotype-dependent selection. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1148-1159.	7.1	146
2308	Efficient but occasionally imperfect vertical transmission of gut mutualistic protists in a woodâ€feeding termite. Molecular Ecology, 2020, 29, 308-324.	3.9	32
2309	Effects of 12-week treatment with dapagliflozin and gliclazide on faecal microbiome: Results of a double-blind randomized trial in patients with type 2 diabetes. Diabetes and Metabolism, 2020, 46, 164-168.	2.9	43
2310	Spatial variability of sediment methane production and methanogen communities within a eutrophic reservoir: Importance of organic matter source and quantity. Limnology and Oceanography, 2020, 65, 1336-1358.	3.1	50

#	Article	IF	CITATIONS
2311	Unexpected mitochondrial genome diversity revealed by targeted single-cell genomics of heterotrophic flagellated protists. Nature Microbiology, 2020, 5, 154-165.	13.3	44
2312	Bacterial and algal symbiont dynamics in early recruits exposed to two adult coral species. Coral Reefs, 2020, 39, 189-202.	2.2	15
2313	Analysis of gut mycobiota in first-episode, drug-na \tilde{A} -ve Chinese patients with schizophrenia: A pilot study. Behavioural Brain Research, 2020, 379, 112374.	2.2	64
2314	Fungi associated with tree species at an Alberta oil sands reclamation area, as determined by sporocarp assessments and high-throughput DNA sequencing. Applied Soil Ecology, 2020, 147, 103359.	4.3	6
2315	Altered Gut Microbiota and Host Metabolite Profiles in Women With Human Immunodeficiency Virus. Clinical Infectious Diseases, 2020, 71, 2345-2353.	5.8	38
2316	Improvements in Metabolic Syndrome by Xanthohumol Derivatives Are Linked to Altered Gut Microbiota and Bile Acid Metabolism. Molecular Nutrition and Food Research, 2020, 64, e1900789.	3.3	32
2317	Towards centralized biogas plants: Co-digestion of sewage sludge and pig manure maintains process performance and active microbiome diversity. Bioresource Technology, 2020, 297, 122442.	9.6	21
2318	A semi-automated protocol for NGS metabarcoding and fungal analysis in forensic. Forensic Science International, 2020, 306, 110052.	2.2	5
2319	Diarrhea as a Potential Cause and Consequence of Reduced Gut Microbial Diversity Among Undernourished Children in Peru. Clinical Infectious Diseases, 2020, 71, 989-999.	5.8	35
2320	Gut Microbiota Features Associated With Campylobacter Burden and Postnatal Linear Growth Deficits in a Peruvian Birth Cohort. Clinical Infectious Diseases, 2020, 71, 1000-1007.	5.8	25
2321	Further insights in the Tardigrada microbiome: phylogenetic position and prevalence of infection of four new Alphaproteobacteria putative endosymbionts. Zoological Journal of the Linnean Society, 2020, 188, 925-937.	2.3	15
2322	A succession of marine bacterial communities in batch reactor experiments during the degradation of five different petroleum types. Marine Pollution Bulletin, 2020, 150, 110775.	5.0	17
2323	Under temperate climate, the conversion of grassland to arable land affects soil nutrient stocks and bacteria in a short term. Science of the Total Environment, 2020, 703, 135494.	8.0	13
2324	Persistent Gut Microbial Dysbiosis in Children with Acute Lymphoblastic Leukemia (ALL) During Chemotherapy. Microbial Ecology, 2020, 79, 1034-1043.	2.8	40
2325	Differential responses of stream water and bed sediment microbial communities to watershed degradation. Environment International, 2020, 134, 105198.	10.0	46
2326	Analysis of Flagellin-Specific Adaptive Immunity Reveals Links to Dysbiosis in Patients With Inflammatory Bowel Disease. Cellular and Molecular Gastroenterology and Hepatology, 2020, 9, 485-506.	4.5	22
2327	Gut Microbiome Fermentation Determines the Efficacy of Exercise for Diabetes Prevention. Cell Metabolism, 2020, 31, 77-91.e5.	16.2	223
2328	Red and processed meat consumption within two different dietary patterns: Effect on the colon microbial community and volatile metabolites in pigs. Food Research International, 2020, 129, 108793.	6.2	7

#	Article	IF	CITATIONS
2329	Accelerated biodegradation testing of slowly degradable polyesters in soil. Polymer Degradation and Stability, 2020, 171, 109031.	5.8	41
2330	Pyrogenic organic matter effects on soil bacterial community composition. Soil Biology and Biochemistry, 2020, 141, 107678.	8.8	48
2331	Fecal short-chain fatty acids in pregnancy and offspring asthma and allergic outcomes. Journal of Allergy and Clinical Immunology: in Practice, 2020, 8, 1100-1102.e13.	3.8	21
2332	Environmental selection shapes the formation of near-surface groundwater microbiomes. Water Research, 2020, 170, 115341.	11.3	95
2333	Assessing the quality of fresh Whitemouth croaker (<i>Micropogonias furnieri</i>) meat based on microâ€organism and histamine analysis using NGS, qPCR and HPLCâ€DAD. Journal of Applied Microbiology, 2020, 128, 1448-1459.	3.1	6
2334	Effects of nebulized dexamethasone on the respiratory microbiota and mycobiota and relative equine herpesvirus $\hat{a} \in \mathbb{R}$, 2, 4, 5 in an equine model of asthma. Journal of Veterinary Internal Medicine, 2020, 34, 307-321.	1.6	12
2335	Short-Term Nitrogen Fertilization Affects Microbial Community Composition and Nitrogen Mineralization Functions in an Agricultural Soil. Applied and Environmental Microbiology, 2020, 86, .	3.1	49
2336	Structural and Functional Dynamics of Soil Microbes following Spruce Beetle Infestation. Applied and Environmental Microbiology, 2020, 86, .	3.1	14
2337	The Effect of Thermal Stress on the Bacterial Microbiome of Exaiptasia diaphana. Microorganisms, 2020, 8, 20.	3.6	18
2338	Influence of Sampling Site and other Environmental Factors on the Bacterial Community Composition of Domestic Washing Machines. Microorganisms, 2020, 8, 30.	3.6	22
2339	Anaerobic digestion of co-ensiled cover crop and barley straw: Effect of co-ensiling ratios, manure addition and impact on microbial community structure. Industrial Crops and Products, 2020, 144, 112025.	5.2	13
2340	Tomato Genotype Modulates Selection and Responses to Root Microbiota. Phytobiomes Journal, 2020, 4, 314-326.	2.7	17
2341	Paleogenomic insights into the red complex bacteria <i>Tannerella forsythia</i> in Pre-Hispanic and Colonial individuals from Mexico. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190580.	4.0	18
2342	The biogeochemical variability of Arctic thermokarst ponds is reflected by stochastic and nicheâ€driven microbial community assembly processes. Environmental Microbiology, 2020, 22, 4847-4862.	3.8	13
2343	Outbreak of acute larval cyathostominosis – A "perfect storm―of inflammation and dysbiosis. Equine Veterinary Journal, 2021, 53, 727-739.	1.7	22
2344	Gut microbiota degrades toxic isothiocyanates in a flea beetle pest. Molecular Ecology, 2020, 29, 4692-4705.	3.9	39
2345	Migration, pathogens and the avian microbiome: A comparative study in sympatric migrants and residents. Molecular Ecology, 2020, 29, 4706-4720.	3.9	25
2346	Changes in root-associated fungal communities in Triticum aestivum ssp. spelta L. and Triticum aestivum ssp. vulgare L. under drought stress and in various soil processing. PLoS ONE, 2020, 15, e0240037.	2.5	14

#	Article	IF	CITATIONS
2347	Exploring the Role of Macroalgal Surface Metabolites on the Settlement of the Benthic Dinoflagellate Ostreopsis cf. ovata. Frontiers in Marine Science, 2020, 7, .	2.5	10
2348	Microbial Communities of the Shallow-Water Hydrothermal Vent Near Naples, Italy, and Chemosynthetic Symbionts Associated With a Free-Living Marine Nematode. Frontiers in Microbiology, 2020, 11, 2023.	3.5	11
2349	Assessment of Inter-Laboratory Variation in the Characterization and Analysis of the Mucosal Microbiota in Crohn's Disease and Ulcerative Colitis. Frontiers in Microbiology, 2020, 11, 2028.	3.5	8
2350	Cross Inoculation of Rumen Fluid to Improve Dry Matter Disappearance and Its Effect on Bacterial Composition Using an in vitro Batch Culture Model. Frontiers in Microbiology, 2020, 11, 531404.	3.5	2
2351	Analyses of the Bacterial Contamination on Belgian Broiler Carcasses at Retail Level. Frontiers in Microbiology, 2020, $11,539540$.	3.5	9
2352	Warming Climate Is Reducing the Diversity of Dominant Microbes in the Largest High Arctic Lake. Frontiers in Microbiology, 2020, 11, 561194.	3.5	13
2353	Successional Change of the Fungal Microbiome Pine Seedling Roots Inoculated With Tricholoma matsutake. Frontiers in Microbiology, 2020, 11, 574146.	3.5	10
2354	PUMAA: A Platform for Accessible Microbiome Analysis in the Undergraduate Classroom. Frontiers in Microbiology, 2020, 11, 584699.	3.5	10
2355	An Overview of Bioinformatics Tools for DNA Meta-Barcoding Analysis of Microbial Communities of Bioaerosols: Digest for Microbiologists. Life, 2020, 10, 185.	2.4	4
2356	Effects of simulated drought on biological soil quality, microbial diversity and yields under long-term conventional and organic agriculture. FEMS Microbiology Ecology, 2020, 96, .	2.7	26
2357	An Improved hgcAB Primer Set and Direct High-Throughput Sequencing Expand Hg-Methylator Diversity in Nature. Frontiers in Microbiology, 2020, 11, 541554.	3.5	33
2358	Environmental and Microbial Interactions Shape Methane-Oxidizing Bacterial Communities in a Stratified Lake. Frontiers in Microbiology, 2020, 11, 579427.	3.5	18
2359	Effects of the husky oil spill on gut microbiota of native fishes in the North Saskatchewan River, Canada. Aquatic Toxicology, 2020, 229, 105658.	4.0	16
2360	Gastroprotective effect of Lycium barbarum polysaccharides and C-phycocyanin in rats with ethanol-induced gastric ulcer. International Journal of Biological Macromolecules, 2020, 165, 1519-1528.	7.5	30
2361	Microbiome dynamics and genomic determinants of bovine mastitis. Genomics, 2020, 112, 5188-5203.	2.9	41
2362	The Nasopharyngeal and Gut Microbiota in Children in a Pediatric Otolaryngology Practice. Pediatric Infectious Disease Journal, 2020, 39, e226-e233.	2.0	10
2363	Microbial succession from a subsequent secondary death event following mass mortality. BMC Microbiology, 2020, 20, 309.	3.3	15
2364	Antibiotic affects the gut microbiota composition and expression of genes related to lipid metabolism and myofiber types in skeletal muscle of piglets. BMC Veterinary Research, 2020, 16, 392.	1.9	14

#	Article	IF	CITATIONS
2365	Microbiota characterization in Blastocystis-colonized and Blastocystis-free school-age children from Colombia. Parasites and Vectors, 2020, 13, 521.	2.5	15
2366	Ontogeny, species identity, and environment dominate microbiome dynamics in wild populations of kissing bugs (Triatominae). Microbiome, 2020, 8, 146.	11.1	25
2367	Trichomes form genotype-specific microbial hotspots in the phyllosphere of tomato. Environmental Microbiomes, 2020, 15, 17.	5.0	14
2368	The "Plastisphere―of Biodegradable Plastics Is Characterized by Specific Microbial Taxa of Alpine and Arctic Soils. Frontiers in Environmental Science, 2020, 8, .	3.3	54
2369	Metagenomic Characterization of the Microbiome and Resistome of Retail Ground Beef Products. Frontiers in Microbiology, 2020, 11, 541972.	3.5	12
2370	A metagenome-wide association study of gut microbiome and visceral fat accumulation. Computational and Structural Biotechnology Journal, 2020, 18, 2596-2609.	4.1	36
2371	Progression of nasopharyngeal and tracheal bacterial microbiotas of feedlot cattle during development of bovine respiratory disease. Veterinary Microbiology, 2020, 248, 108826.	1.9	22
2372	Multiomic features associated with mucosal healing and inflammation in paediatric Crohn's disease. Alimentary Pharmacology and Therapeutics, 2020, 52, 1491-1502.	3.7	20
2373	Longitudinal Metatranscriptomic Analysis of a Meat Spoilage Microbiome Detects Abundant Continued Fermentation and Environmental Stress Responses during Shelf Life and Beyond. Applied and Environmental Microbiology, 2020, 86, .	3.1	11
2374	Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. Cell, 2020, 183, 666-683.e17.	28.9	211
2375	Breeding selection imposed a differential selective pressure on the wheat root-associated microbiome. FEMS Microbiology Ecology, 2020, 96, .	2.7	24
2376	Prophylactic <i>Faecalibacterium prausnitzii</i> treatment prevents the acute breakdown of colonic epithelial barrier in a preclinical model of pelvic radiation disease. Gut Microbes, 2020, 12, 1812867.	9.8	22
2377	The Znt7-null mutation has sex dependent effects on the gut microbiota and goblet cell population in the mouse colon. PLoS ONE, 2020, 15, e0239681.	2.5	3
2378	Coral-Associated Viral Assemblages From the Central Red Sea Align With Host Species and Contribute to Holobiont Genetic Diversity. Frontiers in Microbiology, 2020, 11, 572534.	3.5	16
2379	Soil microbial community restructuring and functional changes in ancient kauri (Agathis australis) forests impacted by the invasive pathogen Phytophthora agathidicida. Soil Biology and Biochemistry, 2020, 150, 108016.	8.8	17
2380	Disruptions of Anaerobic Gut Bacteria Are Associated with Stroke and Post-stroke Infection: a Prospective Case–Control Study. Translational Stroke Research, 2021, 12, 581-592.	4.2	75
2381	TNF Receptor 1 Promotes Early-Life Immunity and Protects against Colitis in Mice. Cell Reports, 2020, 33, 108275.	6.4	10
2382	Effects of chronic exposure to water accommodated fraction (WAF) of light crude oil on gut microbiota composition of the lined sole (Achirus lineatus). Marine Environmental Research, 2020, 161, 105116.	2.5	17

#	Article	IF	CITATIONS
2383	A Potential Role for Stress-Induced Microbial Alterations in IgA-Associated Irritable Bowel Syndrome with Diarrhea. Cell Reports Medicine, 2020, 1, 100124.	6.5	24
2384	Parameters influencing the development of highly conductive and efficient biofilm during microbial electrosynthesis: the importance of applied potential and inorganic carbon source. Npj Biofilms and Microbiomes, 2020, 6, 40.	6.4	45
2385	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. PLoS ONE, 2020, 15, e0239677.	2.5	13
2386	A pioneer calf foetus microbiome. Scientific Reports, 2020, 10, 17712.	3.3	34
2387	Analysis of 16S rRNA genes reveals reduced Fusobacterial community diversity when translocating from saliva to GI sites. Gut Microbes, 2020, 12, 1814120.	9.8	13
2388	A systematic review on bacterial community changes after periodontal therapy with and without systemic antibiotics: An analysis with a wider lens. Journal of Periodontal Research, 2020, 55, 785-800.	2.7	7
2389	Immune Response and Microbiota Profiles during Coinfection with Plasmodium vivax and Soil-Transmitted Helminths. MBio, 2020, 11 , .	4.1	18
2390	Interpretations of Environmental Microbial Community Studies Are Biased by the Selected 16S rRNA (Gene) Amplicon Sequencing Pipeline. Frontiers in Microbiology, 2020, 11, 550420.	3.5	113
2391	Stimulation of methanogenesis in bituminous coal from the upper Silesian coal basin. International Journal of Coal Geology, 2020, 231, 103609.	5.0	8
2392	Strong shifts in microbial community structure are associated with increased litter input rather than temperature in High Arctic soils. Soil Biology and Biochemistry, 2020, 151, 108054.	8.8	28
2393	Influence of probiotic supplementation on the developing microbiota in human preterm neonates. Gut Microbes, 2020, 12, 1826747.	9.8	26
2394	Phragmites australis Associates with Belowground Fungal Communities Characterized by High Diversity and Pathogen Abundance. Diversity, 2020, 12, 363.	1.7	8
2395	Adaption of microbial communities to the hostile environment in the Doce River after the collapse of two iron ore tailing dams. Heliyon, 2020, 6, e04778.	3.2	10
2396	A New "Business as Usual―Climate Scenario and the Stress Response of the Caribbean Coral Montastraea cavernosa. Frontiers in Marine Science, 2020, 7, .	2.5	1
2397	Environmental contamination alters the intestinal microbial community of the livebearer killifish Phalloceros caudimaculatus. Heliyon, 2020, 6, e04190.	3.2	13
2398	The wasted chewing gum bacteriome. Scientific Reports, 2020, 10, 16846.	3.3	10
2399	Plant pathological condition is associated with fungal community succession triggered by root exudates in the plant-soil system. Soil Biology and Biochemistry, 2020, 151, 108046.	8.8	33
2400	Intranasal Application of Lactococcus lactis W136 Is Safe in Chronic Rhinosinusitis Patients With Previous Sinus Surgery. Frontiers in Cellular and Infection Microbiology, 2020, 10, 440.	3.9	26

#	Article	IF	CITATIONS
2401	An Assessment of the Stability of the Canine Oral Microbiota After Probiotic Administration in Healthy Dogs Over Time. Frontiers in Veterinary Science, 2020, 7, 616.	2.2	11
2402	Seasonal and Nutrient Supplement Responses in Rumen Microbiota Structure and Metabolites of Tropical Rangeland Cattle. Microorganisms, 2020, 8, 1550.	3.6	19
2403	Effects of nitrogen and phosphorus addition on microbial community composition and element cycling in a grassland soil. Soil Biology and Biochemistry, 2020, 151, 108041.	8.8	103
2404	Impact of a resistance gene against a fungal pathogen on the plant host residue microbiome: The case of the ⟨i⟩Leptosphaeria maculans–Brassica napus⟨/i⟩ pathosystem. Molecular Plant Pathology, 2020, 21, 1545-1558.	4.2	9
2405	Early-life gut dysbiosis linked to juvenile mortality in ostriches. Microbiome, 2020, 8, 147.	11.1	30
2406	Fungal Community, Metabolic Diversity, and Glomalin-Related Soil Proteins (GRSP) Content in Soil Contaminated With Crude Oil After Long-Term Natural Bioremediation. Frontiers in Microbiology, 2020, 11, 572314.	3.5	28
2407	Grow - Store - Steam - Re-peat: Reuse of spent growing media for circular cultivation of Chrysanthemum. Journal of Cleaner Production, 2020, 276, 124128.	9.3	29
2408	Laboratory and Field Testing Assessment of Next Generation Biocide-Free, Fouling-Resistant Slippery Coatings. ACS Applied Polymer Materials, 2020, 2, 5147-5162.	4.4	14
2409	Temporal dynamics of bacterial communities during seed development and maturation. FEMS Microbiology Ecology, 2020, 96, .	2.7	43
2410	A comprehensive analysis of the microbiota composition and gene expression in colorectal cancer. BMC Microbiology, 2020, 20, 308.	3.3	17
2411	Nutrients and Pharmaceuticals Structure Bacterial Core Communities in Urban and Montane Stream Biofilms. Frontiers in Microbiology, 2020, $11,526545$.	3.5	4
2412	Fermentation profile, microbial populations, taxonomic diversity and aerobic stability of total mixed ration silages based on Cactus and Gliricidia. Journal of Agricultural Science, 2020, 158, 396-405.	1.3	8
2413	eHealth: Disease activity measures are related to the faecal gut microbiota in adult patients with ulcerative colitis. Scandinavian Journal of Gastroenterology, 2020, 55, 1291-1300.	1.5	5
2414	Assessing the Variation within the Oral Microbiome of Healthy Adults. MSphere, 2020, 5, .	2.9	49
2415	Taxonomic profiling of individual nematodes isolated from copse soils using deep amplicon sequencing of four distinct regions of the 18S ribosomal RNA gene. PLoS ONE, 2020, 15, e0240336.	2.5	12
2416	Early Inoculation of Microbial Suspension in Suckling Piglets Affects the Transmission of Maternal Microbiota and the Associated Antibiotic Resistance Genes. Microorganisms, 2020, 8, 1576.	3.6	3
2417	Gut Microbiome in Children from Indigenous and Urban Communities in México: Different Subsistence Models, Different Microbiomes. Microorganisms, 2020, 8, 1592.	3.6	13
2418	Panâ€regional marine benthic cryptobiome biodiversity patterns revealed by metabarcoding Autonomous Reef Monitoring Structures. Molecular Ecology, 2020, 29, 4882-4897.	3.9	19

#	Article	IF	CITATIONS
2419	Fecal Microbiota Transplant in Two Ulcerative Colitis Pediatric Cases: Gut Microbiota and Clinical Course Correlations. Microorganisms, 2020, 8, 1486.	3.6	18
2420	Is a Central Sediment Sample Sufficient? Exploring Spatial and Temporal Microbial Diversity in a Small Lake. Toxins, 2020, 12, 580.	3.4	14
2421	Clostridioides difficile carriage in animals and the associated changes in the host fecal microbiota. Anaerobe, 2020, 66, 102279.	2.1	8
2422	An intensive multilocation temporal dataset of fungal and bacterial communities in the root and rhizosphere of Brassica napus. Data in Brief, 2020, 31, 106143.	1.0	5
2423	Profiling of bacterial assemblages in the marine cage farm environment, with implications on fish, human and ecosystem health. Ecological Indicators, 2020, 118, 106785.	6.3	16
2424	Evaluating Sardinella brasiliensis quality indicators through the quantification of histamine and bacterial communities. Heliyon, 2020, 6, e04461.	3.2	8
2425	Alterations in the gut-associated microbiota of juvenile Caribbean spiny lobsters Panulirus argus (Latreille, 1804) infected with PaV1. Journal of Invertebrate Pathology, 2020, 176, 107457.	3.2	5
2426	A reasonable correlation between cloacal and cecal microbiomes in broiler chickens. Poultry Science, 2020, 99, 6062-6070.	3.4	13
2427	Changes in soil microbial communities in post mine ecological restoration: Implications for monitoring using high throughput DNA sequencing. Science of the Total Environment, 2020, 749, 142262.	8.0	33
2428	Microbiota Supplementation with Bifidobacterium and Lactobacillus Modifies the Preterm Infant Gut Microbiota and Metabolome: An Observational Study. Cell Reports Medicine, 2020, 1, 100077.	6.5	119
2429	Impact of coagulation–ultrafiltration on long-term pipe biofilm dynamics in a full-scale chloraminated drinking water distribution system. Environmental Science: Water Research and Technology, 2020, 6, 3044-3056.	2.4	2
2430	Enhanced microbial degradation of irradiated cellulose under hyperalkaline conditions. FEMS Microbiology Ecology, 2020, 96, .	2.7	9
2431	A converging subset of soil bacterial taxa is permissive to the IncP-1 plasmid pKJK5 across a range of soil copper contamination. FEMS Microbiology Ecology, 2020, 96, .	2.7	9
2432	The Urinary Tract Microbiome in Older Women Exhibits Host Genetic and Environmental Influences. Cell Host and Microbe, 2020, 28, 298-305.e3.	11.0	45
2433	Microglia Require CD4ÂT Cells to Complete the Fetal-to-Adult Transition. Cell, 2020, 182, 625-640.e24.	28.9	191
2434	Allopatric and Sympatric Drivers of Speciation in <i>Alviniconcha</i> Hydrothermal Vent Snails. Molecular Biology and Evolution, 2020, 37, 3469-3484.	8.9	27
2435	Community assembly of the native <scp><i>C</i>. <i>elegans</i></scp> microbiome is influenced by time, substrate and individual bacterial taxa. Environmental Microbiology, 2020, 22, 1265-1279.	3.8	39
2436	Sponge microbiome stability during environmental acquisition of highly specific photosymbionts. Environmental Microbiology, 2020, 22, 3593-3607.	3.8	20

#	Article	IF	CITATIONS
2437	Gut microbiota maturation during early human life induces enterocyte proliferation via microbial metabolites. BMC Microbiology, 2020, 20, 205.	3.3	25
2438	Saccharomyces cerevisiae fermentation products (SCFP) stabilize the ruminal microbiota of lactating dairy cows during periods of a depressed rumen pH. BMC Veterinary Research, 2020, 16, 237.	1.9	22
2439	Metagenomic analysis of gut microbiome and resistome of diarrheal fecal samples from Kolkata, India, reveals the core and variable microbiota including signatures of microbial dark matter. Gut Pathogens, 2020, 12, 32.	3.4	34
2440	Syntrophic acetate oxidation replaces acetoclastic methanogenesis during thermophilic digestion of biowaste. Microbiome, 2020, 8, 105.	11.1	118
2441	The sources and transmission routes of microbial populations throughout a meat processing facility. Npj Biofilms and Microbiomes, 2020, 6, 26.	6.4	63
2442	Niche- and Gender-Dependent Immune Reactions in Relation to the Microbiota Profile in Pediatric Patients with Otitis Media with Effusion. Infection and Immunity, 2020, 88, .	2.2	12
2443	Untargeted Metagenomic Investigation of the Airway Microbiome of Cystic Fibrosis Patients with Moderate-Severe Lung Disease. Microorganisms, 2020, 8, 1003.	3.6	23
2444	The Intestinal Microbiome Restricts Alphavirus Infection and Dissemination through a Bile Acid-Type I IFN Signaling Axis. Cell, 2020, 182, 901-918.e18.	28.9	98
2445	Comprehensive metagenomic insights into a unique mass gathering and bathing event reveals transient influence on a riverine ecosystem. Ecotoxicology and Environmental Safety, 2020, 202, 110938.	6.0	5
2446	Nest microbiota and pathogen abundance in sea turtle hatcheries. Fungal Ecology, 2020, 47, 100964.	1.6	21
2447	Helminth-Induced and Th2-Dependent Alterations of the Gut Microbiota Attenuate Obesity Caused by High-Fat Diet. Cellular and Molecular Gastroenterology and Hepatology, 2020, 10, 763-778.	4.5	27
2448	The supplementation of a corn/barley-based diet with bacterial xylanase did not prevent diarrhoea of ETEC susceptible piglets, but favoured the persistence of Lactobacillus reuteri in the gut. Livestock Science, 2020, 240, 104161.	1.6	4
2449	Colonization kinetics and implantation follow-up of the sewage microbiome in an urban wastewater treatment plant. Scientific Reports, 2020, 10, 11634.	3.3	17
2450	The bacterioplankton community composition and a host genotype dependent occurrence of taxa shape the Daphnia magna gut bacterial community. FEMS Microbiology Ecology, 2020, 96, .	2.7	29
2451	Gut microbiota in a host–brood parasite system: insights from common cuckoos raised by two warbler species. FEMS Microbiology Ecology, 2020, 96, .	2.7	9
2452	CeMbio - The <i>Caenorhabditis elegans</i> Microbiome Resource. G3: Genes, Genomes, Genetics, 2020, 10, 3025-3039.	1.8	96
2453	Denosumab Regulates Gut Microbiota Composition and Cytokines in Dinitrobenzene Sulfonic Acid (DNBS)-Experimental Colitis. Frontiers in Microbiology, 2020, 11, 1405.	3.5	8
2454	Abnormal Food Timing Promotes Alcohol-Associated Dysbiosis and Colon Carcinogenesis Pathways. Frontiers in Oncology, 2020, 10, 1029.	2.8	5

#	Article	IF	CITATIONS
2455	Host Genotype and Colonist Arrival Order Jointly Govern Plant Microbiome Composition and Function. Current Biology, 2020, 30, 3260-3266.e5.	3.9	55
2456	Metabolically-active bacteria in reclaimed water and ponds revealed using bromodeoxyuridine DNA labeling coupled with 16S rRNA and shotgun sequencing. Water Research, 2020, 184, 116185.	11.3	11
2457	Gramâ€negative Microbiota Blooms in Premature Twins Discordant for Parenteral Nutritionâ€associated Cholestasis. Journal of Pediatric Gastroenterology and Nutrition, 2020, 70, 640-644.	1.8	4
2458	Reconstructing marine plankton food web interactions using DNA metabarcoding. Molecular Ecology, 2020, 29, 3380-3395.	3.9	46
2459	Methane Seeps and Independent Methane Plumes in the South China Sea Offshore Taiwan. Frontiers in Marine Science, 2020, 7, .	2.5	12
2460	No correlation between microbiota composition and blood parameters in nesting flatback turtles (Natator depressus). Scientific Reports, 2020, 10, 8333.	3.3	7
2461	Releasing the microbes from old bones: the effect of different DNA extraction protocols on microbial community profiling. Science and Technology of Archaeological Research, 2020, 6, 1-15.	2.4	2
2462	Impact of land use history on the arbuscular mycorrhizal fungal diversity in arid soils of Argentinean farming fields. FEMS Microbiology Letters, 2020, 367, .	1.8	9
2463	Oral or Topical Exposure to Glyphosate in Herbicide Formulation Impacts the Gut Microbiota and Survival Rates of Honey Bees. Applied and Environmental Microbiology, 2020, 86, .	3.1	78
2464	Co-infection of Chicken Layers With Histomonas meleagridis and Avian Pathogenic Escherichia coli Is Associated With Dysbiosis, Cecal Colonization and Translocation of the Bacteria From the Gut Lumen. Frontiers in Microbiology, 2020, 11, 586437.	3.5	16
2465	The Transition From Stochastic to Deterministic Bacterial Community Assembly During Permafrost Thaw Succession. Frontiers in Microbiology, 2020, 11, 596589.	3.5	29
2466	Maternal Linoleic Acid Overconsumption Alters Offspring Gut and Adipose Tissue Homeostasis in Young but Not Older Adult Rats. Nutrients, 2020, 12, 3451.	4.1	5
2467	Jumping the green wall: The use of PNAâ€DNA clamps to enhance microbiome sampling depth in wildlife microbiome research. Ecology and Evolution, 2020, 10, 11779-11786.	1.9	3
2468	Biogeography and Diversity of Multi-Trophic Root Zone Microbiomes in Michigan Apple Orchards: Analysis of Rootstock, Scion, and Local Growing Region. Phytobiomes Journal, 2020, 4, 122-132.	2.7	8
2469	Breeding farm, level of feeding and presence of antibiotics in the feed influence rabbit cecal microbiota. Animal Microbiome, 2020, 2, 40.	3.8	15
2470	Fecal Microbiota Characterization of Seychelles Giant Tortoises (Aldabrachelys gigantea) Living in Both Wild and Controlled Environments. Frontiers in Microbiology, 2020, 11, 569249.	3.5	12
2471	Functional Seasonality of Free-Living and Particle-Associated Prokaryotic Communities in the Coastal Adriatic Sea. Frontiers in Microbiology, 2020, 11, 584222.	3.5	9
2472	Early Life Inoculation With Adult-Derived Microbiota Accelerates Maturation of Intestinal Microbiota and Enhances NK Cell Activation in Broiler Chickens. Frontiers in Veterinary Science, 2020, 7, 584561.	2.2	22

#	Article	IF	CITATIONS
2473	Bacterial Respiration Used as a Proxy to Evaluate the Bacterial Load in Cooling Towers. Sensors, 2020, 20, 6398.	3.8	0
2474	Search for Viral Infections in Cerebrospinal Fluid From Patients With Autoimmune Encephalitis. Open Forum Infectious Diseases, 2020, 7, ofaa468.	0.9	6
2475	Chemical Profiling Provides Insights into the Metabolic Machinery of Hydrocarbon-Degrading Deep-Sea Microbes. MSystems, 2020, 5, .	3.8	16
2476	The Microbiome of Leonardo da Vinci's Drawings: A Bio-Archive of Their History. Frontiers in Microbiology, 2020, 11, 593401.	3.5	24
2477	Can toxin warfare against fungal parasitism influence short-term Dolichospermum bloom dynamics? – A field observation. Harmful Algae, 2020, 99, 101915.	4.8	7
2478	Locality Effect of Coral-Associated Bacterial Community in the Kuroshio Current From Taiwan to Japan. Frontiers in Ecology and Evolution, 2020, 8, .	2.2	8
2479	Microbial Signatures in Deep CO2-Saturated Miocene Sediments of the Active HartouÅiov Mofette System (NW Czech Republic). Frontiers in Microbiology, 2020, 11, 543260.	3.5	5
2480	Early Gut Fungal and Bacterial Microbiota and Childhood Growth. Frontiers in Pediatrics, 2020, 8, 572538.	1.9	13
2481	Differences in Gut Microbiome in Hospitalized Immunocompetent vs. Immunocompromised Children, Including Those With Sickle Cell Disease. Frontiers in Pediatrics, 2020, 8, 583446.	1.9	12
2482	Characterization of Endophytic Microbial Communities in Store-Bought Kale Evaluated by Different Plant Tissue Homogenization Methods. Phytobiomes Journal, 2020, 4, 211-216.	2.7	3
2483	Functional Gene Expression in Shark Bay Hypersaline Microbial Mats: Adaptive Responses. Frontiers in Microbiology, 2020, 11, 560336.	3.5	20
2484	The Native Microbiome is Crucial for Offspring Generation and Fitness of <i>Aurelia aurita</i> . MBio, 2020, 11, .	4.1	25
2485	Indole-3-lactic acid associated with Bifidobacterium-dominated microbiota significantly decreases inflammation in intestinal epithelial cells. BMC Microbiology, 2020, 20, 357.	3.3	117
2486	Genetic selection for growth drives differences in intestinal microbiota composition and parasite disease resistance in gilthead sea bream. Microbiome, 2020, 8, 168.	11.1	48
2487	Perinatal environment shapes microbiota colonization and infant growth: impact on host response and intestinal function. Microbiome, 2020, 8, 167.	11.1	53
2488	Dynamics of the bacterial gut microbiota during controlled human infection with Necator americanus larvae. Gut Microbes, 2020, 12, 1840764.	9.8	6
2489	Vertical Stratification in Urban Green Space Aerobiomes. Environmental Health Perspectives, 2020, 128, 117008.	6.0	35
2490	The Response of Estuarine Ammonia-Oxidizing Communities to Constant and Fluctuating Salinity Regimes. Frontiers in Microbiology, 2020, 11, 574815.	3.5	5

#	Article	IF	CITATIONS
2491	Oral Health, Oral Microbiota, and Incidence of Stroke-Associated Pneumoniaâ€"A Prospective Observational Study. Frontiers in Neurology, 2020, 11, 528056.	2.4	20
2492	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. Microorganisms, 2020, 8, 1861.	3.6	4
2493	Alterations of the gut bacterial microbiota in rhesus macaques with SIV infection and on short- or long-term antiretroviral therapy. Scientific Reports, 2020, 10, 19056.	3.3	18
2494	The Epidome - a species-specific approach to assess the population structure and heterogeneity of Staphylococcus epidermidis colonization and infection. BMC Microbiology, 2020, 20, 362.	3.3	8
2495	Temporal changes in water temperature and salinity drive the formation of a reversible plastic-specific microbial community. FEMS Microbiology Ecology, 2020, 96, .	2.7	27
2496	Ozone Decreased Enteric Methane Production by 20% in an in vitro Rumen Fermentation System. Frontiers in Microbiology, 2020, 11, 571537.	3.5	5
2497	Prokaryotic Diversity and Distribution Along Physical and Nutrient Gradients in the Tunisian Coastal Waters (South Mediterranean Sea). Frontiers in Microbiology, 2020, 11, 593540.	3.5	9
2498	Enhancing Phenol Conversion Rates in Saline Anaerobic Membrane Bioreactor Using Acetate and Butyrate as Additional Carbon and Energy Sources. Frontiers in Microbiology, 2020, 11, 604173.	3.5	10
2499	Anaerobic Respiration of NOX1-Derived Hydrogen Peroxide Licenses Bacterial Growth at the Colonic Surface. Cell Host and Microbe, 2020, 28, 789-797.e5.	11.0	41
2500	The ecogenomics of dsDNA bacteriophages in feces of stabled and feral horses. Computational and Structural Biotechnology Journal, 2020, 18, 3457-3467.	4.1	14
2501	Delivery mode and gut microbial changes correlate with an increased risk of childhood asthma. Science Translational Medicine, 2020, 12, .	12.4	92
2502	Effects of Sex and Diet on Gut Microbiota of Farmland-Dependent Wintering Birds. Frontiers in Microbiology, 2020, 11, 587873.	3.5	25
2503	Preterm Infants Harbour a Rapidly Changing Mycobiota That Includes Candida Pathobionts. Journal of Fungi (Basel, Switzerland), 2020, 6, 273.	3.5	21
2504	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. Nature Communications, 2020, 11 , 5773.	12.8	55
2505	Zero-Valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water. Frontiers in Environmental Science, 2020, 8, .	3.3	7
2506	Microbiome Profiling Reveals a Microbial Dysbiosis During a Natural Outbreak of Tenacibaculosis (Yellow Mouth) in Atlantic Salmon. Frontiers in Microbiology, 2020, 11, 586387.	3.5	32
2507	Diversity Assessment of Toxic Cyanobacterial Blooms during Oxidation. Toxins, 2020, 12, 728.	3.4	22
2508	Characterizing the cirri and gut microbiomes of the intertidal barnacle Semibalanus balanoides. Animal Microbiome, 2020, 2, 41.	3.8	1

#	Article	IF	CITATIONS
2509	Determining Soil Microbial Communities and Their Influence on Ganoderma Disease Incidences in Oil Palm (Elaeis guineensis) via High-Throughput Sequencing. Biology, 2020, 9, 424.	2.8	16
2510	New Insights into the Microbial Profiles of Infected Root Canals in Traumatized Teeth. Journal of Clinical Medicine, 2020, 9, 3877.	2.4	11
2511	16S rRNA gene amplicon dataset of prokaryotic communities from a subantarctic marine ecosystem: Ushuaia Bay and surrounding waters. Data in Brief, 2020, 32, 106171.	1.0	0
2512	Activity and Diversity of Microorganisms in Root Zone of Plant Species Spontaneously Inhabiting Smelter Waste Piles. Molecules, 2020, 25, 5638.	3.8	16
2513	Pomegranate Metabolites Impact Tryptophan Metabolism in Humans and Mice. Current Developments in Nutrition, 2020, 4, nzaa165.	0.3	12
2514	Dietary muramidase degrades bacterial peptidoglycan to NOD-activating muramyl dipeptides and reduces duodenal inflammation in broiler chickens. British Journal of Nutrition, 2021, 126, 641-651.	2.3	13
2515	Response of Horticultural Soil Microbiota to Different Fertilization Practices. Plants, 2020, 9, 1501.	3.5	12
2516	The hemolymph of <i>Biomphalaria</i> snail vectors of schistosomiasis supports a diverse microbiome. Environmental Microbiology, 2020, 22, 5450-5466.	3.8	9
2517	Urban Aerobiomes are Influenced by Season, Vegetation, and Individual Site Characteristics. EcoHealth, 2021, 18, 331-344.	2.0	12
2518	Evaluating the Microbiome of Hemp. Phytobiomes Journal, 2020, 4, 351-363.	2.7	12
2519	Fine Particulate Matter Exposure Alters Pulmonary Microbiota Composition and Aggravates Pneumococcus-Induced Lung Pathogenesis. Frontiers in Cell and Developmental Biology, 2020, 8, 570484.	3.7	23
2520	Microbiome Profiling Reveals Gut Dysbiosis in the Metabotropic Glutamate Receptor 5 Knockout Mouse Model of Schizophrenia. Frontiers in Cell and Developmental Biology, 2020, 8, 582320.	3.7	16
2521	New Frontiers of Anaerobic Hydrocarbon Biodegradation in the Multi-Omics Era. Frontiers in Microbiology, 2020, 11, 590049.	3.5	33
2522	Effect of Mycorrhizal Inoculation and Irrigation on Biological Properties of Sweet Pepper Rhizosphere in Organic Field Cultivation. Agronomy, 2020, 10, 1693.	3.0	8
2523	Identification of Vaginal Microbial Communities Associated with Extreme Cervical Shortening in Pregnant Women. Journal of Clinical Medicine, 2020, 9, 3621.	2.4	12
2524	Decisionâ€making and best practices for taxonomyâ€free environmental DNA metabarcoding in biomonitoring using Hill numbers. Molecular Ecology, 2021, 30, 3326-3339.	3.9	32
2525	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. Genome Biology, 2020, 21, 191.	8.8	67
2526	Composition and Diversity of Natural Bacterial Communities in Mabisi, a Traditionally Fermented Milk. Frontiers in Microbiology, 2020, 11, 1816.	3.5	20

#	Article	IF	Citations
2527	Time since deglaciation and geomorphological disturbances determine the patterns of geochemical, mineralogical and microbial successions in an Icelandic foreland. Geoderma, 2020, 379, 114578.	5.1	15
2528	A large-scale assessment of lakes reveals a pervasive signal of land use on bacterial communities. ISME Journal, 2020, 14, 3011-3023.	9.8	51
2529	Effects of a chemical additive on the fermentation, microbial communities, and aerobic stability of corn silage with or without air stress during storage. Journal of Animal Science, 2020, 98, .	0.5	20
2530	Host plants and <i>Wolbachia</i> shape the population genetics of sympatric herbivore populations. Evolutionary Applications, 2020, 13, 2740-2753.	3.1	13
2531	Modulation of the intestinal microbiota of broilers supplemented with monensin or functional oils in response to challenge by Eimeria spp PLoS ONE, 2020, 15, e0237118.	2.5	16
2532	Microbiota Changes Due to Grape Seed Extract Diet Improved Intestinal Homeostasis and Decreased Fatness in Parental Broiler Hens. Microorganisms, 2020, 8, 1141.	3.6	8
2533	Energy efficiency and biofouling control in a pilot-scale membrane bioreactor using low-frequency reciprocating motion and the succession of biofilm communities resistant to mechanical shear. Bioresource Technology Reports, 2020, 11, 100523.	2.7	6
2534	Distinct mechanisms underlying the assembly of microeukaryotic generalists and specialists in an anthropogenically impacted river. Science of the Total Environment, 2020, 748, 141434.	8.0	49
2535	Composition and activity of nitrifier communities in soil are unresponsive to elevated temperature and CO2, but strongly affected by drought. ISME Journal, 2020, 14, 3038-3053.	9.8	43
2536	Seasonal dynamics of prokaryotes and their associations with diatoms in the Southern Ocean as revealed by an autonomous sampler. Environmental Microbiology, 2020, 22, 3968-3984.	3.8	41
2537	Raw milk and fecal microbiota of commercial Alpine dairy cows varies with herd, fat content and diet. PLoS ONE, 2020, 15, e0237262.	2.5	13
2538	Oral microbiome composition, but not diversity, is associated with adolescent anxiety and depression symptoms. Physiology and Behavior, 2020, 226, 113126.	2.1	51
2539	Versatile cyanobacteria control the timing and extent of sulfide production in a Proterozoic analog microbial mat. ISME Journal, 2020, 14, 3024-3037.	9.8	14
2540	The Gut Microbiome Associates with Immune Checkpoint Inhibition Outcomes in Patients with Advanced Non–Small Cell Lung Cancer. Cancer Immunology Research, 2020, 8, 1243-1250.	3.4	154
2541	Biomethanation processes: new insights on the effect of a high H2 partial pressure on microbial communities. Biotechnology for Biofuels, 2020, 13, 141.	6.2	45
2542	Environmental shaping of the bacterial and fungal community in infant bed dust and correlations with the airway microbiota. Microbiome, 2020, 8, 115.	11.1	36
2543	Lack of significant differences between gastrointestinal tract microbial population structure of Helicobacter pylori â€infected subjects before and 2Âyears after a single eradication event. Helicobacter, 2020, 25, e12748.	3.5	6
2544	SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis. BMC Bioinformatics, 2020, 21, 345.	2.6	41

#	Article	IF	CITATIONS
2545	Investigation of the Ecological Roles of Putative Keystone Taxa during Tailing Revegetation. Environmental Science & Environme	10.0	62
2546	Bacterial and Fungal Dynamics During the Fermentation Process of Sesotho, a Traditional Beer of Southern Africa. Frontiers in Microbiology, 2020, 11, 1451.	3.5	22
2547	Size resolved characteristics of urban and suburban bacterial bioaerosols in Japan as assessed by 16S rRNA amplicon sequencing. Scientific Reports, 2020, 10, 12406.	3.3	17
2548	Biologically mediated release of endogenous N2O and NO2 gases in a hydrothermal, hypoxic subterranean environment. Science of the Total Environment, 2020, 747, 141218.	8.0	21
2549	Monitoring, assessment, and prediction of microbial shifts in coupled catalysis and biodegradation of 1,4-dioxane and co-contaminants. Water Research, 2020, 173, 115540.	11.3	37
2550	Dynamics of uterine microbiota in postpartum dairy cows with clinical or subclinical endometritis. Scientific Reports, 2020, 10, 12353.	3.3	55
2551	Relationship between Rainfall, Fecal Pollution, Antimicrobial Resistance, and Microbial Diversity in an Urbanized Subtropical Bay. Applied and Environmental Microbiology, 2020, 86, .	3.1	20
2552	Association Between the Gut Microbiota and Blood Pressure in a Population Cohort of 6953 Individuals. Journal of the American Heart Association, 2020, 9, e016641.	3.7	67
2553	Gut microbiome composition differences among breeds impact feed efficiency in swine. Microbiome, 2020, 8, 110.	11.1	108
2554	Composition, Structure, and PGPR Traits of the Rhizospheric Bacterial Communities Associated With Wild and Cultivated Echinocactus platyacanthus and Neobuxbaumia polylopha. Frontiers in Microbiology, 2020, 11, 1424.	3.5	9
2555	Metagenomic insights into the fungal assemblages of the northwest Himalayan cold desert. Extremophiles, 2020, 24, 749-758.	2.3	5
2556	Geographical patterns of root nodule bacterial diversity in cultivated and wild populations of a woody legume crop. FEMS Microbiology Ecology, 2020, 96, .	2.7	4
2557	Soil Bacterial Communities Exhibit Strong Biogeographic Patterns at Fine Taxonomic Resolution. MSystems, 2020, 5, .	3.8	33
2558	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, Zostera marina. PLoS ONE, 2020, 15, e0236135.	2.5	35
2559	Microbiome Shifts Associated With the Introduction of Wild Atlantic Horseshoe Crabs (Limulus) Tj ETQq0 0 0 rgE	BT JQverloo	ck 10 Tf 50 18
2560	Hurricane Disturbance Stimulated Nitrification and Altered Ammonia Oxidizer Community Structure in Lake Okeechobee and St. Lucie Estuary (Florida). Frontiers in Microbiology, 2020, 11, 1541.	3.5	15
2561	Replacing Barley and Soybean Meal With By-products, in a Pasture Based Diet, Alters Daily Methane Output and the Rumen Microbial Community in vitro Using the Rumen Simulation Technique (RUSITEC). Frontiers in Microbiology, 2020, 11, 1614.	3.5	8
2562	Evidence of Vent-Adaptation in Sponges Living at the Periphery of Hydrothermal Vent Environments: Ecological and Evolutionary Implications. Frontiers in Microbiology, 2020, 11, 1636.	3.5	15

#	Article	IF	CITATIONS
2563	Organic Farming Sharpens Plant Defenses in the Field. Frontiers in Sustainable Food Systems, 2020, 4, .	3.9	11
2564	Is the Distribution of Two Rare Orchis Sister Species Limited by Their Main Mycobiont?. Diversity, 2020, 12, 262.	1.7	10
2565	The Bacterial Gut Microbiota of Schoolchildren from High and Low Socioeconomic Status: A Study in an Urban Area of Makassar, Indonesia. Microorganisms, 2020, 8, 961.	3.6	13
2566	Extreme storms cause rapid but shortâ€lived shifts in nearshore subtropical bacterial communities. Environmental Microbiology, 2020, 22, 4571-4588.	3.8	11
2567	Immunoglobulin recognition of fecal bacteria in stunted and non-stunted children: findings from the Afribiota study. Microbiome, 2020, $8,113.$	11.1	21
2568	Soil Fungal Communities Investigated by Metabarcoding Within Simulated Forensic Burial Contexts. Frontiers in Microbiology, 2020, $11,1686.$	3.5	13
2569	Marine water environmental DNA metabarcoding provides a comprehensive fish diversity assessment and reveals spatial patterns in a large oceanic area. Ecology and Evolution, 2020, 10, 7560-7584.	1.9	50
2570	Associations between gut microbiota and genetic risk for rheumatoid arthritis in the absence of disease: a cross-sectional study. Lancet Rheumatology, The, 2020, 2, e418-e427.	3.9	91
2571	A Comprehensive Evaluation of the Impact of Bovine Milk Containing Different Beta-Casein Profiles on Gut Health of Ageing Mice. Nutrients, 2020, 12, 2147.	4.1	28
2572	Methanogens Diversity during Anaerobic Sewage Sludge Stabilization and the Effect of Temperature. Processes, 2020, 8, 822.	2.8	10
2573	Eukaryotic plankton communities across reef environments in Bocas del Toro Archipelago, Panam \tilde{A}_i . Coral Reefs, 2020, 39, 1453-1467.	2.2	2
2574	Community Structure of Arbuscular Mycorrhizal Fungi in Soils of Switchgrass Harvested for Bioenergy. Applied and Environmental Microbiology, 2020, 86, .	3.1	9
2575	Impact of Glyphosate on the Honey Bee Gut Microbiota: Effects of Intensity, Duration, and Timing of Exposure. MSystems, 2020, 5, .	3.8	55
2576	Effect of Cyberlindnera jadinii yeast as a protein source on intestinal microbiota and butyrate levels in post-weaning piglets. Animal Microbiome, 2020, 2, 13.	3.8	11
2577	Microbiome Variation Across Two Hemlock Species With Hemlock Woolly Adelgid Infestation. Frontiers in Microbiology, 2020, 11, 1528.	3.5	7
2578	Great Tit (Parus major) Uropygial Gland Microbiomes and Their Potential Defensive Roles. Frontiers in Microbiology, 2020, 11, 1735.	3.5	13
2579	Wildfire effects on soil bacterial community and its potential functions in a permafrost region of Canada. Applied Soil Ecology, 2020, 156, 103713.	4.3	23
2580	Identification of Simplified Microbial Communities That Inhibit Clostridioides difficile Infection through Dilution/Extinction. MSphere, 2020, 5, .	2.9	15

#	Article	IF	CITATIONS
2581	The Gut Microbiota Communities of Wild Arboreal and Ground-Feeding Tropical Primates Are Affected Differently by Habitat Disturbance. MSystems, 2020, 5, .	3.8	36
2582	Different effects of constitutive and induced microbiota modulation on microglia in a mouse model of Alzheimer's disease. Acta Neuropathologica Communications, 2020, 8, 119.	5.2	75
2583	Gastric Microbiota in a Low–Helicobacter pylori Prevalence General Population and Their Associations With Gastric Lesions. Clinical and Translational Gastroenterology, 2020, 11, e00191.	2.5	29
2584	Phosphate fertiliser alters carboxylates and bacterial communities in sweet potato (Ipomoea batatas) Tj ${\sf ETQq1\ 1}$	0.784314 3.7	rgBT /Overl
2585	A footprint of plant eco-geographic adaptation on the composition of the barley rhizosphere bacterial microbiota. Scientific Reports, 2020, 10, 12916.	3.3	48
2586	Intestinal TLR9 deficiency exacerbates hepatic IR injury via altered intestinal inflammation and shortâ€chain fatty acid synthesis. FASEB Journal, 2020, 34, 12083-12099.	0.5	8
2587	Nitrite Oxidizer Activity and Community Are More Responsive Than Their Abundance to Ammonium-Based Fertilizer in an Agricultural Soil. Frontiers in Microbiology, 2020, 11, 1736.	3.5	14
2588	The Composition of Microbial Communities in Six Streams, and Its Association With Environmental Conditions, and Foodborne Pathogen Isolation. Frontiers in Microbiology, 2020, 11, 1757.	3.5	13
2589	Microbiomes and Specific Symbionts of Social Spiders: Compositional Patterns in Host Species, Populations, and Nests. Frontiers in Microbiology, 2020, 11, 1845.	3.5	20
2590	Fungal Endophytic Community Associated with Guarana (Paullinia cupana Var. Sorbilis): Diversity Driver by Genotypes in the Centre of Origin. Journal of Fungi (Basel, Switzerland), 2020, 6, 123.	3.5	3
2591	Holm oak decline and mortality exacerbates drought effects on soil biogeochemical cycling and soil microbial communities across a climatic gradient. Soil Biology and Biochemistry, 2020, 149, 107921.	8.8	16
2592	Airway microbial diversity is decreased in young children with cystic fibrosis compared to healthy controls but improved with CFTR modulation. Heliyon, 2020, 6, e04104.	3.2	11
2593	Application of 16S rRNA next generation sequencing in ticks in Greece. Heliyon, 2020, 6, e04542.	3.2	3
2594	Persistent organic pollutants, metals, and the bacterial community composition associated with microplastics in Muskegon Lake (MI). Journal of Great Lakes Research, 2020, 46, 1444-1458.	1.9	29
2595	Formation and fate of oil-related aggregates (ORAs) in seawater at different temperatures. Marine Pollution Bulletin, 2020, 159, 111483.	5.0	12
2596	Advances in metabarcoding techniques bring us closer to reliable monitoring of the marine benthos. Journal of Applied Ecology, 2020, 57, 2234-2245.	4.0	23
2597	Sequencing effort dictates gene discovery in marine microbial metagenomes. Environmental Microbiology, 2020, 22, 4589-4603.	3.8	13
2598	Consumption of a Western-Style Diet Modulates the Response of the Murine Gut Microbiome to Ciprofloxacin. MSystems, 2020, 5, .	3.8	23

#	Article	IF	CITATIONS
2599	Gut dysbiosis in Huntington's disease: associations among gut microbiota, cognitive performance and clinical outcomes. Brain Communications, 2020, 2, fcaa110.	3.3	98
2600	Altered Patterns of Compositional and Functional Disruption of the Gut Microbiota in Typhoid Fever and Nontyphoidal Febrile Illness. Open Forum Infectious Diseases, 2020, 7, ofaa251.	0.9	4
2601	Exploring the Maternal and Infant Oral Microbiomes. Journal of Perinatal and Neonatal Nursing, 2020, 34, 211-221.	0.7	5
2602	Donor fecal microbiota transplantation ameliorates intestinal graft-versus-host disease in allogeneic hematopoietic cell transplant recipients. Science Translational Medicine, 2020, 12, .	12.4	97
2603	PacBio and Illumina MiSeq Amplicon Sequencing Confirm Full Recovery of the Bacterial Community After Subacute Ruminal Acidosis Challenge in the RUSITEC System. Frontiers in Microbiology, 2020, 11, 1813.	3.5	15
2604	The Influences of Bioinformatics Tools and Reference Databases in Analyzing the Human Oral Microbial Community. Genes, 2020, 11, 878.	2.4	32
2605	Bacteriomic Profiling of Branchial Lesions Induced by Neoparamoeba perurans Challenge Reveals Commensal Dysbiosis and an Association with Tenacibaculum dicentrarchi in AGD-Affected Atlantic Salmon (Salmo salar L.). Microorganisms, 2020, 8, 1189.	3.6	22
2606	Linking rhizosphere bacterial diversity and soil fertility in tobacco plants under different soil types and cropping pattern in Tanzania: A pilot study. Heliyon, 2020, 6, e04278.	3.2	10
2607	The posthatch prophylactic use of ceftiofur affects the cecal microbiota similar to the dietary sanguinarine supplementation in broilers. Poultry Science, 2020, 99, 6013-6021.	3.4	13
2608	Oral and vaginal microbiota in selected field mice of the genus Apodemus: a wild population study. Scientific Reports, 2020, 10, 13246.	3.3	8
2609	Monitoring of biofouling communities in a Portuguese port using a combined morphological and metabarcoding approach. Scientific Reports, 2020, 10, 13461.	3.3	25
2610	Soil microbial composition varies in response to coffee agroecosystem management. FEMS Microbiology Ecology, 2020, 96, .	2.7	16
2611	Short-Chain Fatty Acid Production by Gut Microbiota from Children with Obesity Differs According to Prebiotic Choice and Bacterial Community Composition. MBio, 2020, 11 , .	4.1	49
2612	A Novel Description of the Human Sinus Archaeome During Health and Chronic Rhinosinusitis. Frontiers in Cellular and Infection Microbiology, 2020, 10, 398.	3.9	8
2613	Comparative Microbiomics of Tephritid Frugivorous Pests (Diptera: Tephritidae) From the Field: A Tale of High Variability Across and Within Species. Frontiers in Microbiology, 2020, 11, 1890.	3.5	24
2614	Distinct Temporal Succession of Bacterial Communities in Early Marine Biofilms in a Portuguese Atlantic Port. Frontiers in Microbiology, 2020, 11, 1938.	3.5	29
2615	Gastric Microbiome Diversities in Gastric Cancer Patients from Europe and Asia Mimic the Human Population Structure and Are Partly Driven by Microbiome Quantitative Trait Loci. Microorganisms, 2020, 8, 1196.	3.6	14
2616	Integrating Microbial Community Assembly and Fluid Kinetics to Decouple Nitrogen Dynamics in an Urban Channel Confluence. Environmental Science & Envi	10.0	18

#	Article	IF	CITATIONS
2617	Associations between Diet, the Gut Microbiome, and Short-Chain Fatty Acid Production among Older Caribbean Latino Adults. Journal of the Academy of Nutrition and Dietetics, 2020, 120, 2047-2060.e6.	0.8	28
2618	The role of land management and elevation in shaping soil microbial communities: Insights from the Central European Alps. Soil Biology and Biochemistry, 2020, 150, 107951.	8.8	37
2619	Cystic Fibrosis Lung Transplant Recipients Have Suppressed Airway Interferon Responses during Pseudomonas Infection. Cell Reports Medicine, 2020, 1, 100055.	6.5	12
2620	Stable Isotope Probing Identifies Bacterioplankton Lineages Capable of Utilizing Dissolved Organic Matter Across a Range of Bioavailability. Frontiers in Microbiology, 2020, 11, 580397.	3.5	10
2621	Salt Marsh Elevation Drives Root Microbial Composition of the Native Invasive Grass Elytrigia atherica. Microorganisms, 2020, 8, 1619.	3.6	7
2622	Ecological Structuring of Temperate Bacteriophages in the Inflammatory Bowel Disease-Affected Gut. Microorganisms, 2020, 8, 1663.	3.6	14
2624	Chytrid fungi shape bacterial communities on model particulate organic matter. Biology Letters, 2020, 16, 20200368.	2.3	14
2626	Scheduled Empiric Antibiotics May Alter the Gut Microbiome and Nutrition Outcomes in Pediatric Intestinal Failure. Nutrition in Clinical Practice, 2021, 36, 1230-1239.	2.4	6
2627	Reducing host DNA contamination in 16S rRNA gene surveys of anthozoan microbiomes using PNA clamps. Coral Reefs, 2020, 39, 1817-1827.	2.2	14
2629	Microbiome manipulation by a soil-borne fungal plant pathogen using effector proteins. Nature Plants, 2020, 6, 1365-1374.	9.3	118
2630	Introduced bees (<i>Osmia cornifrons</i>) collect pollen from both coevolved and novel host-plant species within their family-level phylogenetic preferences. Royal Society Open Science, 2020, 7, 200225.	2.4	20
2631	Xanthohumol microbiome and signature in healthy adults (the XMaS trial): a phase I triple-masked, placebo-controlled clinical trial. Trials, 2020, 21, 835.	1.6	10
2632	Local Conditions Influence the Prokaryotic Communities Associated With the Mesophotic Black Coral Antipathella subpinnata. Frontiers in Microbiology, 2020, 11, 537813.	3.5	14
2633	Freshwater Sediment Microbial Communities Are Not Resilient to Disturbance From Agricultural Land Runoff. Frontiers in Microbiology, 2020, 11, 539921.	3.5	21
2634	Testing the Two-Step Model of Plant Root Microbiome Acquisition Under Multiple Plant Species and Soil Sources. Frontiers in Microbiology, 2020, 11, 542742.	3.5	20
2635	Bacterial Communities of Ixodes scapularis from Central Pennsylvania, USA. Insects, 2020, 11, 718.	2.2	8
2636	The Prokaryotic Microbiome of Acropora digitifera is Stable under Short-Term Artificial Light Pollution. Microorganisms, 2020, 8, 1566.	3.6	6
2637	Optimized DNA extraction and purification method for characterization of bacterial and fungal communities in lung tissue samples. Scientific Reports, 2020, 10, 17377.	3.3	15

#	Article	IF	CITATIONS
2639	Response of Salivary Microbiota to Caries Preventive Treatment in Aboriginal and Torres Strait Islander Children. Journal of Oral Microbiology, 2020, 12, 1830623.	2.7	9
2640	Stump removal and tree species composition promote a bacterial microbiome that may be beneficial in the suppression of root disease. FEMS Microbiology Ecology, 2020, 97, .	2.7	3
2641	Dynamics of microbial populations and diversity in NAPL contaminated peat soil under varying water table conditions. Environmental Research, 2020, 191, 110167.	7. 5	15
2642	Identification of plastic-associated species in the Mediterranean Sea using DNA metabarcoding with Nanopore MinION. Scientific Reports, 2020, 10, 17533.	3.3	54
2643	Coffee consumption revealed sex differences in host endogenous metabolism and gut microbiota in healthy adults. Journal of Food Biochemistry, 2020, 44, e13535.	2.9	6
2644	Effect of subtilisin, a protease from Bacillus sp., on soil biochemical parameters and microbial biodiversity. European Journal of Soil Biology, 2020, 101, 103244.	3.2	7
2645	Strong effects of lab-to-field environmental transitions on the bacterial intestinal microbiota of Mus musculus are modulated by Trichuris murisinfection. FEMS Microbiology Ecology, 2020, 96, .	2.7	17
2646	Impact of Yeast-Derived \hat{l}^2 -Glucans on the Porcine Gut Microbiota and Immune System in Early Life. Microorganisms, 2020, 8, 1573.	3.6	26
2647	Association between Aquatic Micropollutant Dissipation and River Sediment Bacterial Communities. Environmental Science & Envir	10.0	37
2648	Islands in the sand: are all hypolithic microbial communities the same?. FEMS Microbiology Ecology, 2020, 97, .	2.7	4
2649	16S rRNA Gene Diversity of Bacterial Endophytes in Parasitic <i>Cuscuta campestris</i> and Its <i>Helianthus annuus</i> Host. Microbiology Resource Announcements, 2020, 9, .	0.6	0
2650	Virome Sequencing of the Human Intestinal Mucosal–Luminal Interface. Frontiers in Cellular and Infection Microbiology, 2020, 10, 582187.	3.9	14
2651	Effect of Inorganic N Top Dressing and Trichoderma harzianum Seed-Inoculation on Crop Yield and the Shaping of Root Microbial Communities of Wheat Plants Cultivated Under High Basal N Fertilization. Frontiers in Plant Science, 2020, 11, 575861.	3.6	32
2652	Seasonal Regime Shift in the Viral Communities of a Permafrost Thaw Lake. Viruses, 2020, 12, 1204.	3.3	5
2653	Daring to be differential: metabarcoding analysis of soil and plant-related microbial communities using amplicon sequence variants and operational taxonomical units. BMC Genomics, 2020, 21, 733.	2.8	58
2654	Compositional and Functional Comparisons of the Microbiota in the Colostrum and Mature Milk of Dairy Goats. Animals, 2020, 10, 1955.	2.3	9
2655	Exploring the resident gut microbiota of stranded odontocetes: high similarities between two dolphin species Tursiops truncatus and Stenella coeruleoalba. Journal of the Marine Biological Association of the United Kingdom, 2020, 100, 1181-1188.	0.8	1
2656	Microbial diversity in water and animal faeces: a metagenomic analysis to assess public health risk. New Zealand Journal of Zoology, 2021, 48, 188-201.	1.1	9

#	Article	IF	CITATIONS
2657	A network of immune and microbial modifications underlies viral persistence in the gastrointestinal tract. Journal of Experimental Medicine, 2020, 217, .	8.5	6
2658	Distinct Polysaccharide Utilization Determines Interspecies Competition between Intestinal Prevotella spp Cell Host and Microbe, 2020, 28, 838-852.e6.	11.0	86
2659	V ^V Reduction by <i>Polaromonas</i> spp. in Vanadium Mine Tailings. Environmental Science &	10.0	47
2660	Identification of Bacteria in Two Food Waste Black Soldier Fly Larvae Rearing Residues. Frontiers in Microbiology, 2020, 11, 582867.	3.5	33
2661	Nutritional profile of rodent diets impacts experimental reproducibility in microbiome preclinical research. Scientific Reports, 2020, 10, 17784.	3.3	24
2662	Deciphering Microbial Community Dynamics and Biochemical Changes During Nyons Black Olive Natural Fermentations. Frontiers in Microbiology, 2020, 11, 586614.	3.5	21
2663	Microbiome Management by Biological and Chemical Treatments in Maize Is Linked to Plant Health. Microorganisms, 2020, 8, 1506.	3.6	17
2664	Assessment of Soil Features on the Growth of Environmental Nontuberculous Mycobacterial Isolates from Hawai'i. Applied and Environmental Microbiology, 2020, 86, .	3.1	18
2665	Modelling technical and biological biases in macroinvertebrate community assessment from bulk preservative using multiple metabarcoding markers. Molecular Ecology, 2021, 30, 3221-3238.	3.9	30
2666	An approach to increase the success rate of cultivation of soil bacteria based on fluorescence-activated cell sorting. PLoS ONE, 2020, 15, e0237748.	2.5	6
2667	Seasonal and Spatial Variations in Bacterial Communities From Tetrodotoxin-Bearing and Non-tetrodotoxin-Bearing Clams. Frontiers in Microbiology, 2020, 11, 1860.	3.5	8
2668	Metagenomic profiling of gut microbiome in early chronic kidney disease. Nephrology Dialysis Transplantation, 2021, 36, 1675-1684.	0.7	29
2669	A preliminary study of the effect of total fishmeal replacement with different dietary sources on the gut microbiota of spotted rose snapper juvenile (<i>Lutjanus guttatus</i> Steindachner, 1869). Aquaculture Research, 2020, 51, 4771-4784.	1.8	2
2670	Niche Partitioning between Coastal and Offshore Shelf Waters Results in Differential Expression of Alkane and Polycyclic Aromatic Hydrocarbon Catabolic Pathways. MSystems, 2020, 5, .	3.8	10
2671	Airborne bacterial emission fluxes from manureâ€fertilized agricultural soil. Microbial Biotechnology, 2020, 13, 1631-1647.	4.2	17
2672	Treadmill exercise has minimal impact on obesogenic diet-related gut microbiome changes but alters adipose and hypothalamic gene expression in rats. Nutrition and Metabolism, 2020, 17, 71.	3.0	9
2673	Characterizing the nectar microbiome of the non-native tropical milkweed, Asclepias curassavica, in an urban environment. PLoS ONE, 2020, 15, e0237561.	2.5	6
2674	Stream microbial communities and ecosystem functioning show complex responses to multiple stressors in wastewater. Global Change Biology, 2020, 26, 6363-6382.	9.5	52

#	Article	IF	CITATIONS
2675	Differential Profiles of Gut Microbiota and Metabolites Associated with Host Shift of Plutella xylostella. International Journal of Molecular Sciences, 2020, 21, 6283.	4.1	26
2676	Human Endogenous Retrovirus Expression Is Associated with Head and Neck Cancer and Differential Survival. Viruses, 2020, 12, 956.	3.3	20
2677	Gut microbiota profile and selected plasma metabolites in type 1 diabetes without and with stratification by albuminuria. Diabetologia, 2020, 63, 2713-2724.	6.3	27
2678	Nutrient Capture from Aqueous Waste and Photocontrolled Fertilizer Delivery to Tomato Plants Using Fe(III)–Polysaccharide Hydrogels. ACS Omega, 2020, 5, 23009-23020.	3.5	7
2679	Evolution of diversity explains the impact of pre-adaptation of a focal species on the structure of a natural microbial community. ISME Journal, 2020, 14, 2877-2889.	9.8	9
2680	Oral microbiome and onset of oral mucositis in patients with squamous cell carcinoma of the head and neck. Cancer, 2020, 126, 5124-5136.	4.1	30
2681	Host age is not a consistent predictor of microbial diversity in the coral Porites lutea. Scientific Reports, 2020, 10, 14376.	3.3	12
2682	1200 high-quality metagenome-assembled genomes from the rumen of African cattle and their relevance in the context of sub-optimal feeding. Genome Biology, 2020, 21, 229.	8.8	38
2683	Microbial environment shapes immune function and cloacal microbiota dynamics in zebra finches Taeniopygia guttata. Animal Microbiome, 2020, 2, 21.	3.8	21
2684	The microbiome of captive hamadryas baboons. Animal Microbiome, 2020, 2, 25.	3.8	5
2685	An observational field study of the cloacal microbiota in adult laying hens with and without access to an outdoor range. Animal Microbiome, 2020, 2, 28.	3.8	13
2686	Influences of claywater and greenwater on the skin microbiome of cultured larval sablefish (Anoplopoma fimbria). Animal Microbiome, 2020, 2, 27.	3.8	5
2687	Antibiotic-induced alterations and repopulation dynamics of yellowtail kingfish microbiota. Animal Microbiome, 2020, 2, 26.	3.8	23
2688	Self-Balance of Intestinal Flora in Spouses of Patients With Rheumatoid Arthritis. Frontiers in Medicine, 2020, 7, 538.	2.6	7
2689	The Microbial Community Associated with Rhizostoma pulmo: Ecological Significance and Potential Consequences for Marine Organisms and Human Health. Marine Drugs, 2020, 18, 437.	4.6	16
2690	Bacterial communities of the Salvia lyrata rhizosphere explained by spatial structure and sampling grain. Microbial Ecology, 2020, 80, 846-858.	2.8	8
2691	Meconium microbiome and its relation to neonatal growth and head circumference catch-up in preterm infants. PLoS ONE, 2020, 15, e0238632.	2.5	13
2692	Nodule and Root Zone Microbiota of Salt-Tolerant Wild Soybean in Coastal Sand and Saline-Alkali Soil. Frontiers in Microbiology, 2020, 11, 2178.	3.5	25

#	Article	IF	CITATIONS
2693	Metagenomic Profiling and Microbial Metabolic Potential of Perdido Fold Belt (NW) and Campeche Knolls (SE) in the Gulf of Mexico. Frontiers in Microbiology, 2020, 11, 1825.	3.5	16
2694	Repurposing Metformin in Nondiabetic People With HIV: Influence on Weight and Gut Microbiota. Open Forum Infectious Diseases, 2020, 7, ofaa338.	0.9	33
2695	Habitat disturbance influences the skin microbiome of a rediscovered neotropical-montane frog. BMC Microbiology, 2020, 20, 292.	3.3	15
2696	The maternal microbiome modulates fetal neurodevelopment in mice. Nature, 2020, 586, 281-286.	27.8	280
2697	Changes in Multi-Level Biodiversity and Soil Features in a Burned Beech Forest in the Southern Italian Coastal Mountain. Forests, 2020, 11, 983.	2.1	23
2698	Depletion of gut microbiota is associated with improved neurologic outcome following traumatic brain injury. Brain Research, 2020, 1747, 147056.	2.2	29
2699	Mothers of Preterm Infants Have Individualized Breast Milk Microbiota that Changes Temporally Based on Maternal Characteristics. Cell Host and Microbe, 2020, 28, 669-682.e4.	11.0	31
2700	Homogeneous environmental selection dominates microbial community assembly in the oligotrophic South Pacific Gyre. Molecular Ecology, 2020, 29, 4680-4691.	3.9	33
2701	Experimental autoimmune encephalomyelitis is associated with changes of the microbiota composition in the gastrointestinal tract. Scientific Reports, 2020, 10, 15183.	3.3	38
2702	Diet posttranslationally modifies the mouse gut microbial proteome to modulate renal function. Science, 2020, 369, 1518-1524.	12.6	108
2703	Distinct fungal communities associated with different organs of the mangrove Sonneratia alba in the Malay Peninsula. IMA Fungus, 2020, 11, 17.	3.8	12
2704	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. PLoS ONE, 2020, 15, e0238648.	2.5	9
2705	The Gut Microbial Community Structure of the North American River Otter (<i>Lontra canadensis</i>) in the Alberta Oil Sands Region in Canada: Relationship with Local Environmental Variables and Metal Body Burden. Environmental Toxicology and Chemistry, 2020, 39, 2516-2526.	4.3	5
2706	Influence of probiotics on biofilm formation and diversity of bacteria colonising crop sorghum ensiled with unsalable vegetables. Applied Microbiology and Biotechnology, 2020, 104, 8825-8836.	3.6	4
2707	The role of seagrass vegetation and local environmental conditions in shaping benthic bacterial and macroinvertebrate communities in a tropical coastal lagoon. Scientific Reports, 2020, 10, 13550.	3.3	32
2708	Low levels of salivary metals, oral microbiome composition and dental decay. Scientific Reports, 2020, 10, 14640.	3.3	14
2709	Spatial patterns of microbial communities across surface waters of the Great Barrier Reef. Communications Biology, 2020, 3, 442.	4.4	30
2710	Biological observations in microbiota analysis are robust to the choice of 16S rRNA gene sequencing processing algorithm: case study on human milk microbiota. BMC Microbiology, 2020, 20, 290.	3.3	15

#	Article	IF	CITATIONS
2711	Anaerobic Conversion of Saline Phenol-Containing Wastewater Under Thermophilic Conditions in a Membrane Bioreactor. Frontiers in Bioengineering and Biotechnology, 2020, 8, 565311.	4.1	11
2712	Stability of Floodplain Subsurface Microbial Communities Through Seasonal Hydrological and Geochemical Cycles. Frontiers in Earth Science, 2020, 8, .	1.8	14
2713	Organic Contaminant Mixture Significantly Changes Microbenthic Community Structure and Increases the Expression of PAH Degradation Genes. Frontiers in Environmental Science, 2020, 8, .	3.3	8
2714	Permafrost Microbial Community Structure Changes Across the Pleistocene-Holocene Boundary. Frontiers in Environmental Science, 2020, 8, .	3.3	8
2715	Antifungal Potential of the Skin Microbiota of Hibernating Big Brown Bats (Eptesicus fuscus) Infected With the Causal Agent of White-Nose Syndrome. Frontiers in Microbiology, 2020, 11, 1776.	3.5	12
2716	Microbiota of the Digestive Gland of Red Abalone (Haliotis rufescens) Is Affected by Withering Syndrome. Microorganisms, 2020, 8, 1411.	3.6	8
2717	Influence of Regional Oceanography and Hydrothermal Activity on Protist Diversity and Community Structure in the Okinawa Trough. Microbial Ecology, 2020, 80, 746-761.	2.8	13
2718	Rumen Microbiome Composition Is Altered in Sheep Divergent in Feed Efficiency. Frontiers in Microbiology, 2020, 11, 1981.	3.5	72
2719	Modulation of Gut Microbiota in Korean Navy Trainees following a Healthy Lifestyle Change. Microorganisms, 2020, 8, 1265.	3.6	11
2720	Investigating Both Mucosal Immunity and Microbiota in Response to Gut Enteritis in Yellowtail Kingfish. Microorganisms, 2020, 8, 1267.	3 . 6	22
2721	Mild hydrostatic-pressure ($15 \text{\^{A}MPa}$) affects the assembly, but not the growth, of oil-degrading coastal microbial communities tested under limiting conditions ($5 \text{\^{A}}^{\circ}\text{C}$, no added nutrients). FEMS Microbiology Ecology, 2020, 96, .	2.7	4
2722	Columbia spotted frogs (<i>Rana luteiventris</i>) have characteristic skin microbiota that may be shaped by cutaneous skin peptides and the environment. FEMS Microbiology Ecology, 2020, 96, .	2.7	10
2723	Three Candidate Probiotic Strains Impact Gut Microbiota and Induce Anergy in Mice with Cow's Milk Allergy. Applied and Environmental Microbiology, 2020, 86, .	3.1	18
2724	Cooperation, Competition, and Specialized Metabolism in a Simplified Root Nodule Microbiome. MBio, 2020, 11, .	4.1	27
2725	Effects of Exogenous Dietary Advanced Glycation End Products on the Cross-Talk Mechanisms Linking Microbiota to Metabolic Inflammation. Nutrients, 2020, 12, 2497.	4.1	40
2726	Comparative Analysis of the Bacterial and Fungal Communities in the Gut and the Crop of Aedes albopictus Mosquitoes: A Preliminary Study. Pathogens, 2020, 9, 628.	2.8	14
2727	Bovine Lactoferrin Supplementation Does Not Disrupt Microbiota Development in Preterm Infants Receiving Probiotics. Journal of Pediatric Gastroenterology and Nutrition, 2020, 71, 216-222.	1.8	5
2728	Berry Polyphenols and Fibers Modulate Distinct Microbial Metabolic Functions and Gut Microbiota Enterotype-Like Clustering in Obese Mice. Frontiers in Microbiology, 2020, 11, 2032.	3.5	87

#	Article	IF	CITATIONS
2729	Effect of glycerol feed-supplementation on seabass metabolism and gut microbiota. Applied Microbiology and Biotechnology, 2020, 104, 8439-8453.	3.6	13
2730	Changes of soil-rhizosphere microbiota after organic amendment application in a Hordeum vulgare L. short-term greenhouse experiment. Plant and Soil, 2020, 455, 489-506.	3.7	17
2731	Paired highâ€throughput, in situ imaging and highâ€throughput sequencing illuminate acantharian abundance and vertical distribution. Limnology and Oceanography, 2020, 65, 2953-2965.	3.1	10
2732	Shifts in the microbiota associated with male mosquitoes (Aedes aegypti) exposed to an obligate gut fungal symbiont (Zancudomyces culisetae). Scientific Reports, 2020, 10, 12886.	3.3	1
2733	Shotgun metagenomics reveals a heterogeneous prokaryotic community and a wide array of antibiotic resistance genes in mangrove sediment. FEMS Microbiology Ecology, 2020, 96, .	2.7	17
2734	Salmonella enterica Serovar Typhimurium Temporally Modulates the Enteric Microbiota and Host Responses To Overcome Colonization Resistance in Swine. Applied and Environmental Microbiology, 2020, 86, .	3.1	18
2735	The Gut Microbiome Is Associated with Clinical Response to Anti–PD-1/PD-L1 Immunotherapy in Gastrointestinal Cancer. Cancer Immunology Research, 2020, 8, 1251-1261.	3.4	155
2736	Dysbiosis in the Dead: Human Postmortem Microbiome Beta-Dispersion as an Indicator of Manner and Cause of Death. Frontiers in Microbiology, 2020, 11, 555347.	3.5	25
2737	Hot in Cold: Microbial Life in the Hottest Springs in Permafrost. Microorganisms, 2020, 8, 1308.	3.6	12
2738	Impact of Viral Lysis on the Composition of Bacterial Communities and Dissolved Organic Matter in Deep-Sea Sediments. Viruses, 2020, 12, 922.	3.3	18
2739	Wood construction more strongly shapes deadwood microbial communities than spatial location over 5 years of decay. Environmental Microbiology, 2020, 22, 4702-4717.	3.8	14
2740	Are substrate-mediated microbial community shifts the future of soilborne disease management?. Acta Horticulturae, 2020, , 83-96.	0.2	1
2741	Diet, Perceived Intestinal Well-Being and Compositions of Fecal Microbiota and Short Chain Fatty Acids in Oat-Using Subjects with Celiac Disease or Gluten Sensitivity. Nutrients, 2020, 12, 2570.	4.1	9
2742	Microbial Communities in Soils and Endosphere of Solanum tuberosum L. and their Response to Long-Term Fertilization. Microorganisms, 2020, 8, 1377.	3.6	17
2743	Microbial Diversity and Community Structures Among Those With Moderate to Severe TBI: A United States-Veteran Microbiome Project Study. Journal of Head Trauma Rehabilitation, 2020, 35, 332-341.	1.7	16
2744	Biosulfidogenesis Mediates Natural Attenuation in Acidic Mine Pit Lakes. Microorganisms, 2020, 8, 1275.	3.6	19
2745	Faecal Microbiota of Dogs Offered a Vegetarian Diet with or without the Supplementation of Feather Meal and either Cornmeal, Rye or Fermented Rye: A Preliminary Study. Microorganisms, 2020, 8, 1363.	3.6	6
2746	Marine Sediments Hold an Untapped Potential for Novel Taxonomic and Bioactive Bacterial Diversity. MSystems, 2020, 5, .	3.8	24

#	Article	IF	CITATIONS
2747	Replicable simulation of distal hot water premise plumbing using convectively-mixed pipe reactors. PLoS ONE, 2020, 15, e0238385.	2.5	4
2748	Microbiota composition in bilateral healthy breast tissue and breast tumors. Cancer Causes and Control, 2020, 31, 1027-1038.	1.8	26
2749	Gut Microbiota Dynamics in Parkinsonian Mice. ACS Chemical Neuroscience, 2020, 11, 3267-3276.	3 . 5	7
2750	Prophylactic effects of oral administration of <i>Lactobacillus casei </i> on house dust mite-induced asthma in mice. Food and Function, 2020, 11, 9272-9284.	4.6	15
2751	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. Ecology and Evolution, 2020, 10, 9721-9739.	1.9	40
2752	Physical drivers facilitating a toxigenic cyanobacterial bloom in a major Great Lakes tributary. Limnology and Oceanography, 2020, 65, 2866-2882.	3.1	19
2753	Anaerobic respiration pathways and response to increased substrate availability of Arctic wetland soils. Environmental Sciences: Processes and Impacts, 2020, 22, 2070-2083.	3.5	6
2754	Dynamic Changes in the Microbiome of Rice During Shoot and Root Growth Derived From Seeds. Frontiers in Microbiology, 2020, 11, 559728.	3.5	29
2755	Microbial Diversity of Fermented Greek Table Olives of Halkidiki and Konservolia Varieties from Different Regions as Revealed by Metagenomic Analysis. Microorganisms, 2020, 8, 1241.	3.6	25
2756	Gut Microbial Changes in Diabetic db/db Mice and Recovery of Microbial Diversity upon Pirfenidone Treatment. Microorganisms, 2020, 8, 1347.	3.6	18
2757	Discovering the indigenous microbial communities associated with the natural fermentation of sap from the cider gum Eucalyptus gunnii. Scientific Reports, 2020, 10, 14716.	3.3	13
2758	A comparative study of the gut microbiome in Egyptian patients with Type I and Type II diabetes. PLoS ONE, 2020, 15, e0238764.	2.5	27
2759	Microbiome and Longevity: High Abundance of Longevity-Linked Muribaculaceae in the Gut of the Long-Living Rodent <i>Spalax leucodon</i> . OMICS A Journal of Integrative Biology, 2020, 24, 592-601.	2.0	59
2760	Nanoparticle treatment of maize analyzed through the metatranscriptome: compromised nitrogen cycling, possible phytopathogen selection, and plant hormesis. Microbiome, 2020, 8, 127.	11.1	26
2761	Microbiological changes along a modular wastewater reuse treatment process with a special focus on bacterial regrowth. Journal of Water Reuse and Desalination, 2020, 10, 380-393.	2.3	11
2762	"Bacterial consortium from hydrothermal vent sediments presents electrogenic activity achieved under sulfate reducing conditions in a microbial fuel cell― Journal of Environmental Health Science & Engineering, 2020, 18, 1189-1205.	3.0	6
2763	Tracking down carbon inputs underground from an arid zone Australian calcrete. PLoS ONE, 2020, 15, e0237730.	2.5	14
2764	Association between temporal patterns in helminth assemblages and successful range expansion of exotic Mus musculus domesticus in Senegal. Biological Invasions, 2020, 22, 3003-3016.	2.4	4

#	Article	IF	CITATIONS
2765	Changes in physiology and microbial diversity in larval ornate chorus frogs are associated with habitat quality., 2020, 8, coaa047.		9
2766	Shotgun metagenomics reveal a diverse assemblage of protists in a model Antarctic soil ecosystem. Environmental Microbiology, 2020, 22, 4620-4632.	3.8	13
2767	Reducing the arbitrary: fuzzy detection of microbial ecotones and ecosystems $\hat{a} \in \text{``focus on the pelagic environment.}$ Environmental Microbiomes, 2020, 15, 16.	5.0	4
2768	Disease-Induced Microbial Shifts in Citrus Indicate Microbiome-Derived Responses to Huanglongbing Across the Disease Severity Spectrum. Phytobiomes Journal, 2020, 4, 375-387.	2.7	53
2769	Microbiota of Four Tissue Types in American Alligators (Alligator mississippiensis) Following Extended Dietary Selenomethionine Exposure. Bulletin of Environmental Contamination and Toxicology, 2020, 105, 381-386.	2.7	1
2770	S100A8 and S100A9 Are Important for Postnatal Development of Gut Microbiota and Immune System in Mice and Infants. Gastroenterology, 2020, 159, 2130-2145.e5.	1.3	64
2771	A specific combination of dual index adaptors decreases the sensitivity of amplicon sequencing with the Illumina platform. DNA Research, 2020, 27, .	3.4	0
2772	The gut mycobiota of rural and urban individuals is shaped by geography. BMC Microbiology, 2020, 20, 257.	3.3	26
2773	Comparative study of neighboring Holm oak and olive trees-belowground microbial communities subjected to different soil management. PLoS ONE, 2020, 15, e0236796.	2.5	10
2774	A core phyllosphere microbiome exists across distant populations of a tree species indigenous to New Zealand. PLoS ONE, 2020, 15, e0237079.	2.5	20
2775	Bacteria but not fungi respond to soil acidification rapidly and consistently in both a spruce and beech forest. FEMS Microbiology Ecology, 2020, 96, .	2.7	15
2776	Termite mounds contain soil-derived methanotroph communities kinetically adapted to elevated methane concentrations. ISME Journal, 2020, 14, 2715-2731.	9.8	21
2777	Comparative genomic analysis of Flavobacteriaceae: insights into carbohydrate metabolism, gliding motility and secondary metabolite biosynthesis. BMC Genomics, 2020, 21, 569.	2.8	53
2778	Diversity in the Extracellular Vesicle-Derived Microbiome of Tissues According to Tumor Progression in Pancreatic Cancer. Cancers, 2020, 12, 2346.	3.7	19
2779	The Response of Red Clover (Trifolium pratense L.) to Separate and Mixed Inoculations with Rhizobium leguminosarum and Azospirillum brasilense in Presence of Polycyclic Aromatic Hydrocarbons. International Journal of Environmental Research and Public Health, 2020, 17, 5751.	2.6	8
2780	Spatial and temporal organization of jejunal microbiota in goats during animal development process. Journal of Applied Microbiology, 2021, 131, 68-79.	3.1	6
2781	A Subset of Roux-en-Y Gastric Bypass Bacterial Consortium Colonizes the Gut of Nonsurgical Rats without Inducing Host-Microbe Metabolic Changes. MSystems, 2020, 5, .	3.8	5
2782	Impacts of Milking and Housing Environment on Milk Microbiota. Animals, 2020, 10, 2339.	2.3	15

#	ARTICLE	IF	CITATIONS
2783	Alteration of Bacterial Communities in Anterior Nares and Skin Sites of Patients Undergoing Arthroplasty Surgery: Analysis by 16S rRNA and Staphylococcal-Specific tuf Gene Sequencing. Microorganisms, 2020, 8, 1977.	3.6	10
2784	Not That Close to Mommy: Horizontal Transmission Seeds the Microbiome Associated with the Marine Sponge Plakina cyanorosea. Microorganisms, 2020, 8, 1978.	3.6	11
2785	Effects of E. coli bivalent vaccine and of host genetic susceptibility to E. coli on the growth performance and faecal microbial profile of weaned pigs. Livestock Science, 2020, 241, 104247.	1.6	6
2786	Dynamic symbioses reveal pathways to coral survival through prolonged heatwaves. Nature Communications, 2020, 11, 6097.	12.8	67
2787	Under the karst: detecting hidden subterranean assemblages using eDNA metabarcoding in the caves of Christmas Island, Australia. Scientific Reports, 2020, 10, 21479.	3.3	12
2788	Composition and geographic variation of the bacterial microbiota associated with the coelomic fluid of the sea urchin Paracentrotus lividus. Scientific Reports, 2020, 10, 21443.	3.3	12
2789	Simultaneous allergic traits in dogs and their owners are associated with living environment, lifestyle and microbial exposures. Scientific Reports, 2020, 10, 21954.	3.3	18
2790	Differential longitudinal establishment of human fecal bacterial communities in germ-free porcine and murine models. Communications Biology, 2020, 3, 760.	4.4	13
2791	DNA-Stable Isotope Probing Shotgun Metagenomics Reveals the Resilience of Active Microbial Communities to Biochar Amendment in Oxisol Soil. Frontiers in Microbiology, 2020, 11, 587972.	3.5	12
2792	Two Food Waste By-Products Selectively Stimulate Beneficial Resident Citrus Host-Associated Microbes in a Zero-Runoff Indoor Plant Production System. Frontiers in Sustainable Food Systems, 2020, 4, .	3.9	6
2793	Urbanized microbiota in infants, immune constitution, and later risk of atopic diseases. Journal of Allergy and Clinical Immunology, 2021, 148, 234-243.	2.9	54
2794	An association between chronic widespread pain and the gut microbiome. Rheumatology, 2021, 60, 3727-3737.	1.9	40
2795	Using the Microbiome Amplification Preference Tool (MAPT) to Reveal Medicago sativa-Associated Eukaryotic Microbes. Phytobiomes Journal, 2020, 4, 340-350.	2.7	3
2796	Alteration of the Gut Microbiome in Normal and Overweight School Children from Selangor with Lactobacillus Fermented Milk Administration. Evolutionary Bioinformatics, 2020, 16, 117693432096594.	1.2	10
2797	Antibiotic Resistance Genes and Bacterial Communities of Farmed Rainbow Trout Fillets (Oncorhynchus mykiss). Frontiers in Microbiology, 2020, 11, 590902.	3.5	16
2798	Microbial Diversity of Pinnacle and Conical Microbial Mats in the Perennially Ice-Covered Lake Untersee, East Antarctica. Frontiers in Microbiology, 2020, 11, 607251.	3.5	10
2799	Gastric Adenocarcinomas and Signet-Ring Cell Carcinoma: Unraveling Gastric Cancer Complexity through Microbiome Analysis—Deepening Heterogeneity for a Personalized Therapy. International Journal of Molecular Sciences, 2020, 21, 9735.	4.1	25
2800	Microbiome Data Enhances Predictive Models of Lung Function in People With Cystic Fibrosis. Journal of Infectious Diseases, 2021, 223, S246-S256.	4.0	12

#	ARTICLE	IF	CITATIONS
2801	Comparison of bacterial diversity and distribution on the gills of Atlantic salmon (<i>Salmo salar</i>) Tj ETQq0 0	O ggBT /O	verlock 10 Tf
2802	You don't have the guts: a diverse set of fungi survive passage through Macrotermes bellicosus termite guts. BMC Evolutionary Biology, 2020, 20, 163.	3.2	7
2803	Relative contributions of various endogenous and exogenous factors to theÂmosquito microbiota. Parasites and Vectors, 2020, 13, 619.	2.5	9
2804	Roundup causes embryonic development failure and alters metabolic pathways and gut microbiota functionality in non-target species. Microbiome, 2020, 8, 170.	11.1	27
2805	Response of Microbial Community to Induced Failure of Anaerobic Digesters Through Overloading With Propionic Acid Followed by Process Recovery. Frontiers in Bioengineering and Biotechnology, 2020, 8, 604838.	4.1	20
2806	Contingent Effects of Liming on N2O-Emissions Driven by Autotrophic Nitrification. Frontiers in Environmental Science, 2020, 8, .	3.3	25
2807	The Total and Active Bacterial Community of the Chlorolichen Cetraria islandica and Its Response to Long-Term Warming in Sub-Arctic Tundra. Frontiers in Microbiology, 2020, 11, 540404.	3.5	11
2808	High-Fat Diets Led to OTU-Level Shifts in Fecal Samples of Healthy Adult Dogs. Frontiers in Microbiology, 2020, 11, 564160.	3.5	9
2809	Understanding Microbial Community Dynamics in Up-Flow Bioreactors to Improve Mitigation Strategies for Oil Souring. Frontiers in Microbiology, 2020, 11, 585943.	3.5	5
2810	Simulation of Microbial Response to Accidental Diesel Spills in Basins Containing Brackish Sea Water and Sediment. Frontiers in Microbiology, 2020, 11, 593232.	3.5	6
2811	Antibiotic Treatment for Chronic Rhinosinusitis: Prescription Patterns and Associations With Patient Outcome and the Sinus Microbiota. Frontiers in Microbiology, 2020, 11, 595555.	3.5	20
2812	Functional Changes of the Community of Microbes With Ni-Dependent Enzyme Genes Accompany Adaptation of the Ruminal Microbiome to Urea-Supplemented Diets. Frontiers in Microbiology, 2020, 11, 596681.	3.5	4
2813	Comparative Microbiome and Metabolome Analyses of the Marine Tunicate Ciona intestinalis from Native and Invaded Habitats. Microorganisms, 2020, 8, 2022.	3.6	17
2814	The Role of Symbiotic Microorganisms, Nutrient Uptake and Rhizosphere Bacterial Community in Response of Pea (Pisum sativum L.) Genotypes to Elevated Al Concentrations in Soil. Plants, 2020, 9, 1801.	3.5	12
2815	Which Are the Central Aspects of Infant Sleep? The Dynamics of Sleep Composites across Infancy. Sensors, 2020, 20, 7188.	3.8	18
2816	The potential role of vitamin D supplementation as a gut microbiota modifier in healthy individuals. Scientific Reports, 2020, 10, 21641.	3.3	100
2817	Exopolysaccharide Producing Bifidobacterium animalis subsp. lactis Strains Modify the Intestinal Microbiota and the Plasmatic Cytokine Levels of BALB/c Mice According to the Type of Polymer Synthesized. Frontiers in Microbiology, 2020, 11, 601233.	3 . 5	5
2818	A Probiotic Mixture Induces Anxiolytic- and Antidepressive-Like Effects in Fischer and Maternally Deprived Long Evans Rats. Frontiers in Behavioral Neuroscience, 2020, 14, 581296.	2.0	6

#	Article	IF	CITATIONS
2819	Alterations in the Gut Microbiota of Zebrafish (Danio rerio) in Response to Water-Soluble Crude Oil Components and Its Mixture With a Chemical Dispersant. Frontiers in Public Health, 2020, 8, 584953.	2.7	11
2820	Microbiome Analysis from Paired Mucosal and Fecal Samples of a Colorectal Cancer Biobank. Cancers, 2020, 12, 3702.	3.7	15
2821	Synthetic Sequencing Standards: A Guide to Database Choice for Rumen Microbiota Amplicon Sequencing Analysis. Frontiers in Microbiology, 2020, 11, 606825.	3.5	14
2822	Hydrogen-Oxidizing Bacteria Are Abundant in Desert Soils and Strongly Stimulated by Hydration. MSystems, 2020, 5, .	3.8	38
2823	The Bacterial and Fungal Microbiota of Saccharina latissima (Laminariales, Phaeophyceae). Frontiers in Marine Science, 2020, 7, .	2.5	19
2824	Exploring Vitamin B1 Cycling and Its Connections to the Microbial Community in the North Atlantic Ocean. Frontiers in Marine Science, 2020, 7, .	2.5	17
2825	Bacterial and fungal diversity in the gut of polystyrene-fed Alphitobius diaperinus (Insecta:) Tj ETQq0 0 0 rgBT /C	verlock 10 0.7) Tf ₉ 50 502 To
2826	Whole beetroot consumption reduces systolic blood pressure and modulates diversity and composition of the gut microbiota in older participants. NFS Journal, 2020, 21, 28-37.	4.3	14
2827	The sad weekend: A perilous North American tradition. Neurobiology of Pain (Cambridge, Mass), 2020, 8, 100053.	2.5	2
2828	Mechanisms governing avian phylosymbiosis: Genetic dissimilarity based on neutral and MHC regions exhibits little relationship with gut microbiome distributions of Galápagos mockingbirds. Ecology and Evolution, 2020, 10, 13345-13354.	1.9	10
2829	Associations between phenotypic characteristics and clinical parameters of broilers and intestinal microbial development throughout a production cycle: A field study. MicrobiologyOpen, 2020, 9, e1114.	3.0	8
2830	Maternal diet alters human milk oligosaccharide composition with implications for the milk metagenome. Scientific Reports, 2020, 10, 22092.	3.3	81
2831	Insights into the mode of action of tannin-based feed additives in broiler chickens: looking for connections with the plasma metabolome and caecal microbiota. Italian Journal of Animal Science, 2020, 19, 1349-1362.	1.9	7
2832	A lowâ€cost pipeline for soil microbiome profiling. MicrobiologyOpen, 2020, 9, e1133.	3.0	8
2833	Social isolation alters behavior, the gut-immune-brain axis, and neurochemical circuits in male and female prairie voles. Neurobiology of Stress, 2020, 13, 100278.	4.0	42
2834	Bio-fertilizer and rotten straw amendments alter the rhizosphere bacterial community and increase oat productivity in a saline–alkaline environment. Scientific Reports, 2020, 10, 19896.	3.3	24
2835	Diet induces parallel changes to the gut microbiota and problem solving performance in a wild bird. Scientific Reports, 2020, 10, 20783.	3.3	34
2836	Bacterial and Fungal Profiles as Markers of Infliximab Drug Response in Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2021, 15, 1019-1031.	1.3	34

#	Article	IF	CITATIONS
2837	Influence of Season and Soil Properties on Fungal Communities of Neighboring Climax Forests (Carpinus cordata and Fraxinus rhynchophylla). Frontiers in Microbiology, 2020, 11, 572706.	3. 5	11
2838	Plant Health and Rhizosphere Microbiome: Effects of the Bionematicide Aphanocladium album in Tomato Plants Infested by Meloidogyne javanica. Microorganisms, 2020, 8, 1922.	3.6	18
2839	Impacts of Wet Market Modernization Levels and Hygiene Practices on the Microbiome and Microbial Safety of Wooden Cutting Boards in Hong Kong. Microorganisms, 2020, 8, 1941.	3.6	12
2840	NetCoMi: network construction and comparison for microbiome data in R. Briefings in Bioinformatics, 2021, 22, .	6.5	222
2841	Associations of the gut microbiome and clinical factors with acute GVHD in allogeneic HSCT recipients. Blood Advances, 2020, 4, 5797-5809.	5.2	42
2842	Falling bacterial communities from the atmosphere. Environmental Microbiomes, 2020, 15, 22.	5.0	28
2843	Organic Matter Composition at Ocean Station Papa Affects Its Bioavailability, Bacterioplankton Growth Efficiency and the Responding Taxa. Frontiers in Marine Science, 2021, 7, .	2.5	17
2844	IMAGINE Network's Mind And Gut Interactions Cohort (MAGIC) Study: a protocol for a prospective observational multicentre cohort study in inflammatory bowel disease and irritable bowel syndrome. BMJ Open, 2020, 10, e041733.	1.9	5
2845	Impact of Water Stress on Microbial Community and Activity in Sandy and Loamy Soils. Agronomy, 2020, 10, 1429.	3.0	55
2846	Evaluation of Metabarcoding Primers for Analysis of Soil Nematode Communities. Diversity, 2020, 12, 388.	1.7	20
2847	The Role of Salmonella Genomic Island 4 in Metal Tolerance of Salmonella enterica Serovar I 4,[5],12:i:-Pork Outbreak Isolate USDA15WA-1. Genes, 2020, 11, 1291.	2.4	14
2848	Occurrence and Analysis of Thermophilic Poly(butylene adipate-co-terephthalate)-Degrading Microorganisms in Temperate Zone Soils. International Journal of Molecular Sciences, 2020, 21, 7857.	4.1	4
2849	Coral Microbiomes Demonstrate Flexibility and Resilience Through a Reduction in Community Diversity Following a Thermal Stress Event. Frontiers in Ecology and Evolution, 2020, 8, .	2.2	34
2850	Sulfate Alters the Competition Among Microbiome Members of Sediments Chronically Exposed to Asphalt. Frontiers in Microbiology, 2020, 11, 556793.	3.5	5
2851	Hormonal contraception alters vaginal microbiota and cytokines in South African adolescents in a randomized trial. Nature Communications, 2020, 11, 5578.	12.8	30
2852	Stream Microbial Community Structured by Trace Elements, Headwater Dispersal, and Large Reservoirs in Sub-Alpine and Urban Ecosystems. Frontiers in Microbiology, 2020, 11, 491425.	3.5	7
2853	A Large-Scale Survey of the Bacterial Communities in Lakes of Western Mongolia with Varying Salinity Regimes. Microorganisms, 2020, 8, 1729.	3.6	9
2854	Impact of air, water and dock microbial communities on boat microbial community composition. Journal of Applied Microbiology, 2021, 131, 768-779.	3.1	2

#	Article	IF	CITATIONS
2855	Sputum microbiota in adults with CF associates with response to inhaled tobramycin. Thorax, 2020, 75, 1058-1064.	5.6	23
2856	Antimicrobial Resistance, an Update from the Ward: Increased Incidence of New Potential Pathogens and Site of Infection-Specific Antibacterial Resistances. Antibiotics, 2020, 9, 631.	3.7	5
2857	Diversity of Acyl Homoserine Lactone Molecules in Anaerobic Membrane Bioreactors Treating Sewage at Psychrophilic Temperatures. Membranes, 2020, 10, 320.	3.0	12
2858	Organic farming practices utilizing spent microbial biomass from an industrial fermentation facility promote transition to copiotrophic soil communities. Journal of Industrial Microbiology and Biotechnology, 2020, 47, 1005-1018.	3.0	3
2859	Airway Microbiota-Host Interactions Regulate Secretory Leukocyte Protease Inhibitor Levels and Influence Allergic Airway Inflammation. Cell Reports, 2020, 33, 108331.	6.4	11
2860	Co-digestion of microalgae with potato processing waste and glycerol: effect of glycerol addition on methane production and the microbial community. RSC Advances, 2020, 10, 37391-37408.	3.6	4
2861	Alternative stable states in the intestinal ecosystem: proof of concept in a rat model and a perspective of therapeutic implications. Microbiome, $2020, 8, 153$.	11.1	21
2862	Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond. Environmental Microbiomes, 2020, 15, 18.	5.0	16
2863	Gut microbiome profiling of a rural and urban South African cohort reveals biomarkers of a population in lifestyle transition. BMC Microbiology, 2020, 20, 330.	3.3	24
2864	Culex pipiens and Culex restuans egg rafts harbor diverse bacterial communities compared to their midgut tissues. Parasites and Vectors, 2020, 13, 532.	2.5	2
2865	Effect of Co-contamination by PAHs and Heavy Metals on Bacterial Communities of Diesel Contaminated Soils of South Shetland Islands, Antarctica. Microorganisms, 2020, 8, 1749.	3.6	28
2866	The Microbial Composition in Circumneutral Thermal Springs from Chignahuapan, Puebla, Mexico Reveals the Presence of Particular Sulfur-Oxidizing Bacterial and Viral Communities. Microorganisms, 2020, 8, 1677.	3.6	10
2867	Functional Anatomical Changes in Ulcerative Colitis Patients Determine Their Gut Microbiota Composition and Consequently the Possible Treatment Outcome. Pharmaceuticals, 2020, 13, 346.	3.8	13
2868	Unmapped RNA Virus Diversity in Termites and Their Symbionts. Viruses, 2020, 12, 1145.	3.3	28
2869	After the bite: bacterial transmission from grey seals (Halichoerus grypus) to harbour porpoises () Tj ETQq0 0 0 r	gBT ₄ /Overl	ogk 10 Tf 50
2870	Skin microbiome of beluga whales: spatial, temporal, and health-related dynamics. Animal Microbiome, 2020, 2, 39.	3.8	14
2871	Effect of fungal, oomycete and nematode interactions on apple root development in replant soil. CABI Agriculture and Bioscience, 2020, 1, .	2.4	10
2872	Response of Soil Microbes and Soil Enzymatic Activity to 20 Years of Fertilization. Agronomy, 2020, 10, 1542.	3.0	7

#	Article	IF	CITATIONS
2873	The Dwindling Microbiota of Aerobic Vaginitis, an Inflammatory State Enriched in Pathobionts with Limited TLR Stimulation. Diagnostics, 2020, 10, 879.	2.6	19
2874	Effect of stevia on the gut microbiota and glucose tolerance in a murine model of diet-induced obesity. FEMS Microbiology Ecology, 2020, 96, .	2.7	22
2875	Vegetation type determines spore deposition within a forest–agricultural mosaic landscape. FEMS Microbiology Ecology, 2020, 96, .	2.7	22
2876	Phenotypic Comparability from Genotypic Variability among Physically Structured Microbial Consortia. Integrative and Comparative Biology, 2020, 60, 288-303.	2.0	5
2877	An <i>In Vitro</i> Pipeline for Screening and Selection of Citrus-Associated Microbiota with Potential Anti-" <i>Candidatus</i> Liberibacter asiaticus―Properties. Applied and Environmental Microbiology, 2020, 86, .	3.1	31
2878	Biogeographic Patterns in Members of Globally Distributed and Dominant Taxa Found in Port Microbial Communities. MSphere, 2020, 5, .	2.9	15
2879	Assessment of the microbial interplay during anaerobic co-digestion of wastewater sludge using common components analysis. PLoS ONE, 2020, 15, e0232324.	2.5	18
2880	Skin Microbiome in Cutaneous T-Cell Lymphoma byÂ16S and Whole-Genome Shotgun Sequencing. Journal of Investigative Dermatology, 2020, 140, 2304-2308.e7.	0.7	22
2881	Denitrification during infiltration for managed aquifer recharge: Infiltration rate controls and microbial response. Science of the Total Environment, 2020, 727, 138642.	8.0	25
2882	Chicken Intestinal Mycobiome: Initial Characterization and Its Response to Bacitracin Methylene Disalicylate. Applied and Environmental Microbiology, 2020, 86, .	3.1	20
2883	Microbial predictors of healing and short-term effect of debridement on the microbiome of chronic wounds. Npj Biofilms and Microbiomes, 2020, 6, 21.	6.4	86
2884	The relationship between cigarette smoking and the tongue microbiome in an East Asian population. Journal of Oral Microbiology, 2020, 12, 1742527.	2.7	18
2885	Sea Cucumber Intestinal Regeneration Reveals Deterministic Assembly of the Gut Microbiome. Applied and Environmental Microbiology, 2020, 86, .	3.1	21
2886	Cystic Fibrosis Patients Infected With Epidemic Pseudomonas aeruginosa Strains Have Unique Microbial Communities. Frontiers in Cellular and Infection Microbiology, 2020, 10, 173.	3.9	8
2887	Marine Microbial Community Composition During the Upwelling Season in the Southern Benguela. Frontiers in Marine Science, 2020, 7, .	2.5	8
2888	Temporal Dynamics of Bacterial Communities in a Pilot-Scale Vermireactor Fed with Distilled Grape Marc. Microorganisms, 2020, 8, 642.	3.6	14
2889	Crop rotation, but not cover crops, influenced soil bacterial community composition in a corn-soybean system in southern Wisconsin. Applied Soil Ecology, 2020, 154, 103603.	4.3	47
2890	Experimental assembly reveals ecological drift as a major driver of root nodule bacterial diversity in a woody legume crop. FEMS Microbiology Ecology, 2020, 96, .	2.7	13

#	Article	IF	CITATIONS
2891	Moderate phosphorus additions consistently affect community composition of arbuscular mycorrhizal fungi in tropical montane forests in southern Ecuador. New Phytologist, 2020, 227, 1505-1518.	7.3	27
2892	Decoding the language of microbiomes using word-embedding techniques, and applications in inflammatory bowel disease. PLoS Computational Biology, 2020, 16, e1007859.	3.2	11
2893	Ecological Assembly Processes of the Bacterial and Fungal Microbiota of Wild and Domesticated Wheat Species. Phytobiomes Journal, 2020, 4, 217-224.	2.7	34
2894	Planting Spartina alterniflora in a salt marsh denuded of vegetation by an oil spill induces a rapid response in the soil microbial community. Ecological Engineering, 2020, 151, 105815.	3 . 6	15
2895	Changes in the cervical microbiota of cervical cancer patients after primary radio-chemotherapy. International Journal of Gynecological Cancer, 2020, 30, 1326-1330.	2.5	12
2896	Lake characteristics influence how methanogens in littoral sediments respond to terrestrial litter inputs. ISME Journal, 2020, 14, 2153-2163.	9.8	8
2897	Tracing the early steps of competition-driven eco-morphological divergence in two sister species of passerines. Evolutionary Ecology, 2020, 34, 501-524.	1.2	9
2898	An intensive multilocation temporal dataset of fungal communities in the root and rhizosphere of Brassica napus. Data in Brief, 2020, 30, 105467.	1.0	3
2899	Effects of Agave Fructans, Inulin, and Starch on Metabolic Syndrome Aspects in Healthy Wistar Rats. ACS Omega, 2020, 5, 10740-10749.	3.5	11
2900	Metagenomic Analysis of Regularly Microwave-Treated and Untreated Domestic Kitchen Sponges. Microorganisms, 2020, 8, 736.	3.6	12
2901	Densely Populated Water Droplets in Heavy-Oil Seeps. Applied and Environmental Microbiology, 2020, 86, .	3.1	12
2902	Viral metagenomic analysis of fecal samples reveals an enteric virome signature in irritable bowel syndrome. BMC Microbiology, 2020, 20, 123.	3.3	20
2903	The Effects of the Marine-Derived Polysaccharides Laminarin and Chitosan on Aspects of Colonic Health in Pigs Challenged with Dextran Sodium Sulphate. Marine Drugs, 2020, 18, 262.	4.6	15
2904	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	27.8	283
2905	Integrative Analysis of Fecal Metagenomics and Metabolomics in Colorectal Cancer. Cancers, 2020, 12, 1142.	3.7	53
2906	Comparison between the intestinal microbiome of healthy fish and fish experimentally infected with <i>Streptococcus agalactiae </i> i>. Aquaculture Research, 2020, 51, 3412-3420.	1.8	14
2907	Microbial community dynamics in mesophilic and thermophilic batch reactors under methanogenic, phenyl acid-forming conditions. Biotechnology for Biofuels, 2020, 13, 81.	6.2	8
2908	Microbiome profile associated with malignant pleural effusion. PLoS ONE, 2020, 15, e0232181.	2.5	7

#	Article	IF	CITATIONS
2909	An Assessment of Environmental Metabarcoding Protocols Aiming at Favoring Contemporary Biodiversity in Inventories of Deep-Sea Communities. Frontiers in Marine Science, 2020, 7, .	2.5	36
2910	Tree Root Zone Microbiome: Exploring the Magnitude of Environmental Conditions and Host Tree Impact. Frontiers in Microbiology, 2020, $11,749$.	3.5	20
2911	The Bacterial Gut Microbiota of Adult Patients Infected, Colonized or Noncolonized by Clostridioides difficile. Microorganisms, 2020, 8, 677.	3.6	25
2912	Reused poultry litter microbiome with competitive exclusion potential against <i>Salmonella</i> Heidelberg. Journal of Environmental Quality, 2020, 49, 869-881.	2.0	39
2913	Bioorthogonal non-canonical amino acid tagging reveals translationally active subpopulations of the cystic fibrosis lung microbiota. Nature Communications, 2020, 11, 2287.	12.8	25
2914	Coâ€occurrence of antibiotic, biocide, and heavy metal resistance genes in bacteria from metal and radionuclide contaminated soils at the Savannah River Site. Microbial Biotechnology, 2020, 13, 1179-1200.	4.2	89
2915	Multi-proxy analyses of a mid-15th century Middle Iron Age Bantu-speaker palaeo-faecal specimen elucidates the configuration of the â€~ancestral' sub-Saharan African intestinal microbiome. Microbiome, 2020, 8, 62.	11.1	14
2916	Whole egg consumption increases plasma choline and betaine without affecting TMAO levels or gut microbiome in overweight postmenopausal women. Nutrition Research, 2020, 78, 36-41.	2.9	36
2917	Adding insult to injury: Effects of chronic oxybenzone exposure and elevated temperature on two reef-building corals. Science of the Total Environment, 2020, 733, 139030.	8.0	44
2918	Fecal microbiota transplant rescues mice from human pathogen mediated sepsis by restoring systemic immunity. Nature Communications, 2020, 11, 2354.	12.8	7 5
2919	Antimicrobial resistance genes in raw milk for human consumption. Scientific Reports, 2020, 10, 7464.	3.3	53
2920	The role of the adaptor molecule STING during Schistosoma mansoni infection. Scientific Reports, 2020, 10, 7901.	3.3	8
2921	Antibiotic exposure postweaning disrupts the neurochemistry and function of enteric neurons mediating colonic motor activity. American Journal of Physiology - Renal Physiology, 2020, 318, G1042-G1053.	3.4	27
2922	Genome reconstruction of the non-culturable spinach downy mildew Peronospora effusa by metagenome filtering. PLoS ONE, 2020, 15, e0225808.	2.5	14
2923	Dietary Soluble and Insoluble Fiber With or Without Enzymes Altered the Intestinal Microbiota in Weaned Pigs Challenged With Enterotoxigenic E. coli F18. Frontiers in Microbiology, 2020, 11, 1110.	3.5	31
2924	Detecting personal microbiota signatures at artificial crime scenes. Forensic Science International, 2020, 313, 110351.	2.2	19
2925	Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. Neurogastroenterology and Motility, 2020, 32, e13914.	3.0	68
2926	Cultivation-independent and cultivation-dependent metagenomes reveal genetic and enzymatic potential of microbial community involved in the degradation of a complex microbial polymer. Microbiome, 2020, 8, 76.	11.1	59

#	Article	IF	CITATIONS
2927	Elucidating the influence of resident seed and soil microbiota on the developing creeping bentgrassAmicrobiome., 2020, 3, e20038.		6
2928	Bacterial communities on the gills of bonefish (Albula vulpes) in the Florida Keys and The Bahamas show spatial structure and differential abundance of disease-associated bacteria. Marine Biology, 2020, 167, 1.	1.5	6
2929	The effect of triploidy on the performance, gut microbiome and behaviour of juvenile Atlantic salmon (Salmo salar) raised at low temperature. Applied Animal Behaviour Science, 2020, 229, 105031.	1.9	10
2930	Cultivation of methanotrophic bacteria in a novel bubble-free membrane bioreactor for microbial protein production. Bioresource Technology, 2020, 310, 123388.	9.6	34
2931	Ecological succession in the vaginal microbiota during pregnancy and birth. ISME Journal, 2020, 14, 2325-2335.	9.8	45
2932	Ecology eclipses phylogeny as a major driver of nematode parasite community structure in a graminivorous primate. Functional Ecology, 2020, 34, 1898-1906.	3 . 6	2
2933	Significant host―and environmentâ€dependent differentiation among highly sporadic fungal endophyte communities in cereal crops―elated wild grasses. Environmental Microbiology, 2020, 22, 3357-3374.	3.8	32
2934	Shortâ€term highâ€intensity interval training exercise does not affect gut bacterial community diversity or composition of lean and overweight men. Experimental Physiology, 2020, 105, 1268-1279.	2.0	30
2935	Gut Microbial Metabolites Induce Donor-Specific Tolerance of Kidney Allografts through Induction of T Regulatory Cells by Short-Chain Fatty Acids. Journal of the American Society of Nephrology: JASN, 2020, 31, 1445-1461.	6.1	50
2936	Significant Short-Term Shifts in the Microbiomes of Smokers With Periodontitis After Periodontal Therapy With Amoxicillin & Description Metronidazole as Revealed by 16S rDNA Amplicon Next Generation Sequencing. Frontiers in Cellular and Infection Microbiology, 2020, 10, 167.	3.9	5
2937	Early Introduction of Solid Feeds: Ingestion Level Matters More Than Prebiotic Supplementation for Shaping Gut Microbiota. Frontiers in Veterinary Science, 2020, 7, 261.	2.2	9
2938	Influence of oil, dispersant, and pressure on microbial communities from the Gulf of Mexico. Scientific Reports, 2020, 10, 7079.	3.3	15
2939	Environmental DNA survey captures patterns of fish and invertebrate diversity across a tropical seascape. Scientific Reports, 2020, 10, 6729.	3.3	60
2940	The probiotic <i>L. casei</i> LC-XCALâ,,¢ improves metabolic health in a diet-induced obesity mouse model without altering the microbiome. Gut Microbes, 2020, 12, 1747330.	9.8	16
2941	Gut Feelings Begin in Childhood: the Gut Metagenome Correlates with Early Environment, Caregiving, and Behavior. MBio, 2020, 11 , .	4.1	40
2942	Microbiota characterization of Exaiptasia diaphana from the Great Barrier Reef. Animal Microbiome, 2020, 2, 10.	3.8	23
2943	Azolla filiculoides L. as a source of metal-tolerantÂmicroorganisms. PLoS ONE, 2020, 15, e0232699.	2.5	24
2944	Detection of 4-Nitrophenol, a Model Toxic Compound, Using Multi-Stage Microbial Fuel Cells. Frontiers in Environmental Science, 2020, 8, .	3.3	18

#	Article	IF	CITATIONS
2945	Cover Crop Impact on Soil Organic Carbon, Nitrogen Dynamics and Microbial Diversity in a Mediterranean Semiarid Vineyard. Sustainability, 2020, 12, 3256.	3.2	30
2946	Intensive land uses modify assembly process and potential metabolic function of edaphic bacterial communities in the Yellow River Delta, China. Science of the Total Environment, 2020, 720, 137713.	8.0	11
2947	Plant litter amendments in restored wetland soils altered microbial communities more than clay additions. Soil Biology and Biochemistry, 2020, 147, 107846.	8.8	9
2948	Community-level signatures of ecological succession in natural bacterial communities. Nature Communications, 2020, 11, 2386.	12.8	33
2949	Shale gas development has limited effects on stream biology and geochemistry in a gradient-based, multiparameter study in Pennsylvania. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3670-3677.	7.1	22
2950	Single-cell amplicon sequencing reveals community structures and transmission trends of protist-associatedÂbacteria in aÂtermite host. PLoS ONE, 2020, 15, e0233065.	2.5	8
2951	Longitudinal Associations of the Cystic Fibrosis Airway Microbiome and Volatile Metabolites: A Case Study. Frontiers in Cellular and Infection Microbiology, 2020, 10, 174.	3.9	19
2952	Cloacal Swabs Are Unreliable Sources for Estimating Lower Gastro-Intestinal Tract Microbiota Membership and Structure in Broiler Chickens. Microorganisms, 2020, 8, 718.	3.6	12
2953	Bacterial community and environmental factors associated to rivers runoff and their possible impacts on coral reef conservation. Marine Pollution Bulletin, 2020, 156, 111233.	5.0	9
2954	Flocs in disguise? High granule abundance found in continuous-flow activated sludge treatment plants. Water Research, 2020, 179, 115865.	11.3	41
2955	Evaluation of fecal Lactobacillus populations in dogs with idiopathic epilepsy: a pilot study. Animal Microbiome, 2020, 2, .	3.8	13
2956	Soil prokaryotes are associated with decreasing Fusarium oxysporum density during anaerobic soil disinfestation in the tomato field. Applied Soil Ecology, 2020, 155, 103632.	4.3	9
2957	Large-scale multivariate dataset on the characterization of microbiota diversity, microbial growth dynamics, metabolic spoilage volatilome and sensorial profiles of two industrially produced meat products subjected to changes in lactate concentration and packaging atmosphere. Data in Brief, 2020, 30, 105453.	1.0	8
2958	Copper accumulation in agricultural soils: Risks for the food chain and soil microbial populations. Science of the Total Environment, 2020, 734, 139434.	8.0	58
2959	Associations between UK tap water and gut microbiota composition suggest the gut microbiome as a potential mediator of health differences linked to water quality. Science of the Total Environment, 2020, 739, 139697.	8.0	11
2960	Longitudinal analysis reveals transition barriers between dominant ecological states in the gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13839-13845.	7.1	47
2961	Crohn's Disease Differentially Affects Region-Specific Composition and Aerotolerance Profiles of Mucosally Adherent Bacteria. Inflammatory Bowel Diseases, 2020, 26, 1843-1855.	1.9	9
2962	Species diversity of fungal endophytes across a stress gradient for plants. New Phytologist, 2020, 228, 210-225.	7.3	28

#	Article	IF	CITATIONS
2963	The features of polyglutamine regions depend on their evolutionary stability. BMC Evolutionary Biology, 2020, 20, 59.	3.2	6
2964	Pathobiomes Revealed that Pseudomonas fuscovaginae and Sarocladium oryzae Are Independently Associated with Rice Sheath Rot. Microbial Ecology, 2020, 80, 627-642.	2.8	14
2965	Large microbiota survey reveals how the microbial ecology of cooked ham is shaped by different processing steps. Food Microbiology, 2020, 91, 103547.	4.2	18
2966	Nitrifying biofilms deprived of organic carbon show higher functional resilience to increases in carbon supply. Scientific Reports, 2020, 10, 7121.	3.3	21
2967	Spatial heterogeneity of the shorebird gastrointestinal microbiome. Royal Society Open Science, 2020, 7, 191609.	2.4	17
2968	The Core Gut Microbiome of Black Soldier Fly (Hermetia illucens) Larvae Raised on Low-Bioburden Diets. Frontiers in Microbiology, 2020, 11, 993.	3.5	91
2969	High levels of primary biogenic organic aerosols are driven by only a few plant-associated microbial taxa. Atmospheric Chemistry and Physics, 2020, 20, 5609-5628.	4.9	16
2970	Longâ€ŧerm stability of microbiome diversity and composition in fecal samples stored in eNAT medium. MicrobiologyOpen, 2020, 9, e1046.	3.0	9
2971	Station and train surface microbiomes of Mexico City's metro (subway/underground). Scientific Reports, 2020, 10, 8798.	3.3	18
2972	Supplementation with Sea Vegetables Palmaria mollis and Undaria pinnatifida Exerts Metabolic Benefits in Diet-Induced Obesity in Mice. Current Developments in Nutrition, 2020, 4, nzaa072.	0.3	8
2973	Analysis of bacterial and archaeal communities associated with Fogo volcanic soils of different ages. FEMS Microbiology Ecology, 2020, 96, .	2.7	4
2974	Environmental DNA surveys detect distinct metazoan communities across abyssal plains and seamounts in the western Clarion Clipperton Zone. Molecular Ecology, 2020, 29, 4588-4604.	3.9	50
2975	Over Winter Microbial Processes in a Svalbard Snow Pack: An Experimental Approach. Frontiers in Microbiology, 2020, 11, 1029.	3.5	4
2976	Eye-Catching Microbesâ€"Polyphasic Analysis of the Microbiota on Microscope Oculars Verifies Their Role as Fomites. Journal of Clinical Medicine, 2020, 9, 1572.	2.4	3
2977	Comparison of lung microbiota between antineutrophil cytoplasmic antibody-associated vasculitis and sarcoidosis. Scientific Reports, 2020, 10, 9466.	3.3	7
2978	Effect of life stage and pesticide exposure on the gut microbiota of Aedes albopictus and Culex pipiens L. Scientific Reports, 2020, 10, 9489.	3.3	12
2979	Heterosis of leaf and rhizosphere microbiomes in fieldâ€grown maize. New Phytologist, 2020, 228, 1055-1069.	7.3	66
2980	Human Milk Oligosaccharides Modulate the Risk for Preterm Birth in a Microbiome-Dependent and -Independent Manner. MSystems, 2020, 5, .	3.8	10

#	Article	IF	CITATIONS
2981	Topography of the respiratory tract bacterial microbiota in cattle. Microbiome, 2020, 8, 91.	11.1	38
2982	Prokaryotic Community Composition and Extracellular Polymeric Substances Affect Soil Microaggregation in Carbonate Containing Semiarid Grasslands. Frontiers in Environmental Science, 2020, 8, .	3.3	17
2983	Altered gut bacterial–fungal interkingdom networks in patients with current depressive episode. Brain and Behavior, 2020, 10, e01677.	2.2	31
2984	Deciphering the rhizosphere microbiome of a bamboo plant in response to different chromium contamination levels. Journal of Hazardous Materials, 2020, 399, 123107.	12.4	32
2985	2,3,7,8-Tetrachlorodibenzo- <i>p</i> dioxin Dechlorination is Differentially Enhanced by Dichlorobenzene Amendment in Passaic River, NJ Sediments. Environmental Science & Envir	10.0	6
2986	Sward type alters the relative abundance of members of the rumen microbial ecosystem in dairy cows. Scientific Reports, 2020, 10, 9317.	3.3	11
2987	Temporal Dynamics of the Gut Bacteriome and Mycobiome in the Weanling Pig. Microorganisms, 2020, 8, 868.	3.6	39
2988	Bacterial community dissimilarity in soils is driven by longâ€ŧerm landâ€useÂpractices. , 2020, 3, e20031.		15
2989	Diverse Thaumarchaeota Dominate Subsurface Ammonia-oxidizing Communities in Semi-arid Floodplains in the Western United States. Microbial Ecology, 2020, 80, 778-792.	2.8	19
2990	Antibiotic-resistant Escherichia coli and Klebsiella spp. in greywater reuse systems and pond water used for agricultural irrigation in the West Bank, Palestinian Territories. Environmental Research, 2020, 188, 109777.	7.5	13
2991	Influence of salt concentration and iodized table salt on the microbiota of fermented cucumbers. Food Microbiology, 2020, 92, 103552.	4.2	19
2992	Toward Standards in Clinical Microbiota Studies: Comparison of Three DNA Extraction Methods and Two Bioinformatic Pipelines. MSystems, 2020, 5, .	3.8	36
2993	Impacts of a novel defensive symbiosis on the nematode host microbiome. BMC Microbiology, 2020, 20, 159.	3.3	8
2994	Eggshell and environmental bacteria contribute to the intestinal microbiota of growing chickens. Journal of Animal Science and Biotechnology, 2020, 11, 60.	5.3	35
2995	Fat, oil, and grease (FOG) deposits yield higher methane than FOG in anaerobic co-digestion with waste activated sludge. Journal of Environmental Management, 2020, 268, 110708.	7.8	19
2996	Response of bacterial communities in Barents Sea sediments in case of a potential CO2 leakage from carbon reservoirs. Marine Environmental Research, 2020, 160, 105050.	2.5	15
2997	Biochar addition reinforces microbial interspecies cooperation in methanation of sugar beet waste (pulp). Science of the Total Environment, 2020, 730, 138921.	8.0	26
2998	Mollusk microbiota shift during Angiostrongylus cantonensis infection in the freshwater snail Biomphalaria glabrata and the terrestrial slug Phillocaulis soleiformis. Parasitology Research, 2020, 119, 2495-2503.	1.6	12

#	Article	IF	CITATIONS
2999	Culture-Independent Analysis of Linuron-Mineralizing Microbiota and Functions in on-Farm Biopurification Systems via DNA-Stable Isotope Probing: Comparison with Enrichment Culture. Environmental Science & Environmental Sci	10.0	19
3000	Amending microbiota by targeting intestinal inflammation with TNF blockade attenuates development of colorectal cancer. Nature Cancer, 2020, 1, 723-734.	13.2	50
3001	Expanding the Diversity of Bacterioplankton Isolates and Modeling Isolation Efficacy with Large-Scale Dilution-to-Extinction Cultivation. Applied and Environmental Microbiology, 2020, 86, .	3.1	34
3002	Sleep fragmentation increases blood pressure and is associated with alterations in the gut microbiome and fecal metabolome in rats. Physiological Genomics, 2020, 52, 280-292.	2.3	61
3003	Biodiversity and Community Structure of Mesozooplankton in the Marine and Coastal National Park Areas of Korea. Diversity, 2020, 12, 233.	1.7	7
3004	Surviving marginalized reefs: assessing the implications of the microbiome on coral physiology and survivorship. Coral Reefs, 2020, 39, 795-807.	2.2	19
3005	Survivor microbial populations in post-chlorinated wastewater are strongly associated with untreated hospital sewage and include ceftazidime and meropenem resistant populations. Science of the Total Environment, 2020, 740, 140186.	8.0	37
3006	A prebiotic-enhanced lipid-based nutrient supplement (LNSp) increases Bifidobacterium relative abundance and enhances short-chain fatty acid production in simulated colonic microbiota from undernourished infants. FEMS Microbiology Ecology, 2020, 96, .	2.7	10
3007	Towards a disease-associated common trait of gut microbiota dysbiosis: The pivotal role of Akkermansia muciniphila. Digestive and Liver Disease, 2020, 52, 1002-1010.	0.9	23
3008	Clay content modulates differences in bacterial community structure in soil aggregates of different size. Geoderma, 2020, 376, 114544.	5.1	33
3009	Changes in microbial community composition, activity, and greenhouse gas production upon inundation of drained iron-rich peat soils. Soil Biology and Biochemistry, 2020, 149, 107862.	8.8	12
3010	Influences of Hillslope Biogeochemistry on Anaerobic Soil Organic Matter Decomposition in a Tundra Watershed. Journal of Geophysical Research G: Biogeosciences, 2020, 125, e2019JG005512.	3.0	4
3011	One year cross-sectional study in adult and neonatal intensive care units reveals the bacterial and antimicrobial resistance genes profiles in patients and hospital surfaces. PLoS ONE, 2020, 15, e0234127.	2.5	18
3012	Impact of DNA Extraction Method on Variation in Human and Built Environment Microbial Community and Functional Profiles Assessed by Shotgun Metagenomics Sequencing. Frontiers in Microbiology, 2020, 11, 953.	3.5	40
3013	Mining the Yucatan Coastal Microbiome for the Identification of Non-Ribosomal Peptides Synthetase (NRPS) Genes. Toxins, 2020, 12, 349.	3.4	9
3014	Characterisation of fungal and bacterial dynamics in an active green wall used for indoor air pollutant removal. Building and Environment, 2020, 179, 106987.	6.9	24
3015	Increased diversity and concordant shifts in community structure of coralâ€associated Symbiodiniaceae and bacteria subjected to chronic human disturbance. Molecular Ecology, 2020, 29, 2477-2491.	3.9	26
3016	Engineering CRISPR/Cas9 to mitigate abundant host contamination for 16S rRNA gene-based amplicon sequencing. Microbiome, 2020, 8, 80.	11.1	27

#	ARTICLE	IF	CITATIONS
3017	Microbial symbiosis and coevolution of an entire clade of ancient vertebrates: the gut microbiota of sea turtles and its relationship to their phylogenetic history. Animal Microbiome, 2020, 2, 17.	3.8	30
3018	Contrasting bacteriome of the hornwort Leiosporoceros dussii in two nearby sites with emphasis on the hornwort-cyanobacterial symbiosis. Symbiosis, 2020, 81, 39-52.	2.3	24
3019	Characterising the soil fungal microbiome in metropolitan green spaces across a vegetation biodiversity gradient. Fungal Ecology, 2020, 47, 100939.	1.6	20
3020	The effect of maternal antibiotic use in sows on intestinal development in offspring. Journal of Animal Science, 2020, 98, .	0.5	12
3021	An empirical Bayes approach to normalization and differential abundance testing for microbiome data. BMC Bioinformatics, 2020, 21, 225.	2.6	11
3022	Characterizing the microbiome of ectoparasitic louse flies feeding on migratory raptors. PLoS ONE, 2020, 15, e0234050.	2.5	5
3023	Assessment of bacterial community composition within and among Acropora loripes colonies in the wild and in captivity. Coral Reefs, 2020, 39, 1245-1255.	2.2	28
3024	Freeze-dried fecal samples are biologically active after long-lasting storage and suited to fecal microbiota transplantation in a preclinical murine model of <i>Clostridioides difficile</i> infection. Gut Microbes, 2020, 11, 1405-1422.	9.8	24
3025	Host genotype explains rhizospheric microbial community composition: the case of wild cotton metapopulations (Gossypium hirsutum L.) in Mexico. FEMS Microbiology Ecology, 2020, 96, .	2.7	7
3026	Short-chain fructo-oligosaccharides supplementation to suckling piglets: Assessment of pre- and post-weaning performance and gut health. PLoS ONE, 2020, 15, e0233910.	2.5	10
3027	A salty start: Brackish water start-up as a microbial management strategy for nitrifying bioreactors with variable salinity. Science of the Total Environment, 2020, 739, 139934.	8.0	21
3028	Prokaryotic and Viral Community Composition of Freshwater Springs in Florida, USA. MBio, 2020, 11, .	4.1	22
3029	Intestinal microbes: an axis of functional diversity among large marine consumers. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192367.	2.6	12
3030	Temperate Forests Dominated by Arbuscular or Ectomycorrhizal Fungi Are Characterized by Strong Shifts from Saprotrophic to Mycorrhizal Fungi with Increasing Soil Depth. Microbial Ecology, 2021, 82, 377-390.	2.8	28
3031	MetaRNAseq analysis of surti buffalo rumen content reveals that transcriptionally active microorganisms need not be abundant. Molecular Biology Reports, 2020, 47, 5101-5114.	2.3	3
3032	Shared bacterial communities between soil, stored drinking water, and hands in rural Bangladeshi households. Water Research X, 2020, 9, 100056.	6.1	5
3033	Gut Microbiome Critically Impacts PCB-induced Changes in Metabolic Fingerprints and the Hepatic Transcriptome in Mice. Toxicological Sciences, 2020, 177, 168-187.	3.1	19
3034	GenePiper, a Graphical User Interface Tool for Microbiome Sequence Data Mining. Microbiology Resource Announcements, 2020, 9, .	0.6	7

#	Article	IF	CITATIONS
3035	Revealing links between gut microbiome and its fungal community in Type 2 Diabetes Mellitus among Emirati subjects: A pilot study. Scientific Reports, 2020, 10, 9624.	3.3	31
3036	Comparison of Bioinformatics Pipelines and Operating Systems for the Analyses of 16S rRNA Gene Amplicon Sequences in Human Fecal Samples. Frontiers in Microbiology, 2020, 11, 1262.	3.5	36
3037	Low-Temperature Pretreatment of Organic Feedstocks with Selected Mineral Wastes Sustains Anaerobic Digestion Stability through Trace Metal Release. Environmental Science & December 1920, 54, 9095-9105.	10.0	10
3038	Maternal Microbiota, Cortisol Concentration, and Post-Partum Weight Recovery Are Dependent on Mode of Delivery. Nutrients, 2020, 12, 1779.	4.1	8
3039	Differential colonization of microbial communities inhabiting Lede stone in the urban and rural environment. Science of the Total Environment, 2020, 733, 139339.	8.0	17
3040	Gut bacterial community profile in Pacific white shrimp Litopenaeus vannamei following 5â€aminolevulinic acid supplementation. Aquaculture Research, 2020, 51, 4075-4086.	1.8	7
3041	Human milk fungi: environmental determinants and inter-kingdom associations with milk bacteria in the CHILD Cohort Study. BMC Microbiology, 2020, 20, 146.	3.3	28
3042	Effects of Intra- and Interspecific Plant Density on Rhizosphere Bacterial Communities. Frontiers in Microbiology, 2020, 11, 1045.	3.5	25
3043	Effect of multispecies probiotic on gut microbiota composition in individuals with intestinal constipation: A double-blind, placebo-controlled randomized trial. Nutrition, 2020, 78, 110890.	2.4	20
3044	Arbuscular mycorrhizal fungus inocula from coastal sand dunes arrest olive cutting growth under salinity stress. Mycorrhiza, 2020, 30, 475-489.	2.8	10
3045	AMF communities associated to Vitis vinifera in an Italian vineyard subjected to integrated pest management at two different phenological stages. Scientific Reports, 2020, 10, 9197.	3.3	16
3046	Heterogeneity of the rice microbial community of the Chinese centuriesâ€old Honghe Hani rice terraces system. Environmental Microbiology, 2020, 22, 3429-3445.	3.8	8
3047	Eutrophication as a driver of microbial community structure in lake sediments. Environmental Microbiology, 2020, 22, 3446-3462.	3.8	51
3048	Xenometabolite signatures in the UC Davis type 2 diabetes mellitus rat model revealed using a metabolomics platform enriched with microbe-derived metabolites. American Journal of Physiology - Renal Physiology, 2020, 319, G157-G169.	3.4	13
3049	The Composition and Function of Microbiomes Within Microcystis Colonies Are Significantly Different Than Native Bacterial Assemblages in Two North American Lakes. Frontiers in Microbiology, 2020, 11, 1016.	3.5	44
3050	Anti-Inflammatory and Gut Microbiota Modulatory Effect of Lactobacillus rhamnosus Strain LDTM 7511 in a Dextran Sulfate Sodium-Induced Colitis Murine Model. Microorganisms, 2020, 8, 845.	3.6	23
3051	Dynamics and resilience of soil mycobiome under multiple organic and inorganic pulse disturbances. Science of the Total Environment, 2020, 733, 139173.	8.0	17
3052	Meconium microbiota predicts clinical early-onset neonatal sepsis in preterm neonates. Journal of Maternal-Fetal and Neonatal Medicine, 2022, 35, 1935-1943.	1.5	11

#	Article	IF	CITATIONS
3053	Spatial Compartmentalization of the Microbiome between the Lumen and Crypts Is Lost in the Murine Cecum following the Process of Surgery, Including Overnight Fasting and Exposure to Antibiotics. MSystems, 2020, 5, .	3.8	21
3054	Fecal microbiota transplantation from high caloric-fed donors alters glucose metabolism in recipient mice, independently of adiposity or exercise status. American Journal of Physiology - Endocrinology and Metabolism, 2020, 319, E203-E216.	3.5	24
3055	Microorganisms Associated With Dust on Alpine Snow. Frontiers in Earth Science, 2020, 8, .	1.8	4
3056	N2 Fixation and New Insights Into Nitrification From the Ice-Edge to the Equator in the South Pacific Ocean. Frontiers in Marine Science, 2020, 7, .	2.5	18
3057	Unraveling the Diversity of Eukaryotic Microplankton in a Large and Deep Perialpine Lake Using a High Throughput Sequencing Approach. Frontiers in Microbiology, 2020, 11, 789.	3.5	20
3058	Persistence of a Core Microbiome Through the Ontogeny of a Multi-Host Parasite. Frontiers in Microbiology, 2020, 11, 954.	3.5	26
3059	Comparison of Bacterial and Fungal Composition and Their Chemical Interaction in Free Tropospheric Air and Snow Over an Entire Winter Season at Mount Sonnblick, Austria. Frontiers in Microbiology, 2020, 11, 980.	3. 5	14
3060	Single-Cell Genomics of Novel Actinobacteria With the Wood–Ljungdahl Pathway Discovered in a Serpentinizing System. Frontiers in Microbiology, 2020, 11, 1031.	3.5	41
3061	Depth-Differentiation and Seasonality of Planktonic Microbial Assemblages in the Monterey Bay Upwelling System. Frontiers in Microbiology, 2020, 11, 1075.	3.5	29
3062	Taxon Appearance From Extraction and Amplification Steps Demonstrates the Value of Multiple Controls in Tick Microbiota Analysis. Frontiers in Microbiology, 2020, 11, 1093.	3.5	25
3063	Crop Management Impacts the Soybean (Glycine max) Microbiome. Frontiers in Microbiology, 2020, 11, 1116.	3. 5	48
3064	Cryoconite Hole Location in East-Antarctic Untersee Oasis Shapes Physical and Biological Diversity. Frontiers in Microbiology, 2020, 11, 1165.	3.5	16
3065	Rhizospheric Organic Acids as Biostimulants: Monitoring Feedbacks on Soil Microorganisms and Biochemical Properties. Frontiers in Plant Science, 2020, 11, 633.	3.6	93
3066	Association of the Salivary Microbiome With Animal Contact During Early Life and Stress-Induced Immune Activation in Healthy Participants. Frontiers in Psychiatry, 2020, 11, 353.	2.6	3
3067	Whole-Genome Deep Sequencing Reveals Host-Driven in-planta Evolution of Columnea Latent Viroid (CLVd) Quasi-Species Populations. International Journal of Molecular Sciences, 2020, 21, 3262.	4.1	7
3068	Effect of Litter Treatment on Campylobacter jejuni in Broilers and on Cecal Microbiota. Pathogens, 2020, 9, 333.	2.8	3
3069	New Soil, Old Plants, and Ubiquitous Microbes: Evaluating the Potential of Incipient Basaltic Soil to Support Native Plant Growth and Influence Belowground Soil Microbial Community Composition. Sustainability, 2020, 12, 4209.	3.2	2
3070	Subgingival microbiome and clinical periodontal status in an elderly cohort: The WHICAP ancillary study of oral health. Journal of Periodontology, 2020, 91, S56-S67.	3.4	31

#	Article	IF	CITATIONS
3071	Inclusion of seasonal variation in river system microbial communities and phototroph activity increases environmental relevance of laboratory chemical persistence tests. Science of the Total Environment, 2020, 733, 139070.	8.0	10
3072	Seasonal contamination of well-water in flood-prone colonias and other unincorporated U.S. communities. Science of the Total Environment, 2020, 740, 140111.	8.0	14
3073	The population of oomycetes in a recycled irrigation water system at a horticultural nursery in southern California. Water Research, 2020, 183, 116050.	11.3	13
3074	Transient effect of single or repeated acute deoxynivalenol and zearalenone dietary challenge on fecal microbiota composition in female finishing pigs. Animal, 2020, 14, 2277-2287.	3.3	11
3075	Evolution of gut microbial community through reproductive life in female rabbits and investigation of the link with offspring survival. Animal, 2020, 14, 2253-2261.	3.3	5
3076	Assessing similarities and disparities in the skin microbiota between wild and laboratory populations of house mice. ISME Journal, 2020, 14, 2367-2380.	9.8	25
3077	Characterizing dysbiosis of gut microbiome in PD: evidence for overabundance of opportunistic pathogens. Npj Parkinson's Disease, 2020, 6, 11.	5. 3	140
3078	Remarkably Complex Microbial Community Composition in Bromeliad Tank Waters Revealed by eDNA Metabarcoding. Journal of Eukaryotic Microbiology, 2020, 67, 593-607.	1.7	3
3079	Oral Microbiota Display Profound Differential Metabolic Kinetics and Community Shifts upon Incubation with Sucrose, Trehalose, Kojibiose, and Xylitol. Applied and Environmental Microbiology, 2020, 86, .	3.1	11
3080	Effect of Gut Microbiota and <i>PNPLA3</i> rs738409 Variant on Nonalcoholic Fatty Liver Disease (NAFLD) in Obese Youth. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e3575-e3585.	3.6	51
3081	Susceptibility of Red Mason Bee Larvae to Bacterial Threats Due to Microbiome Exchange with Imported Pollen Provisions. Insects, 2020, 11, 373.	2.2	23
3082	Growth and rapid succession of methanotrophs effectively limit methane release during lake overturn. Communications Biology, 2020, 3, 108.	4.4	40
3083	Specialized microbiome of the cave-dwelling sponge Plakina kanaky (Porifera, Homoscleromorpha). FEMS Microbiology Ecology, 2020, 96, .	2.7	8
3084	Association of antimicrobial resistance and gut microbiota composition in human and non-human primates at an urban ecotourism site. Gut Pathogens, 2020, 12, 14.	3.4	8
3085	In situ Linkage of Fungal and Bacterial Proliferation to Microbiologically Influenced Corrosion in B20 Biodiesel Storage Tanks. Frontiers in Microbiology, 2020, 11, 167.	3.5	24
3086	Microbiota Composition and Evenness Predict Survival Rate of Oysters Confronted to Pacific Oyster Mortality Syndrome. Frontiers in Microbiology, 2020, 11, 311.	3.5	57
3087	Effect of a Laminarin Rich Macroalgal Extract on the Caecal and Colonic Microbiota in the Post-Weaned Pig. Marine Drugs, 2020, 18, 157.	4.6	29
3088	α-Linolenic Acid-Rich Diet Influences Microbiota Composition and Villus Morphology of the Mouse Small Intestine. Nutrients, 2020, 12, 732.	4.1	21

#	Article	IF	CITATIONS
3089	Characterization of antibiotic resistance and host-microbiome interactions in the human upper respiratory tract during influenza infection. Microbiome, 2020, 8, 39.	11.1	41
3090	Niche Differentiation of Host-Associated Pelagic Microbes and Their Potential Contribution to Biogeochemical Cycling in Artificially Warmed Lakes. Frontiers in Microbiology, 2020, 11, 582.	3.5	15
3091	Geographical separation and physiology drive differentiation of microbial communities of two discrete populations of the bat <i>Leptonycteris yerbabuenae</i>). MicrobiologyOpen, 2020, 9, 1113-1127.	3.0	15
3092	Investigation of the Diet-Gut-Muscle Axis in the Osteoporotic Fractures in Men Study. Journal of Nutrition, Health and Aging, 2020, 24, 445-452.	3.3	19
3093	Context-dependent dynamics lead to the assembly of functionally distinct microbial communities. Nature Communications, 2020, 11, 1440.	12.8	73
3094	Bacterial analysis in the early developmental stages of the black tiger shrimp (Penaeus monodon). Scientific Reports, 2020, 10, 4896.	3.3	38
3095	A bird's-eye view of phylosymbiosis: weak signatures of phylosymbiosis among all 15 species of cranes. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192988.	2.6	31
3096	Effects of synthetic fertilizer and farm compost on soil nematode community in long-term crop rotation plots: A morphological and metabarcoding approach. PLoS ONE, 2020, 15, e0230153.	2.5	19
3097	Household Pet Ownership and the Microbial Diversity of the Human Gut Microbiota. Frontiers in Cellular and Infection Microbiology, 2020, 10, 73.	3.9	32
3098	Influences of Climate on Phyllosphere Endophytic Bacterial Communities of Wild Poplar. Frontiers in Plant Science, 2020, 11, 203.	3.6	25
3099	High Diversity of Testate Amoebae (Amoebozoa, Arcellinida) Detected by ⟨scp⟩HTS⟨/scp⟩ Analyses in a New England Fen using Newly Designed Taxonâ€specific Primers. Journal of Eukaryotic Microbiology, 2020, 67, 450-462.	1.7	9
3100	The effect of diet change and insulin dysregulation on the fecal microbiome of ponies. Journal of Experimental Biology, 2020, 223, .	1.7	4
3101	Metatranscriptomics Reveals Antibiotic-Induced Resistance Gene Expression in the Murine Gut Microbiota. Frontiers in Microbiology, 2020, 11, 322.	3.5	16
3102	A Multi-Omics Analysis Suggests Links Between the Differentiated Surface Metabolome and Epiphytic Microbiota Along the Thallus of a Mediterranean Seaweed Holobiont. Frontiers in Microbiology, 2020, 11, 494.	3.5	45
3103	The Landscape of Adaptive Evolution of a Gut Commensal Bacteria in Aging Mice. Current Biology, 2020, 30, 1102-1109.e5.	3.9	39
3104	Gut Microbiota and Host Gene Mutations in Colorectal Cancer Patients and Controls of Iranian and Finnish Origin. Anticancer Research, 2020, 40, 1325-1334.	1.1	25
3105	Optimization of Preservation Methods Allows Deeper Insights into Changes of Raw Milk Microbiota. Microorganisms, 2020, 8, 368.	3.6	9
3106	Using ggtree to Visualize Data on Treeâ€Like Structures. Current Protocols in Bioinformatics, 2020, 69, e96.	25.8	810

#	Article	IF	Citations
3107	Consequences of Domestication on Gut Microbiome: A Comparative Study Between Wild Gaur and Domestic Mithun. Frontiers in Microbiology, 2020, 11, 133.	3.5	19
3108	Timing of complementary feeding is associated with gut microbiota diversity and composition and short chain fatty acid concentrations Aover the first year of life. BMC Microbiology, 2020, 20, 56.	3.3	70
3109	Diel, daily, and spatial variation of coral reef seawater microbial communities. PLoS ONE, 2020, 15, e0229442.	2.5	22
3110	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. Annals of Clinical and Translational Neurology, 2020, 7, 406-419.	3.7	59
3111	Long-lasting effects of antibiotics on bacterial communities of adult flies. FEMS Microbiology Ecology, 2020, 96, .	2.7	10
3112	Tissue age, orchard location and disease management influence the composition of fungal and bacterial communities present on the bark of apple trees. Environmental Microbiology, 2020, 22, 2080-2093.	3.8	17
3113	Distinct Community Composition of Previously Uncharacterized Denitrifying Bacteria and Fungi across Different Land-Use Types. Microbes and Environments, 2020, 35, n/a.	1.6	10
3114	Cultivation of Bacteria From Aplysina aerophoba: Effects of Oxygen and Nutrient Gradients. Frontiers in Microbiology, 2020, 11, 175.	3.5	12
3115	Changes in Bacterial Populations and Their Metabolism over 90 Sequential Cultures on Wheat-Based Thin Stillage. Journal of Agricultural and Food Chemistry, 2020, 68, 4717-4729.	5.2	7
3116	Trajectory-based differential expression analysis for single-cell sequencing data. Nature Communications, 2020, 11, 1201.	12.8	345
3117	The microbiome and resistome of chimpanzees, gorillas, and humans across host lifestyle and geography. ISME Journal, 2020, 14, 1584-1599.	9.8	78
3118	Impact of UV irradiation at full scale on bacterial communities in drinking water. Npj Clean Water, 2020, 3, .	8.0	35
3119	Differences in Microbiota Between Two Multilocus Lineages of the Sugarcane Aphid (<i>Melanaphis) Tj ETQq0 0 C 113, 257-265.</i>) rgBT /Ove 2.5	erlock 10 Tf
3120	Isopod holobionts as promising models for lignocellulose degradation. Biotechnology for Biofuels, 2020, 13, 49.	6.2	23
3121	Beginning to offer drinking water at birth increases the species richness and the abundance of Faecalibacterium and Bifidobacterium in the gut of preweaned dairy calves. Journal of Dairy Science, 2020, 103, 4262-4274.	3.4	8
3122	Microbiome Profile of Deep Endometriosis Patients: Comparison of Vaginal Fluid, Endometrium and Lesion. Diagnostics, 2020, 10, 163.	2.6	57
3123	Understanding the Response of Nitrifying Communities to Disturbance in the McMurdo Dry Valleys, Antarctica. Microorganisms, 2020, 8, 404.	3.6	13
3124	Naphthenic acid anaerobic biodegrading consortia enriched from pristine sediments underlying oil sands tailings ponds. Journal of Hazardous Materials, 2020, 394, 122546.	12.4	8

#	Article	IF	CITATIONS
3125	PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS, and COI marker genes. GigaScience, 2020, 9, .	6.4	50
3126	Oral biofilms exposure to chlorhexidine results in altered microbial composition and metabolic profile. Npj Biofilms and Microbiomes, 2020, 6, 13.	6.4	50
3127	Similarities and spatial variations of bacterial and fungal communities in field rice planthopper (Hemiptera: Delphacidae) populations. Insect Science, 2020, 27, 947-963.	3.0	15
3128	Comparative genome-centric analysis reveals seasonal variation in the function of coral reef microbiomes. ISME Journal, 2020, 14, 1435-1450.	9.8	40
3129	Niche-based assembly of bacterial consortia on the diatom $\langle i \rangle$ Thalassiosira rotula $\langle i \rangle$ is stable and reproducible. ISME Journal, 2020, 14, 1614-1625.	9.8	59
3130	Maternal carriage of Prevotella during pregnancy associates with protection against food allergy in the offspring. Nature Communications, 2020, 11, 1452.	12.8	84
3131	Chronic disturbance modulates symbiont (Symbiodiniaceae) beta diversity on a coral reef. Scientific Reports, 2020, 10, 4492.	3.3	13
3132	Variations in microbiota composition of laboratory mice influence Citrobacter rodentium infection via variable short-chain fatty acid production. PLoS Pathogens, 2020, 16, e1008448.	4.7	66
3133	Biofilms remember: Osmotic stress priming as a microbial management strategy for improving salinity acclimation in nitrifying biofilms. Water Research, 2020, 176, 115732.	11.3	47
3134	Metagenomic investigation of African dust events in the Caribbean. FEMS Microbiology Letters, 2020, 367, .	1.8	8
3135	Surveying the Sweetpotato Rhizosphere, Endophyte, and Surrounding Soil Microbiomes at Two North Carolina Farms Reveals Underpinnings of Sweetpotato Microbiome Community Assembly. Phytobiomes Journal, 2020, 4, 75-89.	2.7	7
3136	The microbiome of modern microbialites in Bacalar Lagoon, Mexico. PLoS ONE, 2020, 15, e0230071.	2.5	18
3137	Cervicovaginal microbiome and natural history of HPVÂin a longitudinal study. PLoS Pathogens, 2020, 16, e1008376.	4.7	150
3138	Towards Nutrition-Sensitive Agriculture: An evaluation of biocontrol effects, nutritional value, and ecological impact of bacterial inoculants. Science of the Total Environment, 2020, 724, 138127.	8.0	16
3139	Chemolithoautotropic Diazotrophy Dominates the Nitrogen Fixation Process in Mine Tailings. Environmental Science & Environment	10.0	63
3140	Nitrifying niche differentiation in biofilms from full-scale chloraminated drinking water distribution system. Water Research, 2020, 176, 115738.	11.3	26
3141	Targeted Inhibition of Gut Microbial Trimethylamine N-Oxide Production Reduces Renal Tubulointerstitial Fibrosis and Functional Impairment in a Murine Model of Chronic Kidney Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 1239-1255.	2.4	102
3142	The Differential Vertical Distribution of the Airborne Biological Particles Reveals an Atmospheric Reservoir of Microbial Pathogens and Aeroallergens. Microbial Ecology, 2020, 80, 322-333.	2.8	13

#	Article	IF	Citations
3143	Metabolically cohesive microbial consortia and ecosystem functioning. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190245.	4.0	37
3144	Microbial Community Redundancy and Resilience Underpins High-Rate Anaerobic Treatment of Dairy-Processing Wastewater at Ambient Temperatures. Frontiers in Bioengineering and Biotechnology, 2020, 8, 192.	4.1	22
3145	Biotic and abiotic factors shape arbuscular mycorrhizal fungal communities associated with the roots of the widespread fern <scp><i>Botrychium lunaria</i></scp> (Ophioglossaceae). Environmental Microbiology Reports, 2020, 12, 342-354.	2.4	16
3146	Species detection and delineation in the marine planktonic diatoms <scp><i>Chaetoceros</i></scp> and <scp><i>Bacteriastrum</i></scp> through metabarcoding: making biological sense of haplotype diversity. Environmental Microbiology, 2020, 22, 1917-1929.	3.8	15
3147	Changes in the gut microbiota of mice orally exposed to methylimidazolium ionic liquids. PLoS ONE, 2020, 15, e0229745.	2.5	12
3148	Gut Microbiome Profiles Are Associated With Type 2 Diabetes in Urban Africans. Frontiers in Cellular and Infection Microbiology, 2020, 10, 63.	3.9	95
3149	Reliability of stool microbiome methods for DNA yields and sequencing among infants and young children. MicrobiologyOpen, 2020, 9, e1018.	3.0	7
3150	Strong impact of micropollutants on prokaryotic communities at the horizontal but not vertical scales in a subtropical reservoir, China. Science of the Total Environment, 2020, 721, 137767.	8.0	19
3151	Symbiolite formation: a powerful in vitro model to untangle the role of bacterial communities in the photosynthesis-induced formation of microbialites. ISME Journal, 2020, 14, 1533-1546.	9.8	14
3152	Minocycline-induced microbiome alterations predict cafeteria diet-induced spatial recognition memory impairments in rats. Translational Psychiatry, 2020, 10, 92.	4.8	18
3153	Metagenomic analysis of bacterial species in tongue microbiome of current and never smokers. Npj Biofilms and Microbiomes, 2020, 6, 11.	6.4	32
3154	Effects of enrofloxacin treatment on the bacterial microbiota of milk from goats with persistent mastitis. Scientific Reports, 2020, 10, 4421.	3.3	11
3155	Bubble-mediated transport of benthic microorganisms into the water column: Identification of methanotrophs and implication of seepage intensity on transport efficiency. Scientific Reports, 2020, 10, 4682.	3.3	9
3156	Distinct maternal microbiota clusters are associated with diet during pregnancy: impact on neonatal microbiota and infant growth during the first 18 months of life. Gut Microbes, 2020, 11, 962-978.	9.8	75
3157	Reconstructing ribosomal genes from large scale total RNA meta-transcriptomic data. Bioinformatics, 2020, 36, 3365-3371.	4.1	13
3158	Profiling the Salivary microbiome of the Qatari population. Journal of Translational Medicine, 2020, 18, 127.	4.4	33
3159	Bacterial Communities of Mojave Desert Biological Soil Crusts Are Shaped by Dominant Photoautotrophs and the Presence of Hypolithic Niches. Frontiers in Ecology and Evolution, 2020, 7, .	2.2	8
3160	Sulphide addition favours respiratory ammonification (DNRA) over complete denitrification and alters the active microbial community in salt marsh sediments. Environmental Microbiology, 2020, 22, 2124-2139.	3.8	68

#	Article	IF	CITATIONS
3161	Movement ecology and sex are linked to barn owl microbial community composition. Molecular Ecology, 2020, 29, 1358-1371.	3.9	33
3162	Plant responses to insect eggs are not induced by eggâ€associated microbes, but by a secretion attached to the eggs. Plant, Cell and Environment, 2020, 43, 1815-1826.	5.7	20
3163	Multi-kingdom characterization of the core equine fecal microbiota based on multiple equine (sub)species. Animal Microbiome, 2020, 2, 6.	3.8	39
3164	Murine Gut Microbiome Association With APOE Alleles. Frontiers in Immunology, 2020, 11, 200.	4.8	37
3165	Broad and Fine Scale Variability in Bacterial Diversity and Cyanotoxin Quotas in Benthic Cyanobacterial Mats. Frontiers in Microbiology, 2020, 11, 129.	3.5	9
3166	Exploring Rain as Source of Biological Control Agents for Fire Blight on Apple. Frontiers in Microbiology, 2020, 11, 199.	3.5	19
3167	An Integrated Multi-Omics Analysis Defines Key Pathway Alterations in a Diet-Induced Obesity Mouse Model. Metabolites, 2020, 10, 80.	2.9	17
3168	Variations in the Bacterial Communities in Anastrepha obliqua (Diptera: Tephritidae) According to the Insect Life Stage and Host Plant. Current Microbiology, 2020, 77, 1283-1291.	2.2	29
3169	The influence of blood on the human gut microbiome. BMC Microbiology, 2020, 20, 44.	3.3	25
3170	Time series assessment of <i>Thaumarchaeota</i> ecotypes in Monterey Bay reveals the importance of water column position in predicting distribution–environment relationships. Limnology and Oceanography, 2020, 65, 2041-2055.	3.1	21
3171	Microbial composition of enigmatic bird parasites: Wolbachia and Spiroplasma are the most important bacterial associates of quill mites (Acariformes: Syringophilidae). MicrobiologyOpen, 2020, 9, e964.	3.0	12
3172	Tuning up microbiome analysis to monitor WWTPs' biological reactors functioning. Scientific Reports, 2020, 10, 4079.	3.3	42
3173	Soil Fungal Community Characteristics and Mycelial Production Across a Disturbance Gradient in Lowland Dipterocarp Rainforest in Borneo. Frontiers in Forests and Global Change, 2020, 3, .	2.3	6
3174	Seasonal Dynamics of Pelagic Mycoplanktonic Communities: Interplay of Taxon Abundance, Temporal Occurrence, and Biotic Interactions. Frontiers in Microbiology, 2020, 11, 1305.	3.5	23
3175	Analysis of the diversity of intestinal microbiome and its potential value as a biomarker in patients with schizophrenia: A cohort study. Psychiatry Research, 2020, 291, 113260.	3.3	35
3176	Disproportionate increase in freshwater methane emissions induced by experimental warming. Nature Climate Change, 2020, 10, 685-690.	18.8	62
3177	Prevalence and abundance of lactic acid bacteria in raw milk associated with forage types in dairy cow feeding. Journal of Dairy Science, 2020, 103, 5931-5946.	3.4	20
3178	Mobilization of Antibiotic Resistance: Are Current Approaches for Colocalizing Resistomes and Mobilomes Useful?. Frontiers in Microbiology, 2020, 11, 1376.	3.5	33

#	Article	IF	CITATIONS
3179	Evaluation of groundwater bacterial community composition to inform waterborne pathogen vulnerability assessments. Science of the Total Environment, 2020, 743, 140472.	8.0	10
3180	Evaluation of primer pairs for microbiome profiling from soils to humans within the One Health framework. Molecular Ecology Resources, 2020, 20, 1558-1571.	4.8	61
3181	Temporal Variability and Ecological Interactions of Parasitic Marine Syndiniales in Coastal Protist Communities. MSphere, 2020, 5, .	2.9	37
3182	Frog Skin Microbiota Vary With Host Species and Environment but Not Chytrid Infection. Frontiers in Microbiology, 2020, 11, 1330.	3.5	17
3183	Sex-Specific Associations between Gut Prevotellaceae and Host Genetics on Adiposity. Microorganisms, 2020, 8, 938.	3.6	28
3184	Mating changes the genital microbiome in both sexes of the common bedbug <i>Cimex lectularius</i> across populations. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200302.	2.6	5
3185	16S rRNA Amplicon Sequencing of Urban Prokaryotic Communities in the South Bronx River Estuary. Microbiology Resource Announcements, 2020, 9, .	0.6	5
3186	Broad-spectrum antibiotics alter the microbiome, increase intestinal fxr, and decrease hepatic steatosis in zebrafish short bowel syndrome. American Journal of Physiology - Renal Physiology, 2020, 319, G212-G226.	3.4	6
3187	Stress ulcer prophylaxis versus placeboâ€"a blinded randomized control trial to evaluate the safety of two strategies in critically ill infants with congenital heart disease (SUPPRESS-CHD). Trials, 2020, 21, 590.	1.6	4
3188	Gut carriage of antimicrobial resistance genes in women exposed to small-scale poultry farms in rural Uganda: A feasibility study. PLoS ONE, 2020, 15, e0229699.	2.5	3
3189	Only Minor Changes in the Soil Microbiome of a Sub-alpine Forest After 20 Years of Moderately Increased Nitrogen Loads. Frontiers in Forests and Global Change, 2020, 3, .	2.3	19
3190	Impacts of Anthropogenic Pollutants on Benthic Prokaryotic Communities in Mediterranean Touristic Ports. Frontiers in Microbiology, 2020, 11, 1234.	3.5	15
3191	Continent-Scale Sampling Reveals Fine-Scale Turnover in a Beneficial Bug Symbiont. Frontiers in Microbiology, 2020, 11, 1276.	3.5	7
3192	What Can the Bacterial Community of Atta sexdens (Linnaeus, 1758) Tell Us about the Habitats in Which This Ant Species Evolves?. Insects, 2020, 11, 332.	2.2	5
3193	First Detection of Paralytic Shellfish Toxins from Alexandrium pacificum above the Regulatory Limit in Blue Mussels (Mytilus galloprovincialis) in New South Wales, Australia. Microorganisms, 2020, 8, 905.	3.6	8
3194	The Presence of Plant-Associated Bacteria Alters Responses to N-acyl Homoserine Lactone Quorum Sensing Signals that Modulate Nodulation in Medicago Truncatula. Plants, 2020, 9, 777.	3.5	10
3195	Nitrifying and Denitrifying Microbial Communities in Centralized and Decentralized Biological Nitrogen Removing Wastewater Treatment Systems. Water (Switzerland), 2020, 12, 1688.	2.7	11
3196	Metabarcoding Cyanobacteria in coastal waters and sediment in central and southern Adriatic Sea. Acta Botanica Croatica, 2020, 79, 157-169.	0.7	5

#	Article	IF	CITATIONS
3197	Deciphering the relative importance of soil and plant traits on the development of rhizosphere microbial communities. Soil Biology and Biochemistry, 2020, 148, 107909.	8.8	56
3198	Colonic microbiome profiles for improved feed efficiency can be identified despite major effects of farm of origin and contemporary group in pigs. Animal, 2020, 14, 2472-2480.	3.3	14
3199	Assessment of the Urinary Microbiome in Children Younger Than 48 Months. Pediatric Infectious Disease Journal, 2020, 39, 565-570.	2.0	24
3200	Effects of captivity, diet, and relocation on the gut bacterial communities of whiteâ€footed mice. Ecology and Evolution, 2020, 10, 4677-4690.	1.9	22
3201	Fungal Signature of Moisture Damage in Buildings: Identification by Targeted and Untargeted Approaches with Mycobiome Data. Applied and Environmental Microbiology, 2020, 86, .	3.1	12
3202	Chronic kidney disease in cats alters response of the plasma metabolome and fecal microbiome to dietary fiber. PLoS ONE, 2020, 15, e0235480.	2.5	24
3203	Dynamics of active potential bacterial and fungal interactions in the assimilation of acidobacterial EPS in soil. Soil Biology and Biochemistry, 2020, 148, 107916.	8.8	15
3204	Insights in the Global Genetics and Gut Microbiome of Black Soldier Fly, Hermetia illucens: Implications for Animal Feed Safety Control. Frontiers in Microbiology, 2020, 11, 1538.	3.5	34
3205	Uncovered Microbial Diversity in Antarctic Cryptoendolithic Communities Sampling Three Representative Locations of the Victoria Land. Microorganisms, 2020, 8, 942.	3.6	12
3206	Microbiota modulate sympathetic neurons via a gut–brain circuit. Nature, 2020, 583, 441-446.	27.8	227
3207	Gut microbiota composition before infection determines the <i>Salmonella</i> super―and lowâ€shedder phenotypes in chicken. Microbial Biotechnology, 2020, 13, 1611-1630.	4.2	28
3208	How being synanthropic affects the gut bacteriome and mycobiome: comparison of two mouse species with contrasting ecologies. BMC Microbiology, 2020, 20, 194.	3.3	14
3209	New Insight into the Composition of Wheat Seed Microbiota. International Journal of Molecular Sciences, 2020, 21, 4634.	4.1	39
3210	16s rRNA metagenomic analysis reveals predominance of Crtl and CruF genes in Arabian Sea coast of India. Science of the Total Environment, 2020, 743, 140699.	8.0	6
3211	Intestinal Virome Signature Associated With Severity of Nonalcoholic Fatty Liver Disease. Gastroenterology, 2020, 159, 1839-1852.	1.3	103
3212	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. MBio, 2020, 11, .	4.1	27
3213	Characterizing the postmortem human bone microbiome from surface-decomposed remains. PLoS ONE, 2020, 15, e0218636.	2.5	24
3214	Biodegraded peat and ultrafine calcium carbonate result in retained metals and higher microbial diversities in boreal acid sulfate soil. Soil Ecology Letters, 2020, 2, 120-130.	4.5	7

#	Article	IF	CITATIONS
3215	Breastmilk Feeding Practices Are Associated with the Co-Occurrence of Bacteria in Mothers' Milk and the Infant Gut: the CHILD Cohort Study. Cell Host and Microbe, 2020, 28, 285-297.e4.	11.0	148
3216	Insights into dryland biocrust microbiome: geography, soil depth and crust type affect biocrust microbial communities and networks in Mojave Desert, USA. FEMS Microbiology Ecology, 2020, 96, .	2.7	37
3217	Biofilm formation on zirconia and titanium over timeâ€"An in vivo model study. Clinical Oral Implants Research, 2020, 31, 865-880.	4.5	13
3218	Growth velocity in children with Environmental Enteric Dysfunction is associated with specific bacterial and viral taxa of the gastrointestinal tract in Malawian children. PLoS Neglected Tropical Diseases, 2020, 14, e0008387.	3.0	19
3219	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. PLoS ONE, 2020, 15, e0234537.	2.5	0
3220	Meta-Analysis of Microbial Communities in Hot Springs: Recurrent Taxa and Complex Shaping Factors beyond pH and Temperature. Microorganisms, 2020, 8, 906.	3.6	27
3221	The effects of environment and ontogeny on the skin microbiome of two Stegastes damselfishes (Pomacentridae) from the eastern Caribbean Sea. Marine Biology, 2020, 167, 1.	1.5	12
3222	Sierra Nevada mountain lake microbial communities are structured by temperature, resources and geographic location. Molecular Ecology, 2020, 29, 2080-2093.	3.9	14
3223	Study protocol for the ABERRANT study: antibiotic-induced disruption of the maternal and infant microbiome and adverse health outcomes â€" a prospective cohort study among children born at term. BMJ Open, 2020, 10, e036275.	1.9	4
3224	Intestinal permeability, microbial translocation, changes in duodenal and fecal microbiota, and their associations with alcoholic liver disease progression in humans. Gut Microbes, 2020, 12, 1782157.	9.8	83
3225	Zooplankton biogeographic boundaries in the California Current System as determined from metabarcoding. PLoS ONE, 2020, 15, e0235159.	2.5	17
3226	A Differential Metabarcoding Approach to Describe Taxonomy Profiles of Bacteria and Archaea in the Saltern of Margherita di Savoia (Italy). Microorganisms, 2020, 8, 936.	3.6	21
3227	Effect of Washing, Waxing and Low-Temperature Storage on the Postharvest Microbiome of Apple. Microorganisms, 2020, 8, 944.	3.6	54
3228	Macrofaunal control of microbial community structure in continental margin sediments. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15911-15922.	7.1	40
3229	Isolation and Characterization of Extracellular Vesicles Secreted In Vitro by Porcine Microbiota. Microorganisms, 2020, 8, 983.	3.6	9
3230	Relationship between the Oral and Vaginal Microbiota of South African Adolescents with High Prevalence of Bacterial Vaginosis. Microorganisms, 2020, 8, 1004.	3.6	13
3231	Impact of Initial Feeding and Molting on Tachypleus tridentatus Gut Microbiota. Current Microbiology, 2020, 77, 2847-2858.	2.2	16
3232	Effect of ammonia exposure and acclimation on the performance and the microbiome of anaerobic digestion. Bioresource Technology Reports, 2020, 11, 100488.	2.7	10

#	Article	IF	CITATIONS
3233	Proposal for a microcosm biofilm model for the study of vulvovaginal candidiasis. Biofouling, 2020, 36, 610-620.	2.2	4
3234	mAML: an automated machine learning pipeline with a microbiome repository for human disease classification. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	20
3235	Probiotic low-fat fermented goat milk with passion fruit by-product: In vitro effect on obese individuals' microbiota and on metabolites production. Food Research International, 2020, 136, 109453.	6.2	17
3236	Into the wild blueberry (<scp><i>Vaccinium angustifolium</i></scp>) rhizosphere microbiota. Environmental Microbiology, 2020, 22, 3803-3822.	3.8	28
3237	Marked spatiotemporal variations in small phytoplankton structure in contrasted waters of the Southern Ocean (Kerguelen area). Limnology and Oceanography, 2020, 65, 2835-2852.	3.1	14
3238	Fucose Ameliorate Intestinal Inflammation Through Modulating the Crosstalk Between Bile Acids and Gut Microbiota in a Chronic Colitis Murine Model. Inflammatory Bowel Diseases, 2020, 26, 863-873.	1.9	34
3239	Repeated inoculation with fresh rumen fluid before or during weaning modulates the microbiota composition and co-occurrence of the rumen and colon of lambs. BMC Microbiology, 2020, 20, 29.	3.3	41
3240	Host-associated microbiomes are predicted by immune system complexity and climate. Genome Biology, 2020, 21, 23.	8.8	54
3241	Diversity of Bacterial Community in the Oxygen Minimum Zones of Arabian Sea and Bay of Bengal as Deduced by Illumina Sequencing. Frontiers in Microbiology, 2019, 10, 3153.	3.5	37
3242	Applicability of an Unmedicated Feeding Program Aimed to Reduce the Use of Antimicrobials in Nursery Piglets: Impact on Performance and Fecal Microbiota. Animals, 2020, 10, 242.	2.3	2
3243	Comparing Analytical Methods for the Gut Microbiome and Aging: Gut Microbial Communities and Body Weight in the Osteoporotic Fractures in Men (MrOS) Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 1267-1275.	3.6	12
3244	Soil bacterial and fungal community structure of a rice monoculture and rice-pasture rotation systems. Applied Soil Ecology, 2020, 151, 103535.	4.3	35
3245	Historical climate legacies on soil respiration persist despite extreme changes in rainfall. Soil Biology and Biochemistry, 2020, 143, 107752.	8.8	33
3246	Effect of Pepper-Containing Diets on the Diversity and Composition of Gut Microbiome of Drosophila melanogaster. International Journal of Molecular Sciences, 2020, 21, 945.	4.1	8
3247	Hydrocarbon Removal by Two Differently Developed Microbial Inoculants and Comparing Their Actions with Biostimulation Treatment. Molecules, 2020, 25, 661.	3.8	36
3248	Electrogenic sulfide oxidation mediated by cable bacteria stimulates sulfate reduction in freshwater sediments. ISME Journal, 2020, 14, 1233-1246.	9.8	41
3249	Salmon Gravlax Biopreservation With Lactic Acid Bacteria: A Polyphasic Approach to Assessing the Impact on Organoleptic Properties, Microbial Ecosystem and Volatilome Composition. Frontiers in Microbiology, 2019, 10, 3103.	3.5	35
3250	Diversity of Bacterial Biosynthetic Genes in Maritime Antarctica. Microorganisms, 2020, 8, 279.	3.6	9

#	Article	IF	CITATIONS
3251	The Human Oral Microbiome in Health and Disease: From Sequences to Ecosystems. Microorganisms, 2020, 8, 308.	3.6	231
3252	Feedstock thermal pretreatment selectively steers process stability during the anaerobic digestion of waste activated sludge. Applied Microbiology and Biotechnology, 2020, 104, 3675-3686.	3.6	5
3253	Stable biogas production from single-stage anaerobic digestion of food waste. Applied Energy, 2020, 263, 114609.	10.1	63
3254	Enrichment of Nitrogen-Fixing Bacteria in a Nitrogen-Deficient Wastewater Treatment System. Environmental Science & Environmen	10.0	22
3255	c-FLIP is crucial for IL-7/IL-15-dependent NKp46+ ILC development and protection from intestinal inflammation in mice. Nature Communications, 2020, 11, 1056.	12.8	12
3256	Entomopathogenic nematode-associated microbiota: from monoxenic paradigm to pathobiome. Microbiome, 2020, 8, 25.	11.1	49
3257	Different carboxylâ€rich alicyclic molecules proxy compounds select distinct bacterioplankton for oxidation of dissolved organic matter in the mesopelagic Sargasso Sea. Limnology and Oceanography, 2020, 65, 1532-1553.	3.1	44
3258	Is the gut microbiota dysbiotic in patients with classical homocystinuria?. Biochimie, 2020, 173, 3-11.	2.6	10
3259	Microhabitats are associated with diversity–productivity relationships in freshwater bacterial communities. FEMS Microbiology Ecology, 2020, 96, .	2.7	13
3260	Elucidating cryptic dynamics of <i>Theileria</i> communities in African buffalo using a highâ€throughput sequencing informatics approach. Ecology and Evolution, 2020, 10, 70-80.	1.9	19
3261	Spatial variations in bacterial and archaeal abundance and community composition in boreal forest pine mycorrhizospheres. European Journal of Soil Biology, 2020, 97, 103168.	3.2	4
3262	Disturbance in human gut microbiota networks by parasites and its implications in the incidence of depression. Scientific Reports, 2020, 10, 3680.	3.3	22
3263	Insect pollination: an ecological process involved in the assembly of the seed microbiota. Scientific Reports, 2020, 10, 3575.	3.3	34
3264	Impact of in-feed sodium butyrate or sodium heptanoate protected with medium-chain fatty acids on gut health in weaned piglets challenged with Escherichia coli F4+. Archives of Animal Nutrition, 2020, 74, 271-295.	1.8	9
3265	Multitrophic interactions in the rhizosphere microbiome of wheat: from bacteria and fungi to protists. FEMS Microbiology Ecology, 2020, 96, .	2.7	77
3266	Alpine headwaters emerging from glaciers and rock glaciers host different bacterial communities: Ecological implications for the future. Science of the Total Environment, 2020, 717, 137101.	8.0	25
3267	Functional relationships between aboveground and belowground spinach (Spinacia oleracea L., cv.) Tj ETQq0 0 0 137207.	rgBT /Ove 8.0	erlock 10 Tf 5 16
3268	Gut microbial diversity during pregnancy and early infancy: an exploratory study in the Indian population. FEMS Microbiology Letters, 2020, 367, .	1.8	7

#	Article	IF	CITATIONS
3269	Antibiotic use during pregnancy increases offspring asthma severity in a doseâ€dependent manner. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 1979-1990.	5.7	49
3270	Early sexual dimorphism in the developing gut microbiome of northern elephant seals. Molecular Ecology, 2020, 29, 2109-2122.	3.9	37
3271	Effect of long-term destocking on soil fungal functional groups and interactions with plants. Plant and Soil, 2020, 448, 495-508.	3.7	20
3272	Enhanced Resistance to <i>Fusarium graminearum</i> in Transgenic Arabidopsis Plants Expressing a Modified Plant Thionin. Phytopathology, 2020, 110, 1056-1066.	2.2	9
3273	Domestication of Oryza species eco-evolutionarily shapes bacterial and fungal communities in rice seed. Microbiome, 2020, 8, 20.	11.1	101
3274	Performance evaluation of a new custom, multi-component DNA isolation method optimized for use in shotgun metagenomic sequencing-based aerosol microbiome research. Environmental Microbiomes, 2020, 15, 1.	5.0	40
3275	Novel universal primers for metabarcoding environmental DNA surveys of marine mammals and other marine vertebrates. Environmental DNA, 2020, 2, 460-476.	5.8	26
3276	Specific microbiota enhances intestinal IgA levels by inducing TGF $\hat{a}\in\hat{I}^2$ in T follicular helper cells of Peyer's patches in mice. European Journal of Immunology, 2020, 50, 783-794.	2.9	58
3277	Post-antibiotic gut dysbiosis-induced trabecular bone loss is dependent on lymphocytes. Bone, 2020, 134, 115269.	2.9	29
3278	Gut microbiota composition during infancy and subsequent behavioural outcomes. EBioMedicine, 2020, 52, 102640.	6.1	72
3279	Anaerobic reactor applied to laundry wastewater treatment: Unveiling the microbial community by gene and genome-centric approaches. International Biodeterioration and Biodegradation, 2020, 149, 104916.	3.9	15
3280	Intermittent cafeteria diet identifies fecal microbiome changes as a predictor of spatial recognition memory impairment in female rats. Translational Psychiatry, 2020, 10, 36.	4.8	27
3281	Response of the human gut and saliva microbiome to urbanization in Cameroon. Scientific Reports, 2020, 10, 2856.	3.3	27
3282	Cold Case Experiment Demonstrates the Potential Utility of Aquatic Microbial Community Assembly in Estimating a Postmortem Submersion Interval. Journal of Forensic Sciences, 2020, 65, 1210-1220.	1.6	9
3283	Competition experiments in a soil microcosm reveal the impact of genetic and biotic factors on natural yeast populations. ISME Journal, 2020, 14, 1410-1421.	9.8	5
3284	Short-term supplementation of celecoxib-shifted butyrate production on a simulated model of the gut microbial ecosystem and ameliorated in vitro inflammation. Npj Biofilms and Microbiomes, 2020, 6, 9.	6.4	24
3285	Oral Microbiome Profiling in Smokers with and without Head and Neck Cancer Reveals Variations Between Health and Disease. Cancer Prevention Research, 2020, 13, 463-474.	1.5	18
3286	Late weaning is associated with increased microbial diversity and Faecalibacterium prausnitzii abundance in the fecal microbiota of piglets. Animal Microbiome, 2020, 2, 2.	3.8	31

#	Article	IF	CITATIONS
3287	Characterization of gut microbiomes of household pets in the United States using a direct-to-consumer approach. PLoS ONE, 2020, 15, e0227289.	2.5	32
3288	Insights into the microbiome of farmed Asian sea bass (Lates calcarifer) with symptoms of tenacibaculosis and description of Tenacibaculum singaporense sp. nov Antonie Van Leeuwenhoek, 2020, 113, 737-752.	1.7	28
3289	Temporal shotgun metagenomics of an Ecuadorian coffee fermentation process highlights the predominance of lactic acid bacteria. Current Research in Biotechnology, 2020, 2, 1-15.	3.7	42
3290	Effects of bacterial inoculation and nitrogen loading on bacterial-algal consortium composition and functions in an integrated photobioelectrochemical system. Science of the Total Environment, 2020, 716, 137135.	8.0	8
3291	Ocean acidification affects microbial community and invertebrate settlement on biofilms. Scientific Reports, 2020, 10, 3274.	3.3	25
3293	Effect of a polyphenol-rich dietary pattern on intestinal permeability and gut and blood microbiomics in older subjects: study protocol of the MaPLE randomised controlled trial. BMC Geriatrics, 2020, 20, 77.	2.7	39
3294	The Microbial Diversity of Cabbage Pest Delia radicum Across Multiple Life Stages. Frontiers in Microbiology, 2020, 11, 315.	3.5	8
3295	Exotic Spartina alterniflora Loisel. Invasion significantly shifts soil bacterial communities with the successional gradient of saltmarsh in eastern China. Plant and Soil, 2020, 449, 97-115.	3.7	31
3296	18S-V9 DNA metabarcoding detects the effect of water-quality impairment on stream biofilm eukaryotic assemblages. Ecological Indicators, 2020, 113, 106225.	6.3	19
3297	Impact of sampling and DNA extraction methods on skin microbiota assessment. Journal of Microbiological Methods, 2020, 171, 105880.	1.6	4
3298	Poised potential is not an effective strategy to enhance bio-electrochemical denitrification under cyclic substrate limitations. Science of the Total Environment, 2020, 713, 136698.	8.0	5
3299	DNA damage in colon mucosa of Pirc rats, an Apc-driven model of colon tumorigenesis. Toxicology Letters, 2020, 324, 12-19.	0.8	8
3300	Short-Chain <i>N</i> -Acylhomoserine Lactone Quorum-Sensing Molecules Promote Periodontal Pathogens in <i>In Vitro</i> Oral Biofilms. Applied and Environmental Microbiology, 2020, 86, .	3.1	26
3301	Mediterranean seasonality and the halophyte Arthrocnemum macrostachyum determine the bacterial community in salt marsh soils in Southwest Spain. Applied Soil Ecology, 2020, 151, 103532.	4. 3	7
3302	Computational methods for 16S metabarcoding studies using Nanopore sequencing data. Computational and Structural Biotechnology Journal, 2020, 18, 296-305.	4.1	92
3303	Rain induces temporary shifts in epiphytic bacterial communities of cucumber and tomato fruit. Scientific Reports, 2020, 10, 1765.	3.3	25
3304	Diet change affects intestinal microbiota restoration and improves vertical sleeve gastrectomy outcome in diet-induced obese rats. European Journal of Nutrition, 2020, 59, 3555-3564.	3.9	8
3305	Ultradeep Microbial Communities at 4.4 km within Crystalline Bedrock: Implications for Habitability in a Planetary Context. Life, 2020, 10, 2.	2.4	33

#	Article	IF	CITATIONS
3306	Land use as a driver for protist community structure in soils under agricultural use across Europe. Science of the Total Environment, 2020, 717, 137228.	8.0	33
3307	Bacterial community profiling highlights complex diversity and novel organisms in wildlife ticks. Ticks and Tick-borne Diseases, 2020, 11, 101407.	2.7	13
3308	The effect of legume supplementation on the gut microbiota in rural Malawian infants aged 6 to 12 months. American Journal of Clinical Nutrition, 2020, 111, 884-892.	4.7	10
3309	Gut microbiota differences in Island Hispanic Puerto Ricans and mainland non-Hispanic whites during chemoradiation for rectal cancer: A pilot study. Current Problems in Cancer, 2020, 44, 100551.	2.0	9
3310	Characterization of metabolic and inflammatory profiles of transition dairy cows fed an energy-restricted diet. Journal of Animal Science, 2020, 98, .	0.5	11
3311	The influence of hostâ€plant connectivity on fungal assemblages in the root microbiota of Brachypodium pinnatum. Ecology, 2020, 101, e02976.	3.2	10
3312	Characterization of Bacterial and Fungal Communities Reveals Novel Consortia in Tropical Oligotrophic Peatlands. Microbial Ecology, 2021, 82, 188-201.	2.8	8
3313	Bacterial diversity in deep-sea sediments under influence of asphalt seep at the São Paulo Plateau. Antonie Van Leeuwenhoek, 2020, 113, 707-717.	1.7	17
3314	Instances of altered gut microbiomes among Irish cricketers over periods of travel in the lead up to the 2016 World Cup: A sequencing analysis. Travel Medicine and Infectious Disease, 2020, 35, 101553.	3.0	11
3315	Impact of hydraulic retention time on community assembly and function of photogranules for wastewater treatment. Water Research, 2020, 173, 115506.	11.3	79
3316	Prenatal Transfer of Gut Bacteria in Rock Pigeon. Microorganisms, 2020, 8, 61.	3.6	19
3317	Milk Fermented by Lactobacillus paracasei NCC 2461 (ST11) Modulates the Immune Response and Microbiota to Exert its Protective Effects Against Salmonella typhimurium Infection in Mice. Probiotics and Antimicrobial Proteins, 2020, 12, 1398-1408.	3.9	11
3318	Diversity, compositional and functional differences between gut microbiota of children and adults. Scientific Reports, 2020, 10, 1040.	3.3	89
3319	Trimethylamine-N-Oxide Postprandial Response in Plasma and Urine Is Lower After Fermented Compared to Non-Fermented Dairy Consumption in Healthy Adults. Nutrients, 2020, 12, 234.	4.1	27
3320	Metabarcoding analysis of regional variation in gut contents of the copepod Calanus finmarchicus in the North Atlantic Ocean. Deep-Sea Research Part II: Topical Studies in Oceanography, 2020, 180, 104738.	1.4	26
3321	Long-term Proton Pump Inhibitor Administration Caused Physiological and Microbiota Changes in Rats. Scientific Reports, 2020, 10, 866.	3.3	27
3322	Impact of the early-life skin microbiota on the development of canine atopic dermatitis in a high-risk breed birth cohort. Scientific Reports, 2020, 10, 1044.	3.3	11
3323	Comparative Analysis of Gut Microbiota Following Changes in Training Volume Among Swimmers. International Journal of Sports Medicine, 2020, 41, 292-299.	1.7	23

#	Article	IF	CITATIONS
3324	Compositional Flux Within the Intestinal Microbiota and Risk for Bloodstream Infection With Gram-negative Bacteria. Clinical Infectious Diseases, 2021, 73, e4627-e4635.	5.8	74
3325	Top-Down and Bottom-Up Controls on Microeukaryotic Diversity (i.e., Amplicon Analyses of SAR) Tj ETQq1 1 0.784 Frontiers in Marine Science, 2020, 6, .	1314 rgBT 2.5	/Overlock 5
3326	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. Nature Protocols, 2020, 15, 799-821.	12.0	1,019
3327	Integrative analysis of blood and gut microbiota data suggests a non-alcoholic fatty liver disease (NAFLD)-related disorder in French SLAdd minipigs. Scientific Reports, 2020, 10, 234.	3.3	0
3328	Who is eating fructose within the <scp><i>Aedes albopictus</i></scp> gut microbiota?. Environmental Microbiology, 2020, 22, 1193-1206.	3.8	22
3329	Fecal transplant prevents gut dysbiosis and anxiety-like behaviour after spinal cord injury in rats. PLoS ONE, 2020, 15, e0226128.	2.5	77
3330	Host Species and Body Site Explain the Variation in the Microbiota Associated to Wild Sympatric Mediterranean Teleost Fishes. Microbial Ecology, 2020, 80, 212-222.	2.8	25
3331	The composition of the perinatal intestinal microbiota in horse. Scientific Reports, 2020, 10, 441.	3.3	32
3332	Prenatal dietary supplements influence the infant airway microbiota in a randomized factorial clinical trial. Nature Communications, 2020, 11, 426.	12.8	25
3333	A comparison of nonlethal sampling methods for amphibian gut microbiome analyses. Molecular Ecology Resources, 2020, 20, 844-855.	4.8	17
3334	Influences of a Prolific Gut Fungus (<i>Zancudomyces culisetae</i>) on Larval and Adult Mosquito (Aedes aegypti)-Associated Microbiota. Applied and Environmental Microbiology, 2020, 86, .	3.1	13
3335	Prevalence of unclassified bacteria in the soil bacterial community from floodplain meadows (fluvisols) under simulated flood conditions revealed by a metataxonomic approachss. Catena, 2020, 188, 104448.	5.0	35
3336	Interactions between the gut microbiome and host gene regulation in cystic fibrosis. Genome Medicine, 2020, 12, 12.	8.2	73
3337	Positive response of soil microbes to long-term nitrogen input in spruce forest: Results from Gårdsjön whole-catchment N-addition experiment. Soil Biology and Biochemistry, 2020, 143, 107732.	8.8	35
3338	Fungal diversity in canopy soil of silver beech, Nothofagus menziesiiÂ(Nothofagaceae). PLoS ONE, 2020, 15, e0227860.	2.5	4
3339	Tools for Analysis of the Microbiome. Digestive Diseases and Sciences, 2020, 65, 674-685.	2.3	70
3340	Aerobic biodegradation in freshwater and marine environments of textile microfibers generated in clothes laundering: Effects of cellulose and polyester-based microfibers on the microbiome. Marine Pollution Bulletin, 2020, 151, 110826.	5.0	62
3341	Characterization of key bacterial species in the Daphnia magna microbiota using shotgun metagenomics. Scientific Reports, 2020, 10, 652.	3.3	31

#	Article	IF	CITATIONS
3342	Studying the urine microbiome in superficial bladder cancer: samples obtained by midstream voiding versus cystoscopy. BMC Urology, 2020, 20, 5.	1.4	27
3343	Dietary zinc source impacts intestinal morphology and oxidative stress in young broilers. Poultry Science, 2020, 99, 441-453.	3.4	56
3344	Influence of contaminant exposure on the development of aerobic ETBE biodegradation potential in microbial communities from a gasoline-impacted aquifer. Journal of Hazardous Materials, 2020, 388, 122022.	12.4	9
3345	Culture-enriched metagenomic sequencing enables in-depth profiling of the cystic fibrosis lung microbiota. Nature Microbiology, 2020, 5, 379-390.	13.3	57
3346	Experimental DNA Demethylation Associates with Changes in Growth and Gene Expression of Oak Tree Seedlings. G3: Genes, Genomes, Genetics, 2020, 10, 1019-1028.	1.8	11
3347	Characterization of the Gut Microbiota of Individuals at Different T2D Stages Reveals a Complex Relationship with the Host. Microorganisms, 2020, 8, 94.	3.6	44
3348	Fetal membrane bacterial load is increased in histologically confirmed inflammatory chorioamnionitis: A retrospective cohort study. Placenta, 2020, 91, 43-51.	1.5	16
3349	Site-Specific Profiling of the Dental Mycobiome Reveals Strong Taxonomic Shifts during Progression of Early-Childhood Caries. Applied and Environmental Microbiology, 2020, 86, .	3.1	34
3350	CFTR dysregulation drives active selection of the gut microbiome. PLoS Pathogens, 2020, 16, e1008251.	4.7	57
3351	Digestive tract microbiota of beef cattle that differed in feed efficiency. Journal of Animal Science, 2020, 98, .	0.5	35
3352	Microbial resistance and resilience in response to environmental changes under the higher intensity of human activities than global average level. Global Change Biology, 2020, 26, 2377-2389.	9.5	67
3353	Evolutionary signal in the gut microbiomes of 74 bird species from Equatorial Guinea. Molecular Ecology, 2020, 29, 829-847.	3.9	56
3354	The influence of diet on the microbiota of live-feed rotifers (<i>Brachionus plicatilis</i>) used in commercial fish larviculture. FEMS Microbiology Letters, 2020, 367, .	1.8	16
3355	Oral Administration of Heat-Treated Lactobacilli Modifies the Murine Microbiome and Reduces Citrobacter Induced Colitis. Frontiers in Microbiology, 2020, 11, 69.	3.5	18
3356	Evidence for Co-evolutionary History of Early Diverging Lycopodiaceae Plants With Fungi. Frontiers in Microbiology, 2019, 10, 2944.	3.5	18
3357	Core and Differentially Abundant Bacterial Taxa in the Rhizosphere of Field Grown Brassica napus Genotypes: Implications for Canola Breeding. Frontiers in Microbiology, 2019, 10, 3007.	3.5	39
3358	Metagenomics methods for the study of plant-associated microbial communities: A review. Journal of Microbiological Methods, 2020, 170, 105860.	1.6	91
3359	Impact of TCR Diversity on the Development of Transplanted or Chemically Induced Tumors. Cancer Immunology Research, 2020, 8, 192-202.	3.4	15

#	Article	IF	Citations
3360	Discovery of Afifi, the shallowest and southernmost brine pool reported in the Red Sea. Scientific Reports, 2020, 10, 910.	3.3	16
3361	Gut metabolomics profiling of non-small cell lung cancer (NSCLC) patients under immunotherapy treatment. Journal of Translational Medicine, 2020, 18, 49.	4.4	114
3362	Comparing bioinformatic pipelines for microbial 16S rRNA amplicon sequencing. PLoS ONE, 2020, 15, e0227434.	2.5	282
3363	A 28 Day Clinical Assessment of a Lactic Acid-containing Antimicrobial Intimate Gel Wash Formulation on Skin Tolerance and Impact on the Vulvar Microbiome. Antibiotics, 2020, 9, 55.	3.7	12
3364	Distribution of Medically Relevant Antibiotic Resistance Genes and Mobile Genetic Elements in Soils of Temperate Forests and Grasslands Varying in Land Use. Genes, 2020, 11, 150.	2.4	9
3365	Dark septate endophyte improves salt tolerance of native and invasive lineages of <i>Phragmites australis</i> . ISME Journal, 2020, 14, 1943-1954.	9.8	51
3366	Effect of antimicrobial washout from anaerobic digesters on microbial community composition. Environmental Science: Water Research and Technology, 2020, 6, 1658-1671.	2.4	1
3367	Salt tolerance of Cressa cretica and its rhizosphere microbiota. Biologia (Poland), 2020, 75, 355-366.	1.5	8
3368	Patterns in Microbial Assemblages Exported From the Meltwater of Arctic and Sub-Arctic Glaciers. Frontiers in Microbiology, 2020, 11, 669.	3.5	24
3369	Use of polymeric scouring agent as fluidized media in anaerobic fluidized bed membrane bioreactor for wastewater treatment: System performance and microbial community. Journal of Membrane Science, 2020, 606, 118121.	8.2	25
3370	Potential interaction between timing of infant complementary feeding and breastfeeding duration in determination of early childhood gut microbiota composition and <scp>BMI</scp> . Pediatric Obesity, 2020, 15, e12642.	2.8	25
3371	manta: a Clustering Algorithm for Weighted Ecological Networks. MSystems, 2020, 5, .	3.8	7
3372	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. Genome Biology, 2020, 21, 103.	8.8	91
3373	Crewmember microbiome may influence microbial composition of ISS habitable surfaces. PLoS ONE, 2020, 15, e0231838.	2.5	54
3374	Comparison of the Bacterial Gut Microbiome of North American Triatoma spp. With and Without Trypanosoma cruzi. Frontiers in Microbiology, 2020, 11, 364.	3.5	20
3375	The Potato Yam Phyllosphere Ectosymbiont Paraburkholderia sp. Msb3 Is a Potent Growth Promotor in Tomato. Frontiers in Microbiology, 2020, 11, 581.	3.5	16
3376	Microbial Diversity in Moonmilk of Baeg-nyong Cave, Korean CZO. Frontiers in Microbiology, 2020, 11, 613.	3.5	14
3377	Effects of an Eco-Friendly Sanitizing Wash on Spinach Leaf Bacterial Community Structure and Diversity. Applied Sciences (Switzerland), 2020, 10, 2986.	2.5	4

#	Article	IF	CITATIONS
3378	Host Plants Influence the Symbiont Diversity of Eriosomatinae (Hemiptera: Aphididae). Insects, 2020, 11, 217.	2.2	14
3379	Investigating Algal Communities in Lacustrine and Hydro-Terrestrial Environments of East Antarctica Using Deep Amplicon Sequencing. Microorganisms, 2020, 8, 497.	3.6	8
3380	Prebiotic Effects of Partially Hydrolyzed Guar Gum on the Composition and Function of the Human Microbiotaâ€"Results from the PAGODA Trial. Nutrients, 2020, 12, 1257.	4.1	39
3381	Gut microbiota derived metabolites contribute to intestinal barrier maturation at the suckling-to-weaning transition. Gut Microbes, 2020, 11, 1268-1286.	9.8	72
3382	Parenteral lipids shape gut bile acid pools and microbiota profiles in the prevention of cholestasis in preterm pigs. Journal of Lipid Research, 2020, 61, 1038-1051.	4.2	21
3383	Intestinal Microbiota of Fattening Pigs Offered Non-Fermented and Fermented Liquid Feed with and without the Supplementation of Non-Fermented Coarse Cereals. Microorganisms, 2020, 8, 638.	3.6	15
3384	Microbiota Composition and Metabolism Are Associated With Gut Function in Parkinson's Disease. Movement Disorders, 2020, 35, 1208-1217.	3.9	180
3385	Metatax: Metataxonomics with a Compi-Based Pipeline for Precision Medicine. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 252-257.	3.6	2
3386	Development but not diet alters microbial communities in the Neotropical arboreal trap jaw ant Daceton armigerum: an exploratory study. Scientific Reports, 2020, 10, 7350.	3.3	13
3387	The urinary microbiome shows different bacterial genera in renal transplant recipients and non-transplant patients at time of acute kidney injury – a pilot study. BMC Nephrology, 2020, 21, 117.	1.8	11
3388	Timescales of variation in diversity and production of bacterioplankton assemblages in the Lower Mississippi River. PLoS ONE, 2020, 15, e0230945.	2.5	4
3389	Diet and Genotype of an Aquatic Invertebrate Affect the Composition of Free-Living Microbial Communities. Frontiers in Microbiology, 2020, 11, 380.	3.5	32
3390	The Microbiomes of Seven Lichen Genera Reveal Host Specificity, a Reduced Core Community and Potential as Source of Antimicrobials. Frontiers in Microbiology, 2020, 11, 398.	3.5	36
3391	Phylosymbiosis across Deeply Diverging Lineages of Omnivorous Cockroaches (Order Blattodea). Applied and Environmental Microbiology, 2020, 86, .	3.1	27
3392	A Protocol for the Multi-Omic Integration of Cervical Microbiota and Urine Metabolomics to Understand Human Papillomavirus (HPV)-Driven Dysbiosis. Biomedicines, 2020, 8, 81.	3.2	4
3393	Microbial Community Response to a Passive Salt Marsh Restoration. Estuaries and Coasts, 2020, 43, 1439-1455.	2.2	22
3394	Selection on a plant-based diet reveals changes in oral tolerance, microbiota and growth in rainbow trout (Oncorhynchus mykiss) when fed a high soy diet. Aquaculture, 2020, 525, 735287.	3.5	24
3395	Reductions in anti-inflammatory gut bacteria are associated with depression in a sample of young adults. Brain, Behavior, and Immunity, 2020, 88, 308-324.	4.1	115

#	Article	IF	CITATIONS
3396	Cheese whey fermentation into volatile fatty acids in an anaerobic sequencing batch reactor. Bioresource Technology, 2020, 308, 123226.	9.6	43
3397	Differential responses of gut microbiota of male and female fathead minnow (Pimephales promelas) to a short-term environmentally-relevant, aqueous exposure to benzo[a]pyrene. Chemosphere, 2020, 252, 126461.	8.2	37
3398	Response of an aerobic granular and conventional flocculated reactors against changing feed composition from simple composition to more complex. Chemosphere, 2020, 253, 126694.	8.2	12
3399	Commensal Bacteria Modulate Immunoglobulin A Binding in Response to Host Nutrition. Cell Host and Microbe, 2020, 27, 909-921.e5.	11.0	57
3400	The effect of woodchip bioreactors on microbial concentration in subsurface drainage water and the associated risk of antibiotic resistance dissemination. Ecological Engineering: X, 2020, 143, 100017.	3.5	4
3401	The T-shirt microbiome is distinct between individuals and shaped by washing and fabric type. Environmental Research, 2020, 185, 109449.	7.5	15
3402	Comparative analysis of free-living and particle-associated bacterial communities of Lake Baikal during the ice-covered period. Journal of Great Lakes Research, 2020, 46, 508-518.	1.9	14
3403	Meiofauna improve oxygenation and accelerate sulfide removal in the seasonally hypoxic seabed. Marine Environmental Research, 2020, 159, 104968.	2.5	20
3404	Enrichment Versus Bioaugmentation—Microbiological Production of Caproate from Mixed Carbon Sources by Mixed Bacterial Culture and <i>Clostridium kluyveri</i> Technology, 2020, 54, 5864-5873.	10.0	61
3405	Small phytoplankton dominate western North Atlantic biomass. ISME Journal, 2020, 14, 1663-1674.	9.8	74
3406	Site-specific molecular analysis of the bacteriota on worn spectacles. Scientific Reports, 2020, 10, 5577.	3.3	4
3407	Gut, oral and skin microbiome of Indian patrilineal families reveal perceptible association with age. Scientific Reports, 2020, 10, 5685.	3.3	50
3408	Assessment of unconventional antimicrobial compounds for the control of  Candidatus Liberibacter asiaticus', the causative agent of citrus greening disease. Scientific Reports, 2020, 10, 5395.	3.3	17
3409	Intestinal Bacteria Maintain Adult Enteric Nervous System and Nitrergic Neurons via Toll-like Receptor 2-induced Neurogenesis in Mice. Gastroenterology, 2020, 159, 200-213.e8.	1.3	67
3410	Larval density affects phenotype and surrounding bacterial community without altering gut microbiota in Drosophila melanogaster. FEMS Microbiology Ecology, 2020, 96, .	2.7	16
3411	Tomato-Associated Archaea Show a Cultivar-Specific Rhizosphere Effect but an Unspecific Transmission by Seeds. Phytobiomes Journal, 2020, 4, 133-141.	2.7	31
3412	Phylogenetic conservation of soil bacterial responses to simulated global changes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190242.	4.0	46
3413	Linking microbial communities to ecosystem functions: what we can learn from genotype–phenotype mapping in organisms. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190244.	4.0	36

#	Article	IF	CITATIONS
3414	Preconception helminth infection alters offspring microbiota and immune subsets in a mouse model. Parasite Immunology, 2020, 42, e12721.	1.5	13
3415	Legacy of a Butterfly's Parental Microbiome in Offspring Performance. Applied and Environmental Microbiology, 2020, 86, .	3.1	14
3416	Soil Microbial Communities in Diverse Agroecosystems Exposed to the Herbicide Glyphosate. Applied and Environmental Microbiology, 2020, 86, .	3.1	33
3417	Headwater Stream Microbial Diversity and Function across Agricultural and Urban Land Use Gradients. Applied and Environmental Microbiology, 2020, 86, .	3.1	12
3418	Tracking the Dairy Microbiota from Farm Bulk Tank to Skimmed Milk Powder. MSystems, 2020, 5, .	3.8	45
3419	Human Colon Mucosal Biofilms and Murine Host Communicate via Altered mRNA and microRNA Expression during Cancer. MSystems, 2020, 5, .	3.8	25
3420	Intranasal Bacterial Therapeutics Reduce Colonization by the Respiratory Pathogen Mannheimia haemolytica in Dairy Calves. MSystems, 2020, 5, .	3.8	33
3421	Respiratory Viral Infection Alters the Gut Microbiota by Inducing Inappetence. MBio, 2020, 11, .	4.1	122
3422	The Gut Microbiota in Camellia Weevils Are Influenced by Plant Secondary Metabolites and Contribute to Saponin Degradation. MSystems, 2020, 5, .	3.8	44
3423	A High-Fat/High-Protein, Atkins-Type Diet Exacerbates <i>Clostridioides</i> (<i>Clostridium</i>) state of the control of the	3.8	36
3424	Substrate-Dependent Fermentation of Bamboo in Giant Panda Gut Microbiomes: Leaf Primarily to Ethanol and Pith to Lactate. Frontiers in Microbiology, 2020, 11, 530.	3.5	7
3425	Toward Antibiotic Stewardship: Route of Antibiotic Administration Impacts the Microbiota and Resistance Gene Diversity in Swine Feces. Frontiers in Veterinary Science, 2020, 7, 255.	2.2	26
3426	The Microbiology of Hemp retting in a Controlled Environment: Steering the Hemp Microbiome towards More Consistent Fiber Production. Agronomy, 2020, 10, 492.	3.0	15
3427	Transport to the Slaughterhouse Affects the Salmonella Shedding and Modifies the Fecal Microbiota of Finishing Pigs. Animals, 2020, 10, 676.	2.3	13
3428	Distance from the Forest Edge Influences Soil Fungal Communities Colonizing a Reclaimed Soil Borrow Site in Boreal Mixedwood Forest. Forests, 2020, 11, 427.	2.1	7
3429	Long-Term Rewetting of Three Formerly Drained Peatlands Drives Congruent Compositional Changes in Pro- and Eukaryotic Soil Microbiomes through Environmental Filtering. Microorganisms, 2020, 8, 550.	3.6	25
3430	Neonatal diet alters fecal microbiota and metabolome profiles at different ages in infants fed breast milk or formula. American Journal of Clinical Nutrition, 2020, 111, 1190-1202.	4.7	67
3431	Subtle bacterioplankton community responses to elevated <scp>CO₂</scp> and warming in the oligotrophic South Pacific gyre. Environmental Microbiology Reports, 2020, 12, 377-386.	2.4	9

#	Article	IF	CITATIONS
3432	Soil fungal communities differ between shaded and sun-intensive coffee plantations in El Salvador. PLoS ONE, 2020, 15, e0231875.	2.5	13
3433	Epithelium intrinsic vitamin A signaling co-ordinates pathogen clearance in the gut via IL-18. PLoS Pathogens, 2020, 16, e1008360.	4.7	20
3434	Can Gut Microbiota Be a Good Predictor for Parkinson's Disease? A Machine Learning Approach. Brain Sciences, 2020, 10, 242.	2.3	22
3435	Alterations of the Rectal Microbiome Are Associated with the Development of Postoperative Ileus in Patients Undergoing Colorectal Surgery. Journal of Gastrointestinal Surgery, 2020, 24, 1663-1672.	1.7	12
3436	Targeting zonulin and intestinal epithelial barrier function to prevent onset of arthritis. Nature Communications, 2020, 11, 1995.	12.8	253
3437	Long-term effects of stump removal and tree species composition on the diversity and structure of soil fungal communities. FEMS Microbiology Ecology, 2020, 96, .	2.7	8
3438	Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. Agriculture (Switzerland), 2020, 10, 61.	3.1	21
3439	Human gut microbiome composition and tryptophan metabolites were changed differently by fast food and Mediterranean diet in 4 days: a pilot study. Nutrition Research, 2020, 77, 62-72.	2.9	79
3440	Effect of oxytetracycline treatment on the gastrointestinal microbiome of critically endangered white abalone (Haliotis sorenseni) treated for withering syndrome. Aquaculture, 2020, 526, 735411.	3.5	5
3441	Effects of woody biochar on dry thermophilic anaerobic digestion of organic fraction of municipal solid waste. Journal of Environmental Management, 2020, 267, 110633.	7.8	25
3442	Endophytic microbial assemblage in grapevine. FEMS Microbiology Ecology, 2020, 96, .	2.7	60
3443	Tonsillar microbial diversity, abundance, and interrelations in atopic and nonâ€atopic individuals. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 2133-2135.	5.7	5
3444	Comparison of the fecal microbiota of two monogastric herbivorous and five omnivorous mammals. Animal Science Journal, 2020, 91, e13366.	1.4	29
3445	Comparison of Methods To Collect Fecal Samples for Microbiome Studies Using Whole-Genome Shotgun Metagenomic Sequencing. MSphere, 2020, 5, .	2.9	23
3446	Genome-centric resolution of novel microbial lineages in an excavated Centrosaurus dinosaur fossil bone from the Late Cretaceous of North America. Environmental Microbiomes, 2020, 15, 8.	5.0	8
3447	Cloacal swabs and alcohol bird specimens are good proxies for compositional analyses of gut microbial communities of Great tits (Parus major). Animal Microbiome, 2020, 2, 9.	3.8	32
3448	Domesticated equine species and their derived hybrids differ in their fecal microbiota. Animal Microbiome, 2020, 2, 8.	3.8	19
3449	Improvement of Cecal Commensal Microbiome Following the Insect Additive into Chicken Diet. Animals, 2020, 10, 577.	2.3	32

#	Article	IF	CITATIONS
3450	Elucidation of the rhizosphere microbiome linked to Spartina alterniflora phenotype in a salt marsh on Skidaway Island, Georgia, USA. FEMS Microbiology Ecology, 2020, 96, .	2.7	21
3451	The gut microbiome and inflammation in obsessiveâ€compulsive disorder patients compared to age―and sexâ€matched controls: a pilot study. Acta Psychiatrica Scandinavica, 2020, 142, 337-347.	4.5	57
3452	Revegetation of urban green space rewilds soil microbiotas with implications for human health and urban design. Restoration Ecology, 2020, 28, S322.	2.9	43
3453	Adipose tissue derived bacteria are associated with inflammation in obesity and type 2 diabetes. Gut, 2020, 69, 1796-1806.	12.1	149
3454	Characterization of Gut Microbiota Composition in Hemodialysis Patients With Normal Weight Obesity. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2006-2014.	3.6	8
3455	(My Microbiome) Would Walk 10,000Âmiles: Maintenance and Turnover of Microbial Communities in Introduced Dung Beetles. Microbial Ecology, 2020, 80, 435-446.	2.8	27
3456	Characterizing a riverine microbiome impacted by extreme disturbance caused by a mining sludge tsunami. Chemosphere, 2020, 253, 126584.	8.2	15
3457	Water-induced molecular changes of hard coals and lignites. International Journal of Coal Geology, 2020, 224, 103481.	5.0	6
3458	Colitis-Induced Microbial Perturbation Promotes Postinflammatory Visceral Hypersensitivity. Cellular and Molecular Gastroenterology and Hepatology, 2020, 10, 225-244.	4.5	33
3459	Insights into the earthworm gut multi-kingdom microbial communities. Science of the Total Environment, 2020, 727, 138301.	8.0	48
3460	Environmentally clean access to Antarctic subglacial aquatic environments. Antarctic Science, 2020, 32, 329-340.	0.9	13
3461	A fungal pathogen induces systemic susceptibility and systemic shifts in wheat metabolome and microbiome composition. Nature Communications, 2020, 11, 1910.	12.8	85
3462	Oral therapy with colonization factor antigen I prevents development of type 1 diabetes in Non-obese Diabetic mice. Scientific Reports, 2020, 10, 6156.	3.3	9
3463	Microbial modulation of host body composition and plasma metabolic profile. Scientific Reports, 2020, 10, 6545.	3.3	14
3464	Contribution of L-Arginine supplementation during gestation on sow productive performance and on sow microbial faecal profile. Italian Journal of Animal Science, 2020, 19, 330-340.	1.9	9
3465	A novel normalization and differential abundance test framework for microbiome data. Bioinformatics, 2020, 36, 3959-3965.	4.1	12
3466	Insights into the community structure and lifestyle of the fungal root endophytes of tomato by combining amplicon sequencing and isolation approaches with phytohormone profiling. FEMS Microbiology Ecology, 2020, 96, .	2.7	31
3467	Response of aquatic microbial communities and bioindicator modelling of hydraulic fracturing flowback and produced water. FEMS Microbiology Ecology, 2020, 96, .	2.7	12

#	Article	IF	CITATIONS
3468	Local factors drive bacterial and microeukaryotic community composition in lake surface sediment collected across an altitudinal gradient. FEMS Microbiology Ecology, 2020, 96, .	2.7	20
3469	Impacts of Soil Microbiome Variations on Root Colonization by Fungi and Bacteria and on the Metabolome of <i>Populus tremula</i> À— <i>alba</i> Phytobiomes Journal, 2020, 4, 142-155.	2.7	24
3470	A dynamic microbial sulfur cycle in a serpentinizing continental ophiolite. Environmental Microbiology, 2020, 22, 2329-2345.	3.8	33
3471	Microbial community development on model particles in the deep sulfidic waters of the Black Sea. Environmental Microbiology, 2021, 23, 2729-2746.	3.8	11
3472	Different Effects of Soil Fertilization on Bacterial Community Composition in the <i>Penicillium canescens</i> Hyphosphere and in Bulk Soil. Applied and Environmental Microbiology, 2020, 86, .	3.1	14
3473	Observational Cohort Study of Oral Mycobiome and Interkingdom Interactions over the Course of Induction Therapy for Leukemia. MSphere, 2020, 5, .	2.9	18
3474	Oral and Gut Microbial Diversity and Immune Regulation in Patients with HIV on Antiretroviral Therapy. MSphere, 2020, 5, .	2.9	41
3475	Profiling of Oral Bacterial Communities. Journal of Dental Research, 2020, 99, 621-629.	5.2	45
3476	Dissimilarity of the gut–lung axis and dysbiosis of the lower airways in ventilated preterm infants. European Respiratory Journal, 2020, 55, 1901909.	6.7	26
3477	Impact of intestinal parasites on microbiota and cobalamin gene sequences: a pilot study. Parasites and Vectors, 2020, 13, 200.	2.5	33
3478	Genetic and metabolic links between the murine microbiome and memory. Microbiome, 2020, 8, 53.	11.1	56
3479	Resident microbial communities inhibit growth and antibiotic-resistance evolution of Escherichia coli in human gut microbiome samples. PLoS Biology, 2020, 18, e3000465.	5.6	47
3480	Microbial ecology and biogeochemistry of hypersaline sediments in Orca Basin. PLoS ONE, 2020, 15, e0231676.	2.5	14
3481	Lactobacillus reuteri attenuated allergic inflammation induced by HDM in the mouse and modulated gut microbes. PLoS ONE, 2020, 15, e0231865.	2.5	49
3482	Gut microbiota in children with juvenile idiopathic arthritis: characteristics, biomarker identification, and usefulness in clinical prediction. BMC Genomics, 2020, 21, 286.	2.8	30
3483	The penile microbiota of Black South African men: relationship with human papillomavirus and HIV infection. BMC Microbiology, 2020, 20, 78.	3.3	27
3484	Bacterial community composition of vermicompost-treated tomato rhizospheres. PLoS ONE, 2020, 15, e0230577.	2.5	8
3485	Effects of sex and chronic cigarette smoke exposure on the mouse cecal microbiome. PLoS ONE, 2020, 15, e0230932.	2.5	14

#	ARTICLE	IF	CITATIONS
3486	Geology and climate influence rhizobiome composition of the phenotypically diverse tropical tree Tabebuia heterophylla. PLoS ONE, 2020, 15, e0231083.	2.5	5
3487	Metabolic versatility of freshwater sedimentary archaea feeding on different organic carbon sources. PLoS ONE, 2020, 15, e0231238.	2.5	6
3488	Comparative Analysis of Rhizosphere Microbiomes of Southern Highbush Blueberry (Vaccinium) Tj ETQq 000 rgBT Frontiers in Microbiology, 2020, $11,370$.	Overlock	R 10 Tf 50 6 22
3489	Insights Into the Resistome of Bovine Clinical Mastitis Microbiome, a Key Factor in Disease Complication. Frontiers in Microbiology, 2020, 11, 860.	3.5	56
3490	Characterization of the Duodenal Mucosal Microbiome in Obese Adult Subjects by 16S rRNA Sequencing. Microorganisms, 2020, 8, 485.	3.6	36
3491	Identification and characterization of Javanese root-knot nematode (Meloidogyne javanica) suppressive soils in Florida. Applied Soil Ecology, 2020, 154, 103597.	4.3	12
3492	Prevalent root-derived phenolics drive shifts in microbial community composition and prime decomposition in forest soil. Soil Biology and Biochemistry, 2020, 145, 107797.	8.8	69
3493	Sustained RNA virome diversity in Antarctic penguins and their ticks. ISME Journal, 2020, 14, 1768-1782.	9.8	56
3494	Plasma levels of trimethylamine-N-oxide can be increased with †healthy†and †unhealthy†diets and do not correlate with the extent of atherosclerosis but with plaque instability. Cardiovascular Research, 2021, 117, 435-449.	3.8	58
3495	Association of subjective global assessment of nutritional status with gut microbiota in hemodialysis patients: a case–control study. Nephrology Dialysis Transplantation, 2021, 36, 1104-1111.	0.7	15
3496	The legacy of bacterial invasions on soil native communities. Environmental Microbiology, 2021, 23, 669-681.	3.8	21
3497	The fungal airway microbiome in cystic fibrosis and non-cystic fibrosis bronchiectasis. Journal of Cystic Fibrosis, 2021, 20, 295-302.	0.7	36
3498	Wet sieving versus dry crushing: Soil microaggregates reveal different physical structure, bacterial diversity and organic matter composition in a clay gradient. European Journal of Soil Science, 2021, 72, 810-828.	3.9	31
3499	Individual and Site-Specific Variation in a Biogeographical Profile of the Coyote Gastrointestinal Microbiota. Microbial Ecology, 2021, 81, 240-252.	2.8	17
3500	Natural Variation in Physicochemical Profiles and Bacterial Communities Associated with Aedes aegypti Breeding Sites and Larvae on Guadeloupe and French Guiana. Microbial Ecology, 2021, 81, 93-109.	2.8	28
3501	Direct Comparison of Fecal and Gut Microbiota in the Blue Mussel (Mytilus edulis) Discourages Fecal Sampling as a Proxy for Resident Gut Community. Microbial Ecology, 2021, 81, 180-192.	2.8	15
3502	Metabolic effects of duodenojejunal bypass surgery in a rat model of type 1 diabetes. Surgical Endoscopy and Other Interventional Techniques, 2021, 35, 3104-3114.	2.4	1
3503	Environmental and Spatial Influences on Biogeography and Community Structure of Saltmarsh Benthic Diatoms. Estuaries and Coasts, 2021, 44, 147-161.	2.2	10

#	Article	IF	CITATIONS
3504	Bronchopulmonary dysplasia is associated with reduced oral nitrate reductase activity in extremely preterm infants. Redox Biology, 2021, 38, 101782.	9.0	5
3505	Polycyclic aromatic hydrocarbon sorption and bacterial community composition of biodegradable and conventional plastics incubated in coastal sediments. Science of the Total Environment, 2021, 755, 143088.	8.0	17
3506	The human gut microbiota in people with amyotrophic lateral sclerosis. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2021, 22, 186-194.	1.7	49
3507	Unlocking the phylogenetic diversity, primary habitats, and abundances of freeâ€living Symbiodiniaceae on a coral reef. Molecular Ecology, 2021, 30, 343-360.	3.9	33
3508	Increased plant species richness associates with greater soil bacterial diversity in urban green spaces. Environmental Research, 2021, 196, 110425.	7. 5	28
3509	Influence of pipe material on biofilm microbial communities found in drinking water supply system. Environmental Research, 2021, 196, 110433.	7.5	21
3510	Low root functional dispersion enhances functionality of plant growth by influencing bacterial activities in European forest soils. Environmental Microbiology, 2021, 23, 1889-1906.	3.8	16
3511	Changes amid constancy: Flower and leaf microbiomes along land use gradients and between bioregions. Basic and Applied Ecology, 2021, 50, 1-15.	2.7	22
3512	Profiling microbial community structures and functions in bioremediation strategies for treating 1,4-dioxane-contaminated groundwater. Journal of Hazardous Materials, 2021, 408, 124457.	12.4	21
3513	Food or just a free ride? A meta-analysis reveals the global diversity of the Plastisphere. ISME Journal, 2021, 15, 789-806.	9.8	110
3514	The Gut Mycobiome in Parkinson's Disease. Journal of Parkinson's Disease, 2021, 11, 153-158.	2.8	15
3515	The effects of adsorptive materials on microbial community composition and PAH degradation at the sediment cap–water interface. International Journal of Sediment Research, 2021, 36, 555-565.	3 . 5	4
3516	Cover loss in a seagrass Posidonia oceanica meadow accelerates soil organic matter turnover and alters soil prokaryotic communities. Organic Geochemistry, 2021, 151, 104140.	1.8	17
3517	Insufficient dietary choline aggravates disease severity in a mouse model of <i>Citrobacter rodentium</i> -induced colitis. British Journal of Nutrition, 2021, 125, 50-61.	2.3	9
3518	Rare Feature Selection in High Dimensions. Journal of the American Statistical Association, 2021, 116, 887-900.	3.1	19
3519	Comparative analysis of the gut microbiota composition in the Cln1R151X and Cln2R207X mouse models of Batten disease and in three wild-type mouse strains. Archives of Microbiology, 2021, 203, 85-96.	2.2	6
3520	Increased diversity of gut microbiota during active oral immunotherapy in peanutâ€allergic adults. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 927-930.	5.7	20
3521	Synthetic community with six <i>Pseudomonas</i> strains screened from garlic rhizosphere microbiome promotes plant growth. Microbial Biotechnology, 2021, 14, 488-502.	4.2	66

#	Article	IF	Citations
3522	Quantitative profiling of built environment bacterial and fungal communities reveals dynamic material dependent growth patterns and microbial interactions. Indoor Air, 2021, 31, 188-205.	4.3	10
3523	Multi-omics data integration in anorexia nervosa patients before and after weight regain: A microbiome-metabolomics investigation. Clinical Nutrition, 2021, 40, 1137-1146.	5.0	38
3524	Human gut-derived commensal suppresses generation of T-cell response to gliadin in humanized mice by modulating gut microbiota. Anaerobe, 2021, 68, 102237.	2.1	11
3525	Lowâ€dose and longâ€term azithromycin significantly decreases <i>Staphylococcus aureus</i> in the microbiome of refractory CRS patients. International Forum of Allergy and Rhinology, 2021, 11, 93-105.	2.8	10
3526	Muc2 Mucin and Nonmucin Microbiota Confer Distinct Innate Host Defense in Disease Susceptibility and Colonic Injury. Cellular and Molecular Gastroenterology and Hepatology, 2021, 11, 77-98.	4.5	28
3527	Microbial Butyrate Synthesis Indicates Therapeutic Efficacy of Azathioprine in IBD Patients. Journal of Crohn's and Colitis, 2021, 15, 88-98.	1.3	41
3528	Ciliate Diversity From Aquatic Environments in the Brazilian Atlantic Forest as Revealed by High-Throughput DNA Sequencing. Microbial Ecology, 2021, 81, 630-643.	2.8	11
3529	Higher microbial diversity in raw than in pasteurized milk Raclette-type cheese enhances peptide and metabolite diversity after in vitro digestion. Food Chemistry, 2021, 340, 128154.	8.2	21
3530	Ocular surface microbiota in patients with aqueous tear-deficient dry eye. Ocular Surface, 2021, 19, 210-217.	4.4	47
3531	Influence of stormwater infiltration systems on the structure and the activities of groundwater biofilms: Are the effects restricted to rainy periods?. Science of the Total Environment, 2021, 755, 142451.	8.0	1
3532	Sows affect their piglets' faecal microbiota until fattening but not their Salmonella enterica shedding status. Letters in Applied Microbiology, 2021, 72, 113-120.	2.2	1
3533	Metagenomic insights into the antibiotic resistome of mangrove sediments and their association to socioeconomic status. Environmental Pollution, 2021, 268, 115795.	7. 5	17
3534	Mom's diet matters: Maternal prebiotic intake in mice reduces anxiety and alters brain gene expression and the fecal microbiome in offspring. Brain, Behavior, and Immunity, 2021, 91, 230-244.	4.1	20
3535	Co-selection of antibiotic resistance genes, and mobile genetic elements in the presence of heavy metals in poultry farm environments. Science of the Total Environment, 2021, 755, 142702.	8.0	122
3536	Transition of microbial communities and degradation pathways in anaerobic digestion at decreasing retention time. New Biotechnology, 2021, 60, 52-61.	4.4	22
3537	Bacterial communities in the plant phyllosphere harbour distinct responders to a broad-spectrum pesticide. Science of the Total Environment, 2021, 751, 141799.	8.0	46
3538	The mycobiomes and bacteriomes of sputum, saliva, and home dust. Indoor Air, 2021, 31, 357-368.	4.3	3
3539	Root traits explain rhizosphere fungal community composition among temperate grassland plant species. New Phytologist, 2021, 229, 1492-1507.	7.3	102

#	ARTICLE	IF	CITATIONS
3540	Desalinization via freshwater restoration highly improved microbial diversity, co-occurrence patterns and functions in coastal wetland soils. Science of the Total Environment, 2021, 765, 142769.	8.0	23
3541	Acidobacteria are active and abundant members of diverse atmospheric H2-oxidizing communities detected in temperate soils. ISME Journal, 2021, 15, 363-376.	9.8	23
3542	Circulating sDPP-4 is Increased in Obesity and Insulin Resistance but Is Not Related to Systemic Metabolic Inflammation. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e592-e601.	3.6	16
3543	Sourdough cultures as reservoirs of maltose-negative yeasts for low-alcohol beer brewing. Food Microbiology, 2021, 94, 103629.	4.2	27
3544	Host specificity of microbiome assembly and its fitness effects in phytoplankton. ISME Journal, 2021, 15, 774-788.	9.8	48
3545	Interpreting lacustrine bulk sediment $\hat{l}'15N$ values using metagenomics in a tropical hypersaline lake system. Journal of Paleolimnology, 2021, 65, 151-168.	1.6	4
3546	Powdered activated carbon (PAC) amendment enhances naphthalene biodegradation under strictly sulfate-reducing conditions. Environmental Pollution, 2021, 268, 115641.	7.5	10
3547	Functional metagenomic landscape of polluted river reveals potential genes involved in degradation of xenobiotic pollutants. Environmental Research, 2021, 192, 110332.	7.5	24
3548	Microbial communities in field-scale oil-polluted soil remediation using 16S rRNA amplicon sequencing. International Journal of Environmental Studies, 2021, 78, 410-426.	1.6	8
3549	Distinguishing Between the Impacts of Heat and Drought Stress on the Root Microbiome of <i>Sorghum bicolor</i>). Phytobiomes Journal, 2021, 5, 166-176.	2.7	28
3550	Urban ponds as hotspots of antibiotic resistome in the urban environment. Journal of Hazardous Materials, 2021, 403, 124008.	12.4	48
3551	<scp>SCRAPP</scp> : A tool to assess the diversity of microbial samples from phylogenetic placements. Molecular Ecology Resources, 2021, 21, 340-349.	4.8	5
3552	Effects of <i>Lactobacillus hilgardii</i> 4785 and <i>Lactobacillus buchneri</i> 40788 on the bacterial community, fermentation and aerobic stability of highâ€moisture corn silage. Journal of Applied Microbiology, 2021, 130, 1481-1493.	3.1	28
3553	High-throughput sequence analysis of bacterial communities and their predictive functionalities in traditionally preserved fish products of Sikkim, India. Food Research International, 2021, 143, 109885.	6.2	10
3554	Influence of the cold bottom water on taxonomic and functional composition and complexity of microbial communities in the southern Yellow Sea during the summer. Science of the Total Environment, 2021, 759, 143496.	8.0	12
3555	Maternal Diet Shapes the Breast Milk Microbiota Composition and Diversity: Impact of Mode of Delivery and Antibiotic Exposure. Journal of Nutrition, 2021, 151, 330-340.	2.9	52
3556	Rearing water microbiomes in white leg shrimp (<scp><i>Litopenaeus vannamei</i></scp>) larviculture assemble stochastically and are influenced by the microbiomes of live feed products. Environmental Microbiology, 2021, 23, 281-298.	3.8	17
3557	Association of gut microbiome with fasting triglycerides, fasting insulin and obesity status in Mexican children. Pediatric Obesity, 2021, 16, e12748.	2.8	37

#	Article	IF	CITATIONS
3558	<i>Chlamydia pneumoniae</i> hand <i>Mycoplasma pneumoniae</i> ion bacterial respiratory microbiota diversity. Pathogens and Disease, 2021, 79, .	2.0	6
3559	Microbial networks inferred from environmental DNA data for biomonitoring ecosystem change: Strengths and pitfalls. Molecular Ecology Resources, 2021, 21, 762-780.	4.8	17
3560	An integrated metagenomics and metabolomics approach implicates the microbiota-gut-brain axis in the pathogenesis of Huntington's disease. Neurobiology of Disease, 2021, 148, 105199.	4.4	52
3561	Antarctic coastal nanoplankton dynamics revealed by metabarcoding of desalination plant filters: Detection of short-term events and implications for routine monitoring. Science of the Total Environment, 2021, 757, 143809.	8.0	5
3562	Fungal guilds and soil functionality respond to tree community traits rather than to tree diversity in European forests. Molecular Ecology, 2021, 30, 572-591.	3.9	31
3563	Parenteral lipid emulsions induce unique ileal fatty acid and metabolomic profiles but do not increase the risk of necrotizing enterocolitis in preterm pigs. American Journal of Physiology - Renal Physiology, 2021, 320, G227-G239.	3.4	5
3564	The effect of the polarised cathode, formate and ethanol on chain elongation of acetate in microbial electrosynthesis. Applied Energy, 2021, 283, 116310.	10.1	31
3565	Neonicotinoid use on cereals and sugar beet is linked to continued low exposure risk in honeybees. Agriculture, Ecosystems and Environment, 2021, 308, 107205.	5.3	11
3566	Assessing the Diversity of Benthic Sulfate-Reducing Microorganisms in Northwestern Gulf of Mexico by Illumina Sequencing of dsrB Gene. Microbial Ecology, 2021, 81, 908-921.	2.8	6
3567	The microbiome of Chinook salmon (Oncorhynchus tshawytscha) in a recirculation aquaculture system. Aquaculture, 2021, 534, 736227.	3.5	16
3568	Selective Survival of Escherichia coli Phylotypes in Freshwater Beach Sand. Applied and Environmental Microbiology, 2021, 87, .	3.1	9
3569	Soil fungal diversity and functionality are driven by plant species used in phytoremediation. Soil Biology and Biochemistry, 2021, 153, 108102.	8.8	25
3570	Longitudinal Changes in Fecal Calprotectin Levels Among Pregnant Women With and Without Inflammatory Bowel Disease and Their Babies. Gastroenterology, 2021, 160, 1118-1130.e3.	1.3	41
3571	The biogeography of Streptomyces in New Zealand enabled by highâ€throughput sequencing of genusâ€specific rpoB amplicons. Environmental Microbiology, 2021, 23, 1452-1468.	3.8	6
3572	Modified SHI medium supports growth of a diseaseâ€state subgingival polymicrobial community in vitro. Molecular Oral Microbiology, 2021, 36, 37-49.	2.7	11
3573	Differential effect of silver nanoparticles on the microbiome of adult and developing planaria. Aquatic Toxicology, 2021, 230, 105672.	4.0	4
3574	Ecotoxicological assessment of commercial boron nitride nanotubes toward <i>Xenopus laevis</i> tadpoles and host-associated gut microbiota. Nanotoxicology, 2021, 15, 35-51.	3.0	16
3575	Gene expression remodelling and immune response during adaptive divergence in an African cichlid fish. Molecular Ecology, 2021, 30, 274-296.	3.9	5

#	Article	IF	CITATIONS
3576	The Gut Microbiome in Polycystic Ovary Syndrome and Its Association with Metabolic Traits. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 858-871.	3.6	31
3577	In-depth Spatiotemporal Characterization of Planktonic Archaeal and Bacterial Communities in North and South San Francisco Bay. Microbial Ecology, 2021, 81, 601-616.	2.8	11
3578	Abiotic conditions outweigh microbial origin during bacterial assembly in soils. Environmental Microbiology, 2021, 23, 358-371.	3.8	8
3579	Hostâ€association as major driver of microbiome structure and composition in Red Sea seagrass ecosystems. Environmental Microbiology, 2021, 23, 2021-2034.	3.8	9
3580	Impact of a yeastâ€based dietary supplement on the intestinal microbiome of rainbow trout, <i>Oncorhynchus mykiss </i> . Aquaculture Research, 2021, 52, 1594-1604.	1.8	11
3581	Bioaccumulation of trace elements affects chick body condition and gut microbiome in greater flamingos. Science of the Total Environment, 2021, 761, 143250.	8.0	20
3582	Dynamics of microbial stress responses driven by abiotic changes along a temporal gradient in Deception Island, Maritime Antarctica. Science of the Total Environment, 2021, 758, 143671.	8.0	9
3583	CRISPR RNA-guided integrases for high-efficiency, multiplexed bacterial genome engineering. Nature Biotechnology, 2021, 39, 480-489.	17.5	179
3584	Microbes, mutualism, and range margins: testing the fitness consequences of soil microbial communities across and beyond a native plant's range. New Phytologist, 2021, 229, 2886-2900.	7.3	24
3585	The influence of the prebiotic gum acacia on the intestinal microbiome composition in rats with experimental chronic kidney disease. Biomedicine and Pharmacotherapy, 2021, 133, 110992.	5.6	26
3586	Ecological drivers switch from bottom–up to top–down during model microbial community successions. ISME Journal, 2021, 15, 1085-1097.	9.8	21
3587	Effect of chelated iron activated peroxydisulfate oxidation on perchloroethene-degrading microbial consortium. Chemosphere, 2021, 266, 128928.	8.2	5
3588	Substrate type determines microbial activity and community composition in bioreactors for nitrate removal by denitrification at low temperature. Science of the Total Environment, 2021, 755, 143023.	8.0	32
3589	Host plant diet affects growth and induces altered gene expression and microbiome composition in the wood white (Leptidea sinapis) butterfly. Molecular Ecology, 2021, 30, 499-516.	3.9	17
3590	Optimizing the quality of clinical studies on oral microbiome: A practical guide for planning, performing, and reporting. Periodontology 2000, 2021, 85, 210-236.	13.4	51
3591	Intestinal Phospholipid Disequilibrium Initiates an ER Stress Response That Drives Goblet Cell Necroptosis and Spontaneous Colitis in Mice. Cellular and Molecular Gastroenterology and Hepatology, 2021, 11, 999-1021.	4. 5	20
3592	Exploring antibiotic resistance in environmental integron-cassettes through intl-attC amplicons deep sequencing. Brazilian Journal of Microbiology, 2021, 52, 363-372.	2.0	8
3593	Plant resistome profiling in evolutionary old bog vegetation provides new clues to understand emergence of multi-resistance. ISME Journal, 2021, 15, 921-937.	9.8	33

#	Article	IF	CITATIONS
3594	Diversity and biomass dynamics of unicellular marine fungi during a spring phytoplankton bloom. Environmental Microbiology, 2021, 23, 448-463.	3.8	22
3595	Lactobacillus plantarum in black soldier fly (Hermetica illucens) meal modulates gut health and immunity of freshwater crayfish (Cherax cainii). Fish and Shellfish Immunology, 2021, 108, 42-52.	3.6	19
3596	Microplastic pollution alters forest soil microbiome. Journal of Hazardous Materials, 2021, 409, 124606.	12.4	100
3597	Nitrogen addition alters composition, diversity, and functioning of microbial communities in mangrove soils: An incubation experiment. Soil Biology and Biochemistry, 2021, 153, 108076.	8.8	38
3598	Depth Related Structure and Microbial Composition of Microbialites in a Karst Sinkhole, Cenote Azul, Mexico. Geomicrobiology Journal, 2021, 38, 237-251.	2.0	2
3599	Electrochemical evidence for in situ microbial activity at the Deep Mine Microbial Observatory (DeMMO), South Dakota, USA. Geobiology, 2021, 19, 173-188.	2.4	7
3600	Bioaerosols in the Athens Metro: Metagenetic insights into the PM10 microbiome in a naturally ventilated subway station. Environment International, 2021, 146, 106186.	10.0	19
3601	Strong priming of soil organic matter induced by frequent input of labile carbon. Soil Biology and Biochemistry, 2021, 152, 108069.	8.8	70
3602	Plant part and a steep environmental gradient predict plant microbial composition in a tropical watershed. ISME Journal, 2021, 15, 999-1009.	9.8	21
3603	Spatial and temporal variations in Synechococcus microdiversity in the Southern California coastal ecosystem. Environmental Microbiology, 2021, 23, 252-266.	3.8	10
3604	Effects of Antibiotic Treatment with Piperacillin/Tazobactam versus Ceftriaxone on the Composition of the Murine Gut Microbiota. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	17
3605	Impact of high carbon amendments and pre-crops on soil bacterial communities. Biology and Fertility of Soils, 2021, 57, 305-317.	4.3	4
3606	The intestinal microbiome of Australian abalone, Haliotis laevigata and Haliotis laevigata × Haliotis rubra, over a 1-year period in aquaculture Aquaculture, 2021, 534, 736245.	3.5	9
3607	Impact of DNA extraction and sampling methods on bacterial communities monitored by 16S rDNA metabarcoding in cold-smoked salmon and processing plant surfaces. Food Microbiology, 2021, 95, 103705.	4.2	27
3608	Lactobacillus reuteri CCFM1072 and CCFM1040 with the role of Treg cells regulation alleviate airway inflammation through modulating gut microbiota in allergic asthma mice. Journal of Functional Foods, 2021, 76, 104286.	3.4	11
3609	Integrated air cathode microbial fuel cell-aerobic bioreactor set-up for enhanced bioelectrodegradation of azo dye Acid Blue 29. Science of the Total Environment, 2021, 756, 143752.	8.0	46
3610	Microbial community of Hyalomma lusitanicum is dominated by Francisella-like endosymbiont. Ticks and Tick-borne Diseases, 2021, 12, 101624.	2.7	7
3611	Sewage treatment at 4 °C in anaerobic upflow reactors with and without a membrane – performance, function and microbial diversity. Environmental Science: Water Research and Technology, 2021, 7, 156-171.	2.4	7

#	Article	IF	CITATIONS
3612	Microbiological, immunological, and histological changes in the gut of Salmonella Enteritidis-challenged rats fed goat cheese containing Lactobacillus rhamnosus EM1107. Journal of Dairy Science, 2021, 104, 179-197.	3.4	3
3613	Biofilm structure, dynamics, and ecology of an upscaled biocathode wastewater microbial fuel cell. Biotechnology and Bioengineering, 2021, 118, 1305-1316.	3.3	5
3614	Microbiome taxonomic and functional profiles of two domestic sewage treatment systems. Biodegradation, 2021, 32, 17-36.	3.0	7
3615	Composition and functional comparison of vetiver root endophytic microbiota originating from different geographic locations that show antagonistic activity towards Fusarium graminearum. Microbiological Research, 2021, 243, 126650.	5.3	11
3616	Combined removal of organic micropollutants and ammonium in reactive barriers developed for managed aquifer recharge. Water Research, 2021, 190, 116669.	11.3	16
3617	Bacterial Biofilms on Polyamide Nanofibers: Factors Influencing Biofilm Formation and Evaluation. ACS Applied Materials & Diversary (1988).	8.0	28
3618	Metagenomic Approach to Bacterial Diversity and Lipolytic Enzymes' Genes from a Steam Soil of Los Humeros Geothermal Field (Puebla, México). Geomicrobiology Journal, 2021, 38, 304-314.	2.0	0
3619	Contrasting fungal responses to wildfire across different ecosystem types. Molecular Ecology, 2021, 30, 844-854.	3.9	13
3620	Substrate Pre-loading Influences Initial Colonization of GAC Biofilter Biofilms. Frontiers in Microbiology, 2020, 11, 596156.	3.5	2
3621	Phylogenetic and geographical analysis of a retrovirus during the early stages of endogenous adaptation and exogenous spread in a new host. Molecular Ecology, 2021, 30, 2626-2640.	3.9	16
3622	Loss of <i>Arabidopsis</i> matrix metalloproteinaseâ€5 affects root development and root bacterial communities during drought stress. Physiologia Plantarum, 2021, 172, 1045-1058.	5,2	8
3623	Comparing larval microbiomes of the eastern oyster (Crassostrea virginica) raised in different hatcheries. Aquaculture, 2021, 531, 735955.	3.5	22
3624	The Horse Gut Microbiome Responds in a Highly Individualized Manner to Forage Lignification. Journal of Equine Veterinary Science, 2021, 96, 103306.	0.9	8
3625	Influence of photobioreactor set-up on the survival of microalgae inoculum. Bioresource Technology, 2021, 320, 124408.	9.6	26
3626	Rapid microbial community evolution in initial Carex litter decomposition stages in Bayinbuluk alpine wetland during the freeze–thaw period. Ecological Indicators, 2021, 121, 107180.	6.3	25
3627	Gut Microbiota-Derived Metabolite Signature in Suckling and Weaned Piglets. Journal of Proteome Research, 2021, 20, 982-994.	3.7	31
3628	<i>microeco</i> : an R package for data mining in microbial community ecology. FEMS Microbiology Ecology, 2021, 97, .	2.7	398
3629	Association of birth mode of delivery with infant faecal microbiota, potential pathobionts, and short chain fatty acids: a longitudinal study over the first year of life. BJOG: an International Journal of Obstetrics and Gynaecology, 2021, 128, 1293-1303.	2.3	21

#	Article	IF	CITATIONS
3630	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. Molecular Ecology, 2021, 30, 1072-1085.	3.9	43
3631	Enrichment of Hydrogen-Oxidizing Bacteria from High-Temperature and High-Salinity Environments. Applied and Environmental Microbiology, 2021, 87, .	3.1	5
3632	High temperatures enhance the microbial genetic potential to recycle C and N from necromass in highâ€mountain soils. Global Change Biology, 2021, 27, 1365-1386.	9.5	49
3633	Maternal effects shape the seed mycobiome in <i>Quercus petraea</i> . New Phytologist, 2021, 230, 1594-1608.	7. 3	47
3634	Bacterial community dynamics varies with soil management and irrigation practices in grapevines (Vitis vinifera L.). Applied Soil Ecology, 2021, 158, 103807.	4.3	12
3635	Characterization of the Gastric Mucosal Microbiota in Patients with Liver Cirrhosis and Its Associations with Gastrointestinal Symptoms. Engineering, 2021, 7, 507-514.	6.7	0
3636	Molecular monitoring of the poplar wood chip microbiome as a function of storage strategy. International Biodeterioration and Biodegradation, 2021, 156, 105133.	3.9	7
3637	Comparison of intestinal permeability, morphology, and ileal microbial communities of commercial hens housed in conventional cages and cage-free housing systems. Poultry Science, 2021, 100, 1178-1191.	3.4	21
3638	Gut microbiota and metabolic marker alteration following dietary isoflavoneâ€photoperiod interaction. Endocrinology, Diabetes and Metabolism, 2021, 4, e00190.	2.4	8
3639	The utility ofÂenvironmental DNA from sediment and water samples for recovery of observed plant and animal species from four Mojave Desert springs. Environmental DNA, 2021, 3, 214-230.	5.8	14
3640	Linking bacterial diversity to floral identity in the bumble bee pollen basket. Environmental DNA, 2021, 3, 669-680.	5.8	8
3641	Molecular evidence of host-parasite interactions between zooplankton and Syndiniales. Aquatic Ecology, 2021, 55, 125-134.	1.5	15
3642	Pollen diets and niche overlap of honey bees and native bees in protected areas. Basic and Applied Ecology, 2021, 50, 169-180.	2.7	30
3643	Response of oligotrophic coastal microbial populations in the SE Mediterranean Sea to crude oil pollution; lessons from mesocosm studies. Estuarine, Coastal and Shelf Science, 2021, 249, 107102.	2.1	13
3644	Corn-soybean rotation, tillage, and foliar fungicides: Impacts on yield and soil fungi. Field Crops Research, 2021, 262, 108030.	5.1	16
3645	Salivary bacterial shifts in oral leukoplakia resemble the dysbiotic oral cancer bacteriome. Journal of Oral Microbiology, 2021, 13, 1857998.	2.7	24
3646	Molecular Barcoding Reveals the Genus <i>Streptomyces</i> as Associated Root Endophytes of Apple (<i>Malus domestica</i>) Plants Grown in Soils Affected by Apple Replant Disease. Phytobiomes Journal, 2021, 5, 177-189.	2.7	15
3647	Invasive freshwater snails form novel microbial relationships. Evolutionary Applications, 2021, 14, 770-780.	3.1	9

#	Article	IF	CITATIONS
3648	Host population size is linked to orchid mycorrhizal fungal communities in roots and soil, which are shaped by microenvironment. Mycorrhiza, 2021, 31, 17-30.	2.8	20
3649	Distribution of airborne pollen, fungi and bacteria at four altitudes using high-throughput DNA sequencing. Atmospheric Research, 2021, 249, 105306.	4.1	8
3650	Arsenic behavior in groundwater in Hanoi (Vietnam) influenced by a complex biogeochemical network of iron, methane, and sulfur cycling. Journal of Hazardous Materials, 2021, 407, 124398.	12.4	31
3651	The relevance of environment vs. composition on dissolved organic matter degradation in freshwaters. Limnology and Oceanography, 2021, 66, 306-320.	3.1	31
3652	Do environmental pharmaceuticals affect the composition of bacterial communities in a freshwater stream? A case study of the Knivsta river in the south of Sweden. Science of the Total Environment, 2021, 763, 142991.	8.0	11
3653	Microbiome and environment explain the absence of correlations between consumers and their diet in Bornean microsnails. Ecology, 2021, 102, e03237.	3.2	3
3654	Pollution shapes the microbial communities in river water and sediments from the Olifants River catchment, South Africa. Archives of Microbiology, 2021, 203, 295-303.	2.2	3
3655	Commercial wash of leafy vegetables do not significantly decrease bacterial load but leads to shifts in bacterial species composition. Food Microbiology, 2021, 94, 103667.	4.2	24
3656	Postmortem submersion interval (PMSI) estimation from the microbiome of Sus scrofa bone in a freshwater river. Forensic Science International, 2021, 318, 110480.	2.2	18
3657	Comparing DNA Extraction and 16S rRNA Gene Amplification Methods for Plant-Associated Bacterial Communities. Phytobiomes Journal, 2021, 5, 190-201.	2.7	5
3658	Chasing Waterborne Pathogens in Antarctic Human-Made and Natural Environments, with Special Reference to <i>Legionella</i> spp. Applied and Environmental Microbiology, 2021, 87, .	3.1	13
3659	Spatio-temporal resolution of taxonomic and functional microbiome of Lonar soda lake of India reveals metabolic potential for bioremediation. Chemosphere, 2021, 264, 128574.	8.2	13
3660	Ultimate pH effects on dry-aged beef quality. Meat Science, 2021, 172, 108365.	5.5	28
3661	Scale-Dependent Influences of Distance and Vegetation on the Composition of Aboveground and Belowground Tropical Fungal Communities. Microbial Ecology, 2021, 81, 874-883.	2.8	10
3662	Physiologic colonic uptake of 18F-FDG on PET/CT is associated with clinical response and gut microbiome composition in patients with advanced non-small cell lung cancer treated with immune checkpoint inhibitors. European Journal of Nuclear Medicine and Molecular Imaging, 2021, 48, 1550-1559.	6.4	15
3663	Drivers of diazotroph community structure and co-occurrence in a Northern Great Plains pulse crop rotation system. Applied Soil Ecology, 2021, 157, 103737.	4.3	9
3664	How the  kitome' influences the characterization of bacterial communities in lepidopteran samples with low bacterial biomass. Journal of Applied Microbiology, 2021, 130, 1780-1793.	3.1	9
3665	Molecular Evidence for an Active Microbial Methane Cycle in Subsurface Serpentinite-Hosted Groundwaters in the Samail Ophiolite, Oman. Applied and Environmental Microbiology, 2021, 87, .	3.1	29

#	Article	IF	CITATIONS
3666	Depicting Temporal, Functional, and Phylogenetic Patterns in Estuarine Diazotrophic Communities from Environmental DNA and RNA. Microbial Ecology, 2021, 81, 36-51.	2.8	14
3667	Long-term liming promotes drastic changes in the composition of the microbial community in a tropical savanna soil. Biology and Fertility of Soils, 2021, 57, 31-46.	4.3	10
3668	Niche Partitioning of Microbial Communities at an Ancient Vitrified Hillfort: Implications for Vitrified Radioactive Waste Disposal. Geomicrobiology Journal, 2021, 38, 36-56.	2.0	5
3669	A network approach to elucidate and prioritize microbial dark matter in microbial communities. ISME Journal, 2021, 15, 228-244.	9.8	91
3670	Interactions between nitrogen availability, bacterial communities, and nematode indicators of soil food web function in response to organic amendments. Applied Soil Ecology, 2021, 157, 103767.	4.3	20
3671	Microbial communities in rare earth mining soil after in-situ leaching mining. Science of the Total Environment, 2021, 755, 142521.	8.0	38
3672	Litter-inhabiting fungi show high level of specialization towards biopolymers composing plant and fungal biomass. Biology and Fertility of Soils, 2021, 57, 77-88.	4.3	30
3673	Type 2–high asthma is associated with a specific indoor mycobiome and microbiome. Journal of Allergy and Clinical Immunology, 2021, 147, 1296-1305.e6.	2.9	41
3674	Metagenome Across a Geochemical Gradient of Indian Stone Ruins Found at Historic Sites in Tamil Nadu, India. Microbial Ecology, 2021, 81, 385-395.	2.8	15
3675	Depth-Dependent Variables Shape Community Structure and Functionality in the Prince Edward Islands. Microbial Ecology, 2021, 81, 396-409.	2.8	5
3676	Intraspecific Variability in Root Traits and Edaphic Conditions Influence Soil Microbiomes Across 12 Switchgrass Cultivars. Phytobiomes Journal, 2021, 5, 108-120.	2.7	18
3677	Spatiotemporal Changes in the Bacterial Community of the Meromictic Lake Uchum, Siberia. Microbial Ecology, 2021, 81, 357-369.	2.8	6
3678	Crop, genotype, and field environmental conditions shape bacterial and fungal seed epiphytic microbiomes. Canadian Journal of Microbiology, 2021, 67, 161-173.	1.7	29
3679	Metagenomic Alterations in Gut Microbiota Precede and Predict Onset of Colitis in the IL10 Gene-Deficient Murine Model. Cellular and Molecular Gastroenterology and Hepatology, 2021, 11, 491-502.	4.5	7
3680	The Microbiome in Health and Disease. , 2021, , 232-246.		1
3681	Resolving broad patterns of prokaryotic community structure in New Zealand pasture soils. New Zealand Journal of Agricultural Research, 2021, 64, 143-161.	1.6	2
3682	Diversity of bacteria associated with Hormaphidinae aphids (Hemiptera: Aphididae). Insect Science, 2021, 28, 165-179.	3.0	20
3683	Current challenges and best-practice protocols for microbiome analysis. Briefings in Bioinformatics, 2021, 22, 178-193.	6.5	268

#	ARTICLE	IF	CITATIONS
3684	Metagenomics Approaches to Investigate the Gut Microbiome of COVID-19 Patients. Bioinformatics and Biology Insights, 2021, 15, 117793222199942.	2.0	8
3685	ResistoXplorer: a web-based tool for visual, statistical and exploratory data analysis of resistome data. NAR Genomics and Bioinformatics, 2021, 3, lqab018.	3.2	9
3686	The Use of Data Science for Decision Making in Medicine: The Microbial Community of the Gut and Autism Spectrum Disorders. Communications in Computer and Information Science, 2021, , 79-91.	0.5	2
3687	Influence of reductive soil disinfestation or biochar amendment on bacterial communities and their utilization of plant-derived carbon in the rhizosphere of tomato. Applied Microbiology and Biotechnology, 2021, 105, 815-825.	3.6	11
3688	Bacterial and Fungal Microbiome Profiling in Chilhuacle Negro Chili (<i>Capsicum annuum</i> L.) Associated With Fruit Rot Disease. Plant Disease, 2021, 105, 2618-2627.	1.4	3
3689	Signatures of landscape and captivity in the gut microbiota of Southern Hairy-nosed Wombats (Lasiorhinus latifrons). Animal Microbiome, 2021, 3, 4.	3.8	9
3691	A Longitudinal Study of the Human Oropharynx Microbiota Over Time Reveals a Common Core and Significant Variations With Self-Reported Disease. Frontiers in Microbiology, 2020, 11, 573969.	3.5	9
3693	Application of extracellular polymers on soil communities exposed to oil and nickel contamination. Brazilian Journal of Microbiology, 2021, 52, 651-661.	2.0	1
3695	Identification of novel bacterial biomarkers to detect bird scavenging by invasive rats. Ecology and Evolution, 2021, 11, 1814-1828.	1.9	4
3696	Microbial retention and resistances in stormwater quality improvement devices treating road runoff. FEMS Microbes, 2021, 2, .	2.1	1
3697	Citizen-science based study of the oral microbiome in Cystic fibrosis and matched controls reveals major differences in diversity and abundance of bacterial and fungal species. Journal of Oral Microbiology, 2021, 13, 1897328.	2.7	11
3698	The Effect of a High-Grain Diet on the Rumen Microbiome of Goats with a Special Focus on Anaerobic Fungi. Microorganisms, 2021, 9, 157.	3.6	17
3699	Seaâ€ice microbial communities in the Central Arctic Ocean: Limited responses to shortâ€term pCO 2 perturbations. Limnology and Oceanography, 2021, 66, S383.	3.1	6
3700	Influence of Plant Host and Organ, Management Strategy, and Spore Traits on Microbiome Composition. Phytobiomes Journal, 2021, 5, 202-219.	2.7	13
3702	Postâ€epizootic microbiome associations across communities of neotropical amphibians. Molecular Ecology, 2021, 30, 1322-1335.	3.9	6
3703	Paternal Methyl Donor Supplementation in Rats Improves Fertility, Physiological Outcomes, Gut Microbial Signatures and Epigenetic Markers Altered by High Fat/High Sucrose Diet. International Journal of Molecular Sciences, 2021, 22, 689.	4.1	8
3704	Distinct microbial communities colonize tonsillar squamous cell carcinoma. Oncolmmunology, 2021, 10, 1945202.	4.6	13
3705	Identification of the core rumen bacterial taxa and their population dynamics during the fattening period in Japanese Black cattle. Animal Science Journal, 2021, 92, e13601.	1.4	12

#	Article	IF	CITATIONS
3706	Ethnicity influences the gut microbiota of individuals sharing a geographical location: a cross-sectional study from a middle-income country. Scientific Reports, 2021, 11, 2618.	3.3	73
3707	The Bacterial Community of the Foliose Macro-lichen Peltigera frigida Is More than a Mere Extension of the Microbiota of the Subjacent Substrate. Microbial Ecology, 2021, 81, 965-976.	2.8	19
3708	Environment has a Stronger Effect than Host Plant Genotype in Shaping Spring <i>Brassica napus</i> Seed Microbiomes. Phytobiomes Journal, 2021, 5, 220-230.	2.7	26
3709	Biogeographical Landscape of the Human Face Skin Microbiome Viewed in High Definition. Acta Dermato-Venereologica, 2021, 101, adv00603.	1.3	1
3710	The gut microbiome of COVID-19 recovered patients returns to uninfected status in a minority-dominated United States cohort. Gut Microbes, 2021, 13, 1-15.	9.8	46
3711	Effects of Rare Microbiome Taxa Filtering on Statistical Analysis. Frontiers in Microbiology, 2020, 11, 607325.	3.5	65
3712	Interactions between soil compositions and the wheat root microbiome under drought stress: From an in silico to in planta perspective. Computational and Structural Biotechnology Journal, 2021, 19, 4235-4247.	4.1	7
3713	Linking Bacterial Communities Associated with the Environment and the Ecosystem Engineer Orchestia gammarellus at Contrasting Salt Marsh Elevations. Microbial Ecology, 2021, 82, 537-548.	2.8	3
3714	Significant and Conflicting Correlation of IL-9 With Prevotella and Bacteroides in Human Colorectal Cancer. Frontiers in Immunology, 2020, 11, 573158.	4.8	37
3715	Strain-Level Profiling of Oral Microbiota with Targeted Sequencing. Methods in Molecular Biology, 2021, 2327, 239-252.	0.9	2
3716	Compensatory intestinal immunoglobulin response after vancomycin treatment in humans. Gut Microbes, 2021, 13, 1-14.	9.8	6
3717	Identification of microbial signatures linked to oilseed rape yield decline at the landscape scale. Microbiome, 2021, 9, 19.	11.1	31
3718	Enrichment and description of novel bacteria performing syntrophic propionate oxidation at high ammonia level. Environmental Microbiology, 2021, 23, 1620-1637.	3.8	21
3719	Deprivation of dietary fiber in specific-pathogen-free mice promotes susceptibility to the intestinal mucosal pathogen <i>Citrobacter rodentium < li>. Gut Microbes, 2021, 13, 1966263.</i>	9.8	35
3720	Modeling transfer of vaginal microbiota from mother to infant in early life. ELife, 2021, 10, .	6.0	35
3721	Microbial Communities' Characterization in Urban Recreational Surface Waters Using Next Generation Sequencing. Microbial Ecology, 2021, 81, 847-863.	2.8	12
3722	Gut microbiome is affected by inter-sexual and inter-seasonal variation in diet for thick-billed murres (Uria lomvia). Scientific Reports, 2021, 11, 1200.	3.3	40
3723	Mesopelagic microbial carbon production correlates with diversity across different marine particle fractions. ISME Journal, 2021, 15, 1695-1708.	9.8	31

#	Article	IF	CITATIONS
3724	Merging Fungal and Bacterial Community Profiles via an Internal Control. Microbial Ecology, 2021, 82, 484-497.	2.8	5
3725	Phosphate-Arsenic Interactions in Halophilic Microorganisms of the Microbial Mat from Laguna Tebenquiche: from the Microenvironment to the Genomes. Microbial Ecology, 2021, 81, 941-953.	2.8	11
3726	Intestinal microbiota fingerprint in subjects with irritable bowel syndrome responders to a low FODMAP diet. Food and Function, 2021, 12, 3206-3218.	4.6	10
3727	Associations of observed home dampness and mold with the fungal and bacterial dust microbiomes. Environmental Sciences: Processes and Impacts, 2021, 23, 491-500.	3.5	3
3728	Longitudinal assessment of the bovine ocular bacterial community dynamics in calves. Animal Microbiome, 2021, 3, 16.	3.8	17
3729	Impact of healthy aging on active bacterial assemblages throughout the gastrointestinal tract. Gut Microbes, 2021, 13, 1966261.	9.8	7
3730	Competitive Exclusion and Metabolic Dependency among Microorganisms Structure the Cellulose Economy of an Agricultural Soil. MBio, 2021, 12, .	4.1	23
3731	The Effect of Incubation Temperature on the Species Composition of Phytophthora, Phytopythium, and Pythium Communities Associated with Soybean. Phytobiomes Journal, 2021, 5, 133-144.	2.7	4
3733	Rigorous Plasma Microbiome Analysis Method Enables Disease Association Discovery in Clinic. Frontiers in Microbiology, 2020, 11, 613268.	3.5	12
3734	Biocontrol of Two Bacterial Inoculant Strains and Their Effects on the Rhizosphere Microbial Community of Field-Grown Wheat. BioMed Research International, 2021, 2021, 1-12.	1.9	9
3737	Effects of Dysbiosis and Dietary Manipulation on the Digestive Microbiota of a Detritivorous Arthropod. Microorganisms, 2021, 9, 148.	3.6	3
3738	Limited carbon sources prevent sulfate remediation in circumneutral abandoned mine drainage. FEMS Microbiology Ecology, 2021, 97, .	2.7	2
3739	Selection and re-acclimation of bioprospected acid-tolerant green microalgae suitable for growth at low pH. Extremophiles, 2021, 25, 129-141.	2.3	8
3740	Cast iron drinking water pipe biofilms support diverse microbial communities containing antibiotic resistance genes, metal resistance genes, and class 1 integrons. Environmental Science: Water Research and Technology, 2021, 7, 584-598.	2.4	10
3742	Bacterial dysbiosis predicts the diagnosis of Crohn's disease in Saudi children. Saudi Journal of Gastroenterology, 2021, 27, 144.	1.1	1
3743	The effect of legacy gold mining on methylmercury cycling and microbial community structure in northern freshwater lakes. Environmental Sciences: Processes and Impacts, 2021, 23, 1220-1230.	3.5	4
3744	Natural Bacterial Assemblages in Arabidopsis thaliana Tissues Become More Distinguishable and Diverse during Host Development. MBio, 2021, 12, .	4.1	18
3745	Differential response of digesta- and mucosa-associated intestinal microbiota to dietary insect meal during the seawater phase of Atlantic salmon. Animal Microbiome, 2021, 3, 8.	3.8	54

#	ARTICLE	IF	CITATIONS
3746	Metabarcoding of Soil Fungal Communities Associated with Alpine Field-Grown Saffron (Crocus) Tj ETQq0 0 0 rgB	T/Qverloc	:k ₁₃ 0 Tf 50 7
3747	Variability of the Atmospheric PM10 Microbiome in Three Climatic Regions of France. Frontiers in Microbiology, 2020, 11, 576750.	3.5	6
3748	Application of culture, PCR, and PacBio sequencing for determination of microbial composition of milk from subclinical mastitis dairy cows of smallholder farms. Open Life Sciences, 2021, 16, 800-808.	1.4	4
3750	Early life environmental exposures have a minor impact on the gut ecosystem following a natural birth. Gut Microbes, $2021, 13, 1-15$.	9.8	7
3751	Diarrhea prevalence in a randomized, controlled prospective trial of point-of-use water filters in homes and schools in the Dominican Republic. Tropical Medicine and Health, 2021, 49, 1.	2.8	44
3752	Induction of antibiotic specialized metabolism by coâ€eulturing in a collection of phyllosphere bacteria. Environmental Microbiology, 2021, 23, 2132-2151.	3.8	12
3753	A Novel Signaling Pathway Required for Arabidopsis Endodermal Root Organization Shapes the Rhizosphere Microbiome. Plant and Cell Physiology, 2021, 62, 248-261.	3.1	17
3754	Short-Term Exposure to Sterile Seawater Reduces Bacterial Community Diversity in the Sea Anemone, Exaiptasia diaphana. Frontiers in Marine Science, 2021, 7, .	2.5	11
3755	Fungal sporocarps house diverse and host-specific communities of fungicolous fungi. ISME Journal, 2021, 15, 1445-1457.	9.8	24
3756	Antibiotics and the developing intestinal microbiome, metabolome and inflammatory environment in a randomized trial of preterm infants. Scientific Reports, 2021, 11, 1943.	3.3	40
3757	Curbing gastrointestinal infections by defensin fragment modifications without harming commensal microbiota. Communications Biology, 2021, 4, 47.	4.4	4
3758	Bradyrhizobium as the Only Rhizobial Inhabitant of Mung Bean (Vigna radiata) Nodules in Tropical Soils: A Strategy Based on Microbiome for Improving Biological Nitrogen Fixation Using Bio-Products. Frontiers in Plant Science, 2020, 11, 602645.	3.6	16
3759	The effect of early probiotic exposure on the preterm infant gut microbiome development. Gut Microbes, 2021, 13, 1951113.	9.8	26
3760	Microbial community analysis of soils under different soybean cropping regimes in the Argentinean south-eastern Humid Pampas. FEMS Microbiology Ecology, 2021, 97, .	2.7	12
3761	Metagenomic sequencing reveals a lack of virus exchange between native and invasive freshwater fish across the Murray–Darling Basin, Australia. Virus Evolution, 2021, 7, veab034.	4.9	27
3762	Distribution and comparison of bacterial communities in HVAC systems of two university buildings: Implications for indoor air quality and public health. Environmental Monitoring and Assessment, 2021, 193, 47.	2.7	11
3763	Clostridioides difficile exploits toxin-mediated inflammation to alter the host nutritional landscape and exclude competitors from the gut microbiota. Nature Communications, 2021, 12, 462.	12.8	94
3764	Coupling the endophytic microbiome with the host transcriptome in olive roots. Computational and Structural Biotechnology Journal, 2021, 19, 4777-4789.	4.1	8

#	Article	IF	CITATIONS
3765	Anthelmintic drugs modulate the acute phase immune response but not the microbiota in wild Song Sparrows. Auk, 2021, 138, .	1.4	1
3766	The microbiome of the seagrass Halophila ovalis: community structuring from plant parts to regional scales. Aquatic Microbial Ecology, 2021, 87, 139-150.	1.8	3
3767	Highly abundant core taxa in the blow within and across captive bottlenose dolphins provide evidence for a temporally stable airway microbiota. BMC Microbiology, 2021, 21, 20.	3.3	5
3768	Maternal antibiotic exposure disrupts microbiota and exacerbates hyperoxia-induced lung injury in neonatal mice. Pediatric Research, 2021, 90, 776-783.	2.3	3
3769	Contamination Sources and Transmission Routes for Campylobacter on (Mixed) Broiler Farms in Belgium, and Comparison of the Gut Microbiota of Flocks Colonized and Uncolonized with Campylobacter. Pathogens, 2021, 10, 66.	2.8	9
3770	Relative qPCR to quantify colonization of plant roots by arbuscular mycorrhizal fungi. Mycorrhiza, 2021, 31, 137-148.	2.8	18
3771	Effect of heavy metal-induced stress on two extremophilic microbial communities from Caviahue-Copahue, Argentina. Environmental Pollution, 2021, 268, 115709.	7.5	3
3772	Effects of brewers' spent grain protein hydrolysates on gas production, ruminal fermentation characteristics, microbial protein synthesis and microbial community in an artificial rumen fed a high grain diet. Journal of Animal Science and Biotechnology, 2021, 12, 1.	5. 3	54
3773	Metagenomics and Culture Dependent Insights into the Distribution of Firmicutes across Two Different Sample Types Located in the Black Hills Region of South Dakota, USA. Microorganisms, 2021, 9, 113.	3.6	8
3775	Phylogenetic Integration Reveals the Zebrafish Core Microbiome and Its Sensitivity to Environmental Exposures. Toxics, 2021, 9, 10.	3.7	25
3776	Prebiotic Enriched Exclusive Enteral Nutrition Suppresses Colitis via Gut Microbiome Modulation and Expansion of Anti-inflammatory T Cells in a Mouse Model of Colitis. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 1251-1266.	4.5	16
3777	Evidence That Microorganisms at the Animal-Water Interface Drive Sea Star Wasting Disease. Frontiers in Microbiology, 2020, 11, 610009.	3.5	36
3778	Ethnic variability associating gut and oral microbiome with obesity in children. Gut Microbes, 2021, 13, 1-15.	9.8	19
3779	The Oral Bacterial Community in Melanophryniscus admirabilis (Admirable Red-Belly Toads): Implications for Conservation. Microorganisms, 2021, 9, 220.	3.6	4
3780	Altered gut microbiota correlate with different immune responses to HAART in HIV-infected individuals. BMC Microbiology, 2021, 21, 11.	3.3	28
3781	Concurrent Prebiotic Intake Reverses Insulin Resistance Induced by Early-Life Pulsed Antibiotic in Rats. Biomedicines, 2021, 9, 66.	3.2	5
3782	Association of Baseline Luminal Narrowing With Ileal Microbial Shifts and Gene Expression Programs and Subsequent Transmural Healing in Pediatric Crohn Disease. Inflammatory Bowel Diseases, 2021, 27, 1707-1718.	1.9	9
3783	Gut Microbiome Diversity and Composition Are Associated with Habitual Dairy Intakes: A Cross-Sectional Study in Men. Journal of Nutrition, 2021, 151, 3400-3412.	2.9	6

#	Article	IF	Citations
3784	Environmental influences shaping microbial communities in low oxygen, highly stratified marine embayment. Aquatic Microbial Ecology, 0, , .	1.8	6
3785	Shift of Maternal Gut Microbiota of Tibetan Antelope (Pantholops hodgsonii) During the Periparturition Period. Current Microbiology, 2021, 78, 727-738.	2.2	13
3786	Protist communities along freshwater–marine transition zones in Hudson Bay (Canada). Elementa, 2021, 9, .	3.2	9
3787	Temporal changes in the gut microbiota in farmed Atlantic cod (Gadus morhua) outweigh the response to diet supplementation with macroalgae. Animal Microbiome, 2021, 3, 7.	3.8	13
3788	Chicory inulin enhances fermentation of 2′-fucosyllactose by infant fecal microbiota and differentially influences immature dendritic cell and T-cell cytokine responses under normal and Th2-polarizing conditions. Food and Function, 2021, 12, 9018-9029.	4.6	6
3789	Gut bacteria-derived 5-hydroxyindole is a potent stimulant of intestinal motility via its action on L-type calcium channels. PLoS Biology, 2021, 19, e3001070.	5.6	21
3790	Microbial and genetic-based framework identifies drug targets in inflammatory bowel disease. Theranostics, 2021, 11, 7491-7506.	10.0	13
3791	Recovery and Community Succession of the <i>Zostera marina</i> Rhizobiome after Transplantation. Applied and Environmental Microbiology, 2021, 87, .	3.1	10
3792	Profiling the Human in Tissue and Using ITS2 DNA Metabarcoding Compared to a Fungal-Specific Database. Methods in Molecular Biology, 2021, 2327, 253-269.	0.9	0
3793	The Microbiome of Size-Fractionated Airborne Particles from the Sahara Region. Environmental Science &	10.0	12
3794	Relationship Between Peat Type and Microbial Ecology in Sphagnum-Containing Peatlands of the Adirondack Mountains, NY, USA. Microbial Ecology, 2021, 82, 429-441.	2.8	4
3795	Differences in the bacteriome of swab, saliva, and tissue biopsies in oral cancer. Scientific Reports, 2021, 11, 1181.	3.3	30
3796	Monoassociation with bacterial isolates reveals the role of colonization, community complexity and abundance on locomotor behavior in larval zebrafish. Animal Microbiome, 2021, 3, 12.	3.8	10
3797	Democratization of fungal highway columns as a tool to investigate bacteria associated with soil fungi. FEMS Microbiology Ecology, 2021, 97, .	2.7	15
3798	Zebra Mussel Holobionts Fix and Recycle Nitrogen in Lagoon Sediments. Frontiers in Microbiology, 2020, 11, 610269.	3 . 5	15
3799	Host-associated microbiota of yellow stingrays (Urobatis jamaicensis) is shaped by their environment and life history. Marine and Freshwater Research, 2021, 72, 658.	1.3	4
3800	Can Cyanobacterial Diversity in the Source Predict the Diversity in Sludge and the Risk of Toxin Release in a Drinking Water Treatment Plant?. Toxins, 2021, 13, 25.	3.4	18
3801	An altered fecal microbial profiling in rosacea patients compared to matched controls. Journal of the Formosan Medical Association, 2021, 120, 256-264.	1.7	26

#	Article	IF	CITATIONS
3802	The effect of a single, early-life administration of a probiotic on piglet growth performance and faecal microbiota until weaning. Italian Journal of Animal Science, 2021, 20, 1373-1385.	1.9	3
3803	Seasonal shifts in the gut microbiome indicate plastic responses to diet in wild geladas. Microbiome, 2021, 9, 26.	11.1	105
3804	Propionate attenuates atherosclerosis by immune-dependent regulation of intestinal cholesterol metabolism. European Heart Journal, 2022, 43, 518-533.	2.2	113
3805	Dietary intake of yacon roots (<i>Smallanthus sonchifolius</i>) affects gut microbiota and fecal mucin and prevents intestinal inflammation in mice. Journal of Clinical Biochemistry and Nutrition, 2021, 69, 272-279.	1.4	7
3807	The upper respiratory tract microbiome of indigenous Orang Asli in north-eastern Peninsular Malaysia. Npj Biofilms and Microbiomes, 2021, 7, 1.	6.4	49
3808	Microbial diversity of co-occurring heterotrophs in cultures of marine picocyanobacteria. Environmental Microbiomes, 2021, $16, 1.$	5.0	28
3809	Relationship between dental and periodontal health status and the salivary microbiome: bacterial diversity, co-occurrence networks and predictive models. Scientific Reports, 2021, 11, 929.	3.3	28
3810	The Impact of Migration on the Gut Metagenome of South Asian Canadians. Gut Microbes, 2021, 13, 1-29.	9.8	14
3811	Heterochronic Fecal Microbiota Transfer Reverses Hallmarks of the Aging Murine Gut, Eye and Brain. SSRN Electronic Journal, 0, , .	0.4	3
3812	Lignin intermediates lead to phenyl acid formation and microbial community shifts in meso- and thermophilic batch reactors. Biotechnology for Biofuels, 2021, 14, 27.	6.2	8
3814	Diversity of putative ericoid mycorrhizal fungi increases with soil age and progressive phosphorus limitation across a 4.1-million-year chronosequence. FEMS Microbiology Ecology, 2021, 97, .	2.7	10
3815	Low-dosage ozonation in gas-phase biofilter promotes community diversity and robustness. Microbiome, 2021, 9, 14.	11.1	9
3816	Characterization of the Food Microbiota in Ready-to-Eat Mexican Foods. Proceedings (mdpi), 2020, 66, 32.	0.2	1
3817	Capturing the diversity of the human milk microbiota through culture-enriched molecular profiling: a feasibility study. FEMS Microbiology Letters, 2021, 368, .	1.8	2
3819	Microbial intrusion and seasonal dynamics in the groundwater microbiome of a porous basaltic rock aquifer used as municipal water reservoir. FEMS Microbiology Ecology, 2021, 97, .	2.7	5
3821	Subgingival microbiota in a population with and without cognitive dysfunction. Journal of Oral Microbiology, 2021, 13, 1854552.	2.7	24
3822	Elevation Correlates With Significant Changes in Relative Abundance in Hummingbird Fecal Microbiota, but Composition Changes Little. Frontiers in Ecology and Evolution, 2021, 8, .	2.2	13
3823	Exploring Changes in the Microbiota of Aedes albopictus: Comparison Among Breeding Site Water, Larvae, and Adults. Frontiers in Microbiology, 2021, 12, 624170.	3.5	24

#	Article	IF	CITATIONS
3824	Bioinformatics for Human Microbiome., 2021,, 333-350.		2
3825			

#	Article	IF	CITATIONS
3843	Gut Microbiota Dysbiosis Associated with Persistent Fatigue in Hematopoietic Cell Transplantation Survivors. Transplantation and Cellular Therapy, 2021, 27, 498.e1-498.e8.	1.2	10
3844	Gut Microbiota Profile and Changes in Body Weight in Elderly Subjects with Overweight/Obesity and Metabolic Syndrome. Microorganisms, 2021, 9, 346.	3.6	14
3845	Intracellular bacteria are common and taxonomically diverse in cultured and <i>in hospite</i> endosymbionts of coral reefs. ISME Journal, 2021, 15, 2028-2042.	9.8	61
3846	Metagenomic Analysis of the Gut Microbiota of Wild Mice, a Newly Identified Reservoir of Campylobacter. Frontiers in Cellular and Infection Microbiology, 2020, 10, 596149.	3.9	11
3847	Composition and acquisition of the microbiome in solitary, ground-nesting alkali bees. Scientific Reports, 2021, 11, 2993.	3.3	26
3848	Environmental DNA simultaneously informs hydrological and biodiversity characterization of an Alpine catchment. Hydrology and Earth System Sciences, 2021, 25, 735-753.	4.9	5
3851	Comparison of beta diversity measures in clustering the high-dimensional microbial data. PLoS ONE, 2021, 16, e0246893.	2.5	9
3852	Sulfadiazine dissipation as a function of soil bacterial diversity. Environmental Pollution, 2021, 271, 116374.	7.5	6
3854	Diving into Inflammation: A Pilot Study Exploring the Dynamics of the Immune–Microbiota Axis in Ileal Tissue Layers of Patients with Crohn's Disease. Journal of Crohn's and Colitis, 2021, 15, 1500-1516.	1.3	19
3855	Seasonality of the Microbial Community Composition in the North Atlantic. Frontiers in Marine Science, 2021, 8, .	2.5	32
3856	Signatures of vaginal microbiota by 16S rRNA gene: potential bio-geographical application in Chinese Han from three regions of China. International Journal of Legal Medicine, 2021, 135, 1213-1224.	2.2	10
3857	Influence of Acidification and Warming of Seawater on Biofouling by Bacteria Grown over API 5L Steel. Indian Journal of Microbiology, 2021, 61, 151-159.	2.7	3
3858	Volatile aroma composition and sensory profile of Shiraz and Cabernet Sauvignon wines produced with novel <i>Metschnikowia pulcherrima</i> yeast starter cultures. Australian Journal of Grape and Wine Research, 2021, 27, 406-418.	2.1	11
3859	Long-term stability of the urogenital microbiota of asymptomatic European women. BMC Microbiology, 2021, 21, 64.	3.3	18
3860	Size fractionation of bioaerosol emissions from green-waste composting. Environment International, 2021, 147, 106327.	10.0	22
3861	Association of Maternal Microbiota and Diet in Cord Blood Cytokine and Immunoglobulin Profiles. International Journal of Molecular Sciences, 2021, 22, 1778.	4.1	15
3862	Microbiota Assessments for the Identification and Confirmation of Slit Defect-Causing Bacteria in Milk and Cheddar Cheese. MSystems, 2021, 6, .	3.8	9
3864	Equivolumetric Protocol Generates Library Sizes Proportional to Total Microbial Load in 16S Amplicon Sequencing. Frontiers in Microbiology, 2021, 12, 638231.	3.5	13

#	ARTICLE	IF	CITATIONS
3865	Co-Occurrence of Listeria spp. and Spoilage Associated Microbiota During Meat Processing Due to Cross-Contamination Events. Frontiers in Microbiology, 2021, 12, 632935.	3.5	26
3866	Distinctive Microbial Signatures and Gut-Brain Crosstalk in Pediatric Patients with Coeliac Disease and Type 1 Diabetes Mellitus. International Journal of Molecular Sciences, 2021, 22, 1511.	4.1	10
3867	Colonization of Naive Roots from <i>Populus tremula</i> $\tilde{A}-$ <i>alba</i> Involves Successive Waves of Fungi and Bacteria with Different Trophic Abilities. Applied and Environmental Microbiology, 2021, 87, .	3.1	13
3868	Fecal microbiota transplantation in HIV: A pilot placebo-controlled study. Nature Communications, 2021, 12, 1139.	12.8	49
3869	Effect of polymer type on the colonization of plastic pellets by marine bacteria. FEMS Microbiology Letters, 2021, 368, .	1.8	25
3870	Reduction of Sb(V) by coupled biotic-abiotic processes under sulfidogenic conditions. Heliyon, 2021, 7, e06275.	3.2	10
3871	Inconsistent effects of agricultural practices on soil fungal communities across 12 <scp>European</scp> longâ€ŧerm experiments. European Journal of Soil Science, 2021, 72, 1902-1923.	3.9	26
3872	Endolithic microbial composition in Helliwell Hills, a newly investigated Marsâ€like area in Antarctica. Environmental Microbiology, 2021, 23, 4002-4016.	3.8	21
3873	Comparison between 16S rRNA and shotgun sequencing data for the taxonomic characterization of the gut microbiota. Scientific Reports, 2021, 11, 3030.	3.3	208
3874	Feedback mechanisms stabilise degraded turf algal systems at a CO2 seep site. Communications Biology, 2021, 4, 219.	4.4	12
3876	Reduced tillage, cover crops and organic amendments affect soil microbiota and improve soil health in Uruguayan vegetable farming systems. FEMS Microbiology Ecology, 2021, 97, .	2.7	10
3877	A timeâ€agged association between the gut microbiome, nestling weight and nestling survival in wild great tits. Journal of Animal Ecology, 2021, 90, 989-1003.	2.8	16
3878	Stomach and colonic microbiome of wild Japanese macaques. American Journal of Primatology, 2021, 83, e23242.	1.7	4
3879	The skin microbiome of Xenopus laevis and the effects of husbandry conditions. Animal Microbiome, 2021, 3, 17.	3.8	8
3880	Impact of Zero-Valent Iron on Freshwater Bacterioplankton Metabolism as Predicted from 16S rRNA Gene Sequence Libraries. Current Microbiology, 2021, 78, 979-991.	2.2	2
3881	Toward Best Practice in Livestock Microbiota Research: A Comprehensive Comparison of Sample Storage and DNA Extraction Strategies. Frontiers in Microbiology, 2021, 12, 627539.	3.5	11
3882	Diversity and plant growth-promoting potential of (un)culturable bacteria in the Hedera helix phylloplane. BMC Microbiology, 2021, 21, 66.	3.3	10
3883	The uropygial gland microbiome of house sparrows with malaria infection. Journal of Avian Biology, 2021, 52, .	1.2	11

#	Article	IF	CITATIONS
3884	Hierarchical spatial sampling reveals factors influencing arbuscular mycorrhizal fungus diversity in CÃ'te d'Ivoire cocoa plantations. Mycorrhiza, 2021, 31, 289-300.	2.8	7
3885	Alterations in the gut microbiome and metabolic profile in rats acclimated to high environmental temperature. Microbial Biotechnology, 2022, 15, 276-288.	4.2	15
3886	Tillage shapes the soil and rhizosphere microbiome of barleyâ€"but not its susceptibility towards <i>Blumeria graminis</i> f. sp. <i>hordei</i> FEMS Microbiology Ecology, 2021, 97, .	2.7	23
3887	Tree Species Richness and Neighborhood Effects on Ectomycorrhizal Fungal Richness and Community Structure in Boreal Forest. Frontiers in Microbiology, 2021, 12, 567961.	3.5	13
3888	The acidified drinking water-induced changes in the behavior and gut microbiota of wild-type mice depend on the acidification mode. Scientific Reports, 2021, 11, 2877.	3.3	15
3890	Exploring the faecal microbiome of the Eurasian nuthatch (Sitta europaea). Archives of Microbiology, 2021, 203, 2119-2127.	2.2	2
3891	Maturation of the neonatal oral mucosa involves unique epithelium-microbiota interactions. Cell Host and Microbe, 2021, 29, 197-209.e5.	11.0	24
3892	Considerations for mosquito microbiome research from the Mosquito Microbiome Consortium. Microbiome, 2021, 9, 36.	11.1	25
3893	Effect of Amplicon Sequencing Depth in Environmental Microbiome Research. Current Microbiology, 2021, 78, 1026-1033.	2.2	12
3894	The regional diversity of gut microbiome along the GI tract of male C57BL/6 mice. BMC Microbiology, 2021, 21, 44.	3.3	52
3895	Sulfur bacteria promote dissolution of authigenic carbonates at marine methane seeps. ISME Journal, 2021, 15, 2043-2056.	9.8	9
3896	Ripened Pu-erh Tea Extract Promotes Gut Microbiota Resilience against Dextran Sulfate Sodium Induced Colitis. Journal of Agricultural and Food Chemistry, 2021, 69, 2190-2203.	5.2	39
3897	The Gut Microbial Composition Is Species-Specific and Individual-Specific in Two Species of Estrildid Finches, the Bengalese Finch and the Zebra Finch. Frontiers in Microbiology, 2021, 12, 619141.	3.5	13
3898	Antibiotic-associated dysbiosis affects the ability of the gut microbiota to control intestinal inflammation upon fecal microbiota transplantation in experimental colitis models. Microbiome, 2021, 9, 39.	11.1	52
3899	Distinct Changes Occur in the Human Breast Milk Microbiome Between Early and Established Lactation in Breastfeeding Guatemalan Mothers. Frontiers in Microbiology, 2021, 12, 557180.	3.5	26
3900	Decadeâ€scale stability and change in a marine bivalve microbiome. Molecular Ecology, 2021, 30, 1237-1250.	3.9	15
3901	Electro-bioremediation of nitrate and arsenite polluted groundwater. Water Research, 2021, 190, 116748.	11.3	34
3902	Microfiber structure for enhanced immobilization of nitrifying bacteria in a post-nitrification reactor. Environmental Technology and Innovation, 2021, 21, 101373.	6.1	6

#	Article	IF	CITATIONS
3904	Functional capacities of microbial communities to carry out large scale geochemical processes are maintained during ex situ anaerobic incubation. PLoS ONE, 2021, 16, e0245857.	2.5	11
3905	Meta-omics characteristics of intestinal microbiota associated to HBeAg seroconversion induced by oral antiviral therapy. Scientific Reports, 2021, 11, 3253.	3.3	1
3906	Identification and Metabolism of Naturally Prevailing Microorganisms in Zinc and Copper Mineral Processing. Minerals (Basel, Switzerland), 2021, 11, 156.	2.0	10
3907	Comparative study of the hemolymph microbiome between live and recently dead American lobsters Homarus americanus. Diseases of Aquatic Organisms, 2021, 143, 147-158.	1.0	7
3908	Balance between geographic, soil, and host tree parameters to shape soil microbiomes associated to clonal oak varies across soil zones along a European North–South transect. Environmental Microbiology, 2021, 23, 2274-2292.	3.8	3
3909	Exploring the Gut Microbiome Alteration of the European Hare (Lepus europaeus) after Short-Term Diet Modifications. Biology, 2021, 10, 148.	2.8	0
3910	Longitudinal Microbiome Analysis in a Dextran Sulfate Sodium-Induced Colitis Mouse Model. Microorganisms, 2021, 9, 370.	3.6	16
3911	A multi-omic investigation of male lower urinary tract symptoms: Potential role for JC virus. PLoS ONE, 2021, 16, e0246266.	2.5	7
3912	Amazonia Seasons Have an Influence in the Composition of Bacterial Gut Microbiota of Mangrove Oysters (Crassostrea gasar). Frontiers in Genetics, 2020, 11, 602608.	2.3	8
3913	Diversity and dynamics of bacterial and fungal communities in cider for distillation. International Journal of Food Microbiology, 2021, 339, 108987.	4.7	9
3915	Molecular analysis of the blood meals and bacterial communities of bed bugs (Cimex lectularius L.) to assess interactions with alternative hosts. Parasitology Research, 2021, 120, 1209-1217.	1.6	6
3916	Linked networks reveal dual roles of insect dispersal and species sorting for bacterial communities in flowers. Oikos, 2021, 130, 697-707.	2.7	22
3917	The role of oral microbiome in pemphigus vulgaris. Archives of Microbiology, 2021, 203, 2237-2247.	2.2	6
3919	PPIT: an R package for inferring microbial taxonomy from <i>nifH</i> sequences. Bioinformatics, 2021, 37, 2289-2298.	4.1	13
3920	Gut Microbiota in Decapod Shrimps: Evidence of Phylosymbiosis. Microbial Ecology, 2021, 82, 994-1007.	2.8	8
3921	Associations between diet, the gut microbiome and short chain fatty acids in youth with islet autoimmunity and type 1 diabetes. Pediatric Diabetes, 2021, 22, 425-433.	2.9	5
3922	Insights into the structure and role of seed-borne bacteriome during maize germination. FEMS Microbiology Ecology, 2021, 97, .	2.7	14
3923	Local Geomorphological Gradients and Land Use Patterns Play Key Role on the Soil Bacterial Community Diversity and Dynamics in the Highly Endemic Indigenous Afrotemperate Coastal Scarp Forest Biome. Frontiers in Microbiology, 2021, 12, 592725.	3.5	16

#	Article	IF	CITATIONS
3924	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. Nature Metabolism, 2021, 3, 274-286.	11.9	278
3925	Gulf of Mexico blue hole harbors high levels of novel microbial lineages. ISME Journal, 2021, 15, 2206-2232.	9.8	13
3926	Relationships of gut microbiota, short-chain fatty acids, inflammation, and the gut barrier in Parkinson's disease. Molecular Neurodegeneration, 2021, 16, 6.	10.8	197
3927	Inhibition of Batrachochytrium dendrobatidis Infection by Skin Bacterial Communities in Wild Amphibian Populations. Microbial Ecology, 2021, 82, 666-676.	2.8	14
3928	Taxonomic and functional analyses of intact microbial communities thriving in extreme, astrobiology-relevant, anoxic sites. Microbiome, 2021, 9, 50.	11.1	14
3929	Lung microbiota associations with clinical features of COPD in the SPIROMICS cohort. Npj Biofilms and Microbiomes, 2021, 7, 14.	6.4	33
3930	Anoxic chlorophyll maximum enhances local organic matter remineralization and nitrogen loss in Lake Tanganyika. Nature Communications, 2021, 12, 830.	12.8	24
3931	Development of a robust protocol for the characterization of the pulmonary microbiota. Communications Biology, 2021, 4, 164.	4.4	7
3932	Biological soil crusts structure the subsurface microbiome in a sandy agroecosystem. Plant and Soil, 2021, 462, 311-329.	3.7	17
3933	Comparative Fungal Community Analyses Using Metatranscriptomics and Internal Transcribed Spacer Amplicon Sequencing from Norway Spruce. MSystems, 2021, 6, .	3.8	16
3934	Fungal Communities on Standing Litter Are Structured by Moisture Type and Constrain Decomposition in a Hyper-Arid Grassland. Frontiers in Microbiology, 2021, 12, 596517.	3. 5	14
3935	Antibacterial effect of a brominated self-etch adhesive on carious dentin - An in vivo study. Journal of Dentistry, 2021, 105, 103555.	4.1	1
3936	Microbial composition of a hydropower cooling water system reveals thermophilic bacteria with a possible role in primary biofilm formation. Biofouling, 2021, 37, 246-256.	2.2	4
3939	Bacterial shifts on broiler carcasses at retail upon frozen storage. International Journal of Food Microbiology, 2021, 340, 109051.	4.7	5
3940	Interplay Between Class II HLA Genotypes and the Microbiome and Immune Phenotypes in Individuals With PTEN Hamartoma Tumor Syndrome. JCO Precision Oncology, 2021, 5, 357-369.	3.0	2
3942	Gut Microbiota Profile in Children with IgE-Mediated Cow's Milk Allergy and Cow's Milk Sensitization and Probiotic Intestinal Persistence Evaluation. International Journal of Molecular Sciences, 2021, 22, 1649.	4.1	15
3943	Repeatability and reproducibility assessment in a large-scale population-based microbiota study: case study on human milk microbiota. Microbiome, 2021, 9, 41.	11.1	13
3945	Disentangling the Association of Corn Root Mycobiome With Plant Productivity and the Importance of Soil Physicochemical Balance in Shaping Their Relationship. Frontiers in Sustainable Food Systems, 2021, 5, .	3.9	7

#	ARTICLE	IF	CITATIONS
3946	Western Kenyan Anopheles gambiae showing intense permethrin resistance harbour distinct microbiota. Malaria Journal, 2021, 20, 77.	2.3	27
3947	The Lung Microbiome in Young Children with Cystic Fibrosis: A Prospective Cohort Study. Microorganisms, 2021, 9, 492.	3.6	12
3948	Chance or Necessity—The Fungi Coâ^'Occurring with Formica polyctena Ants. Insects, 2021, 12, 204.	2.2	6
3949	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. Frontiers in Microbiology, 2021, 12, 635781.	3.5	51
3950	Impacts of replanting American ginseng on fungal assembly and abundance in response to disease outbreaks. Archives of Microbiology, 2021, 203, 2157-2170.	2.2	22
3951	Microbial and clinical factors are related to recurrence of symptoms after childhood lower respiratory tract infection. ERJ Open Research, 2021, 7, 00939-2020.	2.6	4
3952	Builders, tenants, and squatters: the origins of genetic material in modern stromatolites. Geobiology, 2021, 19, 261-277.	2.4	7
3953	Warming mediates the resistance of aquatic bacteria to invasion during community coalescence. Molecular Ecology, 2021, 30, 1345-1356.	3.9	9
3954	Microbiota restoration reduces antibiotic-resistant bacteria gut colonization in patients with recurrent Clostridioides difficile infection from the open-label PUNCH CD study. Genome Medicine, 2021, 13, 28.	8.2	51
3955	Rainfall as a trigger of ecological cascade effects in an Australian groundwater ecosystem. Scientific Reports, 2021, 11, 3694.	3.3	20
3956	North American Fireflies Host Low Bacterial Diversity. Microbial Ecology, 2021, 82, 793-804.	2.8	3
3957	Soil microbial inoculation during flood events shapes headwater stream microbial communities and diversity. Microbial Ecology, 2021, 82, 591-601.	2.8	10
3958	Description of the temporal dynamics in microbial community composition and beer chemistry in sour beer production via barrel ageing of finished beers. International Journal of Food Microbiology, 2021, 339, 109030.	4.7	23
3959	Shotgun metagenomic analysis of kombucha mutualistic community exposed to Marsâ€ike environment outside the International Space Station. Environmental Microbiology, 2021, 23, 3727-3742.	3.8	17
3960	Local dynamics of a white syndrome outbreak and changes in the microbial community associated with colonies of the scleractinian brain coral <i>Pseudodiploria strigosa</i> . PeerJ, 2021, 9, e10695.	2.0	17
3961	The cancer microbiome atlas: a pan-cancer comparative analysis to distinguish tissue-resident microbiota from contaminants. Cell Host and Microbe, 2021, 29, 281-298.e5.	11.0	109
3962	Characterization of Bacterial Communities of Cold-Smoked Salmon during Storage. Foods, 2021, 10, 362.	4.3	19
3963	Interactive Effects of Scion and Rootstock Genotypes on the Root Microbiome of Grapevines (Vitis spp.) Tj ETQq1	1.0.78431 2.5	14 rgBT /Ove

#	Article	IF	CITATIONS
3965	The applicability of eDNA metabarcoding approaches for sessile benthic surveying in the Kimberley region, northâ€western Australia. Environmental DNA, 2022, 4, 34-49.	5.8	15
3968	Microbiomes of different ages in Rendzic Leptosols in the Crimean Peninsula. PeerJ, 2021, 9, e10871.	2.0	2
3971	Soil microbial composition and carbon mineralization are associated with vegetation type and temperature regime in mesocosms of a semiarid ecosystem. FEMS Microbiology Letters, 2021, 368, .	1.8	3
3973	Evidence for strong environmental control on bacterial microbiomes of Antarctic springtails. Scientific Reports, 2021, 11, 2973.	3.3	5
3974	Host immunity modulates the efficacy of microbiota transplantation for treatment of Clostridioides difficile infection. Nature Communications, 2021, 12, 755.	12.8	40
3975	Comparison of Two 16S rRNA Primers (V3–V4 and V4–V5) for Studies of Arctic Microbial Communities. Frontiers in Microbiology, 2021, 12, 637526.	3.5	77
3976	Impact of Metronidazole Treatment and <i>Dientamoeba Fragilis</i> Colonization on Gut Microbiota Diversity. Journal of Pediatric Gastroenterology and Nutrition, 2021, 73, 23-29.	1.8	8
3978	The Pediatric Obesity Microbiome and Metabolism Study (POMMS): Methods, Baseline Data, and Early Insights. Obesity, 2021, 29, 569-578.	3.0	19
3979	Effects of parity, blood progesterone, and non-steroidal anti-inflammatory treatment on the dynamics of the uterine microbiota of healthy postpartum dairy cows. PLoS ONE, 2021, 16, e0233943.	2.5	19
3980	The microbial community associated with pea seeds (Pisum sativum) of different geographical origins. Plant and Soil, 2021, 462, 405-427.	3.7	15
3981	Resolving cryptic species complexes in marine protists: phylogenetic haplotype networks meet global DNA metabarcoding datasets. ISME Journal, 2021, 15, 1931-1942.	9.8	29
3982	A 16S rRNA Gene and Draft Genome Database for the Murine Oral Bacterial Community. MSystems, 2021, 6, .	3.8	14
3983	Distinct rhizomicrobiota assemblages and plant performance in lettuce grown in soils with different agricultural management histories. FEMS Microbiology Ecology, 2021, 97, .	2.7	7
3984	Bacterial microbiota similarity between predators and prey in a blue tit trophic network. ISME Journal, 2021, 15, 1098-1107.	9.8	16
3985	Multiple techniques point to oxygenic phototrophs dominating the Isopora palifera skeletal microbiome. Coral Reefs, 2021, 40, 275-282.	2.2	21
3986	The colorectal cancer-associated faecal microbiome of developing countries resembles that of developed countries. Genome Medicine, 2021, 13, 27.	8.2	25
3987	Comparative analysis of the alveolar microbiome in COPD, ECOPD, Sarcoidosis, and ILD patients to identify respiratory illnesses specific microbial signatures. Scientific Reports, 2021, 11, 3963.	3.3	42
3988	Disruptions in oral and nasal microbiota in biomass and tobacco smoke associated chronic obstructive pulmonary disease. Archives of Microbiology, 2021, 203, 2087-2099.	2.2	9

#	Article	IF	CITATIONS
3989	Staphylococcal Communities on Skin Are Associated with Atopic Dermatitis and Disease Severity. Microorganisms, 2021, 9, 432.	3.6	25
3990	Flexibility and resilience of great tit (Parus major) gut microbiomes to changing diets. Animal Microbiome, 2021, 3, 20.	3.8	30
3991	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature Microbiology, 2021, 6, 499-511.	13.3	116
3992	Depth Profile of Nitrifying Archaeal and Bacterial Communities in the Remote Oligotrophic Waters of the North Pacific. Frontiers in Microbiology, 2021, 12, 624071.	3.5	14
3993	Differences in the Concentration of the Fecal Neurotransmitters GABA and Glutamate Are Associated with Microbial Composition among Healthy Human Subjects. Microorganisms, 2021, 9, 378.	3.6	21
3995	Gut microbiota of patients with different subtypes of gastric cancer and gastrointestinal stromal tumors. Gut Pathogens, 2021, 13, 11.	3.4	23
3996	Immune status, well-being and gut microbiota in military supplemented with synbiotic ice cream and submitted to field training: a randomised clinical trial. British Journal of Nutrition, 2021, 126, 1794-1808.	2.3	11
3997	Climate change alters temporal dynamics of alpine soil microbial functioning and biogeochemical cycling via earlier snowmelt. ISME Journal, 2021, 15, 2264-2275.	9.8	51
3998	Dust-borne microbes affect Ulva ohnoi's growth and physiological state. FEMS Microbiology Ecology, 2021, 97, .	2.7	2
3999	Low-dose exposure of glyphosate-based herbicides disrupt the urine metabolome and its interaction with gut microbiota. Scientific Reports, 2021, 11, 3265.	3.3	32
4000	Prostaglandin E $\langle \text{sub} \rangle 2 \langle \text{sub} \rangle$ promotes intestinal inflammation via inhibiting microbiota-dependent regulatory T cells. Science Advances, 2021, 7, .	10.3	44
4001	Functional shifts of soil microbial communities associated with Alliaria petiolata invasion. Pedobiologia, 2021, 84, 150700.	1.2	15
4003	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. Genome Medicine, 2021, 13, 36.	8.2	31
4004	The effect of ultrasonic antifouling control on the growth and microbiota of farmed European sea bass (Dicentrarchus labrax). Marine Pollution Bulletin, 2021, 164, 112072.	5.0	10
4005	Population Dynamics and Yeast Diversity in Early Winemaking Stages without Sulfites Revealed by Three Complementary Approaches. Applied Sciences (Switzerland), 2021, 11, 2494.	2.5	18
4006	Impact of Covid-19 Lockdown on Availability of Drinking Water in the Arsenic-Affected Ganges River Basin. International Journal of Environmental Research and Public Health, 2021, 18, 2832.	2.6	19
4007	Phenolic acid-degrading <i>Paraburkholderia</i> prime decomposition in forest soil. ISME Communications, 2021, 1, .	4.2	17
4009	Microbial Community Composition Correlates with Metal Sorption in an Ombrotrophic Boreal Bog: Implications for Radionuclide Retention. Soil Systems, 2021, 5, 19.	2.6	7

#	ARTICLE	IF	CITATIONS
4010	Persistence of the ground beetle (Coleoptera: Carabidae) microbiome to diet manipulation. PLoS ONE, 2021, 16, e0241529.	2.5	9
4011	Controls on diatom biogeography on South Carolina (USA) barrier island beaches. Marine Ecology - Progress Series, 2021, 661, 17-33.	1.9	1
4012	Gut dysbiosis and mortality in hemodialysis patients. Npj Biofilms and Microbiomes, 2021, 7, 20.	6.4	26
4013	Alkylphenols and Chlorophenols Remediation in Vertical Flow Constructed Wetlands: Removal Efficiency and Microbial Community Response. Water (Switzerland), 2021, 13, 715.	2.7	5
4015	Akkermansia, a Possible Microbial Marker for Poor Glycemic Control in Qataris Children Consuming Arabic Dietâ€"A Pilot Study on Pediatric T1DM in Qatar. Nutrients, 2021, 13, 836.	4.1	9
4016	Effective low-cost preservation of human stools in field-based studies for helminth and microbiota analysis. International Journal for Parasitology, 2021, 51, 741-748.	3.1	5
4017	Fermentation of African nightshade leaves with lactic acid bacterial starter cultures. International Journal of Food Microbiology, 2021, 342, 109056.	4.7	16
4018	Associations Between Dysmenorrhea Symptom-Based Phenotypes and Vaginal Microbiome. Nursing Research, 2021, Publish Ahead of Print, 248-255.	1.7	3
4019	Plant and microbial impacts of an invasive species vary across an environmental gradient. Journal of Ecology, 2021, 109, 2163-2176.	4.0	12
4020	A Statistical Perspective on the Challenges in Molecular Microbial Biology. Journal of Agricultural, Biological, and Environmental Statistics, 2021, 26, 131-160.	1.4	10
4021	Placentas delivered by preâ€pregnant obese women have reduced abundance and diversity in the microbiome. FASEB Journal, 2021, 35, e21524.	0.5	14
4022	Gut microbiota resilience in horse athletes following holidays out to pasture. Scientific Reports, 2021, 11, 5007.	3.3	19
4023	Deep-sea microbes as tools to refine the rules of innate immune pattern recognition. Science Immunology, 2021, 6, .	11.9	21
4024	Multiple co-occurring and persistently detected cyanotoxins and associated cyanobacteria in adjacent California lakes. Toxicon, 2021, 192, 1-14.	1.6	15
4026	Methotrexate impacts conserved pathways in diverse human gut bacteria leading to decreased host immune activation. Cell Host and Microbe, 2021, 29, 362-377.e11.	11.0	70
4027	Conserved and reproducible bacterial communities associate with extraradical hyphae of arbuscular mycorrhizal fungi. ISME Journal, 2021, 15, 2276-2288.	9.8	91
4031	Age and sex-associated variation in the multi-site microbiome of an entire social group of free-ranging rhesus macaques. Microbiome, 2021, 9, 68.	11.1	42
4032	Composition and potential functions of the dominant microbiota in deep-sea hagfish gut from the South China Sea. Deep-Sea Research Part I: Oceanographic Research Papers, 2021, 169, 103488.	1.4	5

#	Article	IF	CITATIONS
4034	animalcules: interactive microbiome analytics and visualization in R. Microbiome, 2021, 9, 76.	11.1	18
4035	Importance of environmental factors over habitat connectivity in shaping bacterial communities in microbial mats and bacterioplankton in an Antarctic freshwater system. FEMS Microbiology Ecology, 2021, 97, .	2.7	13
4036	Comparative Metagenomics Reveals Microbial Signatures of Sugarcane Phyllosphere in Organic Management. Frontiers in Microbiology, 2021, 12, 623799.	3. 5	17
4037	Dysbiosis and Enhanced Beta-Defensin Production in Hair Follicles of Patients with Lichen Planopilaris and Frontal Fibrosing Alopecia. Biomedicines, 2021, 9, 266.	3.2	7
4040	The Cheese Production Facility Microbiome Exhibits Temporal and Spatial Variability. Frontiers in Microbiology, 2021, 12, 644828.	3.5	13
4041	Age Matters: Community Assembly in the Pig Fecal Microbiome in the First Month of Life. Frontiers in Microbiology, 2021, 12, 564408.	3.5	13
4043	Gut microbiota profiles in diarrheic patients with co-occurrence of Clostridioides difficile and Blastocystis. PLoS ONE, 2021, 16, e0248185.	2.5	19
4044	The Banana Root Endophytome: Differences between Mother Plants and Suckers and Evaluation of Selected Bacteria to Control Fusarium oxysporum f.sp. cubense. Journal of Fungi (Basel, Switzerland), 2021, 7, 194.	3.5	26
4046	<i>Trifolium repens</i> and <i>T. subterraneum</i> modify their nodule microbiome in response to soil pH. Journal of Applied Microbiology, 2021, 131, 1858-1869.	3.1	5
4047	Evaluating domestication and ploidy effects on the assembly of the wheat bacterial microbiome. PLoS ONE, 2021, 16, e0248030.	2.5	28
4048	New Insights into Microbial Diversity of the Traditional Packed Table Olives Aloreña de Málaga through Metataxonomic Analysis. Microorganisms, 2021, 9, 561.	3.6	10
4049	Evaluating a Laboratory Flume Microbiome as a Window Into Natural Riverbed Biogeochemistry. Frontiers in Water, 2021, 3, .	2.3	3
4050	Soil Microbiome Composition along the Natural Norway Spruce Forest Life Cycle. Forests, 2021, 12, 410.	2.1	6
4052	Geographic Variation of Bacterial Communities Associated with Cotton Fleahopper, Pseudatomoscelis seriatus 1. Southwestern Entomologist, 2021, 46, .	0.2	1
4053	Early socialization and environmental enrichment of lactating piglets affects the caecal microbiota and metabolomic response after weaning. Scientific Reports, 2021, 11, 6113.	3.3	10
4055	Single-cell metabarcoding reveals biotic interactions of the Arctic calcifier <i>Neogloboquadrina pachyderma</i> with the eukaryotic pelagic community. Journal of Plankton Research, 2021, 43, 113-125.	1.8	13
4056	Effects of Clinical Wastewater on the Bacterial Community Structure from Sewage to the Environment. Microorganisms, 2021, 9, 718.	3.6	8
4057	Using neural networks to mine text and predict metabolic traits for thousands of microbes. PLoS Computational Biology, 2021, 17, e1008757.	3.2	4

#	Article	IF	CITATIONS
4058	Relative contributions of egg-associated and substrate-associated microorganisms to black soldier fly larval performance and microbiota. FEMS Microbiology Ecology, 2021, 97, .	2.7	12
4059	Drivers of the variability of dimethylsulfonioproprionate (DMSP) and dimethylsulfoxide (DMSO) in the Southern North Sea. Continental Shelf Research, 2021, 216, 104360.	1.8	1
4060	The vaginal and fecal microbiota of a murine cervical carcinoma model under synergistic effect of 17β-Estradiol and E7 oncogene expression. Microbial Pathogenesis, 2021, 152, 104763.	2.9	3
4061	Alterations in skin microbiome mediated by radiotherapy and their potential roles in the prognosis of radiotherapy-induced dermatitis: a pilot study. Scientific Reports, 2021, 11, 5179.	3.3	14
4062	Transient Effect of Infant Formula Supplementation on the Intestinal Microbiota. Nutrients, 2021, 13, 807.	4.1	8
4063	Localization of Bacterial Communities within Gut Compartments across <i>Cephalotes</i> Turtle Ants. Applied and Environmental Microbiology, 2021, 87, .	3.1	14
4064	Methanogens and Their Syntrophic Partners Dominate Zones of Enhanced Magnetic Susceptibility at a Petroleum Contaminated Site. Frontiers in Earth Science, 2021, 9, .	1.8	10
4065	Undaria pinnatifida exudates trigger shifts in seawater chemistry and microbial communities from Atlantic Patagonian coasts. Biological Invasions, 2021, 23, 1781-1801.	2.4	9
4066	Exploration of applying growth-promotion bacteria of Chlorella sorokiniana to open cultivation systems. Bioprocess and Biosystems Engineering, 2021, 44, 1567-1576.	3.4	7
4067	Forensic Microbiome Database: A Tool for Forensic Geolocation Meta-Analysis Using Publicly Available 16S rRNA Microbiome Sequencing. Frontiers in Microbiology, 2021, 12, 644861.	3 . 5	16
4068	Gut microbiota determines the social behavior of mice and induces metabolic and inflammatory changes in their adipose tissue. Npj Biofilms and Microbiomes, 2021, 7, 28.	6.4	35
4069	Highly parallelized droplet cultivation and prioritization of antibiotic producers from natural microbial communities. ELife, 2021, 10, .	6.0	44
4070	Climate change alters the haemolymph microbiome of oysters. Marine Pollution Bulletin, 2021, 164, 111991.	5.0	35
4071	Stool metabolome-microbiota evaluation among children and adolescents with obesity, overweight, and normal-weight using 1H NMR and 16S rRNA gene profiling. PLoS ONE, 2021, 16, e0247378.	2.5	13
4072	Benzoxazinoids selectively affect maize root-associated nematode taxa. Journal of Experimental Botany, 2021, 72, 3835-3845.	4.8	15
4073	Probiotics mediated gut microbiota diversity shifts are associated with reduction in histopathology and shedding of Lawsonia intracellularis. Animal Microbiome, 2021, 3, 22.	3.8	7
4074	Rumen Epithelial Communities Share a Core Bacterial Microbiota: A Meta-Analysis of 16S rRNA Gene Illumina MiSeq Sequencing Datasets. Frontiers in Microbiology, 2021, 12, 625400.	3.5	23
4075	Microbial Community Shifts Reflect Losses of Native Soil Carbon with Pyrogenic and Fresh Organic Matter Additions and Are Greatest in Low-Carbon Soils. Applied and Environmental Microbiology, 2021, 87, .	3.1	9

#	ARTICLE	IF	CITATIONS
4076	Geographic distribution of Ophiothela brittle stars (Echinodermata: Ophiuroidea): substrate use plasticity and implications for the silent invasion of O. mirabilis in the Atlantic. Hydrobiologia, 2021, 848, 2093-2103.	2.0	6
4077	The Adult Phenylketonuria (PKU) Gut Microbiome. Microorganisms, 2021, 9, 530.	3.6	19
4078	Fungal and metabolome diversity of the rhizosphere and endosphere of Phragmites australis in an AMD-polluted environment. Heliyon, 2021, 7, e06399.	3.2	21
4079	Fire alters plant microbiome assembly patterns: integrating the plant and soil microbial response to disturbance. New Phytologist, 2021, 230, 2433-2446.	7. 3	29
4080	Microbial ecology in selenateâ€reducing biofilm communities: Rare biosphere and their interactions with abundant phylotypes. Biotechnology and Bioengineering, 2021, 118, 2460-2471.	3.3	4
4081	Chemical Properties and Bacterial Community Reaction to Acidified Cattle Slurry Fertilization in Soil from Maize Cultivation. Agronomy, 2021, 11, 601.	3.0	6
4082	Time in the Laboratory, but Not Exposure to a Chytrid Fungus, Results in Rapid Change in Spring Peeper (Pseudacris crucifer) Skin Bacterial Communities. Ichthyology and Herpetology, 2021, 109, .	0.8	3
4083	The nasopharyngeal microbiota of preweaned dairy calves with and without ultrasonographic lung lesions. Journal of Dairy Science, 2021, 104, 3386-3402.	3.4	6
4084	Predicting spatial patterns of soil bacteria under current and future environmental conditions. ISME Journal, 2021, 15, 2547-2560.	9.8	27
4085	A Mouse Model Suggests That Heart Failure and Its Common Comorbidity Sleep Fragmentation Have No Synergistic Impacts on the Gut Microbiome. Microorganisms, 2021, 9, 641.	3.6	4
4086	Different Effects of Mineral Versus Vegetal Granular Activated Carbon Filters on the Microbial Community Composition of a Drinking Water Treatment Plant. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	3
4087	Microbial predation accelerates granulation and modulates microbial community composition. BMC Microbiology, 2021, 21, 91.	3.3	9
4088	Bugs and Brains, the Gut and Mental Health Study: a mixed-methods study investigating microbiota composition and function in anxiety, depression and irritable bowel syndrome. BMJ Open, 2021, 11, e043221.	1.9	5
4091	Gut microbiota in two recently diverged passerine species: evaluating the effects of species identity, habitat use and geographic distance. Bmc Ecology and Evolution, 2021, 21, 41.	1.6	6
4095	Graphene-Based Nanomaterials Modulate Internal Biofilm Interactions and Microbial Diversity. Frontiers in Microbiology, 2021, 12, 623853.	3.5	5
4096	Monitoring the variation in the gut microbiota of captive woolly monkeys related to changes in diet during a reintroduction process. Scientific Reports, 2021, 11, 6522.	3.3	9
4097	Vaginal microbiome and serum metabolite differences in late gestation commercial sows at risk for pelvic organ prolapse. Scientific Reports, 2021, 11, 6189.	3.3	9
4098	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	1.6	16

#	Article	IF	CITATIONS
4099	Biomat Resilience to Desiccation and Flooding Within a Shallow, Unit Process Open Water Engineered Wetland. Water (Switzerland), 2021, 13, 815.	2.7	5
4101	Identification of cutaneous fungi and mites in adult atopic dermatitis: analysis by targeted 18S rRNA amplicon sequencing. BMC Microbiology, 2021, 21, 72.	3.3	12
4102	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. Genome Medicine, 2021, 13, 37.	8.2	34
4103	Supplementation of tuna hydrolysate and insect larvae improves fishmeal replacement efficacy of poultry by-product in Lates calcarifer (Bloch, 1790) juveniles. Scientific Reports, 2021, 11, 4997.	3.3	35
4104	In situ characterisation of pathogen dynamics during a Pacific oyster mortality syndrome episode. Marine Environmental Research, 2021, 165, 105251.	2.5	12
4105	Drought and rewetting events enhance nitrate leaching and seepage-mediated translocation of microbes from beech forest soils. Soil Biology and Biochemistry, 2021, 154, 108153.	8.8	22
4106	Maize germplasm chronosequence shows crop breeding history impacts recruitment of the rhizosphere microbiome. ISME Journal, 2021, 15, 2454-2464.	9.8	49
4107	A guide to minimize contamination issues in microbiome restoration studies. Restoration Ecology, 2021, 29, e13358.	2.9	6
4108	Bacterial community analysis of purulent material from liver abscesses of crossbred cattle and Holstein steers fed finishing diets with or without tylosin. Journal of Animal Science, 2021, 99, .	0.5	14
4109	Temporal Soil Bacterial Community Responses to Cropping Systems and Crop Identity in Dryland Agroecosystems of the Northern Great Plains. Frontiers in Sustainable Food Systems, 2021, 5, .	3.9	7
4111	Hydrogen as a Co-electron Donor for Chain Elongation With Complex Communities. Frontiers in Bioengineering and Biotechnology, 2021, 9, 650631.	4.1	30
4112	Porcine reproductive and respiratory syndrome virus impacts on gut microbiome in a strain virulenceâ€dependent fashion. Microbial Biotechnology, 2022, 15, 1007-1016.	4.2	9
4113	Casein phosphopeptide–amorphous calcium phosphate fluoride treatment enriches the symbiotic dental plaque microbiome in children. Journal of Dentistry, 2021, 106, 103582.	4.1	11
4114	Investigation of Fungal Strains Composition in Fruit Pollens for Artificial Pollination. Mycobiology, 2021, 49, 249-257.	1.7	2
4116	Ensiling sorghum with unsalable pumpkin improves feed digestibility with minimal influence on the rumen microbial population using the rumen simulation technique. Applied Microbiology and Biotechnology, 2021, 105, 3289-3300.	3.6	4
4117	Microbiological findings in early and late implant loss: an observational clinical case-controlled study. BMC Oral Health, 2021, 21, 112.	2.3	16
4118	Microbiota Changes in Fathers Consuming a High Prebiotic Fiber Diet Have Minimal Effects on Male and Female Offspring in Rats. Nutrients, 2021, 13, 820.	4.1	5
4119	Associations between the gut microbiome and fatigue in cancer patients. Scientific Reports, 2021, 11, 5847.	3.3	24

#	Article	IF	CITATIONS
4120	Gut microbiota diversity but not composition is related to saliva cortisol stress response at the age of 2.5 months. Stress, 2021, 24, 551-560.	1.8	18
4121	Geographicalâ€based variations in white truffle <i>Tuber magnatum</i> aroma is explained by quantitative differences in key volatile compounds. New Phytologist, 2021, 230, 1623-1638.	7.3	24
4122	Vaginal Microbiota and Cytokine Levels Predict Preterm Delivery in Asian Women. Frontiers in Cellular and Infection Microbiology, 2021, 11, 639665.	3.9	34
4123	Neonatal hyperoxia induces gut dysbiosis and behavioral changes in adolescent mice. Journal of the Chinese Medical Association, 2021, 84, 290-298.	1.4	11
4124	Investigating the microbial ecology of coastal hotspots of marine nitrogen fixation in the western North Atlantic. Scientific Reports, 2021, 11, 5508.	3.3	4
4125	Long-term storage of feces at \hat{a}° 80 \hat{A}° C versus \hat{a}° 20 \hat{A}° C is negligible for 16S rRNA amplicon profiling of the equine bacterial microbiome. Peerl, 2021, 9, e10837.	2.0	7
4126	Microbial community composition interacts with local abiotic conditions to drive colonization resistance in human gut microbiome samples. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20203106.	2.6	12
4127	Enterolignan Production in a Flaxseed Intervention Study in Postmenopausal US Women of African Ancestry and European Ancestry. Nutrients, 2021, 13, 919.	4.1	9
4128	Modelâ€based biclustering for overdispersed count data with application in microbial ecology. Methods in Ecology and Evolution, 2021, 12, 1050-1061.	5.2	2
4130	Bacterial gut dysbiosis is associated with Crohn's disease symptoms but not with elevated fecal calprotectin. Clinics and Research in Hepatology and Gastroenterology, 2021, 45, 101669.	1.5	3
4131	Gut Microbiome of a Multiethnic Community Possessed No Predominant Microbiota. Microorganisms, 2021, 9, 702.	3.6	3
4132	Temporal oral microbiome changes with brushing in children with cleft lip and palate. Heliyon, 2021, 7, e06513.	3.2	7
4133	HIV-Exposed Seronegative Sex Workers Express Low T-Cell Activation and an Intact Ectocervical Tissue Microenvironment. Vaccines, 2021, 9, 217.	4.4	3
4134	Multipleâ€trophic patterns of primary succession following retreat of a highâ€elevation glacier. Ecosphere, 2021, 12, e03400.	2.2	15
4135	Microbial Succession under Freeze–Thaw Events and Its Potential for Hydrocarbon Degradation in Nutrient-Amended Antarctic Soil. Microorganisms, 2021, 9, 609.	3.6	4
4136	Host–microbial systems as glass cannons: Explaining microbiome stability in corals exposed to extrinsic perturbations. Journal of Animal Ecology, 2021, 90, 1044-1057.	2.8	8
4137	Benchmarking DNA isolation kits used in analyses of the urinary microbiome. Scientific Reports, 2021, 11, 6186.	3.3	20
4138	Diversity of Weissella confusa in Pozol and Its Carbohydrate Metabolism. Frontiers in Microbiology, 2021, 12, 629449.	3.5	6

#	Article	IF	CITATIONS
4139	Biocrust cyanobacterial composition, diversity, and environmental drivers in two contrasting climatic regions in Brazil. Geoderma, 2021, 386, 114914.	5.1	20
4140	Transitions in oral and gut microbiome of HPV+ oropharyngeal squamous cell carcinoma following definitive chemoradiotherapy (ROMA LA-OPSCC study). British Journal of Cancer, 2021, 124, 1543-1551.	6.4	19
4141	Relationship between Nutrient Intake and Human Gut Microbiota in Monozygotic Twins. Medicina (Lithuania), 2021, 57, 275.	2.0	8
4142	Gone with the Wind: Microbial Communities Associated with Dust from Emissive Farmlands. Microbial Ecology, 2021, 82, 859-869.	2.8	9
4143	Characterization of the bacterial microbiome of Rhipicephalus (Boophilus) microplus collected from Pecari tajacu "Sajino―Madre de Dios, Peru. Scientific Reports, 2021, 11, 6661.	3.3	9
4144	Effects of phenylbutazone alone or in combination with a nutritional therapeutic on gastric ulcers, intestinal permeability, and fecal microbiota in horses. Journal of Veterinary Internal Medicine, 2021, 35, 1121-1130.	1.6	8
4145	Changes in Gut Microbiota after a Four-Week Intervention with Vegan vs. Meat-Rich Diets in Healthy Participants: A Randomized Controlled Trial. Microorganisms, 2021, 9, 727.	3.6	16
4146	Meta-analysis of the Parkinson's disease gut microbiome suggests alterations linked to intestinal inflammation. Npj Parkinson's Disease, 2021, 7, 27.	5.3	315
4147	A comparative analysis of biogas production from tomato bio-waste in mesophilic batch and continuous anaerobic digestion systems. PLoS ONE, 2021, 16, e0248654.	2.5	18
4148	Composition and structure of the skin microbiota of rorquals off the Eastern South Pacific. FEMS Microbiology Ecology, 2021, 97, .	2.7	4
4149	Tree diversity and functional leaf traits drive herbivoreâ€associated microbiomes in subtropical China. Ecology and Evolution, 2021, 11, 6153-6166.	1.9	1
4150	Penicillium oxalicum XD-3.1 removes pharmaceutical compounds from hospital wastewater and outcompetes native bacterial and fungal communities in fluidised batch bioreactors. International Biodeterioration and Biodegradation, 2021, 158, 105179.	3.9	14
4151	Microbial population shift and metabolic characterization of silver diamine fluoride treatment failure on dental caries. PLoS ONE, 2021, 16, e0242396.	2.5	8
4152	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. Genome Biology, 2021, 22, 93.	8.8	122
4153	Social networks strongly predict the gut microbiota of wild mice. ISME Journal, 2021, 15, 2601-2613.	9.8	64
4154	Inorganic Chemical Fertilizer Application to Wheat Reduces the Abundance of Putative Plant Growth-Promoting Rhizobacteria. Frontiers in Microbiology, 2021, 12, 642587.	3.5	23
4155	Leafâ€associated fungal and viral communities of wild plant populations differ between cultivated and natural ecosystems. Plant-Environment Interactions, 2021, 2, 87-99.	1.5	14
4156	Mucosa-associated gut microbiome in Japanese patients with functional constipation. Journal of Clinical Biochemistry and Nutrition, 2021, 68, 187-192.	1.4	11

#	Article	IF	CITATIONS
4157	Glacier clear ice bands indicate englacial channel microbial distribution. Journal of Glaciology, 2021, 67, 811-823.	2.2	1
4158	The Composition and Diversity of the Gut Microbiota in Children Is Modifiable by the Household Dogs: Impact of a Canine-Specific Probiotic. Microorganisms, 2021, 9, 557.	3.6	13
4159	Microbial Diversity and Mercury Methylation Activity in Periphytic Biofilms at a Run-of-River Hydroelectric Dam and Constructed Wetlands. MSphere, $2021, 6, .$	2.9	7
4160	Hybrid assembly of an agricultural slurry virome reveals a diverse and stable community with the potential to alter the metabolism and virulence of veterinary pathogens. Microbiome, 2021, 9, 65.	11.1	182
4161	The Airway Microbiota Modulates Effect of Azithromycin Treatment for Episodes of Recurrent Asthma-like Symptoms in Preschool Children: A Randomized Clinical Trial. American Journal of Respiratory and Critical Care Medicine, 2021, 204, 149-158.	5.6	27
4162	Long-term changes in population genetic features of a rapidly expanding marine invader: implication for invasion success. Biological Invasions, 2021, 23, 2541.	2.4	4
4163	Effects of DNA preservation solution and DNA extraction methods on microbial community profiling of soil. Folia Microbiologica, 2021, 66, 597-606.	2.3	14
4165	Impact of Chronic Exposure to Sublethal Doses of Glyphosate on Honey Bee Immunity, Gut Microbiota and Infection by Pathogens. Microorganisms, 2021, 9, 845.	3.6	35
4166	Rootstocks Shape Their Microbiomeâ€"Bacterial Communities in the Rhizosphere of Different Grapevine Rootstocks. Microorganisms, 2021, 9, 822.	3.6	18
4168	Evidence of thermophilic waste decomposition at a landfill exhibiting elevated temperature regions. Waste Management, 2021, 124, 26-35.	7.4	14
4169	Casing soil microbiome mediates suppression of bacterial blotch of mushrooms during consecutive cultivation cycles. Soil Biology and Biochemistry, 2021, 155, 108161.	8.8	9
4170	Photooxidation and biodegradation potential of a light crude oil in first-year sea ice. Marine Pollution Bulletin, 2021, 165, 112154.	5.0	10
4171	A prevalent and culturable microbiota links ecological balance to clinical stability of the human lung after transplantation. Nature Communications, 2021, 12, 2126.	12.8	31
4172	Identification of new eligible indicator organisms for combined sewer overflow via 16S rRNA gene amplicon sequencing in Kanda River, Tokyo. Journal of Environmental Management, 2021, 284, 112059.	7.8	10
4173	<i>Macrobdella decora</i> : Old World Leech Gut Microbial Community Structure Conserved in a New World Leech. Applied and Environmental Microbiology, 2021, 87, .	3.1	4
4174	Species-specific but not phylosymbiotic gut microbiomes of New Guinean passerine birds are shaped by diet and flight-associated gut modifications. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210446.	2.6	29
4175	Eukaryotic viruses in the fecal virome at the onset of type 1 diabetes: A study from four geographically distant African and Asian countries. Pediatric Diabetes, 2021, 22, 558-566.	2.9	11
4176	A step towards the validation of bacteria biotic indices using DNA metabarcoding for benthic monitoring. Molecular Ecology Resources, 2021, 21, 1889-1903.	4.8	15

#	Article	IF	CITATIONS
4177	Infant Feeding Alters the Longitudinal Impact of Birth Mode on the Development of the Gut Microbiota in the First Year of Life. Frontiers in Microbiology, 2021, 12, 642197.	3.5	28
4178	Characterization and Performance of Lactate-Feeding Consortia for Reductive Dechlorination of Trichloroethene. Microorganisms, 2021, 9, 751.	3.6	10
4179	The larval environment strongly influences the bacterial communities of Aedes triseriatus and Aedes japonicus (Diptera: Culicidae). Scientific Reports, 2021, 11, 7910.	3.3	9
4180	The Reaction of Cellulolytic and Potentially Cellulolytic Spore-Forming Bacteria to Various Types of Crop Management and Farmyard Manure Fertilization in Bulk Soil. Agronomy, 2021, 11, 772.	3.0	17
4181	Bifidobacterium Lactis Probio-M8 regulates gut microbiota to alleviate Alzheimer's disease in the APP/PS1 mouse model. European Journal of Nutrition, 2021, 60, 3757-3769.	3.9	37
4182	Bark-dwelling methanotrophic bacteria decrease methane emissions from trees. Nature Communications, 2021, 12, 2127.	12.8	51
4183	Diversity and composition of pollen loads carried by pollinators are primarily driven by insect traits, not floral community characteristics. Oecologia, 2021, 196, 131-143.	2.0	25
4184	Habitat Quality Determines Dispersal Decisions and Fitness in a Beetle – Fungus Mutualism. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	10
4185	Long-term evolution and short-term adaptation of microbiota strains and sub-strains in mice. Cell Host and Microbe, 2021, 29, 650-663.e9.	11.0	58
4186	Metabarcoding meiofauna biodiversity assessment in four beaches of Northern Colombia: effects of sampling protocols and primer choice. Hydrobiologia, 2021, 848, 3407.	2.0	10
4187	Many small rather than few large sources identified in long-term bee pollen diets in agroecosystems. Agriculture, Ecosystems and Environment, 2021, 310, 107296.	5.3	29
4188	Fiber Derived Microbial Metabolites Prevent Acute Kidney Injury Through G-Protein Coupled Receptors and HDAC Inhibition. Frontiers in Cell and Developmental Biology, 2021, 9, 648639.	3.7	26
4189	Genetically determined hypertensive phenotype affects gut microbiota composition, but not vice versa. Journal of Hypertension, 2021, 39, 1790-1799.	0.5	7
4190	Soil Microsite Outweighs Cultivar Genotype Contribution to Brassica Rhizobacterial Community Structure. Frontiers in Microbiology, 2021, 12, 645784.	3.5	1
4192	Rank normalization empowers a t-test for microbiome differential abundance analysis while controlling for false discoveries. Briefings in Bioinformatics, 2021, 22, .	6.5	2
4193	Nutritional Programming with Dietary Soybean Meal and Its Effect on Gut Microbiota in Zebrafish (<i>Danio rerio</i>). Zebrafish, 2021, 18, 125-138.	1.1	13
4194	Limited influence of marine sediment lyophilization on prokaryotic community structure assessed via amplicon sequencing: an example from environmentally contrasted sediment layers in Toulon harbor (France). Peerl, 2021, 9, e11075.	2.0	1
4195	Safety and Modulatory Effects of Humanized Galacto-Oligosaccharides on the Gut Microbiome. Frontiers in Nutrition, 2021, 8, 640100.	3.7	9

#	Article	IF	CITATIONS
4196	Divergent airway microbiomes in lung transplant recipients with or without pulmonary infection. Respiratory Research, 2021, 22, 118.	3.6	8
4197	Mycoplankton Biome Structure and Assemblage Processes Differ Along a Transect From the Elbe River Down to the River Plume and the Adjacent Marine Waters. Frontiers in Microbiology, 2021, 12, 640469.	3.5	7
4198	Comparison of Hydrocarbon-Degrading Consortia from Surface and Deep Waters of the Eastern Mediterranean Sea: Characterization and Degradation Potential. Energies, 2021, 14, 2246.	3.1	7
4199	The Effects of Nisin-Producing Lactococcus lactis Strain Used as Probiotic on Gilthead Sea Bream (Sparus aurata) Growth, Gut Microbiota, and Transcriptional Response. Frontiers in Marine Science, 2021, 8, .	2.5	21
4200	In vitro Fermentation Reveals Changes in Butyrate Production Dependent on Resistant Starch Source and Microbiome Composition. Frontiers in Microbiology, 2021, 12, 640253.	3.5	27
4202	Characterization of maize root microbiome in two different soils by minimizing plant DNA contamination in metabarcoding analysis. Biology and Fertility of Soils, 2021, 57, 731-737.	4.3	5
4203	Oak decaying wood harbors taxonomically and functionally different bacterial communities in sapwood and heartwood. Soil Biology and Biochemistry, 2021, 155, 108160.	8.8	12
4204	Pollinators mediate floral microbial diversity and microbial network under agrochemical disturbance. Molecular Ecology, 2021, 30, 2235-2247.	3.9	23
4205	Composition and temporal dynamics of sand-dwelling dinoflagellate communities from three Mediterranean beaches. Aquatic Microbial Ecology, 2021, 86, 85-98.	1.8	6
4206	Loss of Interleukin-10 (IL-10) Signaling Promotes IL-22-Dependent Host Defenses against Acute Clostridioides difficile Infection. Infection and Immunity, 2021, 89, .	2.2	6
4207	The hierarchy of root branching order determines bacterial composition, microbial carrying capacity and microbial filtering. Communications Biology, 2021, 4, 483.	4.4	30
4208	Inter- and Intra-Annual Bacterioplankton Community Patterns in a Deepwater Sub-Arctic Region: Persistent High Background Abundance of Putative Oil Degraders. MBio, 2021, 12, .	4.1	10
4210	Host resistance to <i>Bacillus thuringiensis</i> is linked to altered bacterial community within a specialist insect herbivore. Molecular Ecology, 2021, 30, 5438-5453.	3.9	23
4212	Drift of the Subgingival Periodontal Microbiome during Chronic Periodontitis in Type 2 Diabetes Mellitus Patients. Pathogens, 2021, 10, 504.	2.8	16
4213	One dog's waste is another dog's wealth: A pilot study of fecal microbiota transplantation in dogs with acute hemorrhagic diarrhea syndrome. PLoS ONE, 2021, 16, e0250344.	2.5	18
4214	Foliar Aphid Herbivory Alters the Tomato Rhizosphere Microbiome, but Initial Soil Community Determines the Legacy Effects. Frontiers in Sustainable Food Systems, 2021, 5, .	3.9	13
4215	EzMAP: Easy Microbiome Analysis Platform. BMC Bioinformatics, 2021, 22, 179.	2.6	1
4216	Gut microbial alterations in neonatal jaundice pre- and post-treatment. Bioscience Reports, 2021, 41, .	2.4	4

#	Article	IF	CITATIONS
4217	Prediction, enrichment and isolation identify a responsive, competitive community of cellulolytic microorganisms from a municipal landfill. FEMS Microbiology Ecology, 2021, 97, .	2.7	3
4218	The influence of maize genotype on the rhizosphere eukaryotic community. FEMS Microbiology Ecology, 2021, 97, .	2.7	8
4219	Effect of xylanase and xylo-oligosaccharide supplementation on growth performance and faecal bacterial community composition in growing pigs. Animal Feed Science and Technology, 2021, 274, 114822.	2.2	9
4220	Dietary conjugated linoleic acid links reduced intestinal inflammation to amelioration of CNS autoimmunity. Brain, 2021, 144, 1152-1166.	7.6	28
4221	Protist diversity and community complexity in the rhizosphere of switchgrass are dynamic as plants develop. Microbiome, 2021, 9, 96.	11.1	54
4222	Nasopharyngeal microbiome analyses in otitis-prone and otitis-free children. International Journal of Pediatric Otorhinolaryngology, 2021, 143, 110629.	1.0	9
4223	Influence of pipe materials on the microbial community in unchlorinated drinking water and biofilm. Water Research, 2021, 194, 116922.	11.3	35
4224	An in vitro model for microbial fructoselysine degradation shows substantial interindividual differences in metabolic capacities of human fecal slurries. Toxicology in Vitro, 2021, 72, 105078.	2.4	9
4225	Do Rural Second Homes Shape Commensal Microbiota of Urban Dwellers? A Pilot Study among Urban Elderly in Finland. International Journal of Environmental Research and Public Health, 2021, 18, 3742.	2.6	6
4226	Meta-analysis suggests the microbiome responds to Evolve and Resequence experiments in Drosophila melanogaster. BMC Microbiology, 2021, 21, 108.	3.3	10
4227	Shortâ€ŧerm exposure to synthetic flaxseed lignan LGM2605 alters gut microbiota in mice. MicrobiologyOpen, 2021, 10, e1185.	3.0	6
4228	Brassica napus phyllosphere bacterial composition changes with growth stage. Plant and Soil, 2021, 464, 501-516.	3.7	13
4229	Fungal biodiversity and metabolic potential of selected fluvisols from the Vistula River valley in Lubelskie, Poland. Applied Soil Ecology, 2021, 160, 103866.	4.3	5
4230	Host phylogeny and host ecology structure the mammalian gut microbiota at different taxonomic scales. Animal Microbiome, 2021, 3, 33.	3.8	30
4231	Nitrateâ€rich diet alters the composition of the oral microbiota in periodontal recall patients. Journal of Periodontology, 2021, 92, 1536-1545.	3.4	17
4232	Screening of probiotic candidates in a simulated piglet small intestine <i>in vitro</i> model. FEMS Microbiology Letters, 2021, 368, .	1.8	5
4233	Microbiome-Assisted Breeding to Understand Cultivar-Dependent Assembly in Cucurbita pepo. Frontiers in Plant Science, 2021, 12, 642027.	3.6	24
4234	Effect of dietary supplementation with a blend of protected aromatic compounds, including benzoic acid, on growth performance and faecal microbial profile of weaned piglets as an alternative to Zinc Oxide. Livestock Science, 2021, 246, 104455.	1.6	10

#	Article	IF	CITATIONS
4235	A Substrate-Independent Benthic Sampler (SIBS) for Hard and Mixed-Bottom Marine Habitats: A Proof-of-Concept Study. Frontiers in Marine Science, 2021, 8, .	2.5	10
4236	Characterizing rumen microbiota and CAZyme profile of Indian dromedary camel (Camelus) Tj ETQq1 1 0.784314	rgBT /Ove	erlock 10 Tf
4237	Dissecting the contribution of host genetics and the microbiome in complex behaviors. Cell, 2021, 184, 1740-1756.e16.	28.9	109
4238	SARS-CoV-2 infection and viral load are associated with the upper respiratory tract microbiome. Journal of Allergy and Clinical Immunology, 2021, 147, 1226-1233.e2.	2.9	58
4239	Diet and gut microbiome enterotype are associated at the population level in African buffalo. Nature Communications, 2021, 12, 2267.	12.8	31
4240	Re-Analysis of 16S rRNA Gene Sequence Data Sets Uncovers Disparate Laboratory-Specific Microbiomes Associated with the Yellow Fever Mosquito (Aedes aegypti). Microbial Ecology, 2022, 83, 167-181.	2.8	5
4241	From the Andes to the desert: 16S rRNA metabarcoding characterization of aquatic bacterial communities in the Rimac river, the main source of water for Lima, Peru. PLoS ONE, 2021, 16, e0250401.	2.5	8
4242	Coral microbiome changes over the day–night cycle. Coral Reefs, 2021, 40, 921-935.	2.2	6
4243	Pathogen infection influences a distinct microbial community composition in sorghum RILs. Plant and Soil, 2021, 463, 555-572.	3.7	18
4244	Metabarcoding analysis of gut microbiota of healthy individuals reveals impact of probiotic and maltodextrin consumption. Beneficial Microbes, 2021, 12, 121-136.	2.4	13
4245	Distinct community structures of soil nematodes from three ecologically different sites revealed by high-throughput amplicon sequencing of four 18S ribosomal RNA gene regions. PLoS ONE, 2021, 16, e0249571.	2.5	5
4246	2,4-Dichlorophenoxyacetic acid degradation in methanogenic mixed cultures obtained from Brazilian Amazonian soil samples. Biodegradation, 2021, 32, 419-433.	3.0	13
4247	Comparing Sediment Microbiomes in Contaminated and Pristine Wetlands along the Coast of Yucatan. Microorganisms, 2021, 9, 877.	3.6	4
4248	Patterns of Microbiome Variation Among Infrapopulations of Permanent Bloodsucking Parasites. Frontiers in Microbiology, 2021, 12, 642543.	3.5	6
4249	Host-specific symbioses and the microbial prey of a pelagic tunicate ($\langle i \rangle$ Pyrosoma atlanticum $\langle i \rangle$). ISME Communications, 2021, 1, .	4.2	10
4250	Influence of environmental factors on benthic nitrogen fixation and role of sulfur reducing diazotrophs in a eutrophic tropical estuary. Marine Pollution Bulletin, 2021, 165, 112126.	5.0	11
4251	Increasing Freshwater Salinity Impacts Aerosolized Bacteria. Environmental Science & Environmental Sci	10.0	8
4252	Seasonal marine microorganisms change neighbours under contrasting environmental conditions. Environmental Microbiology, 2021, 23, 2592-2604.	3.8	18

#	Article	IF	Citations
4253	Metabarcoding analysis suggests that flexible food web interactions in the eukaryotic plankton community are more common than specific predator–prey relationships at Helgoland Roads, North Sea. ICES Journal of Marine Science, 0, , .	2.5	10
4254	The influence of estuary eutrophication on the benthic diatom community: a molecular approach. African Journal of Marine Science, 2021, 43, 171-186.	1.1	5
4255	Effects of monochloramine on culturability, viability and persistence of Pseudomonas putida and tap water mixed bacterial community. Applied Microbiology and Biotechnology, 2021, 105, 3799-3810.	3.6	1
4256	Targeted Manipulation of Abundant and Rare Taxa in the <i>Daphnia magna</i> Microbiota with Antibiotics Impacts Host Fitness Differentially. MSystems, 2021, 6, .	3.8	13
4257	Antibiotic resistance gene load and irrigation intensity determine the impact of wastewater irrigation on antimicrobial resistance in the soil microbiome. Water Research, 2021, 193, 116818.	11.3	38
4258	Cascading effects of composts and cover crops on soil chemistry, bacterial communities and the survival of foodborne pathogens. Journal of Applied Microbiology, 2021, 131, 1564-1577.	3.1	18
4259	Diversity structure of the microbial communities in the guts of four neotropical termite species. PeerJ, 2021, 9, e10959.	2.0	14
4260	Dietary Curdlan Enhances Bifidobacteria and Reduces Intestinal Inflammation in Mice. Nutrients, 2021, 13, 1305.	4.1	10
4261	Gut microbiota profiles and characterization of cultivable fungal isolates in IBS patients. Applied Microbiology and Biotechnology, 2021, 105, 3277-3288.	3.6	31
4262	The Liquid Diet Composition Affects the Fecal Bacterial Community in Pre-weaning Dairy Calves. Frontiers in Animal Science, 2021, 2, .	1.9	6
4263	Resistance, Resilience, and Recovery of Dryland Soil Bacterial Communities Across Multiple Disturbances. Frontiers in Microbiology, 2021, 12, 648455.	3.5	13
4264	Spatial Memory and Gut Microbiota Alterations Are Already Present in Early Adulthood in a Pre-clinical Transgenic Model of Alzheimer's Disease. Frontiers in Neuroscience, 2021, 15, 595583.	2.8	28
4265	Bacterial–fungal interactions in the neonatal gut influence asthma outcomes later in life. ELife, 2021, 10, .	6.0	22
4266	Differences in the Genital Microbiota in Women Who Naturally Clear Chlamydia trachomatis Infection Compared to Women Who Do Not Clear; A Pilot Study. Frontiers in Cellular and Infection Microbiology, 2021, 11, 615770.	3.9	13
4267	Shifts in the Oral Microbiota During a Four-Week Commercial Saturation Dive to 200 Meters. Frontiers in Physiology, 2021, 12, 669355.	2.8	4
4269	The Fungicide Chlorothalonil Changes the Amphibian Skin Microbiome: A Potential Factor Disrupting a Host Disease-Protective Trait. Applied Microbiology, 2021, 1, 26-37.	1.6	9
4270	Evenness-Richness Scatter Plots: a Visual and Insightful Representation of Shannon Entropy Measurements for Ecological Community Analysis. MSphere, 2021, 6, .	2.9	16
4272	Evaluating sediment and water sampling methods for the estimation of deep-sea biodiversity using environmental DNA. Scientific Reports, 2021, 11, 7856.	3.3	18

#	Article	IF	CITATIONS
4273	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. ISME Journal, 2021, 15, 2817-2829.	9.8	10
4274	Metabolic capabilities mute positive response to direct and indirect impacts of warming throughout the soil profile. Nature Communications, 2021, 12, 2089.	12.8	36
4275	Fungal diversity living in the root and sporophore of the endemic Korean fern Mankyua chejuense. Fungal Ecology, 2021, 50, 101038.	1.6	3
4276	Biofilters are potential hotspots for H2S production in brackish and marine water RAS. Aquaculture, 2021, 536, 736490.	3.5	15
4277	Comparison of Argentinean microbiota with other geographical populations reveals different taxonomic and functional signatures associated with obesity. Scientific Reports, 2021, 11, 7762.	3.3	8
4278	Human Milk Microbiota in an Indigenous Population Is Associated with Maternal Factors, Stage of Lactation, and Breastfeeding Practices. Current Developments in Nutrition, 2021, 5, nzab013.	0.3	5
4279	Parasites, niche modification and the host microbiome: A field survey of multiple parasites. Molecular Ecology, 2021, 30, 2404-2416.	3.9	8
4280	Host preferences of coexisting Perkinsea parasitoids during coastal dinoflagellate blooms. Molecular Ecology, 2021, 30, 2417-2433.	3.9	13
4281	The Composition of the Microbiota in the Full-Term Fetal Gut and Amniotic Fluid: A Bovine Cesarean Section Study. Frontiers in Microbiology, 2021, 12, 626421.	3.5	25
4282	Harnessing the Potential of Native Microbial Communities for Bioremediation of Oil Spills in the Iberian Peninsula NW Coast. Frontiers in Microbiology, 2021, 12, 633659.	3.5	20
4283	Composition of Rhizosphere Microbial Communities Associated With Healthy and Verticillium Wilt Diseased Cotton Plants. Frontiers in Microbiology, 2021, 12, 618169.	3.5	31
4284	Multiple distinct, scaleâ€dependent links between fungi and decomposition. Ecology Letters, 2021, 24, 1352-1362.	6.4	12
4285	Human breast microbiome correlates with prognostic features and immunological signatures in breast cancer. Genome Medicine, 2021, 13, 60.	8.2	101
4286	High-severity wildfire reduces richness and alters composition of ectomycorrhizal fungi in low-severity adapted ponderosa pine forests. Forest Ecology and Management, 2021, 485, 118923.	3.2	36
4287	Metatranscriptomic analyses reveal ruminal pH regulates fiber degradation and fermentation by shifting the microbial community and gene expression of carbohydrate-active enzymes. Animal Microbiome, 2021, 3, 32.	3.8	17
4288	Salmon gut microbiota correlates with disease infection status: potential for monitoring health in farmed animals. Animal Microbiome, 2021, 3, 30.	3.8	84
4289	A Novel Laboratory-Scale Mesocosm Setup to Study Methane Emission Mitigation by Sphagnum Mosses and Associated Methanotrophs. Frontiers in Microbiology, 2021, 12, 652486.	3.5	3
4290	Postmortem submersion interval (PMSI) estimation from the microbiome of <i>sus scrofa</i> bone in a freshwater lake. Journal of Forensic Sciences, 2021, 66, 1334-1347.	1.6	8

#	Article	IF	CITATIONS
4291	Developing a non-destructive metabarcoding protocol for detection of pest insects in bulk trap catches. Scientific Reports, 2021, 11, 7946.	3.3	32
4292	Field multi-omics analysis reveals a close association between bacterial communities and mineral properties in the soybean rhizosphere. Scientific Reports, 2021, 11, 8878.	3.3	14
4293	The fecal microbiota of piglets during weaning transition and its association with piglet growth across various farm environments. PLoS ONE, 2021, 16, e0250655.	2.5	21
4295	Microbial Community Characteristics Largely Unaffected by X-Ray Computed Tomography of Sediment Cores. Frontiers in Microbiology, 2021, 12, 584676.	3.5	0
4296	Complementary Contribution of Fungi and Bacteria to Lignocellulose Digestion in the Food Stored by a Neotropical Higher Termite. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	9
4297	Land-Use System and Forest Floor Explain Prokaryotic Metacommunity Structuring and Spatial Turnover in Amazonian Forest-to-Pasture Conversion Areas. Frontiers in Microbiology, 2021, 12, 657508.	3.5	4
4298	Microbiota-associated risk factors for asymptomatic gut colonisation with multi-drug-resistant organisms in a Dutch nursing home. Genome Medicine, 2021, 13, 54.	8.2	19
4300	Response to Holmes – practical considerations for vector microbiome studies. Molecular Ecology, 2021, 30, 2214-2219.	3.9	1
4301	A Mixture of Manganese, Silica and Phosphorus Supplementation Alters the Plankton Density, Species Diversity, Gut Microbiota and Improved the Health Status of Cultured Marron (Cherax cainii, Austin) Tj ETQq0 0 0	rgBT/Ove	erløck 10 Tf 5
4302	The microbiota of intertidal macroalgae Fucus distichus is siteâ€specific and resistant to change following transplant. Environmental Microbiology, 2021, 23, 2617-2631.	3.8	6
4303	Metazoan diversity and seasonality through eDNA metabarcoding at a Mediterranean long-term ecological research site. ICES Journal of Marine Science, 2021, 78, 3303-3316.	2.5	19
4304	Anode Surface Bioaugmentation Enhances Deterministic Biofilm Assembly in Microbial Fuel Cells. MBio, 2021, 12, .	4.1	9
4305	In vitro and in vivo digestion of red cured cooked meat: oxidation, intestinal microbiota and fecal metabolites. Food Research International, 2021, 142, 110203.	6.2	16
4306	Understanding the Holobiont: Crosstalk Between Gut Microbiota and Mitochondria During Long Exercise in Horse. Frontiers in Molecular Biosciences, 2021, 8, 656204.	3.5	14
4307	Direct cell extraction from fresh and stored soil samples: Impact on microbial viability and community compositions. Soil Biology and Biochemistry, 2021, 155, 108178.	8.8	12
4308	The effects of air stress during storage and low packing density on the fermentation and aerobic stability of corn silage inoculated with Lactobacillus buchneri 40788. Journal of Dairy Science, 2021, 104, 4206-4222.	3.4	15
4309	Genome-Based Targeted Sequencing as a Reproducible Microbial Community Profiling Assay. MSphere, 2021, 6, .	2.9	4
4311	Microbiomes of willow-galling sawflies: effects of host plant, gall type, and phylogeny on community structure and function. Genome, 2021, 64, 615-626.	2.0	7

#	Article	IF	Citations
4312	Changes in the ceca microbiota of broilers vaccinated for coccidiosis or supplemented with salinomycin. Poultry Science, 2021, 100, 100969.	3.4	20
4313	Establishment of <i>Culex modestus</i> in Belgium and a Glance into the Virome of Belgian Mosquito Species. MSphere, 2021, 6, .	2.9	19
4314	Shifts in the Skin Microbiota after UVB Treatment in Adult Atopic Dermatitis. Dermatology, 2022, 238, 109-120.	2.1	10
4316	Effect of tectonic processes on biosphere–geosphere feedbacks across a convergent margin. Nature Geoscience, 2021, 14, 301-306.	12.9	32
4317	Surface Topography, Bacterial Carrying Capacity, and the Prospect of Microbiome Manipulation in the Sea Anemone Coral Model Aiptasia. Frontiers in Microbiology, 2021, 12, 637834.	3.5	21
4318	Bioinformatic pipelines combining denoising and clustering tools allow for more comprehensive prokaryotic and eukaryotic metabarcoding. Molecular Ecology Resources, 2021, 21, 1904-1921.	4.8	43
4319	A Î²â€łactamase gene of <i>Fusarium oxysporum</i> alters the rhizosphere microbiota of soybean. Plant Journal, 2021, 106, 1588-1604.	5.7	4
4322	Exposure to airborne bacteria depends upon vertical stratification and vegetation complexity. Scientific Reports, 2021, 11, 9516.	3.3	31
4323	Monitoring vertebrate biodiversity of a protected coastal wetland using eDNA metabarcoding. Environmental DNA, 2022, 4, 77-92.	5.8	14
4324	Randomised, double-blind, placebo-controlled trial of Probiotics To Eliminate COVID-19 Transmission in Exposed Household Contacts (PROTECT-EHC): a clinical trial protocol. BMJ Open, 2021, 11, e047069.	1.9	26
4325	Interactions between soil properties, agricultural management and cultivar type drive structural and functional adaptations of the wheat rhizosphere microbiome to drought. Environmental Microbiology, 2021, 23, 5866-5882.	3.8	36
4326	Does the Composition of the Gut Bacteriome Change during the Growth of Tuna?. Microorganisms, 2021, 9, 1157.	3.6	6
4327	Press Xenobiotic 3-Chloroaniline Disturbance Favors Deterministic Assembly with a Shift in Function and Structure of Bacterial Communities in Sludge Bioreactors. ACS ES&T Water, 2021, 1, 1429-1437.	4.6	11
4328	Low microbial biomass within the reproductive tract of mid-lactation dairy cows: A study approach. Journal of Dairy Science, 2021, 104, 6159-6174.	3.4	6
4329	Rhizosphere Bacterial Networks, but Not Diversity, Are Impacted by Pea-Wheat Intercropping. Frontiers in Microbiology, 2021, 12, 674556.	3.5	23
4331	Infant Gut Microbiota Associated with Fine Motor Skills. Nutrients, 2021, 13, 1673.	4.1	19
4332	Long-Term Effects of Dietary Supplementation with Olive Oil and Hydrogenated Vegetable Oil on the Rumen Microbiome of Dairy Cows. Microorganisms, 2021, 9, 1121.	3.6	7
4333	High biodiversity in a benzene-degrading nitrate-reducing culture is sustained by a few primary consumers. Communications Biology, 2021, 4, 530.	4.4	11

#	Article	IF	CITATIONS
4334	Associations of healthy food choices with gut microbiota profiles. American Journal of Clinical Nutrition, 2021, 114, 605-616.	4.7	42
4336	Community Assembly Processes as a Mechanistic Explanation of the Predator-Prey Diversity Relationship in Marine Microbes. Frontiers in Marine Science, 2021, 8, .	2.5	4
4337	Characterization of oral and cloacal microbial communities in cold-stunned Kemp's ridley sea turtles (Lepidochelys kempii) during the time course of rehabilitation. PLoS ONE, 2021, 16, e0252086.	2.5	12
4338	The impact of Opisthorchis felineus infection and praziquantel treatment on the intestinal microbiota in children. Acta Tropica, 2021, 217, 105835.	2.0	5
4339	Unveiling Taxonomic Diversity and Functional Composition Differences of Microbial Mat Communities Through Comparative Metagenomics. Geomicrobiology Journal, 2021, 38, 639-648.	2.0	3
4340	Shifts in the rhizobiome during consecutive <i>inÂplanta</i> enrichment for phosphateâ€solubilizing bacteria differentially affect maize P status. Microbial Biotechnology, 2021, 14, 1594-1612.	4.2	21
4341	Microbial Sharing between Pediatric Patients and Therapy Dogs during Hospital Animal-Assisted Intervention Programs. Microorganisms, 2021, 9, 1054.	3.6	9
4342	Evaluation of saliva as a source of accurate wholeâ€genome and microbiome sequencing data. Genetic Epidemiology, 2021, 45, 537-548.	1.3	2
4343	Fetal meconium does not have a detectable microbiota before birth. Nature Microbiology, 2021, 6, 865-873.	13.3	95
4344	Microbial Composition of SCOBY Starter Cultures Used by Commercial Kombucha Brewers in North America. Microorganisms, 2021, 9, 1060.	3.6	47
4345	Gut microbiota characterization in Chinese patients with alopecia areata. Journal of Dermatological Science, 2021, 102, 109-115.	1.9	19
4346	Understanding the differences in 2G ethanol fermentative scales through omics data integration. FEMS Yeast Research, 2021, 21, .	2.3	6
4347	Influence of genetic background and dietary oleic acid on gut microbiota composition in Duroc and Iberian pigs. PLoS ONE, 2021, 16, e0251804.	2.5	4
4348	Biogeochemical dynamics and microbial community development under sulfate- and iron-reducing conditions based on electron shuttle amendment. PLoS ONE, 2021, 16, e0251883.	2.5	6
4349	Urban wastewater bacterial communities assemble into seasonal steady states. Microbiome, 2021, 9, 116.	11.1	35
4350	The ecological impacts of multiple environmental stressors on coastal biofilm bacteria. Global Change Biology, 2021, 27, 3166-3178.	9.5	10
4351	Diversity Metrics Are Robust to Differences in Sampling Location and Depth for Environmental DNA of Plants in Small Temperate Lakes. Frontiers in Environmental Science, 2021, 9, .	3.3	12
4353	Early life stress in mice alters gut microbiota independent of maternal microbiota inheritance. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2021, 320, R663-R674.	1.8	17

#	Article	IF	CITATIONS
4354	Tapirus bairdii-Associated Fecal Microbiome from a Critical Conservation Area: Calakmul, México. Current Microbiology, 2021, 78, 2648-2659.	2.2	4
4355	Meta-analysis to identify the core microbiome in diverse wastewater. International Journal of Environmental Science and Technology, 2022, 19, 5079-5096.	3.5	13
4356	Applications of Blocker Nucleic Acids and Non-Metazoan PCR Improves the Discovery of the Eukaryotic Microbiome in Ticks. Microorganisms, 2021, 9, 1051.	3.6	2
4358	Soil Microbial Diversity Impacts Plant Microbiota More than Herbivory. Phytobiomes Journal, 2021, 5, 408-417.	2.7	15
4359	Targeted metagenomics reveals inferior resilience of farm soil resistome compared to soil microbiome after manure application. Science of the Total Environment, 2021, 770, 145399.	8.0	27
4360	Linking Pélardon artisanal goat cheese microbial communities to aroma compounds during cheese-making and ripening. International Journal of Food Microbiology, 2021, 345, 109130.	4.7	30
4361	Taxonomic variations in the gut microbiome of gout patients with and without tophi might have a functional impact on urate metabolism. Molecular Medicine, 2021, 27, 50.	4.4	31
4362	Bacterial and Archaeal Communities in Polymetallic Nodules, Sediments, and Bottom Waters of the Abyssal Clarion-Clipperton Zone: Emerging Patterns and Future Monitoring Considerations. Frontiers in Marine Science, 2021, 8, .	2.5	6
4364	Nicotine concentration and mentholation affect bacterial community diversity in SPECTRUM research cigarettes. Applied Microbiology and Biotechnology, 2021, 105, 4241-4253.	3.6	2
4365	Microbiome characterization of defensive tissues in the model anemone Exaiptasia diaphana. BMC Microbiology, 2021, 21, 152.	3.3	14
4367	Effect of Differences in the Microbiome of Cyp17a1-Deficient Mice on Atherosclerotic Background. Cells, 2021, 10, 1292.	4.1	3
4369	Spatial and Structural Factors Shape Seagrass-Associated Bacterial Communities in Singapore and Peninsular Malaysia. Frontiers in Marine Science, 2021, 8, .	2.5	10
4370	Effects of Peroxyacetic Acid Spray and Storage Temperature on the Microbiota and Sensory Properties of Vacuum-Packed Subprimal Cuts of Meat. Applied and Environmental Microbiology, 2021, 87, .	3.1	9
4371	<i>Megasphaera</i> in the Stool Microbiota Is Negatively Associated With Diarrheal Cryptosporidiosis. Clinical Infectious Diseases, 2021, 73, e1242-e1251.	5.8	33
4372	Gut Microbiota Induced by Pterostilbene and Resveratrol in High-Fat-High-Fructose Fed Rats: Putative Role in Steatohepatitis Onset. Nutrients, 2021, 13, 1738.	4.1	15
4373	Compositional shifts in the strawberry fruit microbiome in response to near-harvest application of Metschnikowia fructicola, a yeast biocontrol agent. Postharvest Biology and Technology, 2021, 175, 111469.	6.0	50
4374	Dual RNAseq highlights the kinetics of skin microbiome and fish host responsiveness to bacterial infection. Animal Microbiome, 2021, 3, 35.	3.8	2
4375	Characterising Post-mortem Bacterial Translocation Under Clinical Conditions Using 16S rRNA Gene Sequencing in Two Animal Models. Frontiers in Microbiology, 2021, 12, 649312.	3.5	2

#	Article	IF	CITATIONS
4377	Long-term dynamic changes in attached and planktonic microbial communities in a contaminated aquifer. Environmental Pollution, 2021, 277, 116765.	7.5	6
4378	Bacterial sepsis increases hippocampal fibrillar amyloid plaque load and neuroinflammation in a mouse model of Alzheimer's disease. Neurobiology of Disease, 2021, 152, 105292.	4.4	21
4379	Degradation of the Indospicine Toxin from Indigofera spicata by a Mixed Population of Rumen Bacteria. Toxins, 2021, 13, 389.	3.4	1
4380	Compositional and Functional Microbiome Variation Between Tubes of an Intertidal Polychaete and Surrounding Marine Sediment. Frontiers in Marine Science, 2021, 8, .	2.5	4
4381	Gut microbiota restoration through fecal microbiota transplantation: a new atopic dermatitis therapy. Experimental and Molecular Medicine, 2021, 53, 907-916.	7.7	45
4382	Rhizosphere Microbiomes in a Historical Maize-Soybean Rotation System Respond to Host Species and Nitrogen Fertilization at the Genus and Subgenus Levels. Applied and Environmental Microbiology, 2021, 87, e0313220.	3.1	17
4384	Shifts in composition and function of soil fungal communities and edaphic properties during the reclamation chronosequence of an open-cast coal mining dump. Science of the Total Environment, 2021, 767, 144465.	8.0	10
4385	Spatio-temporal variations in chemical pollutants found among urban deposits match changes in thiopurine S-methyltransferase-harboring bacteria tracked by the tpm metabarcoding approach. Science of the Total Environment, 2021, 767, 145425.	8.0	4
4386	Impact of Application of Abscisic Acid, Benzothiadiazole and Chitosan on Berry Quality Characteristics and Plant Associated Microbial Communities of Vitis vinifera L var. Mouhtaro Plants. Sustainability, 2021, 13, 5802.	3.2	11
4387	Critical evaluation of faecal microbiome preservation using metagenomic analysis. ISME Communications, 2021, 1, .	4.2	8
4388	Modulating T Follicular Cells In Vivo Enhances Antigen-Specific Humoral Immunity. Journal of Immunology, 2021, 206, 2583-2595.	0.8	0
4389	Depletion of the gut microbiota differentially affects the impact of whey protein on highâ€fat dietâ€induced obesity and intestinal permeability. Physiological Reports, 2021, 9, e14867.	1.7	12
4390	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. ISME Journal, 2021, 15, 2986-3004.	9.8	89
4391	Covariation of the Fecal Microbiome with Diet in Nonpasserine Birds. MSphere, 2021, 6, .	2.9	22
4392	Specific and conserved patterns of microbiota-structuring by maize benzoxazinoids in the field. Microbiome, 2021, 9, 103.	11.1	57
4393	Metformin Affects Gut Microbiome Composition and Function and Circulating Short-Chain Fatty Acids: A Randomized Trial. Diabetes Care, 2021, 44, 1462-1471.	8.6	77
4394	Driving factors influencing the rhizobacteriome community structure of plants adapted to multiple climatic stressors in edaphic savannas. Science of the Total Environment, 2021, 769, 145214.	8.0	14
4395	Immune Gene Expression Covaries with Gut Microbiome Composition in Stickleback. MBio, 2021, 12, .	4.1	15

#	Article	IF	CITATIONS
4396	Effect of a bioconverted product of Lotus corniculatus seed on the axillary microbiome and body odor. Scientific Reports, 2021, 11, 10138.	3.3	3
4397	Patients With Common Variable Immunodeficiency (CVID) Show Higher Gut Bacterial Diversity and Levels of Low-Abundance Genes Than the Healthy Housemates. Frontiers in Immunology, 2021, 12, 671239.	4.8	13
4398	Children Tooth Brushing Behavior and Oral Microbiota: A Pilot Study. Oral, 2021, 1, 112-121.	0.6	0
4399	Comparative analyses of sooty mould communities from Brazil and Central Europe. Mycological Progress, 2021, 20, 869-887.	1.4	12
4400	Sex differences in gut microbiota modulation of aversive conditioning, open field activity, and basolateral amygdala dendritic spine density. Journal of Neuroscience Research, 2021, 99, 1780-1801.	2.9	12
4401	Metagenomic analysis of urban wastewater resistome and mobilome: A support for antimicrobial resistance surveillance in an endemic country. Environmental Pollution, 2021, 276, 116736.	7.5	30
4402	Factors Influencing the Succession of the Fecal Microbiome in Broilers. Livestock Science, 2021, 247, 104486.	1.6	10
4403	Organic Matter Type Defines the Composition of Active Microbial Communities Originating From Anoxic Baltic Sea Sediments. Frontiers in Microbiology, 2021, 12, 628301.	3.5	13
4404	Investigating variability in microbial community composition in replicate environmental DNA samples down lake sediment cores. PLoS ONE, 2021, 16, e0250783.	2.5	15
4405	Consistent patterns of fungal communities within ant-plants across a large geographic range strongly suggest a multipartite mutualism. Mycological Progress, 2021, 20, 681-699.	1.4	5
4406	Gut Microbiota of Drosophila subobscura Contributes to Its Heat Tolerance and Is Sensitive to Transient Thermal Stress. Frontiers in Microbiology, 2021, 12, 654108.	3. 5	25
4407	Prevotella histicola Protects From Arthritis by Expansion of Allobaculum and Augmenting Butyrate Production in Humanized Mice. Frontiers in Immunology, 2021, 12, 609644.	4.8	53
4408	Shiftwork, functional bowel symptoms, and the microbiome. PeerJ, 2021, 9, e11406.	2.0	5
4409	Seasonal Dynamics of the Honey Bee Gut Microbiota in Colonies Under Subtropical Climate. Microbial Ecology, 2022, 83, 492-500.	2.8	11
4410	Global Diversity and Biogeography of the <i>Zostera marina</i> Mycobiome. Applied and Environmental Microbiology, 2021, 87, e0279520.	3.1	19
4411	Cable bacteria at oxygenâ€releasing roots of aquatic plants: a widespread and diverse plant–microbe association. New Phytologist, 2021, 232, 2138-2151.	7.3	32
4412	Alteration of gut microbiota with a broadâ€spectrum antibiotic does not impair maternal care in the European earwig. Journal of Evolutionary Biology, 2021, 34, 1034-1045.	1.7	6
4413	Combined Effect of Activated Carbon Particles and Non-Adsorptive Spherical Beads as Fluidized Media on Fouling, Organic Removal and Microbial Communities in Anaerobic Membrane Bioreactor. Membranes, 2021, 11, 365.	3.0	8

#	Article	IF	CITATIONS
4414	Dadaist2: A Toolkit to Automate and Simplify Statistical Analysis and Plotting of Metabarcoding Experiments. International Journal of Molecular Sciences, 2021, 22, 5309.	4.1	12
4415	Exploring benthic cyanobacterial diversity and co-occurring potentially harmful dinoflagellates in six islands of the South Pacific. Hydrobiologia, 2021, 848, 2815-2829.	2.0	11
4416	Choice of Commercial DNA Extraction Method Does Not Affect 16S Sequencing Outcomes in Cloacal Swabs. Animals, 2021, 11, 1372.	2.3	0
4417	Large and interacting effects of temperature and nutrient addition on stratified microbial ecosystems in a small, replicated, and liquidâ€dominated Winogradsky column approach. MicrobiologyOpen, 2021, 10, e1189.	3.0	5
4418	Gut Microbiota-Related Effects of Tanhuo Decoction in Acute Ischemic Stroke. Oxidative Medicine and Cellular Longevity, 2021, 2021, 1-18.	4.0	28
4420	Experimental Infection of the Biomphalaria glabrata Vector Snail by Schistosoma mansoni Parasites Drives Snail Microbiota Dysbiosis. Microorganisms, 2021, 9, 1084.	3.6	22
4421	The Effect of Antimicrobial Treatment upon the Gill Bacteriome of Atlantic Salmon (Salmo salar L.) and Progression of Amoebic Gill Disease (AGD) In Vivo. Microorganisms, 2021, 9, 987.	3.6	11
4422	The Rhizosphere Responds: Rich Fen Peat and Root Microbial Ecology after Long-Term Water Table Manipulation. Applied and Environmental Microbiology, 2021, 87, e0024121.	3.1	4
4423	The Rhinobiome of Exacerbated Wheezers and Asthmatics: Insights From a German Pediatric Exacerbation Network. Frontiers in Allergy, 2021, 2, 667562.	2.8	7
4424	Machine Learning Algorithms Reveals Country-Specific Metagenomic Taxa from American Gut Project Data. Studies in Health Technology and Informatics, 2021, 281, 382-386.	0.3	0
4425	Galacto-oligosaccharides supplementation in prefrail older and healthy adults increased faecal bifidobacteria, but did not impact immune function and oxidative stress. Clinical Nutrition, 2021, 40, 3019-3031.	5.0	25
4426	Phylogeny- and Abundance-Based Metrics Allow for the Consistent Comparison of Core Gut Microbiome Diversity Indices Across Host Species. Frontiers in Microbiology, 2021, 12, 659918.	3.5	14
4427	Effect on gut microbiota of a 1-y lifestyle intervention with Mediterranean diet compared with energy-reduced Mediterranean diet and physical activity promotion: PREDIMED-Plus Study. American Journal of Clinical Nutrition, 2021, 114, 1148-1158.	4.7	60
4428	Effect of plant biostimulants on root and plant health and the rhizosphere microbiome of citrus trees in huanglongbing-endemic conditions. Trees - Structure and Function, 2021, 35, 1525-1539.	1.9	16
4429	Fast and pervasive transcriptomic resilience and acclimation of extremely heat-tolerant coral holobionts from the northern Red Sea. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	63
4430	Submesoscale physicochemical dynamics directly shape bacterioplankton community structure in space and time. Limnology and Oceanography, 2021, 66, 2901-2913.	3.1	12
4431	Comprehensive Ecological and Geographic Characterization of Eukaryotic and Prokaryotic Microbiomes in African Anopheles. Frontiers in Microbiology, 2021, 12, 635772.	3.5	5
4432	The lower respiratory tract microbiome of critically ill patients with COVID-19. Scientific Reports, 2021, 11, 10103.	3.3	52

#	Article	IF	CITATIONS
4433	Convergence of the turkey gut microbiota following cohabitation under commercial settings. Journal of Animal Science and Biotechnology, 2021, 12, 59.	5.3	2
4434	Deep Soil Layers of Drought-Exposed Forests Harbor Poorly Known Bacterial and Fungal Communities. Frontiers in Microbiology, 2021, 12, 674160.	3.5	41
4435	Microbiomes in Suspended Soils of Vascular Epiphytes Differ from Terrestrial Soil Microbiomes and from Each Other. Microorganisms, 2021, 9, 1033.	3.6	10
4438	Impacts of radiation exposure on the bacterial and fungal microbiome of small mammals in the Chernobyl Exclusion Zone. Journal of Animal Ecology, 2021, 90, 2172-2187.	2.8	12
4439	Composition of cutaneous bacterial microbiome in seborrheic dermatitis patients: A cross-sectional study. PLoS ONE, 2021, 16, e0251136.	2.5	12
4440	Chitin- and Keratin-Rich Soil Amendments Suppress Rhizoctonia solani Disease via Changes to the Soil Microbial Community. Applied and Environmental Microbiology, 2021, 87, .	3.1	25
4441	Post-reclamation microbial diversity and functions in hexachlorocyclohexane (HCH) contaminated soil in relation to spontaneous HCH tolerant vegetation. Science of the Total Environment, 2021, 767, 144653.	8.0	16
4442	Investigation of Early Supplementation of Nucleotides on the Intestinal Maturation of Weaned Piglets. Animals, 2021, 11, 1489.	2.3	3
4444	Speciesâ€level ichthyoplankton dynamics for 97 fishes in two major river basins of the Amazon using quantitative metabarcoding. Molecular Ecology, 2022, 31, 1627-1648.	3.9	17
4445	Variation in Human Milk Composition Is Related to Differences in Milk and Infant Fecal Microbial Communities. Microorganisms, 2021, 9, 1153.	3.6	34
4446	Comparable response of wild rodent gut microbiome to anthropogenic habitat contamination. Molecular Ecology, 2021, 30, 3485-3499.	3.9	15
4447	Sweet spheres: succession and <scp>CAZyme</scp> expression of marine bacterial communities colonizing a mix of alginate and pectin particles. Environmental Microbiology, 2021, 23, 3130-3148.	3.8	17
4448	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. ISME Journal, 2021, 15, 3339-3356.	9.8	48
4449	Bacillus Subtilis 29784 as a Feed Additive for Broilers Shifts the Intestinal Microbial Composition and Supports the Production of Hypoxanthine and Nicotinic Acid. Animals, 2021, 11, 1335.	2.3	11
4450	Altered Nasal Microbiota Composition Associated with Development of Polyserositis by Mycoplasma hyorhinis. Pathogens, 2021, 10, 603.	2.8	10
4451	Methane oxidation in the waters of a humic-rich boreal lake stimulated by photosynthesis, nitrite, Fe(III) and humics. Biogeosciences, 2021, 18, 3087-3101.	3.3	20
4452	Microbial linkages to soil biogeochemical processes in a poorly drained agricultural ecosystem. Soil Biology and Biochemistry, 2021, 156, 108228.	8.8	22
4455	Molecular diet analysis of neotropical bats based on fecal DNA metabarcoding. Ecology and Evolution, 2021, 11, 7474-7491.	1.9	45

#	Article	IF	Citations
4456	Maternal Vegetable and Fruit Consumption during Pregnancy and Its Effects on Infant Gut Microbiome. Nutrients, 2021, 13, 1559.	4.1	19
4457	Effects of increasing lime application rates on microbial diversity and community structure in paddy soils. Applied Soil Ecology, 2021, 161, 103837.	4.3	5
4458	Exploring the pathogenic function of Pantoea ananatis endogenous plasmid by an efficient and simple plasmid elimination strategy. Microbiological Research, 2021, 246, 126710.	5.3	5
4460	Long-term storage affects resource availability and occurrence of bacterial taxa linked to pollutant degradation and human health in landscaping materials. Urban Forestry and Urban Greening, 2021, 60, 127065.	5.3	4
4461	Processed Animal Proteins from Insect and Poultry By-Products in a Fish Meal-Free Diet for Rainbow Trout: Impact on Intestinal Microbiota and Inflammatory Markers. International Journal of Molecular Sciences, 2021, 22, 5454.	4.1	43
4462	Comparison study of differential abundance testing methods using two large Parkinson disease gut microbiome datasets derived from 16S amplicon sequencing. BMC Bioinformatics, 2021, 22, 265.	2.6	39
4463	Microbial communities of wild-captured Kemp's ridley (Lepidochelys kempii) and green sea turtles (Chelonia mydas). Endangered Species Research, 2021, 45, 21-36.	2.4	7
4464	Prokaryotic diversity and biogeochemical characteristics of field living and laboratory cultured stromatolites from the hypersaline Laguna Interna, Salar de Atacama (Chile). Extremophiles, 2021, 25, 327-342.	2.3	3
4465	Water Quality Dynamics in Response to Rainfall along an Estuarine Ecocline. ACS ES&T Water, 2021, 1, 1503-1514.	4.6	0
4466	Isotopic tracing reveals single-cell assimilation of a macroalgal polysaccharide by a few marine Flavobacteria and Gammaproteobacteria. ISME Journal, 2021, 15, 3062-3075.	9.8	16
4467	Effects of three flower field types on bumblebees and their pollen diets. Basic and Applied Ecology, 2021, 52, 95-108.	2.7	16
4468	Assessment of the gut bacterial microbiome and metabolome of girls and women with Rett Syndrome. PLoS ONE, 2021, 16, e0251231.	2.5	11
4469	Artificial neural network analysis of microbial diversity in the central and southern Adriatic Sea. Scientific Reports, 2021, 11, 11186.	3.3	13
4470	Taxonomic signatures of cause-specific mortality risk in human gut microbiome. Nature Communications, 2021, 12, 2671.	12.8	55
4473	Dynamic plant–soil microbe interactions: the neglected effect of soil conditioning time. New Phytologist, 2021, 231, 1546-1558.	7.3	20
4475	Use of metabarcoding and source tracking to identify desirable or spoilage autochthonous microorganism sources during black olive fermentations. Food Research International, 2021, 144, 110344.	6.2	13
4476	Experimental Evidence Pointing to Rain as a Reservoir of Tomato Phyllosphere Microbiota. Phytobiomes Journal, 2021, 5, 382-399.	2.7	17
4478	Influence of seasonal changes and salinity on spinach phyllosphere bacterial functional assemblage. PLoS ONE, 2021, 16, e0252242.	2.5	5

#	Article	IF	CITATIONS
4479	Differences in Precipitation Regime Shape Microbial Community Composition and Functional Potential in Namib Desert Soils. Microbial Ecology, 2022, 83, 689-701.	2.8	18
4480	Circulating bacterial signature is linked to metabolic disease and shifts with metabolic alleviation after bariatric surgery. Genome Medicine, 2021, 13, 105.	8.2	14
4483	Short-lived detection of an introduced vertebrate eDNA signal in a nearshore rocky reef environment. PLoS ONE, 2021, 16, e0245314.	2.5	22
4484	Taxonomic, phylogenetic and functional diversity of rootâ€associated fungi in bromeliads: effects of host identity, life forms and nutritional modes. New Phytologist, 2021, 231, 1195-1209.	7.3	13
4486	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. GigaScience, 2021, 10, .	6.4	9
4487	Influential Insider: Wolbachia, an Intracellular Symbiont, Manipulates Bacterial Diversity in Its Insect Host. Microorganisms, 2021, 9, 1313.	3.6	7
4489	The Effect of a Total Fishmeal Replacement by Arthrospira platensis on the Microbiome of African Catfish (Clarias gariepinus). Life, 2021, 11, 558.	2.4	8
4490	Managing Contamination and Diverse Bacterial Loads in 16S rRNA Deep Sequencing of Clinical Samples: Implications of the Law of Small Numbers. MBio, 2021, 12, e0059821.	4.1	8
4493	Gut colonization in preterm infants supplemented with bovine colostrum in the first week of life: An explorative pilot study. Journal of Parenteral and Enteral Nutrition, 2022, 46, 592-599.	2.6	5
4494	Spheres of Influence: Host Tree Proximity and Soil Chemistry Shape rRNA, but Not DNA, Communities of Symbiotic and Free-Living Soil Fungi in a Mixed Hardwood-Conifer Forest. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	3
4496	The Urinary Microbiome in Postmenopausal Women with Recurrent Urinary Tract Infections. Journal of Urology, 2021, 206, 1222-1231.	0.4	30
4497	Microbial community structure in hadal sediments: high similarity along trench axes and strong changes along redox gradients. ISME Journal, 2021, 15, 3455-3467.	9.8	29
4498	Changes in the Gut Microbiota Following Bariatric Surgery Are Associated with Increased Alcohol Intake in a Female Rat Model. Alcohol and Alcoholism, 2021, 56, 605-613.	1.6	7
4499	Sediment archives reveal irreversible shifts in plankton communities after World War II and agricultural pollution. Current Biology, 2021, 31, 2682-2689.e7.	3.9	25
4500	Fenofibrate promotes PPARα-targeted recovery of the intestinal epithelial barrier at the host-microbe interface in dogs with diabetes mellitus. Scientific Reports, 2021, 11, 13454.	3.3	10
4501	Plant Age Influences Microbiome Communities More Than Plant Compartment in Greenhouse-Grown Creeping Bentgrass. Phytobiomes Journal, 2021, 5, 373-381.	2.7	7
4502	Probiotic Bacteria with High Alpha-Gal Content Protect Zebrafish against Mycobacteriosis. Pharmaceuticals, 2021, 14, 635.	3.8	14
4503	The Effect of Inoculation of a Diazotrophic Bacterial Consortium on the Indigenous Bacterial Community Structure of Sugarcane Apoplast Fluid. Current Microbiology, 2021, 78, 3079-3091.	2.2	2

#	Article	IF	CITATIONS
4504	DNA metabarcoding reveals trophic niche diversity of micro and mesozooplankton species. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210908.	2.6	21
4505	Investigation of Spaceflight Induced Changes to Astronaut Microbiomes. Frontiers in Microbiology, 2021, 12, 659179.	3.5	28
4506	Bacterial communities associated with sugarcane under different agricultural management exhibit a diversity of plant growth-promoting traits and evidence of synergistic effect. Microbiological Research, 2021, 247, 126729.	5.3	14
4507	Socioeconomic position links circulatory microbiota differences with biological age. Scientific Reports, 2021, 11, 12629.	3.3	14
4508	Weaning-associated feed deprivation stress causes microbiota disruptions in a novel mucin-containing in vitro model of the piglet colon (MPigut-IVM). Journal of Animal Science and Biotechnology, 2021, 12, 75.	5.3	7
4509	Microbiome response differs among selected lines of Sydney rock oysters to ocean warming and acidification. FEMS Microbiology Ecology, 2021, 97, .	2.7	18
4510	Allergyâ€related diseases and early gut fungal and bacterial microbiota abundances in children. Clinical and Translational Allergy, 2021, 11, e12041.	3.2	4
4511	Reindeer control over subarctic treeline alters soil fungal communities with potential consequences for soil carbon storage. Global Change Biology, 2021, 27, 4254-4268.	9.5	10
4512	Passive Immunization of Chickens with Anti-Enterobactin Egg Yolk Powder for Campylobacter Control. Vaccines, 2021, 9, 569.	4.4	7
4513	Influence of shrub willow buffers strategically integrated in an Illinois corn-soybean field on soil health and microbial community composition. Science of the Total Environment, 2021, 772, 145674.	8.0	6
4514	Successive plant growth amplifies genotype-specific assembly of the tomato rhizosphere microbiome. Science of the Total Environment, 2021, 772, 144825.	8.0	38
4516	Metataxonomic characterization of bacterial and archaeal community involved in hydrogen and methane production from citrus peel waste (Citrus sinensis L. Osbeck) in batch reactors. Biomass and Bioenergy, 2021, 149, 106091.	5.7	13
4517	Microbial and geo-archaeological records reveal the growth rate, origin and composition of desert rock surface communities. Biogeosciences, 2021, 18, 3331-3342.	3.3	1
4518	Manipulation of Unfrozen Water Retention for Enhancing Petroleum Hydrocarbon Biodegradation in Seasonally Freezing and Frozen Soil. Environmental Science & Environmental Scie	10.0	1
4519	Structure and function of Shark Bay microbial communities following tropical cyclone Olwyn: A metatranscriptomic and organic geochemical perspective. Geobiology, 2021, 19, 642-664.	2.4	6
4520	Effect of bioactive compounds released from Brassicaceae defatted seed meals on bacterial load in pig manure. Environmental Science and Pollution Research, 2021, 28, 62353-62367.	5.3	5
4521	An Examination of Fungal and Bacterial Assemblages in Bulk and Rhizosphere Soils under Solanum tuberosum in Southeastern Wyoming, USA. Applied Microbiology, 2021, 1, 162-176.	1.6	6
4522	Microbiota and Metabolite Modifications after Dietary Exclusion of Dairy Products and Reduced Consumption of Fermented Food in Young and Older Men. Nutrients, 2021, 13, 1905.	4.1	4

#	Article	IF	CITATIONS
4524	Metagenomics of mine tailing rhizospheric communities and its selection for plant establishment towards bioremediation. Microbiological Research, 2021, 247, 126732.	5.3	15
4525	Transmitting silks of maize have a complex and dynamic microbiome. Scientific Reports, 2021, 11, 13215.	3.3	10
4526	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. MSystems, 2021, 6, e0130620.	3.8	17
4527	Association Between Gut Microbial Abundance and Sight-Threatening Diabetic Retinopathy. , 2021, 62, 19.		19
4528	Elevated Atmospheric CO2 Modifies Mostly the Metabolic Active Rhizosphere Soil Microbiome in the Giessen FACE Experiment. Microbial Ecology, 2022, 83, 619-634.	2.8	9
4529	The Microbiome Associated with the Reef Builder Neogoniolithon sp. in the Eastern Mediterranean. Microorganisms, 2021, 9, 1374.	3.6	3
4530	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. MSystems, 2021, 6, .	3.8	8
4533	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. Lab Animal, 2021, 50, 185-195.	0.4	17
4535	Evaluating the lettuce metatranscriptome with MinION sequencing for future spaceflight food production applications. Npj Microgravity, 2021, 7, 22.	3.7	5
4537	Comparison of Diazotrophic Composition and Distribution in the South China Sea and the Western Pacific Ocean. Biology, 2021, 10, 555.	2.8	4
4539	Response of fungal endophyte communities within Andropogon gerardii (Big bluestem) to nutrient addition and herbivore exclusion. Fungal Ecology, 2021, 51, 101043.	1.6	3
4540	Protein and Microbial Biomarkers in Sputum Discern Acute and Latent Tuberculosis in Investigation of Pastoral Ethiopian Cohort. Frontiers in Cellular and Infection Microbiology, 2021, 11, 595554.	3.9	5
4542	Effect of Aeration on Yeast Community Structure and Volatile Composition in Uninoculated Chardonnay Wines. Fermentation, 2021, 7, 97.	3.0	6
4543	Transmission of Seed and Soil Microbiota to Seedling. MSystems, 2021, 6, e0044621.	3.8	38
4544	Testing cophylogeny between coral reef invertebrates and their bacterial and archaeal symbionts. Molecular Ecology, 2021, 30, 3768-3782.	3.9	11
4546	Investigating the association between the urinary microbiome and bladder cancer: An exploratory study. Urologic Oncology: Seminars and Original Investigations, 2021, 39, 370.e9-370.e19.	1.6	36
4547	Microbial Profile Evaluation of Beef Steaks From Different Packaging and Retail Lighting Display Conditions. Meat and Muscle Biology, 2021, 5, .	1.9	3
4548	Specialized microbiomes facilitate natural rhizosphere microbiome interactions counteracting high salinity stress in plants. Environmental and Experimental Botany, 2021, 186, 104430.	4.2	28

#	Article	IF	CITATIONS
4549	Human encroachment into wildlife gut microbiomes. Communications Biology, 2021, 4, 800.	4.4	36
4550	Effect of condensed tannins on growth performance, intestinal immune capacity and bacterial microbiomes of <i>Lateolabrax japonicus</i> . Aquaculture Research, 2021, 52, 5321-5331.	1.8	21
4551	Soil Microbial Community Response to Permafrost Degradation in Palsa Fields of the Hudson Bay Lowlands: Implications for Greenhouse Gas Production in a Warming Climate. Global Biogeochemical Cycles, 2021, 35, e2021GB006954.	4.9	6
4552	Root-Associated Bacterial Community Shifts in Hydroponic Lettuce Cultured with Urine-Derived Fertilizer. Microorganisms, 2021, 9, 1326.	3.6	8
4553	The Effect of Biochar-Based Organic Amendments on the Structure of Soil Bacterial Community and Yield of Maize (Zea mays L.). Agronomy, 2021, 11, 1286.	3.0	11
4555	The surface bacterial community of an Australian kelp shows cross-continental variation and relative stability within regions. FEMS Microbiology Ecology, 2021, 97, .	2.7	13
4556	The Microbiota of Modified-Atmosphere-Packaged Cooked Charcuterie Products throughout Their Shelf-Life Period, as Revealed by a Complementary Combination of Culture-Dependent and Culture-Independent Analysis. Microorganisms, 2021, 9, 1223.	3.6	12
4557	Maternal Antibiotic Treatment Disrupts the Intestinal Microbiota and Intestinal Development in Neonatal Mice. Frontiers in Microbiology, 2021, 12, 684233.	3.5	8
4558	Effect of concentration and hydraulic reaction time on the removal of pharmaceutical compounds in a membrane bioreactor inoculated with activated sludge. Microbial Biotechnology, 2021, 14, 1707-1721.	4.2	16
4559	Exposure to traffic-related air pollution and bacterial diversity in the lower respiratory tract of children. PLoS ONE, 2021, 16, e0244341.	2.5	9
4560	Characterization of the microbiome of the invasive Asian toad in Madagascar across the expansion range and comparison with a native co-occurring species. PeerJ, 2021, 9, e11532.	2.0	7
4561	Phosphorus Availability Alters the Effect of Tree Girdling on the Diversity of Phosphorus Solubilizing Soil Bacterial Communities in Temperate Beech Forests. Frontiers in Forests and Global Change, 2021, 4, .	2.3	5
4562	Altered IgA Response to Gut Bacteria Is Associated with Childhood Asthma in Peru. Journal of Immunology, 2021, 207, 398-407.	0.8	5
4563	Exploring Viral Diversity in a Gypsum Karst Lake Ecosystem Using Targeted Single-Cell Genomics. Genes, 2021, 12, 886.	2.4	6
4564	Longitudinal Changes in Diet Cause Repeatable and Largely Reversible Shifts in Gut Microbial Communities of Laboratory Mice and Are Observed across Segments of the Entire Intestinal Tract. International Journal of Molecular Sciences, 2021, 22, 5981.	4.1	10
4565	Farnesol induces protection against murine CNS inflammatory demyelination and modifies gut microbiome. Clinical Immunology, 2022, 235, 108766.	3.2	13
4566	Decreased Abundance of <i>Akkermansia muciniphila</i> Leads to the Impairment of Insulin Secretion and Glucose Homeostasis in Lean Type 2 Diabetes. Advanced Science, 2021, 8, e2100536.	11,2	68
4567	The profile of the soil microbiota in the Cerrado is influenced by land use. Applied Microbiology and Biotechnology, 2021, 105, 4791-4803.	3.6	15

#	Article	IF	CITATIONS
4568	Effect of Fecal Microbiota Transplantation Combined With Mediterranean Diet on Insulin Sensitivity in Subjects With Metabolic Syndrome. Frontiers in Microbiology, 2021, 12, 662159.	3.5	22
4569	Gullies and Moraines Are Islands of Biodiversity in an Arid, Mountain Landscape, Asgard Range, Antarctica. Frontiers in Microbiology, 2021, 12, 654135.	3.5	6
4571	Comparative Genomic Insights Into the Taxonomic Classification, Diversity, and Secondary Metabolic Potentials of Kitasatospora, a Genus Closely Related to Streptomyces. Frontiers in Microbiology, 2021, 12, 683814.	3.5	11
4572	Longitudinal sampling of external mucosae in farmed European seabass reveals the impact of water temperature on bacterial dynamics. ISME Communications, $2021, 1, \dots$	4.2	10
4573	Taxonomic and Functional Variations Induced by an Overloading Event in Anaerobic Codigestion of Municipal Wastewater Sludge with Fats, Oils, and Grease. ACS ES&T Engineering, 2021, 1, 1205-1216.	7.6	5
4574	Reproducible Microbial Community Dynamics of Two Drinking Water Systems Treating Similar Source Waters. ACS ES&T Water, 2021, 1, 1617-1627.	4.6	8
4575	Structure and variation of root-associated bacterial communities of Cyperus rotundus L. in the contaminated soils around Pb/Zn mine sites. Environmental Science and Pollution Research, 2021, 28, 58523-58535.	5.3	13
4576	Impact of dietary carbohydrate type and protein–carbohydrate interaction on metabolic health. Nature Metabolism, 2021, 3, 810-828.	11.9	42
4577	Directional Selection of Microbial Community Reduces Propionate Accumulation in Glycerol and Glucose Anaerobic Bioconversion Under Elevated pCO2. Frontiers in Microbiology, 2021, 12, 675763.	3.5	12
4579	Root-associated (rhizosphere and endosphere) microbiomes of the Miscanthus sinensis and their response to the heavy metal contamination. Journal of Environmental Sciences, 2021, 104, 387-398.	6.1	53
4580	The impact of propagule pressure on whole community invasions in biomethane-producing communities. IScience, 2021, 24, 102659.	4.1	7
4581	Diversity and substrate-specificity of green algae and other micro-eukaryotes colonizing amphibian clutches in Germany, revealed by DNA metabarcoding. Die Naturwissenschaften, 2021, 108, 29.	1.6	6
4582	Environment and host-related factors modulate gut and carapace bacterial diversity of the invasive red swamp crayfish (Procambarus clarkii). Hydrobiologia, 2021, 848, 4045-4057.	2.0	8
4583	Effects of Lumacaftor–Ivacaftor on Lung Clearance Index, Magnetic Resonance Imaging, and Airway Microbiome in Phe508del Homozygous Patients with Cystic Fibrosis. Annals of the American Thoracic Society, 2021, 18, 971-980.	3.2	65
4584	Plant phenology influences rhizosphere microbial community and is accelerated by serpentine microorganisms in <i>Plantago erecta</i> . FEMS Microbiology Ecology, 2021, 97, .	2.7	5
4586	The response of soil microbial communities to the infection of kauri (<i>Agathis australis</i>) seedlings with <i>Phytophthora agathidicida</i>). Forest Pathology, 2021, 51, e12708.	1.1	0
4587	Salivary Microbiome Diversity in Kuwaiti Adolescents with Varied Body Mass Index—A Pilot Study. Microorganisms, 2021, 9, 1222.	3.6	5
4588	Bacterial and Viral Respiratory Tract Microbiota and Host Characteristics in Adults With Lower Respiratory Tract Infections: A Case-Control Study. Clinical Infectious Diseases, 2022, 74, 776-784.	5.8	14

#	Article	IF	CITATIONS
4589	Detection of cell-free microbial DNA using a contaminant-controlled analysis framework. Genome Biology, 2021, 22, 187.	8.8	22
4590	Whole-Genome Metagenomic Analysis of the Gut Microbiome in HIV-1-Infected Individuals on Antiretroviral Therapy. Frontiers in Microbiology, 2021, 12, 667718.	3.5	15
4591	Soil, senescence and exudate utilisation: characterisation of theÂParagon var. spring bread wheat root microbiome. Environmental Microbiomes, 2021, 16, 12.	5.0	19
4592	Microbial exposures in moistureâ€damaged schools and associations with respiratory symptoms in students: A multiâ€country environmental exposure study. Indoor Air, 2021, 31, 1952-1966.	4.3	13
4593	Larval Diet Abundance Influences Size and Composition of the Midgut Microbiota of Aedes aegypti Mosquitoes. Frontiers in Microbiology, 2021, 12, 645362.	3.5	19
4594	Soil Reservoir Dynamics of Ophidiomyces ophidiicola, the Causative Agent of Snake Fungal Disease. Journal of Fungi (Basel, Switzerland), 2021, 7, 461.	3.5	15
4595	Investigating the Effects of a Phytobiotics-Based Product on the Fecal Bacterial Microbiome of Weaned Pigs. Animals, 2021, 11, 1950.	2.3	8
4596	Probiotic Yeasts and Vibrio anguillarum Infection Modify the Microbiome of Zebrafish Larvae. Frontiers in Microbiology, 2021, 12, 647977.	3.5	13
4597	Human variation in gingival inflammation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118 , .	7.1	25
4598	Feeding diversified protein sources exacerbates hepatic insulin resistance via increased gut microbial branched-chain fatty acids and mTORC1 signaling in obese mice. Nature Communications, 2021, 12, 3377.	12.8	42
4599	On pickles: biological and sociocultural links between fermented foods and the human gut microbiome. Journal of Ethnobiology and Ethnomedicine, 2021, 17, 39.	2.6	8
4600	Maternal Microbiota Transfer Programs Offspring Eating Behavior. Frontiers in Microbiology, 2021, 12, 672224.	3.5	9
4601	The Equine Faecal Microbiota of Healthy Horses and Ponies in The Netherlands: Impact of Host and Environmental Factors. Animals, 2021, 11, 1762.	2.3	19
4602	Validity and safety of ID-JPL934 in lower gastrointestinal symptom improvement. Scientific Reports, 2021, 11, 13046.	3.3	6
4603	Fecal microbiota transfer for refractory intestinal graftâ€versusâ€host disease â€" Experience from two German tertiary centers. European Journal of Haematology, 2021, 107, 229-245.	2.2	20
4604	The microbiome mediates the interaction between predation and heavy metals. Science of the Total Environment, 2021, 775, 145144.	8.0	5
4605	The infant gut resistome associates withÂE. coli, environmental exposures, gut microbiome maturity, and asthma-associated bacterial composition. Cell Host and Microbe, 2021, 29, 975-987.e4.	11.0	64
4606	Application of manure from cattle administered antibiotics has sustained multi-year impacts on soil resistome and microbial community structure. Soil Biology and Biochemistry, 2021, 157, 108252.	8.8	39

#	Article	IF	CITATIONS
4607	Characterization of Supragingival Plaque and Oral Swab Microbiomes in Children With Severe Early Childhood Caries. Frontiers in Microbiology, 2021, 12, 683685.	3.5	19
4608	Climate warming dominates over plant genotype in shaping the seasonal trajectory of foliar fungal communities on oak. New Phytologist, 2021, 231, 1770-1783.	7.3	31
4609	A phylogenetic framework to investigate the microsporidian communities through metabarcoding and its application to lake ecosystems. Environmental Microbiology, 2021, 23, 4344-4359.	3.8	22
4612	A globally ubiquitous symbiont can drive experimental host evolution. Molecular Ecology, 2021, 30, 3882-3892.	3.9	6
4613	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. Nature Communications, 2021, 12, 3562.	12.8	30
4614	Coupled DNA-labeling and sequencing approach enables the detection of viable-but-non-culturable Vibrio spp. in irrigation water sources in the Chesapeake Bay watershed. Environmental Microbiomes, 2021, 16, 13.	5.0	6
4615	Defining the resilience of the human salivary microbiota by a 520-day longitudinal study in a confined environment: the Mars500 mission. Microbiome, 2021, 9, 152.	11.1	5
4617	Biogeochemical Mobility of Contaminants from a Replica Radioactive Waste Trench in Response to Rainfall-Induced Redox Oscillations. Environmental Science & Environmental Science & 2021, 55, 8793-8805.	10.0	9
4618	Spatial abundance and distribution of picocyanobacterial communities in two contrasting lakes revealed using environmental DNA metabarcoding. FEMS Microbiology Ecology, 2021, 97, .	2.7	7
4619	Gut microbiota signature in treatment-na \tilde{A} -ve attention-deficit/hyperactivity disorder. Translational Psychiatry, 2021, 11, 382.	4.8	25
4620	Valorization of pulp and paper industry wastewater using sludge enriched with nitrogenâ€fixing bacteria. Water Environment Research, 2021, 93, 1734-1747.	2.7	5
4622	Gut Microbiota Dynamics in Natural Populations of Pintomyia evansi under Experimental Infection with Leishmania infantum. Microorganisms, 2021, 9, 1214.	3.6	6
4623	Changes in Digestive Microbiota, Rumen Fermentations and Oxidative Stress around Parturition Are Alleviated by Live Yeast Feed Supplementation to Gestating Ewes. Journal of Fungi (Basel, Switzerland), 2021, 7, 447.	3. 5	8
4624	Characterizing the Effects of Calcium and Prebiotic Fiber on Human Gut Microbiota Composition and Function Using a Randomized Crossover Design—A Feasibility Study. Nutrients, 2021, 13, 1937.	4.1	10
4625	Ocular Surface Microbiota in Contact Lens Users and Contact-Lens-Associated Bacterial Keratitis. Vision (Switzerland), 2021, 5, 27.	1.2	10
4626	Tannery Wastewater Recalcitrant Compounds Foster the Selection of Fungi in Non-Sterile Conditions: A Pilot Scale Long-Term Test. International Journal of Environmental Research and Public Health, 2021, 18, 6348.	2.6	5
4627	Effect of sequentially fed high protein, hydrolyzed protein, and high fiber diets on the fecal microbiota of healthy dogs: a cross-over study. Animal Microbiome, 2021, 3, 42.	3.8	9
4628	Vertically transmitted microbiome protects eggs from fungal infection and egg failure. Animal Microbiome, 2021, 3, 43.	3.8	23

#	Article	IF	CITATIONS
4629	Metabarcoding as a tool to examine cryptic algae in the diets of two common grazing surgeonfishes, <i>Acanthurustriostegus</i> and <i>A</i> . <i>nigrofuscus</i> . Environmental DNA, 2022, 4, 135-146.	5 . 8	8
4630	Composition and Associations of the Infant Gut Fungal Microbiota with Environmental Factors and Childhood Allergic Outcomes. MBio, 2021, 12, e0339620.	4.1	31
4632	High-throughput 16S rRNA gene sequencing of the microbial community associated with palm oil mill effluents of two oil processing systems. Scientific Reports, 2021, 11, 13232.	3.3	4
4633	Unravelling the Importance of Diazotrophy in Corals $\hat{a} \in \text{``Combined Assessment of Nitrogen}$ Assimilation, Diazotrophic Community and Natural Stable Isotope Signatures. Frontiers in Microbiology, 2021, 12, 631244.	3.5	8
4634	Prospective Observational Study of Bisphosphonate-Related Osteonecrosis of the Jaw in Multiple Myeloma: Microbiota Profiling and Cytokine Expression. Frontiers in Oncology, 2021, 11, 704722.	2.8	7
4637	Structureâ€Specific Fermentation of Galactoâ€Oligosaccharides, Isomaltoâ€Oligosaccharides and Isomalto/Maltoâ€Polysaccharides by Infant Fecal Microbiota and Impact on Dendritic Cell Cytokine Responses. Molecular Nutrition and Food Research, 2021, 65, e2001077.	3.3	13
4638	Soil Buffering Capacity Can Be Used To Optimize Biostimulation of Psychrotrophic Hydrocarbon Remediation. Environmental Science & Environmental Scienc	10.0	4
4639	mbImpute: an accurate and robust imputation method for microbiome data. Genome Biology, 2021, 22, 192.	8.8	23
4640	Profiling temporal dynamics of acetogenic communities in anaerobic digesters using next-generation sequencing and T-RFLP. Scientific Reports, 2021, 11, 13298.	3.3	12
4641	Staphylococcus aureus ventilator-associated pneumonia in patients with COVID-19: clinical features and potential inference with lung dysbiosis. Critical Care, 2021, 25, 197.	5 . 8	41
4642	No Durable Impact of COVID-19 on Intestinal Disease Activity in Subjects With IBD. Clinical Gastroenterology and Hepatology, 2021, 19, 2312-2314.e3.	4.4	12
4643	Oral Ferric Maltol Does Not Adversely Affect the Intestinal Microbiome of Patients or Mice, but Ferrous Sulphate Does. Nutrients, 2021, 13, 2269.	4.1	10
4647	Succession patterns of the bacterial community in poultry litter after bird removal and sodium bisulfate application. Journal of Environmental Quality, 2021, 50, 923-933.	2.0	4
4648	Recommendations for interpreting zooplankton metabarcoding and integrating molecular methods with morphological analyses. ICES Journal of Marine Science, 2021, 78, 3387-3396.	2.5	12
4649	Climatic Zone and Soil Properties Determine the Biodiversity of the Soil Bacterial Communities Associated to Native Plants from Desert Areas of North-Central Algeria. Microorganisms, 2021, 9, 1359.	3.6	18
4650	Effect of mupirocin for Staphylococcus aureus decolonization on the microbiome of the nose and throat in community and nursing home dwelling adults. PLoS ONE, 2021, 16, e0252004.	2.5	4
4652	Consistency of Bacterial Communities in a Parasitic Worm: Variation Throughout the Life Cycle and Across Geographic Space. Microbial Ecology, 2022, 83, 724-738.	2.8	8
4653	Fungal diversity and occurrence of mycotoxin producing fungi in tropical vineyards. World Journal of Microbiology and Biotechnology, 2021, 37, 112.	3.6	7

#	Article	IF	CITATIONS
4654	Microbiota long-term dynamics and prediction of acute graft-versus-host disease in pediatric allogeneic stem cell transplantation. Microbiome, 2021, 9, 148.	11.1	35
4655	The Plastid-Localized AtFtsHi3 Pseudo-Protease of Arabidopsis thaliana Has an Impact on Plant Growth and Drought Tolerance. Frontiers in Plant Science, 2021, 12, 694727.	3.6	5
4656	Cross-Sectional Variations in Structure and Function of Coral Reef Microbiome With Local Anthropogenic Impacts on the Kenyan Coast of the Indian Ocean. Frontiers in Microbiology, 2021, 12, 673128.	3.5	4
4657	Microbial Phosphorus Mobilization Strategies Across a Natural Nutrient Limitation Gradient and Evidence for Linkage With Iron Solubilization Traits. Frontiers in Microbiology, 2021, 12, 572212.	3.5	8
4658	Longitudinal Survey of Fecal Microbiota in Healthy Dogs Administered a Commercial Probiotic. Frontiers in Veterinary Science, 2021, 8, 664318.	2.2	4
4659	Associations between urinary 3-indoxyl sulfate, a gut microbiome-derived biomarker, and patient outcomes after intensive care unit admission. Journal of Critical Care, 2021, 63, 15-21.	2.2	4
4660	A pilot experiment to assess the efficiency of pharmaceutical plant wastewater treatment and the decreasing effluent toxicity to periphytic biofilms. Journal of Hazardous Materials, 2021, 411, 125121.	12.4	11
4661	Individual diet specialization drives population trophic niche responses to environmental change in a predator fish population. Food Webs, 2021, 27, e00193.	1.2	12
4662	Bacterial transfer from Pristionchus entomophagus nematodes to the invasive ant Myrmica rubra and the potential for colony mortality in coastal Maine. IScience, 2021, 24, 102663.	4.1	4
4663	Seasonal Dynamics Are the Major Driver of Microbial Diversity and Composition in Intensive Freshwater Aquaculture. Frontiers in Microbiology, 2021, 12, 679743.	3. 5	11
4664	Dietary fat and low fiber in purified diets differently impact the gut-liver axis to promote obesity-linked metabolic impairments. American Journal of Physiology - Renal Physiology, 2021, 320, G1014-G1033.	3.4	12
4665	A Multiomic Approach to Investigate the Effects of a Weight Loss Program on the Intestinal Health of Overweight Horses. Frontiers in Veterinary Science, 2021, 8, 668120.	2.2	7
4666	Seasonal Prokaryotic Community Linkages Between Surface and Deep Ocean Water. Frontiers in Marine Science, 2021, 8, .	2.5	10
4667	Assembly of the <i>Populus</i> Microbiome Is Temporally Dynamic and Determined by Selective and Stochastic Factors. MSphere, 2021, 6, e0131620.	2.9	25
4669	Insights into Autotrophic Activities and Carbon Flow in Iron-Rich Pelagic Aggregates (Iron Snow). Microorganisms, 2021, 9, 1368.	3.6	2
4671	Exploring the Potential of Micrococcus luteus Culture Supernatant With Resuscitation-Promoting Factor for Enhancing the Culturability of Soil Bacteria. Frontiers in Microbiology, 2021, 12, 685263.	3.5	12
4672	Interkingdom Gut Microbiome and Resistome of the Cockroach <i>Blattella germanica</i> . MSystems, 2021, 6, .	3.8	13
4674	Longâ€ŧerm nitrogen addition does not sustain host tree stem radial growth but doubles the abundance of highâ€biomass ectomycorrhizal fungi. Global Change Biology, 2021, 27, 4125-4138.	9.5	23

#	Article	IF	Citations
4675	Cross-Hemisphere Study Reveals Geographically Ubiquitous, Plastic-Specific Bacteria Emerging from the Rare and Unexplored Biosphere. MSphere, 2021, 6, e0085120.	2.9	20
4678	Pollen DNA metabarcoding identifies regional provenance and high plant diversity in Australian honey. Ecology and Evolution, 2021, 11, 8683-8698.	1.9	22
4679	Nematode fauna associated with freshwater microbialites in Bacalar Lake, Quintana Roo, Mexico. Limnology, 2021, 22, 347-355.	1.5	2
4680	The Selective Advantage of the lac Operon for Escherichia coli Is Conditional on Diet and Microbiota Composition. Frontiers in Microbiology, 2021, 12, 709259.	3.5	6
4681	Using Plate-Wash PCR and High-Throughput Sequencing to Measure Cultivated Diversity for Natural Product Discovery Efforts. Frontiers in Microbiology, 2021, 12, 675798.	3.5	4
4683	Impact of gut fungal and bacterial communities on the outcome of allogeneic hematopoietic cell transplantation. Mucosal Immunology, 2021, 14, 1127-1132.	6.0	9
4684	16S rRNA Gene Metabarcoding Indicates Species-Characteristic Microbiomes in Deep-Sea Benthic Foraminifera. Frontiers in Microbiology, 2021, 12, 694406.	3. 5	2
4685	Microbiome pattern of Lucilia sericata (Meigen) (Diptera: Calliphoridae) and feeding substrate in the presence of the foodborne pathogen Salmonella enterica. Scientific Reports, 2021, 11, 15296.	3.3	4
4686	Rapid ecosystem-scale consequences of acute deoxygenation on a Caribbean coral reef. Nature Communications, 2021, 12, 4522.	12.8	42
4688	Addition of Activated Carbon into a Cattle Diet to Mitigate GHG Emissions and Improve Production. Sustainability, 2021, 13, 8254.	3.2	7
4689	Sustainable plant-based diets promote rainbow trout gut microbiota richness and do not alter resistance to bacterial infection. Animal Microbiome, 2021, 3, 47.	3.8	18
4690	Investigation into the bacterial diversity of sediment samples obtained from Berg River, Western Cape, South Africa. Folia Microbiologica, 2021, 66, 931-947.	2.3	1
4691	Captivity reduces diversity and shifts composition of the Brown Kiwi microbiome. Animal Microbiome, 2021, 3, 48.	3.8	36
4692	Diet-induced microbiome shifts of sympatric overwintering birds. Applied Microbiology and Biotechnology, 2021, 105, 5993-6005.	3. 6	17
4694	Phosphate Availability Modulates Root Exudate Composition and Rhizosphere Microbial Community in a Teosinte and a Modern Maize Cultivar. Phytobiomes Journal, 2022, 6, 83-94.	2.7	16
4695	Nitrogen Fertilization and Native C4 Grass Species Alter Abundance, Activity, and Diversity of Soil Diazotrophic Communities. Frontiers in Microbiology, 2021, 12, 675693.	3.5	13
4696	A Comparison of Primers in 16S rRNA Gene Surveys of Bacteria and Archaea from Volcanic Caves. Geomicrobiology Journal, 2021, 38, 741-754.	2.0	8
4698	Exploring the Individual Bacterial Microbiota of Questing Ixodes ricinus Nymphs. Microorganisms, 2021, 9, 1526.	3.6	2

#	Article	IF	CITATIONS
4699	Digital Droplet PCR-Based Environmental DNA Tool for Monitoring Cryptocaryon irritans in a Marine Fish Farm from Hong Kong. Diversity, 2021, 13, 350.	1.7	7
4701	The infant gut resistome is associated with E. coli and early-life exposures. BMC Microbiology, 2021, 21, 201.	3.3	30
4702	Reshaping of Gut Microbiota in Gilthead Sea Bream Fed Microbial and Processed Animal Proteins as the Main Dietary Protein Source. Frontiers in Marine Science, 2021, 8, .	2.5	18
4703	Periodontitis induces endothelial dysfunction in mice. Scientific Reports, 2021, 11, 14993.	3.3	9
4704	Temporal Comparison of Microbial Community Structure in an Australian Winery. Fermentation, 2021, 7, 134.	3.0	2
4705	Patterns of the fecal microbiota in the Juan FernÃ;ndez fur seal (<i>Arctocephalus philippii</i>). MicrobiologyOpen, 2021, 10, e1215.	3.0	11
4706	Metagenomic and metatranscriptomic analysis reveals enrichment for <scp>xenobioticâ€degrading</scp> bacterial specialists and <scp>xenobioticâ€degrading</scp> genes in a Canadian Prairie <scp>twoâ€eell</scp> biobed system. Environmental Microbiology Reports, 2021, 13, 720-727.	2.4	11
4707	Temporal and spatial variation in bacterial communities on uniform substrates in nonâ€wadeable rivers. Environmental DNA, 2021, 3, 1023-1034.	5.8	1
4708	Tree species mixing causes a shift in fineâ€root soil exploitation strategies across European forests. Functional Ecology, 2021, 35, 1886-1902.	3.6	19
4709	The bacterial and fungal nest microbiomes in populations of the social spider Stegodyphus dumicola. Systematic and Applied Microbiology, 2021, 44, 126222.	2.8	12
4710	Time outweighs the effect of host developmental stage on microbial community composition. FEMS Microbiology Ecology, 2021, 97, .	2.7	13
4711	eDNA metabarcoding illuminates species diversity and composition of three phyla (chordata, mollusca) Tj ETQq1	l 0.78431 2.6	4 ₁₈ BT /Ove
4712	16S rRNA Gene Amplicon Sequencing Data from Flooded Rice Paddy Mesocosms Treated with Different Silicon-Rich Soil Amendments. Microbiology Resource Announcements, 2021, 10, e0017821.	0.6	3
4713	Going Beyond Soil Conservation with the Use of Cover Crops in Mediterranean Sloping Olive Orchards. Agronomy, 2021, 11, 1387.	3.0	4
4714	Environmental biomonitoring of reef fish community structure with eDNA metabarcoding in the Coral Triangle. Environmental Biology of Fishes, 2021, 104, 887-903.	1.0	19
4715	Oily Bilge Wastes Harbor a Set of Persistent Hydrocarbonoclastic Bacteria Accompanied by a Variable alkB Gene Composition in Marine Vessel Samples from Southwestern Atlantic Port of Mar del Plata, Argentina. Water, Air, and Soil Pollution, 2021, 232, 1.	2.4	4
4716	Fecal sample collection methods and time of day impact microbiome composition and short chain fatty acid concentrations. Scientific Reports, 2021, 11, 13964.	3.3	30
4717	Coral-associated nitrogen fixation rates and diazotrophic diversity on a nutrient-replete equatorial reef. ISME Journal, 2022, 16, 233-246.	9.8	29

#	Article	IF	CITATIONS
4720	Phytohormones selectively affect plant parasitic nematodes associated with Arabidopsis roots. New Phytologist, 2021, 232, 1272-1285.	7.3	11
4721	Effects of truffle inoculation on a nursery culture substrate environment and seedling ofÂCarya illinoinensis. Fungal Biology, 2021, 125, 576-584.	2.5	1
4722	Extended Ecological Restoration of Bacterial Communities in the Godavari River During the COVID-19 Lockdown Period: a Spatiotemporal Meta-analysis. Microbial Ecology, 2021, 82, 365-376.	2.8	11
4724	Anxiety-like behavior and intestinal microbiota changes as strain-and sex-dependent sequelae of mild food allergy in mouse models of cow's milk allergy. Brain, Behavior, and Immunity, 2021, 95, 122-141.	4.1	8
4726	Responses of cucumber (<i>Cucumis sativus</i> L.) rhizosphere microbial community to some agronomic management practices. FEMS Microbiology Ecology, 2021, 97, .	2.7	4
4727	Temporal Variation in the Microbiome of Tropical and Temperate Octocorals. Microbial Ecology, 2022, 83, 1073-1087.	2.8	8
4728	Ubiquitousness of Haloferax and Carotenoid Producing Genes in Arabian Sea Coastal Biosystems of India. Marine Drugs, 2021, 19, 442.	4.6	5
4729	Evaluation of Two Amendments (Biochar and Acid Mine Drainage Sludge) on Arsenic Contaminated Soil Using Chemical, Biological, and Ecological Assessments. Materials, 2021, 14, 4111.	2.9	0
4730	Occurrence and dynamics of potentially pathogenic vibrios in the wet-dry tropics of northern Australia. Marine Environmental Research, 2021, 169, 105405.	2.5	6
4731	Impact of Long-Term Manure and Sewage Sludge Application to Soil as Organic Fertilizer on the Incidence of Pathogenic Microorganisms and Antibiotic Resistance Genes. Agronomy, 2021, 11, 1423.	3.0	6
4732	Oral Vaccination Reduces the Effects of Lawsonia intracellularis Challenge on the Swine Small and Large Intestine Microbiome. Frontiers in Veterinary Science, 2021, 8, 692521.	2.2	2
4734	Bacterial diversity and community structure along the glacier foreland of Midtre Lovénbreen, Svalbard, Arctic. Ecological Indicators, 2021, 126, 107704.	6.3	25
4735	Stress-related changes in the gut microbiome after trauma. Journal of Trauma and Acute Care Surgery, 2021, 91, 192-199.	2.1	9
4736	Infants' First Solid Foods: Impact on Gut Microbiota Development in Two Intercontinental Cohorts. Nutrients, 2021, 13, 2639.	4.1	22
4737	Silica/Lignin Carrier as a Factor Increasing the Process Performance and Genetic Diversity of Microbial Communities in Laboratory-Scale Anaerobic Digesters. Energies, 2021, 14, 4429.	3.1	9
4738	Contribution of microbial photosynthesis to peatland carbon uptake along a latitudinal gradient. Journal of Ecology, 2021, 109, 3424-3441.	4.0	10
4739	Microzooplankton diversity and potential role in carbon cycling of contrasting Southern Ocean productivity regimes. Journal of Marine Systems, 2021, 219, 103531.	2.1	9
4740	Field evaluation of the gut microbiome composition of pre-school and school-aged children in Tha Song Yang, Thailand, following oral MDA for STH infections. PLoS Neglected Tropical Diseases, 2021, 15, e0009597.	3.0	9

#	Article	IF	CITATIONS
4741	Gut Microbiome Signatures of Risk and Prodromal Markers of Parkinson Disease. Annals of Neurology, 2021, 90, E1-E12.	5. 3	41
4742	Temporal differences in microbial composition of Époisses cheese rinds during ripening and storage. Journal of Dairy Science, 2021, 104, 7500-7508.	3.4	11
4744	Seasonal niche differentiation among closely related marine bacteria. ISME Journal, 2022, 16, 178-189.	9.8	36
4746	Circular utilization of food waste to biochar enhances thermophilic co-digestion performance. Bioresource Technology, 2021, 332, 125130.	9.6	13
4748	Comparison of Preservation and Extraction Methods on Five Taxonomically Disparate Coral Microbiomes. Frontiers in Marine Science, 2021, 8, .	2.5	5
4749	Accessing Dietary Effects on the Rumen Microbiome: Different Sequencing Methods Tell Different Stories. Veterinary Sciences, 2021, 8, 138.	1.7	3
4750	A Pilot Study on the Microbiome of Amblyomma hebraeum Tick Stages Infected and Non-Infected with Rickettsia africae. Pathogens, 2021, 10, 941.	2.8	3
4751	Shades of grey: host phenotype dependent effect of urbanization on the bacterial microbiome of a wild mammal. Animal Microbiome, 2021, 3, 46.	3.8	10
4752	Holocene life and microbiome profiling in ancient tropical Lake Chalco, Mexico. Scientific Reports, 2021, 11, 13848.	3.3	8
4753	Variations in the oral microbiome are associated with depression in young adults. Scientific Reports, 2021, 11, 15009.	3.3	44
4754	Nutrient load acts as a driver of gut microbiota load, community composition and metabolic functionality in the simulator of the human intestinal microbial ecosystem. FEMS Microbiology Ecology, 2021, 97, .	2.7	7
4755	Links between fecal microbiota and the response to vaccination against influenza A virus in pigs. Npj Vaccines, 2021, 6, 92.	6.0	13
4756	Effects of rearing system and microbial inoculation on black soldier fly larvae growth and microbiota when reared on agri-food by-products. Journal of Insects As Food and Feed, 2022, 8, 113-127.	3.9	8
4757	The microbial metabolite p-Cresol induces autistic-like behaviors in mice by remodeling the gut microbiota. Microbiome, 2021, 9, 157.	11.1	78
4758	Molecular characterization of the bacterial communities present in sheep's milk and cheese produced in South Brazilian Region via 16S rRNA gene metabarcoding sequencing. LWT - Food Science and Technology, 2021, 147, 111579.	5.2	11
4759	Tree-aggregated predictive modeling of microbiome data. Scientific Reports, 2021, 11, 14505.	3.3	13
4760	Competition and community succession link N transformation and greenhouse gas emissions in urine patches. Science of the Total Environment, 2021, 779, 146318.	8.0	6
4763	Influence of Estuarine Water on the Microbial Community Structure of Patagonian Fjords. Frontiers in Marine Science, 2021, 8, .	2.5	5

#	Article	IF	CITATIONS
4764	Monitoring Infection and Antibiotic Treatment in the Skin Microbiota of Farmed European Seabass (Dicentrarchus Labrax) Fingerlings. Microbial Ecology, 2022, 83, 789-797.	2.8	4
4766	Earthworms drastically change fungal and bacterial communities during vermicomposting of sewage sludge. Scientific Reports, 2021, 11, 15556.	3.3	32
4767	Changes in Skin and Nasal Microbiome and Staphylococcal Species Following Treatment of Atopic Dermatitis with Dupilumab. Microorganisms, 2021, 9, 1487.	3.6	29
4768	16S and 18S rRNA Gene Metabarcoding Provide Congruent Information on the Responses of Sediment Communities to Eutrophication. Frontiers in Marine Science, 2021, 8, .	2.5	6
4769	Microbiome diversity and host immune functions influence survivorship of sponge holobionts under future ocean conditions. ISME Journal, 2022, 16, 58-67.	9.8	27
4770	A Standard Scale to Measure Equine Keeper Status and the Effect of Metabolic Tendency on Gut Microbiome Structure. Animals, 2021, 11, 1975.	2.3	0
4771	Profiles and interrelationships of functional soil microbiomes involved in phosphorus cycling in diversified agricultural landâ€use systems. Food and Energy Security, 2021, 10, e315.	4.3	2
4772	Microplastics accumulate fungal pathogens in terrestrial ecosystems. Scientific Reports, 2021, 11, 13214.	3.3	95
4773	The role of plant–pollinator interactions in structuring nectar microbial communities. Journal of Ecology, 2021, 109, 3379-3395.	4.0	22
4774	Low dose antibiotic ingestion potentiates systemic and microbiome changes induced by silver nanoparticles. NanoImpact, 2021, 23, 100343.	4.5	1
4777	Processing of leafy vegetables matters: Damage and microbial community structure from field to bag. Food Control, 2021, 125, 107894.	5.5	13
4778	Pathogen Challenge and Dietary Shift Alter Microbiota Composition and Activity in a Mucin-Associated in vitro Model of the Piglet Colon (MPigut-IVM) Simulating Weaning Transition. Frontiers in Microbiology, 2021, 12, 703421.	3.5	8
4779	Seeding as a start-up strategy for improving the acclimation of freshwater nitrifying bioreactors to salinity stress. Aquaculture, 2021, 540, 736663.	3.5	11
4780	Deciphering the Role of Skin Surface Microbiome in Skin Health: An Integrative Multiomics Approach Reveals Three Distinct Metaboliteâ€'Microbe Clusters. Journal of Investigative Dermatology, 2022, 142, 469-479.e5.	0.7	30
4781	"More Guts Than Brains?â€â€"The Role of Gut Microbiota in Idiopathic Intracranial Hypertension. Journal of Neuro-Ophthalmology, 2022, 42, e70-e77.	0.8	2
4782	Effects of dietary supplementation with a laminarin-rich extract on the growth performance and gastrointestinal health in broilers. Poultry Science, 2021, 100, 101179.	3.4	14
4783	Spatial and Temporal Variations in Pigment and Species Compositions of Snow Algae on Mt. Tateyama in Toyama Prefecture, Japan. Frontiers in Plant Science, 2021, 12, 689119.	3.6	12
4784	Environmentally enriched housing conditions affect pig welfare, immune system and gut microbiota in early life. Animal Microbiome, 2021, 3, 52.	3.8	24

#	Article	IF	Citations
4785	A Temporally Dynamic Gut Microbiome in Atlantic Salmon During Freshwater Recirculating Aquaculture System (RAS) Production and Post-seawater Transfer. Frontiers in Marine Science, 2021, 8, .	2.5	20
4787	Manipulating exudate composition from root apices shapes the microbiome throughout the root system. Plant Physiology, 2021, 187, 2279-2295.	4.8	44
4788	Microbial metabolism and adaptations in <i>Atribacteria</i> i>â€dominated methane hydrate sediments. Environmental Microbiology, 2021, 23, 4646-4660.	3.8	20
4789	Environmental DNA reveals the fine-grained and hierarchical spatial structure of kelp forest fish communities. Scientific Reports, 2021, 11, 14439.	3.3	22
4790	Evaluation of Three Prokaryote Primers for Identification of Prokaryote Community Structure and Their Abode Preference in Three Distinct Wetland Ecosystems. Frontiers in Microbiology, 2021, 12, 643945.	3.5	4
4791	Evaluating extraction methods to study canine urine microbiota. PLoS ONE, 2021, 16, e0253989.	2.5	11
4792	Unraveling the bacterial community composition across aquatic sediments in the Southwestern coast of India by employing high-throughput 16S rRNA gene sequencing. Regional Studies in Marine Science, 2021, 46, 101890.	0.7	4
4793	Microbial Diversity and Activity During the Biodegradation in Seawater of Various Substitutes to Conventional Plastic Cotton Swab Sticks. Frontiers in Microbiology, 2021, 12, 604395.	3.5	28
4794	Specific Detection of Coral-Associated Ruegeria, a Potential Probiotic Bacterium, in Corals and Subtropical Seawater. Marine Biotechnology, 2021, 23, 576-589.	2.4	10
4795	Unstable regulatory T cells, enriched for na \tilde{A} -ve and Nrp1 <code>^{neg}</code> cells, are purged after fate challenge. Science Immunology, 2021, 6, .	11.9	13
4796	Using a next-generation sequencing approach to DNA metabarcoding for identification of adulteration and potential sources of mercury in commercial cat and dog foods. Science of the Total Environment, 2021, 778, 146102.	8.0	4
4797	Geographic differences in gut microbiota composition impact susceptibility to enteric infection. Cell Reports, 2021, 36, 109457.	6.4	33
4798	AÂMetatranscriptomicsÂSurvey of Microbial Diversity on Surfaces Post-Intervention ofÂcleanSURFACES® Technology in an Intensive Care Unit. Frontiers in Cellular and Infection Microbiology, 2021, 11, 705593.	3.9	3
4799	Isolation and Characterization of Pseudomonas chlororaphis Strain ST9; Rhizomicrobiota and in Planta Studies. Plants, 2021, 10, 1466.	3.5	7
4800	Structure of rhizospheric microbial community and N cycling functional gene shifts with reduced N input in sugarcane-soybean intercropping in South China. Agriculture, Ecosystems and Environment, 2021, 314, 107413.	5.3	19
4801	Southwestern Bats and Their External Bacteria. Western North American Naturalist, 2021, 81, .	0.4	1
4802	Function-adaptive clustered nanoparticles reverse Streptococcus mutans dental biofilm and maintain microbiota balance. Communications Biology, 2021, 4, 846.	4.4	13
4803	Nutritional and ecological perspectives of the interrelationships between diet and the gut microbiome in multiple sclerosis: Insights from marmosets. IScience, 2021, 24, 102709.	4.1	9

#	Article	IF	Citations
4804	Production and diversity of microorganisms associated with sinking particles in the subtropical North Pacific Ocean. Limnology and Oceanography, 2021, 66, 3255-3270.	3.1	12
4805	Probiotics impact the antibiotic resistance gene reservoir along the human GI tract in a person-specific and antibiotic-dependent manner. Nature Microbiology, 2021, 6, 1043-1054.	13.3	109
4806	microViz: an R package for microbiome data visualization and statistics. Journal of Open Source Software, 2021, 6, 3201.	4.6	101
4807	Simultaneous nitrification-denitrification (SND) using a thermoplastic gel as support: pollutants removal and microbial community in a pilot-scale biofilm membrane bioreactor. Environmental Technology (United Kingdom), 2022, 43, 4411-4425.	2.2	11
4810	Comparative analysis of the bronchoalveolar microbiome in Portuguese patients with different chronic lung disorders. Scientific Reports, 2021, 11, 15042.	3.3	5
4812	Strong host-specific selection and over-dominance characterize arbuscular mycorrhizal fungal root colonizers of coastal sand dune plants of the Mediterranean region. FEMS Microbiology Ecology, 2021, 97, .	2.7	7
4813	Clinically Healthy Human Gingival Tissues Show Significant Inter-individual Variability in GCF Chemokine Expression and Subgingival Plaque Microbial Composition. Frontiers in Oral Health, 2021, 2, 689475.	3.0	7
4814	Native AMF Communities in an Italian Vineyard at Two Different Phenological Stages of Vitis vinifera. Frontiers in Microbiology, 2021, 12, 676610.	3.5	3
4815	The mycobiome of Pocillopora acuta in Singapore. Coral Reefs, 2021, 40, 1419-1427.	2.2	11
4816	Landscape analyses using eDNA metabarcoding and Earth observation predict community biodiversity in California. Ecological Applications, 2021, 31, e02379.	3.8	23
4817	Land use and season drive changes in soil microbial communities and related functions in agricultural soils. Environmental DNA, 2021, 3, 1214-1228.	5.8	14
4818	Improvement of Cutaneous Wound Healing via Topical Application of Heat-Killed Lactococcus chungangensis CAU 1447 on Diabetic Mice. Nutrients, 2021, 13, 2666.	4.1	24
4819	Differential Effects of Western and Mediterranean-Type Diets on Gut Microbiota: A Metagenomics and Metabolomics Approach. Nutrients, 2021, 13, 2638.	4.1	32
4821	MFGM components promote gut Bifidobacterium growth in infant and in vitro. European Journal of Nutrition, 2022, 61, 277-288.	3.9	12
4823	First Evidence That Nematode Communities in Deadwood Are Related to Tree Species Identity and to Co-Occurring Fungi and Prokaryotes. Microorganisms, 2021, 9, 1454.	3.6	8
4824	An Ecological Basis for Dual Genetic Code Expansion in Marine Deltaproteobacteria. Frontiers in Microbiology, 2021, 12, 680620.	3.5	4
4825	Gut microbes impact stroke severity via the trimethylamine N-oxide pathway. Cell Host and Microbe, 2021, 29, 1199-1208.e5.	11.0	78
4826	Prolonged drought imparts lasting compositional changes to the rice root microbiome. Nature Plants, 2021, 7, 1065-1077.	9.3	111

#	Article	IF	CITATIONS
4827	Bacterial communities in the rumen and feces of lactating Holstein dairy cows are not affected when fed reduced-fat dried distillers' grains with solubles. Animal, 2021, 15, 100281.	3.3	5
4828	Feeding sites promoting wildlife-related tourism might highly expose the endangered Yunnan snub-nosed monkey (Rhinopithecus bieti) to parasite transmission. Scientific Reports, 2021, 11, 15817.	3.3	5
4829	Fasting increases microbiome-based colonization resistance and reduces host inflammatory responses during an enteric bacterial infection. PLoS Pathogens, 2021, 17, e1009719.	4.7	14
4830	Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning. ISME Communications, 2021, 1 , .	4.2	28
4831	Fungal microbiomes are determined by host phylogeny and exhibit widespread associations with the bacterial microbiome. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210552.	2.6	12
4833	Effect of an Increased Particulate COD Load on the Aerobic Granular Sludge Process: A Full Scale Study. Processes, 2021, 9, 1472.	2.8	6
4834	Contamination of Hospital Surfaces with Bacterial Pathogens under the Current COVID-19 Outbreak. International Journal of Environmental Research and Public Health, 2021, 18, 9042.	2.6	6
4835	Probiotic Lactobacilli Administration Induces Changes in the Fecal Microbiota of Preweaned Dairy Calves. Probiotics and Antimicrobial Proteins, 2022, 14, 804-815.	3.9	7
4836	Horizontal Gene Transfer Is the Main Driver of Antimicrobial Resistance in Broiler Chicks Infected with Salmonella enterica Serovar Heidelberg. MSystems, 2021, 6, e0072921.	3.8	8
4837	A Holistic Assessment of Polyethylene Fiber Ingestion in Larval and Juvenile Japanese Medaka Fish. Frontiers in Physiology, 2021, 12, 668645.	2.8	6
4838	Gut microbiome is affected by gut region but robust to host physiological changes in captive active-season ground squirrels. Animal Microbiome, 2021, 3, 56.	3.8	5
4839	Potential oxygen consumption and community composition of sediment bacteria in a seasonally hypoxic enclosed bay. PeerJ, 2021, 9, e11836.	2.0	4
4840	Disentangling the Possible Drivers of Indri indri Microbiome: A Threatened Lemur Species of Madagascar. Frontiers in Microbiology, 2021, 12, 668274.	3.5	3
4842	Tissue-dependent transcriptional and bacterial associations in primary sclerosing cholangitis-associated inflammatory bowel disease. Wellcome Open Research, 0, 6, 199.	1.8	0
4843	The structure of Brazilian Amazonian gut microbiomes in the process of urbanisation. Npj Biofilms and Microbiomes, 2021, 7, 65.	6.4	7
4844	Analysis of bacterial communities associated with Mountain Chickadees (<i>Poecile gambeli</i>) across urban and rural habitats. Canadian Journal of Microbiology, 2021, 67, 572-583.	1.7	4
4845	Importance of microbial communities at the root-soil interface for extracellular polymeric substances and soil aggregation in semiarid grasslands. Soil Biology and Biochemistry, 2021, 159, 108301.	8.8	18
4846	Effects of biochar amendment on tomato rhizosphere bacterial communities and their utilization of plant-derived carbon in a calcareous soil. Geoderma, 2021, 396, 115082.	5.1	22

#	Article	IF	CITATIONS
4847	SalmoSim: the development of a three-compartment in vitro simulator of the Atlantic salmon GI tract and associated microbial communities. Microbiome, 2021, 9, 179.	11.1	5
4848	Type 1 diabetes in pregnancy is associated with distinct changes in the composition and function of the gut microbiome. Microbiome, 2021, 9, 167.	11.1	23
4849	Associations between the gut microbiome and metabolome in early life. BMC Microbiology, 2021, 21, 238.	3.3	23
4850	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. PLoS ONE, 2021, 16, e0237556.	2.5	4
4851	Do initial concentration and activated sludge seasonality affect pharmaceutical biotransformation rate constants?. Applied Microbiology and Biotechnology, 2021, 105, 6515-6527.	3.6	11
4852	Spatial analysis of the root system coupled to microbial community inoculation shed light on rhizosphere bacterial community assembly. Biology and Fertility of Soils, 2021, 57, 973-989.	4.3	12
4853	Comparative study of gut microbiota from captive and confiscated-rescued wild pangolins. Journal of Genetics and Genomics, 2021, 48, 825-835.	3.9	20
4854	Commensal microbiota regulates skin barrier function and repair via signaling through the aryl hydrocarbon receptor. Cell Host and Microbe, 2021, 29, 1235-1248.e8.	11.0	119
4855	"Touch microbiome―as a potential tool for forensic investigation: A pilot study. Journal of Clinical Forensic and Legal Medicine, 2021, 82, 102223.	1.0	15
4856	Effect of copper and zinc as sulfate or nitrate salts on soil microbiome dynamics and bla-positive Pseudomonas aeruginosa survival. Journal of Hazardous Materials, 2021, 415, 125631.	12.4	11
4857	Describing the intestinal microbiota of Holstein Fasciola-positive and -negative cattle from a hyperendemic area of fascioliasis in central Colombia. PLoS Neglected Tropical Diseases, 2021, 15, e0009658.	3.0	8
4858	Characterizing the Cattle Gut Microbiome in Farms with a High and Low Prevalence of Shiga Toxin Producing Escherichia coli. Microorganisms, 2021, 9, 1737.	3.6	8
4862	Contribution of stochastic processes to the microbial community assembly on fieldâ€collected microplastics. Environmental Microbiology, 2021, 23, 6707-6720.	3.8	60
4863	Standard methods for pollen research. Journal of Apicultural Research, 2021, 60, 1-109.	1.5	25
4864	GATA6 Deficiency Leads to Epithelial Barrier Dysfunction and Enhances Susceptibility to Gut Inflammation. Journal of Crohn's and Colitis, 2022, 16, 301-311.	1.3	15
4865	Drivers of change and stability in the gut microbiota of an omnivorous avian migrant exposed to artificial food supplementation. Molecular Ecology, 2021, 30, 4723-4739.	3.9	16
4866	The rice foot rot pathogen <scp><i>Dickeya zeae</i></scp> alters the inâ€field plant microbiome. Environmental Microbiology, 2021, 23, 7671-7687.	3.8	14
4868	Cutaneous Effects of In Utero and Lactational Exposure of C57BL/6J Mice to 2,3,7,8-Tetrachlorodibenzo-p-dioxin. Toxics, 2021, 9, 192.	3.7	3

#	Article	IF	CITATIONS
4869	Microbial composition differs between production systems and is associated with growth performance and carcass quality in pigs. Animal Microbiome, 2021, 3, 57.	3.8	7
4871	Herbivory shapes the rhizosphere bacterial microbiota in potato plants. Environmental Microbiology Reports, 2021, 13, 805-811.	2.4	16
4872	A Central Role for Atg5 in Microbiota-Dependent Foxp3+ RORγt+ Treg Cell Preservation to Maintain Intestinal Immune Homeostasis. Frontiers in Immunology, 2021, 12, 705436.	4.8	5
4874	Decline in plankton diversity and carbon flux with reduced sea ice extent along the Western Antarctic Peninsula. Nature Communications, 2021, 12, 4948.	12.8	24
4876	DAnIEL: A User-Friendly Web Server for Fungal ITS Amplicon Sequencing Data. Frontiers in Microbiology, 2021, 12, 720513.	3.5	10
4879	The Impact of Enriched Resistant Starch Typeâ€2 Cookies on the Gut Microbiome in Hemodialysis Patients: A Randomized Controlled Trial. Molecular Nutrition and Food Research, 2021, 65, e2100374.	3.3	19
4881	Characterizing rhizosphere microbiota of peanut (Arachis hypogaea L.) from pre-sowing to post-harvest of crop under field conditions. Scientific Reports, 2021, 11, 17457.	3.3	10
4882	Aboveground and belowground responses to cyanobacterial biofertilizer supplement in a semiâ€arid, perennial bioenergy cropping system. GCB Bioenergy, 2021, 13, 1908-1923.	5.6	4
4883	Spatiotemporal Assembly of Bacterial and Fungal Communities of Seed-Seedling-Adult in Rice. Frontiers in Microbiology, 2021, 12, 708475.	3.5	16
4884	Silicon-rich soil amendments impact microbial community composition and the composition of arsM bearing microbes. Plant and Soil, 2021, 468, 147-164.	3.7	7
4885	Resistance, resilience, and functional redundancy of freshwater bacterioplankton communities facing a gradient of agricultural stressors in a mesocosm experiment. Molecular Ecology, 2021, 30, 4771-4788.	3.9	12
4887	Dietary inflammatory index and its relationship with gut microbiota in individuals with intestinal constipation: a cross-sectional study. European Journal of Nutrition, 2022, 61, 341-355.	3.9	13
4888	Partial Substitution of Meat with Insect (Alphitobius diaperinus) in a Carnivore Diet Changes the Gut Microbiome and Metabolome of Healthy Rats. Foods, 2021, 10, 1814.	4.3	12
4889	Shifts in arbuscular mycorrhizal fungal community composition and edaphic variables during reclamation chronosequence of an open-cast coal mining dump. Catena, 2021, 203, 105301.	5.0	8
4891	Microbiome diversity declines while distinct expansions of Th17, iNKT, and dendritic cell subpopulations emerge after anastomosis surgery. Gut Pathogens, 2021, 13, 51.	3.4	4
4892	Effect of Vancomycin on the Gut Microbiome and Plasma Concentrations of Gut-Derived Uremic Solutes. Kidney International Reports, 2021, 6, 2122-2133.	0.8	11
4893	Salivary microbiome differences in prepubertal children with and without adrenal androgen excess. Pediatric Research, 2022, 91, 1797-1803.	2.3	3
4894	Groundwater bacterial communities evolve over time in response to recharge. Water Research, 2021, 201, 117290.	11.3	35

#	ARTICLE	IF	Citations
4895	A population-based study on associations of stool microbiota with atopic diseases in school-age children. Journal of Allergy and Clinical Immunology, 2021, 148, 612-620.	2.9	29
4896	Post-weaning shifts in microbiome composition and metabolism revealed by over 25 000 pig gut metagenome-assembled genomes. Microbial Genomics, 2021, 7, .	2.0	9
4897	Rhizosphere microbial communities explain positive effects of diverse crop rotations on maize and soybean performance. Soil Biology and Biochemistry, 2021, 159, 108309.	8.8	48
4898	The composition of the gut microbiota following early-life antibiotic exposure affects host health and longevity in later life. Cell Reports, 2021, 36, 109564.	6.4	31
4899	Evolution of fungal community associated with ready-to-eat pineapple during storage under different temperature conditions. Food Microbiology, 2021, 97, 103736.	4.2	6
4900	Comparison of enteric methane yield and diversity of ruminal methanogens in cattle and buffaloes fed on the same diet. PLoS ONE, 2021, 16, e0256048.	2.5	17
4901	Chronic $\langle i \rangle$ Toxoplasma gondii $\langle i \rangle$ infection enhances susceptibility to colitis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
4902	Comparison between cage and free-range egg production on microbial composition, diversity and the presence of Salmonella enterica. Food Microbiology, 2021, 97, 103754.	4.2	5
4903	Declining fungal diversity in Arctic freshwaters along a permafrost thaw gradient. Global Change Biology, 2021, 27, 5889-5906.	9.5	10
4905	Captive Common Marmosets (Callithrix jacchus) Are Colonized throughout Their Lives by a Community of <i>Bifidobacterium</i> Species with Species-Specific Genomic Content That Can Support Adaptation to Distinct Metabolic Niches. MBio, 2021, 12, e0115321.	4.1	8
4906	Spatial variation in the gastrointestinal microbiome, diet, and nutritional condition of a juvenile flatfish among coastal habitats. Marine Environmental Research, 2021, 170, 105413.	2.5	6
4907	Distribution of ETBE-degrading microorganisms and functional capability in groundwater, and implications for characterising aquifer ETBE biodegradation potential. Environmental Science and Pollution Research, 2022, 29, 1223-1238.	5.3	6
4908	Fecal Supernatant from Adult with Autism Spectrum Disorder Alters Digestive Functions, Intestinal Epithelial Barrier, and Enteric Nervous System. Microorganisms, 2021, 9, 1723.	3.6	11
4909	Metagenomic Investigation Uncovers Presence of Probiotic-Type Microbiome in Kalparasa \hat{A}^{\otimes} (Fresh) Tj ETQq $1\ 1$	0.784314	rgBT /Overlo
4910	Vascular endothelial tissue factor contributes to trimethylamine N-oxide-enhanced arterial thrombosis. Cardiovascular Research, 2022, 118, 2367-2384.	3.8	45
4911	Impact of onboard chitosan treatment of whole cod (Gadus morhua) on the shelf life and spoilage bacteria of loins stored superchilled under different atmospheres. Food Microbiology, 2021, 97, 103723.	4.2	13
4912	Characterization of the vaginal and endometrial microbiome in patients with chronic endometritis. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2021, 263, 25-32.	1.1	37
4913	Plumage manipulation alters associations between behaviour, physiology, the internal microbiome and fitness. Animal Behaviour, 2021, 178, 11-36.	1.9	10

#	Article	IF	CITATIONS
4914	Microbial Involvement in Carbon Transformation via CH4 and CO2 in Saline Sedimentary Pool. Biology, 2021, 10, 792.	2.8	3
4916	Niche partitioning by photosynthetic plankton as a driver of CO2-fixation across the oligotrophic South Pacific Subtropical Ocean. ISME Journal, 2022, 16, 465-476.	9.8	10
4917	An Innovative Solid-State Micro-Anaerobic Digestion Process to Valorize Food Waste: Technical Development Constraints and Consequences on Biological Performances. Waste and Biomass Valorization, 2022, 13, 617-630.	3.4	5
4918	Conservation Strip Tillage Leads to Persistent Alterations in the Rhizosphere Microbiota of Brassica napus Crops. Frontiers in Soil Science, 2021, 1, .	2.2	0
4919	Hierarchical modelling of immunoglobulin coated bacteria in dogs with chronic enteropathy shows reduction in coating with disease remission but marked inter-individual and treatment-response variability. PLoS ONE, 2021, 16, e0255012.	2.5	0
4920	Analysis of Human Gut Microbiota Composition Associated to the Presence of Commensal and Pathogen Microorganisms in CÃ′te d'Ivoire. Microorganisms, 2021, 9, 1763.	3.6	7
4921	Metagenomic Survey of the Highly Polyphagous Anastrepha ludens Developing in Ancestral and Exotic Hosts Reveals the Lack of a Stable Microbiota in Larvae and the Strong Influence of Metamorphosis on Adult Gut Microbiota. Frontiers in Microbiology, 2021, 12, 685937.	3.5	10
4922	The Effect of First Feeding Exposure of Larval Largemouth Bass to a Formulated Soybean Mealâ€Based or Soy Saponinâ€Supplemented Diet on Fish Growth Performance and Gut Microbiome. North American Journal of Aquaculture, 2021, 83, 312.	1.4	9
4923	Metagenomic analysis of a mega-city river network reveals microbial compositional heterogeneity among urban and peri-urban river stretch. Science of the Total Environment, 2021, 783, 146960.	8.0	12
4924	Bacterial Community Patterns in the Agaricus bisporus Cultivation System, from Compost Raw Materials to Mushroom Caps. Microbial Ecology, 2022, 84, 20-32.	2.8	17
4926	Seasonality and episodic variation in picoeukaryote diversity and structure reveal community resilience to disturbances in the North Pacific Subtropical Gyre. Limnology and Oceanography, 2022, 67, .	3.1	9
4927	Lifelong dietary omega-3 fatty acid suppresses thrombotic potential through gut microbiota alteration in aged mice. IScience, 2021, 24, 102897.	4.1	15
4928	Manure derived nutrients alter microbial community composition and increase the presence of potential pathogens in freshwater sediment. Journal of Applied Microbiology, 2021, , .	3.1	0
4929	Altered Fecal Microbiotas and Organic Acid Concentrations Indicate Possible Gut Dysbiosis in University Rugby Players: An Observational Study. Microorganisms, 2021, 9, 1687.	3.6	5
4930	The  black box' of plant demography: how do seed type, climate and seed fungal communities affect grass seed germination?. New Phytologist, 2021, 231, 2319-2332.	7.3	6
4931	Paternal high protein diet modulates body composition, insulin sensitivity, epigenetics, and gut microbiota intergenerationally in rats. FASEB Journal, 2021, 35, e21847.	0.5	13
4932	Composition of the Gut Microbiome Influences Production of Sulforaphane-Nitrile and Iberin-Nitrile from Glucosinolates in Broccoli Sprouts. Nutrients, 2021, 13, 3013.	4.1	12
4933	Microbiological Surveillance of Biogas Plants: Targeting Acetogenic Community. Frontiers in Microbiology, 2021, 12, 700256.	3.5	8

#	ARTICLE	IF	CITATIONS
4934	Resource–diversity relationships in bacterial communities reflect the network structure of microbial metabolism. Nature Ecology and Evolution, 2021, 5, 1424-1434.	7.8	65
4935	First report of novel assemblages and mixed infections of Giardia duodenalis in human isolates from New Zealand. Acta Tropica, 2021, 220, 105969.	2.0	21
4936	Gut microbiome is associated with multiple sclerosis activity in children. Annals of Clinical and Translational Neurology, 2021, 8, 1867-1883.	3.7	21
4937	Lipocalin 2 Deficiency Restrains Aging-Related Reshaping of Gut Microbiota Structure and Metabolism. Biomolecules, 2021, 11, 1286.	4.0	3
4943	Quantifying the diet diversity of herbivorous coral reef fishes using systematic review and DNA metabarcoding. Environmental DNA, 2022, 4, 191-205.	5.8	13
4944	Bifidobacterium animalis subsp. lactis BB-12 Protects against Antibiotic-Induced Functional and Compositional Changes in Human Fecal Microbiome. Nutrients, 2021, 13, 2814.	4.1	22
4945	Genome-Resolved Metagenomic Analyses Reveal the Presence of a Putative Bacterial Endosymbiont in an Avian Nasal Mite (Rhinonyssidae; Mesostigmata). Microorganisms, 2021, 9, 1734.	3.6	1
4946	Maternal Immune Activation Causes Social Behavior Deficits and Hypomyelination in Male Rat Offspring with an Autism-Like Microbiota Profile. Brain Sciences, 2021, 11, 1085.	2.3	36
4947	Spatially resolved correlative microscopy and microbial identification reveal dynamic depth―and mineralâ€dependent anabolic activity in salt marsh sediment. Environmental Microbiology, 2021, 23, 4756-4777.	3.8	8
4948	<i>Enterococcus</i> peptidoglycan remodeling promotes checkpoint inhibitor cancer immunotherapy. Science, 2021, 373, 1040-1046.	12.6	158
4949	Healthcare-Associated Infections-Related Bacteriome and Antimicrobial Resistance Profiling: Assessing Contamination Hotspots in a Developing Country Public Hospital. Frontiers in Microbiology, 2021, 12, 711471.	3.5	4
4950	Scat DNA provides important data for effective monitoring of mammal and bird biodiversity. Biodiversity and Conservation, 2021, 30, 3585-3602.	2.6	10
4952	Effect of elevation, season and accelerated snowmelt on biogeochemical processes during isolated conifer needle litter decomposition. Peerl, 2021, 9, e11926.	2.0	1
4953	Exploring plant diversity through soil DNA in Thai national parks for influencing land reform and agriculture planning. PeerJ, 2021, 9, e11753.	2.0	3
4954	Pearl Oyster Bacterial Community Structure Is Governed by Location and Tissue-Type, but Vibrio Species Are Shared Among Oyster Tissues. Frontiers in Microbiology, 2021, 12, 723649.	3.5	6
4955	Fecal microbiota transplantation does not alter bacterial translocation and visceral adipose tissue inflammation in individuals with obesity. Obesity Science and Practice, 2022, 8, 56-65.	1.9	4
4956	Long-term maize-Desmodium intercropping shifts structure and composition of soil microbiome with stronger impact on fungal communities. Plant and Soil, 2021, 467, 437-450.	3.7	21
4957	Divergent, age-associated fungal communities of Pinus flexilis and Pinus longaeva. Forest Ecology and Management, 2021, 494, 119277.	3.2	18

#	ARTICLE	IF	CITATIONS
4958	Interactions between temperature and energy supply drive microbial communities in hydrothermal sediment. Communications Biology, 2021, 4, 1006.	4.4	10
4959	Fish performance, intestinal bacterial community, digestive function and skin and fillet attributes during cold storage of gilthead seabream (Sparus aurata) fed diets supplemented with Gracilaria by-products. Aquaculture, 2021, 541, 736808.	3.5	10
4960	Bog ecosystems as a playground for plant–microbe coevolution: bryophytes and vascular plants harbour functionally adapted bacteria. Microbiome, 2021, 9, 170.	11.1	28
4961	Blastocystis in the faeces of children from six distant countries: prevalence, quantity, subtypes and the relation to the gut bacteriome. Parasites and Vectors, 2021, 14, 399.	2.5	14
4962	Microbially mediated nitrogen removal and retention in the York River Estuary. FEMS Microbiology Ecology, 2021, 97, .	2.7	7
4963	Do hostâ€associated microbes show a contrarian latitudinal diversity gradient? Insights from <i>Mytilus californianus</i> , an intertidal foundation host. Journal of Biogeography, 2021, 48, 2839-2852.	3.0	6
4964	Soil microbial community coalescence and fertilization interact to drive the functioning of the legume–rhizobium symbiosis. Journal of Applied Ecology, 2021, 58, 2590-2602.	4.0	10
4965	Microbes toâ€go: slugs as source for <i>Caenorhabditis elegans</i> microbiota acquisition. Environmental Microbiology, 2021, 23, 6721-6733.	3.8	7
4966	Comparison of 16S and whole genome dog microbiomes using machine learning. BioData Mining, 2021, 14, 41.	4.0	4
4967	Gut Microbiota in Military International Travelers with Doxycycline Malaria Prophylaxis: Towards the Risk of a Simpson Paradox in the Human Microbiome Field. Pathogens, 2021, 10, 1063.	2.8	2
4968	Towards reproducible metabarcoding data: Lessons from an international crossâ€laboratory experiment. Molecular Ecology Resources, 2021, , .	4.8	25
4969	Evidence for the genetic similarity rule at an expanding mangrove range limit. American Journal of Botany, 2021, 108, 1331-1342.	1.7	2
4970	Facial Skin Microbiota-Mediated Host Response to Pollution Stress Revealed by Microbiome Networks of Individual. MSystems, 2021, 6, e0031921.	3.8	7
4971	Extremophilic taxa predominate in a microbial community of photovoltaic panels in a tropical region. FEMS Microbiology Letters, 2021, 368, .	1.8	7
4972	Contrasting heat stress response patterns of coral holobionts across the Red Sea suggest distinct mechanisms of thermal tolerance. Molecular Ecology, 2021, 30, 4466-4480.	3.9	68
4973	Identification of an Intestinal Microbiota Signature Associated With the Severity of Necrotic Enteritis. Frontiers in Microbiology, 2021, 12, 703693.	3.5	20
4974	Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS. MSphere, 2021, 6, e0021921.	2.9	12
4975	Coral microbiome manipulation elicits metabolic and genetic restructuring to mitigate heat stress and evade mortality. Science Advances, 2021, 7, .	10.3	114

#	Article	IF	CITATIONS
4976	Changes in the Fecal Microbiota Associated with a Broad-Spectrum Antimicrobial Administration in Hospitalized Neonatal Foals with Probiotics Supplementation. Animals, 2021, 11, 2283.	2.3	2
4977	Neonatal exposure to a wild-derived microbiome protects mice against diet-induced obesity. Nature Metabolism, 2021, 3, 1042-1057.	11.9	23
4978	The associations of butyrate-producing bacteria of the gut microbiome with diet quality and muscle health. Gut Microbiome, 2021, 2, .	3.2	8
4979	Multiple analysis of root exudates and microbiome in rice (Oryza sativa) under low P conditions. Archives of Microbiology, 2021, 203, 5599-5611.	2.2	7
4980	Soil protist function varies with elevation in the Swiss Alps. Environmental Microbiology, 2022, 24, 1689-1702.	3.8	10
4981	Dependency of hydration and growth conditions on the mechanical properties of oral biofilms. Scientific Reports, 2021, 11, 16234.	3.3	5
4982	Long-Term Biocide Efficacy and Its Effect on a Souring Microbial Community. Applied and Environmental Microbiology, 2021, 87, e0084221.	3.1	4
4983	Impact of Poly I:C induced maternal immune activation on offspring's gut microbiome diversity – Implications for schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2021, 110, 110306.	4.8	19
4984	Effects of organic loading rate and hydraulic retention time on bioaugmentation performance to tackle ammonia inhibition in anaerobic digestion. Bioresource Technology, 2021, 334, 125246.	9.6	20
4985	Profile of Bacterial Infections in COVID-19 Patients: Antimicrobial Resistance in the Time of SARS-CoV-2. Biology, 2021, 10, 822.	2.8	9
4986	In vitro Colon Fermentation of Soluble Arabinoxylan Is Modified Through Milling and Extrusion. Frontiers in Nutrition, 2021, 8, 707763.	3.7	10
4987	Dietary Exposure of Pacific Oyster (Crassostrea gigas) Larvae to Compromised Microalgae Results in Impaired Fitness and Microbiome Shift. Frontiers in Microbiology, 2021, 12, 706214.	3.5	6
4988	Omouma: a prospective mother and child cohort aiming to identify early biomarkers of pregnancy complications in women living in Qatar. BMC Pregnancy and Childbirth, 2021, 21, 570.	2.4	3
4989	Modulation of the Mucosa-Associated Microbiome Linked to the PTPN2 Risk Gene in Patients with Primary Sclerosing Cholangitis and Ulcerative Colitis. Microorganisms, 2021, 9, 1752.	3.6	6
4990	The metabolic footprint of Clostridia and Erysipelotrichia reveals their role in depleting sugar alcohols in the cecum. Microbiome, 2021, 9, 174.	11.1	17
4991	Contrasting gut microbiota in captive Eurasian otters (Lutra lutra) by age. Archives of Microbiology, 2021, 203, 5405-5416.	2.2	3
4992	Multiple thresholds and trajectories of microbial biodiversity predicted across browning gradients by neural networks and decision tree learning. ISME Communications, $2021, 1, \ldots$	4.2	3
4993	Exposure to Parasitic Protists and Helminths Changes the Intestinal Community Structure of Bacterial Communities in a Cohort of Mother-Child Binomials from a Semirural Setting in Mexico. MSphere, 2021, 6, e0008321.	2.9	9

#	ARTICLE	IF	Citations
4994	Molecular and culture-based assessment of the microbiome in a zebrafish (Danio rerio) housing system during set-up and equilibration. Animal Microbiome, 2021, 3, 55.	3.8	5
4997	Pathogenic <i>Vibrio </i> Species Are Associated with Distinct Environmental Niches and Planktonic Taxa in Southern California (USA) Aquatic Microbiomes. MSystems, 2021, 6, e0057121.	3.8	13
4998	Candidatus Methylumidiphilus Drives Peaks in Methanotrophic Relative Abundance in Stratified Lakes and Ponds Across Northern Landscapes. Frontiers in Microbiology, 2021, 12, 669937.	3.5	11
4999	Marine biofilms on different fouling control coating types reveal differences in microbial community composition and abundance. MicrobiologyOpen, 2021, 10, e1231.	3.0	16
5000	Engineered methanotrophic syntrophy in photogranule communities removes dissolved methane. Water Research X, 2021, 12, 100106.	6.1	19
5001	Tree mycorrhizal type and tree diversity shape the forest soil microbiota. Environmental Microbiology, 2022, 24, 4236-4255.	3.8	22
5002	Differential response of soil microbial and animal communities along the chronosequence of Cunninghamia lanceolata at different soil depth levels in subtropical forest ecosystem. Journal of Advanced Research, 2021, 38, 41-54.	9.5	11
5003	Ferries and Environmental DNA: Underway Sampling From Commercial Vessels Provides New Opportunities for Systematic Genetic Surveys of Marine Biodiversity. Frontiers in Marine Science, 2021, 8, .	2.5	10
5005	Dietary and Pharmacologic Manipulations of Host Lipids and Their Interaction With the Gut Microbiome in Non-human Primates. Frontiers in Medicine, 2021, 8, 646710.	2.6	6
5007	Oral Phenotype and Salivary Microbiome of Individuals With Papillon–LefÔvre Syndrome. Frontiers in Cellular and Infection Microbiology, 2021, 11, 720790.	3.9	3
5008	Unraveling the plant diversity of the Amazonian <i>canga</i> through DNA barcoding. Ecology and Evolution, 2021, 11, 13348-13362.	1.9	6
5009	Dynamics of the Human Nasal Microbiota and Staphylococcus aureus CC398 Carriage in Pig Truck Drivers across One Workweek. Applied and Environmental Microbiology, 2021, 87, e0122521.	3.1	8
5011	Reindeer grazing history determines the responses of subarctic soil fungal communities to warming and fertilization. New Phytologist, 2021, 232, 788-801.	7.3	9
5012	Spatial and Temporal Dynamics of Prokaryotic and Viral Community Assemblages in a Lotic System (Manatee Springs, Florida). Applied and Environmental Microbiology, 2021, 87, e0064621.	3.1	10
5013	UCYN-A/haptophyte symbioses dominate N2 fixation in the Southern California Current System. ISME Communications, 2021, 1 , .	4.2	17
5014	Gut-microbiota-targeted diets modulate human immune status. Cell, 2021, 184, 4137-4153.e14.	28.9	482
5015	The fungal community outperforms the bacterial community in predicting plant health status. Applied Microbiology and Biotechnology, 2021, 105, 6499-6513.	3.6	18
5016	The gut microbiome in sickle cell disease: Characterization and potential implications. PLoS ONE, 2021, 16, e0255956.	2.5	24

#	Article	IF	CITATIONS
5017	High Taxonomic Diversity in Ship Bilges Presents Challenges for Monitoring Microbial Corrosion and Opportunity To Utilize Community Functional Profiling. Applied and Environmental Microbiology, 2021, 87, e0089021.	3.1	1
5018	Biogeographic structure of fungal communities in seagrass <i>Halophilia ovalis</i> across the Malay Peninsula. Environmental Microbiology Reports, 2021, 13, 871-877.	2.4	5
5019	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. MSphere, 2021, 6, e0045521.	2.9	12
5020	Influence of Tall Fescue Epichloë Endophytes on Rhizosphere Soil Microbiome. Microorganisms, 2021, 9, 1843.	3 . 6	10
5022	Natural contaminants in bee pollen: DNA metabarcoding as a tool to identify floral sources of pyrrolizidine alkaloids and fungal diversity. Food Research International, 2021, 146, 110438.	6.2	6
5023	Whatâ∈™s for dinner this time?: DNA authentication of â∈œwild mushroomsâ∈in food products sold in the USA. PeerJ, 2021, 9, e11747.	2.0	7
5024	Different patterns in root and soil fungal diversity drive plant productivity of the desert truffle <i>Terfezia claveryi</i> in plantation. Environmental Microbiology, 2021, 23, 5917-5933.	3.8	9
5025	Associations between Afrotropical bats, eukaryotic parasites, and microbial symbionts. Molecular Ecology, 2022, 31, 1939-1950.	3.9	10
5026	Effects of dietary exposure to the engineered nanomaterials CeO2, SiO2, Ag, and TiO2 on the murine gut microbiome. Nanotoxicology, 2021, 15, 1-17.	3.0	6
5027	Microbial Shift in the Enteric Bacteriome of Coral Reef Fish Following Climate-Driven Regime Shifts. Microorganisms, 2021, 9, 1711.	3.6	6
5029	Lake microbial communities are not resistant or resilient to repeated largeâ€scale natural pulse disturbances. Molecular Ecology, 2021, 30, 5137-5150.	3.9	8
5030	Altered Microbial Composition of Drug-Sensitive and Drug-Resistant TB Patients Compared with Healthy Volunteers. Microorganisms, 2021, 9, 1762.	3.6	3
5031	Comparison of Chicken Cecal Microbiota after Metaphylactic Treatment or Following Administration of Feed Additives in a Broiler Farm with Enterococcal Spondylitis History. Pathogens, 2021, 10, 1068.	2.8	5
5032	Endophytic Microbiome Variation Among Single Plant Seeds. Phytobiomes Journal, 2022, 6, 45-55.	2.7	24
5033	Impact of a Vancomycin-Induced Shift of the Gut Microbiome in a Gram-Negative Direction on Plasma Factor VIII:C Levels: Results from a Randomized Controlled Trial. Thrombosis and Haemostasis, 2022, 122, 540-551.	3.4	4
5034	Pulmonary immune cell trafficking promotes host defense against alcohol-associated Klebsiella pneumonia. Communications Biology, 2021, 4, 997.	4.4	15
5035	Conditioning Film and Early Biofilm Succession on Plastic Surfaces. Environmental Science & Emp; Technology, 2021, 55, 11006-11018.	10.0	45
5036	Frogs Respond to Commercial Formulations of the Biopesticide <i>Bacillus thuringiensis</i> var <i>. israelensis</i> , Especially Their Intestine Microbiota. Environmental Science & Environmental Scien	10.0	12

#	Article	IF	CITATIONS
5037	Geographical separation and ethnic origin influence the human gut microbial composition: a meta-analysis from a Malaysian perspective. Microbial Genomics, 2021, 7, .	2.0	11
5038	Exploring Changes in the Host Gut Microbiota During a Controlled Human Infection Model for Campylobacter jejuni. Frontiers in Cellular and Infection Microbiology, 2021, 11, 702047.	3.9	6
5039	The Rhizobial Microbiome from the Tropical Savannah Zones in Northern Côte d'lvoire. Microorganisms, 2021, 9, 1842.	3.6	7
5040	Characterization of cellulose-degrading microbiota from the eastern subterranean termite and soil. F1000Research, 0, 6, 2082.	1.6	O
5041	Effects of Inhaled Corticosteroid/Long-Acting \hat{l}^2 ₂ -Agonist Combination on the Airway Microbiome of Patients with Chronic Obstructive Pulmonary Disease: A Randomized Controlled Clinical Trial (DISARM). American Journal of Respiratory and Critical Care Medicine, 2021, 204, 1143-1152.	5.6	44
5042	Borrelia afzelii Infection in the Rodent Host Has Dramatic Effects on the Bacterial Microbiome of Ixodes ricinus Ticks. Applied and Environmental Microbiology, 2021, 87, e0064121.	3.1	13
5043	Application of nanofiber carriers for sampling of microbial biomass from contaminated groundwater. Science of the Total Environment, 2021, 780, 146518.	8.0	5
5044	Manipulation of the soil microbiome regulates the colonization of plants by arbuscular mycorrhizal fungi. Mycorrhiza, 2021, 31, 545-558.	2.8	6
5045	The spleen bacteriome of wild rodents and shrews from Marigat, Baringo County, Kenya. PeerJ, 2021, 9, e12067.	2.0	2
5046	Lack of Phylogenetic Differences in Ectomycorrhizal Fungi among Distinct Mediterranean Pine Forest Habitats. Journal of Fungi (Basel, Switzerland), 2021, 7, 793.	3.5	4
5048	Living to the High Extreme: Unraveling the Composition, Structure, and Functional Insights of Bacterial Communities Thriving in the Arsenic-Rich Salar de Huasco Altiplanic Ecosystem. Microbiology Spectrum, 2021, 9, e0044421.	3.0	16
5050	Gut microbiota alterations in response to sleep length among African-origin adults. PLoS ONE, 2021, 16, e0255323.	2.5	18
5051	Subacute Exposure to an Environmentally Relevant Dose of Di-(2-ethylhexyl) Phthalate during Gestation Alters the Cecal Microbiome, but Not Pregnancy Outcomes in Mice. Toxics, 2021, 9, 215.	3.7	5
5052	Chinese gut microbiota and its associations with staple food type, ethnicity, and urbanization. Npj Biofilms and Microbiomes, 2021, 7, 71.	6.4	37
5053	Associations Between Human Milk Oligosaccharides at 1 Month and Infant Development Throughout the First Year of Life in a Brazilian Cohort. Journal of Nutrition, 2021, 151, 3543-3554.	2.9	6
5054	Microbes mediating the sulfur cycle in the Atlantic Ocean and their link to chemolithoautotrophy. Environmental Microbiology, 2021, 23, 7152-7167.	3.8	3
5055	New insights into the role of constitutive bacterial rhizobiome and phenolic compounds in two Pinus spp. with contrasting susceptibility to pine pitch canker. Tree Physiology, 2021, , .	3.1	4
5057	Complex species and strain ecology of the vaginal microbiome from pregnancy to postpartum and association with preterm birth. Med, 2021, 2, 1027-1049.e7.	4.4	29

#	ARTICLE	IF	Citations
5058	Biogeography rather than substrate type determines bacterial colonization dynamics of marine plastics. Peerl, 2021, 9, e12135.	2.0	15
5059	A statistical model for describing and simulating microbial community profiles. PLoS Computational Biology, 2021, 17, e1008913.	3.2	21
5061	Environmental DNA gives comparable results to morphology-based indices of macroinvertebrates in a large-scale ecological assessment. PLoS ONE, 2021, 16, e0257510.	2.5	25
5062	Distinct Endophytic Bacterial Communities Inhabiting Seagrass Seeds. Frontiers in Microbiology, 2021, 12, 703014.	3.5	21
5063	Detection of Sulfate-Reducing Bacteria as an Indicator for Successful Mitigation of Sulfide Production. Applied and Environmental Microbiology, 2021, 87, e0174821.	3.1	3
5064	Kefir modulates gut microbiota and reduces DMH-associated colorectal cancer via regulation of intestinal inflammation in adulthood offsprings programmed by neonatal overfeeding. Food Research International, 2022, 152, 110708.	6.2	8
5065	Ruminal and Fecal Bacteriome of Dairy Calves Fed Different Levels and Sources of NDF. Animals, 2021, 11, 2705.	2.3	2
5066	Relationships Between the Microbial Composition and the Geochemistry and Mineralogy of the Cobalt-Bearing Legacy Mine Tailings in Northeastern Ontario. Frontiers in Microbiology, 2021, 12, 660190.	3.5	5
5067	Dynamics of the Upper Respiratory Tract Microbiota and Its Association with Mortality in COVID-19. American Journal of Respiratory and Critical Care Medicine, 2021, 204, 1379-1390.	5.6	46
5068	A protocol for characterization of extremely preterm infant gut microbiota in double-blind clinical trials. STAR Protocols, 2021, 2, 100652.	1.2	3
5069	Gut Metabolites Are More Predictive of Disease and Cohoused States than Gut Bacterial Features in a Polycystic Ovary Syndrome-Like Mouse Model. MSystems, 2021, 6, e0114920.	3.8	8
5071	Increasing Hydrostatic Pressure Impacts the Prokaryotic Diversity during Emiliania huxleyi Aggregates Degradation. Water (Switzerland), 2021, 13, 2616.	2.7	8
5072	The Foliar Microbiome Suggests that Fungal and Bacterial Agents May be Involved in the Beech Leaf Disease Pathosystem. Phytobiomes Journal, 2021, 5, 335-349.	2.7	12
5073	Machine Learning Predicts the Presence of 2,4,6-Trinitrotoluene in Sediments of a Baltic Sea Munitions Dumpsite Using Microbial Community Compositions. Frontiers in Microbiology, 2021, 12, 626048.	3.5	6
5075	Prokaryotic diversity and activity in contrasting productivity regimes in late summer in the Kerguelen region (Southern Ocean). Journal of Marine Systems, 2021, 221, 103561.	2.1	6
5076	Microbial Abundance and Diversity in Subsurface Lower Oceanic Crust at Atlantis Bank, Southwest Indian Ridge. Applied and Environmental Microbiology, 2021, 87, e0151921.	3.1	5
5077	Distinctive prokaryotic microbiomes in sympatric plant roots from a Yucatan cenote. BMC Research Notes, 2021, 14, 333.	1.4	2
5078	18S rRNA amplicon sequence data (V1–V3) of the Bronx river estuary, New York. Metabarcoding and Metagenomics, 0, 5, .	0.0	3

#	ARTICLE	IF	CITATIONS
5080	Environmental factors shaping bacterial, archaeal and fungal community structure in hydrothermal sediments of Guaymas Basin, Gulf of California. PLoS ONE, 2021, 16, e0256321.	2.5	14
5081	Alpha-synuclein alters the faecal viromes of rats in a gut-initiated model of Parkinson's disease. Communications Biology, 2021, 4, 1140.	4.4	6
5082	Exploring Semi-Quantitative Metagenomic Studies Using Oxford Nanopore Sequencing: A Computational and Experimental Protocol. Genes, 2021, 12, 1496.	2.4	11
5083	Breeding Strategy Shapes the Composition of Bacterial Communities in Female Nile Tilapia Reared in a Recirculating Aquaculture System. Frontiers in Microbiology, 2021, 12, 709611.	3.5	2
5084	Altered milk yield and rumen microbial abundance in response to concentrate supplementation during the cold season in Tibetan sheep. Electronic Journal of Biotechnology, 2021, 53, 80-86.	2.2	12
5085	Signatures of Adaptation and Acclimatization to Reef Flat and Slope Habitats in the Coral Pocillopora damicornis. Frontiers in Marine Science, 2021, 8, .	2.5	17
5086	Probiotic properties of an indigenous Pediococcus pentosaceus strain on Tenebrio molitor larval growth and survival. Journal of Insects As Food and Feed, 2021, 7, 975-986.	3.9	15
5087	Shifts in Soil Structure, Biological, and Functional Diversity Under Long-Term Carbon Deprivation. Frontiers in Microbiology, 2021, 12, 735022.	3.5	7
5088	Bacterial community dynamics on bats and the implications for pathogen resistance. Environmental Microbiology, 2022, 24, 1484-1498.	3.8	12
5089	Community response of arbuscular mycorrhizal fungi to extreme drought in a coldâ€ŧemperate grassland. New Phytologist, 2022, 234, 2003-2017.	7.3	35
5090	Optimizing an enclosed bead beating extraction method for microbial and fish environmental DNA. Environmental DNA, 2022, 4, 291-303.	5.8	6
5091	Microbiome of a Reef-Building Coral Displays Signs of Acclimation to a Stressful Shallow Hydrothermal Vent Habitat. Frontiers in Marine Science, 2021, 8, .	2.5	4
5092	Deciphering the molecular signal from past and alive bacterial communities in aquatic sedimentary archives. Molecular Ecology Resources, 2022, 22, 877-890.	4.8	9
5093	Cyanobacteria and nitrates in karstic systems of Yucatan (Mexico) and Texas (USA). Aquatic Sciences, 2021, 83, 1.	1.5	1
5094	Parallel sequencing reveals Campylobacter in commercial meat chickens less than 8 days old Applied and Environmental Microbiology, 2021, 87, e0106021.	3.1	4
5095	Associations between Maternal Diet, Body Composition and Gut Microbial Ecology in Pregnancy. Nutrients, 2021, 13, 3295.	4.1	18
5096	The core seed mycobiome of <i>Pseudotsuga menziesii </i> var. <i>menziesii </i> across provenances of the Pacific Northwest, USA. Mycologia, 2021, 113, 1-12.	1.9	4
5097	Vaginal microbiota differences associated with pelvic organ prolapse risk during late gestation in commercial sows. Biology of Reproduction, 2021, 105, 1545-1561.	2.7	6

#	Article	IF	CITATIONS
5098	Fire and herbivory drive fungal and bacterial communities through distinct above- and belowground mechanisms. Science of the Total Environment, 2021, 785, 147189.	8.0	9
5101	Elucidating gene expression adaptation of phylogenetically divergent coral holobionts under heat stress. Nature Communications, 2021, 12, 5731.	12.8	29
5102	Effect of functional oils or probiotics on performance and microbiota profile of newly weaned piglets. Scientific Reports, 2021, 11, 19457.	3.3	6
5103	The value of gut microbiota to predict feed efficiency and growth of rabbits under different feeding regimes. Scientific Reports, 2021, 11, 19495.	3.3	13
5104	Dynamics of integron structures across a wastewater network – Implications to resistance gene transfer. Water Research, 2021, 206, 117720.	11.3	18
5105	Metagenomic Analysis of Biochemical Passive Reactors During Acid Mine Drainage Bioremediation Reveals Key Co-selected Metabolic Functions. Microbial Ecology, 2022, 84, 465-472.	2.8	2
5106	Saline mine-water alters the structure and function of prokaryote communities in shallow groundwater below a tropical stream. Environmental Pollution, 2021, 284, 117318.	7.5	8
5107	Ecological memory of recurrent drought modifies soil processes via changes in soil microbial community. Nature Communications, 2021, 12, 5308.	12.8	108
5108	Shoot and root insect herbivory change the plant rhizosphere microbiome and affects cabbage–insect interactions through plant–soil feedback. New Phytologist, 2021, 232, 2475-2490.	7.3	23
5109	Taxonomic Compositions and Co-occurrence Relationships of Protists in Bulk Soil and Rhizosphere of Soybean Fields in Different Regions of China. Frontiers in Microbiology, 2021, 12, 738129.	3.5	7
5110	Effects of laboratory domestication on the rodent gut microbiome. ISME Communications, 2021, 1, .	4.2	21
5112	Local versus site-level effects of algae on coral microbial communities. Royal Society Open Science, 2021, 8, 210035.	2.4	4
5114	Dietary advanced glycation endproducts (AGEs) increase their concentration in plasma and tissues, result in inflammation and modulate gut microbial composition in mice; evidence for reversibility. Food Research International, 2021, 147, 110547.	6.2	41
5115	Aquatic microbial community is partially functionally redundant: Insights from an in situ reciprocal transplant experiment. Science of the Total Environment, 2021, 786, 147433.	8.0	3
5116	Temperature differently affected methanogenic pathways and microbial communities in sub-Antarctic freshwater ecosystems. Environment International, 2021, 154, 106575.	10.0	21
5117	Dysregulation of ILC3s unleashes progression and immunotherapy resistance in colon cancer. Cell, 2021, 184, 5015-5030.e16.	28.9	102
5118	Complex photobiont diversity in the marine lichen <i>Lichina pygmaea</i> . Journal of the Marine Biological Association of the United Kingdom, 2021, 101, 667-674.	0.8	9
5119	Anaerobic co-digestion of raw glycerol and swine manure: microbial communities. Biomass Conversion and Biorefinery, 2023, 13, 7127-7138.	4.6	5

#	Article	IF	CITATIONS
5120	The taxonomic distribution of histamine-secreting bacteria in the human gut microbiome. BMC Genomics, 2021, 22, 695.	2.8	22
5121	Effects of Recreational Boating on Microbial and Meiofauna Diversity in Coastal Shallow Ecosystems of the Baltic Sea. MSphere, 2021, 6, e0012721.	2.9	4
5122	Lineage-Specific Growth Curves Document Large Differences in Response of Individual Groups of Marine Bacteria to the Top-Down and Bottom-Up Controls. MSystems, 2021, 6, e0093421.	3.8	10
5124	Gut microbiota depletion exacerbates cholestatic liver injury via loss of FXR signalling. Nature Metabolism, 2021, 3, 1228-1241.	11.9	65
5125	DNA metabarcoding reveals the dietary composition in the endangered black-faced spoonbill. Scientific Reports, 2021, 11, 18773.	3.3	2
5126	Liraglutide and sitagliptin have no effect on intestinal microbiota composition: A 12-week randomized placebo-controlled trial in adults with type 2 diabetes. Diabetes and Metabolism, 2021, 47, 101223.	2.9	25
5127	Factors associated with suppression of Fusarium basal rot of onion in New Zealand soils: literature review and greenhouse experiments. New Zealand Journal of Crop and Horticultural Science, 2023, 51, 137-155.	1.3	2
5128	Longitudinal patterns in sediment type and quality during daily flow regimes and following natural hazards in an urban estuary: a Hurricane Harvey retrospective. Environmental Science and Pollution Research, 2021, , 1.	5. 3	1
5129	What's under the Christmas Tree? A Soil Sulfur Amendment Lowers Soil pH and Alters Fir Tree Rhizosphere Bacterial and Eukaryotic Communities, Their Interactions, and Functional Traits. Microbiology Spectrum, 2021, 9, e0016621.	3.0	6
5130	Microbial Communities in a Serpentinizing Aquifer Are Assembled through Strong Concurrent Dispersal Limitation and Selection. MSystems, 2021, 6, e0030021.	3.8	12
5131	Glycosaminoglycan biosynthesis pathway in host genome is associated with Helicobacter pylori infection. Scientific Reports, 2021, 11, 18235.	3.3	0
5133	Chemical, biochemical, and microbiological properties of Technosols produced from urban inorganic and organic wastes. Journal of Soils and Sediments, 2022, 22, 146-161.	3.0	3
5134	Relationship between the Microbiome and Indoor Temperature/Humidity in a Traditional Japanese House with a Thatched Roof in Kyoto, Japan. Diversity, 2021, 13, 475.	1.7	9
5135	A Six-Day, Lifestyle-Based Immersion Program Mitigates Cardiovascular Risk Factors and Induces Shifts in Gut Microbiota, Specifically Lachnospiraceae, Ruminococcaceae, Faecalibacterium prausnitzii: A Pilot Study. Nutrients, 2021, 13, 3459.	4.1	31
5136	Highly comparable metabarcoding results from MGI-Tech and Illumina sequencing platforms. PeerJ, 2021, 9, e12254.	2.0	13
5137	Visualization of the seasonal shift of a variety of airborne pollens in western Tokyo. Science of the Total Environment, 2021, 788, 147623.	8.0	13
5139	RNA virome abundance and diversity is associated with host age in a bird species. Virology, 2021, 561, 98-106.	2.4	19
5140	Diversity and flexibility of algal symbiont community in globally distributed larger benthic foraminifera of the genus Amphistegina. BMC Microbiology, 2021, 21, 243.	3.3	5

#	Article	IF	CITATIONS
5141	Transient antibiotic-induced changes in the neonatal swine intestinal microbiota impact islet expression profiles reducing subsequent function. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2021, 321, R303-R316.	1.8	1
5142	Short-term improvement of clinical parameters and microbial diversity in periodontitis patients following Indocyanine green-based antimicrobial photodynamic therapy: A randomized single-blind split-mouth cohort. Photodiagnosis and Photodynamic Therapy, 2021, 35, 102349.	2.6	6
5145	The effect of benzo[a]pyrene on the gut microbiota of Nile tilapia (Oreochromis niloticus). Applied Microbiology and Biotechnology, 2021, 105, 7935-7947.	3.6	5
5146	Fungi in soil and understory have coupled distribution patterns. PeerJ, 2021, 9, e11915.	2.0	4
5147	Diversity and characteristics of raw milk microbiota from Korean dairy farms using metagenomic and culturomic analysis. Food Control, 2021, 127, 108160.	5.5	12
5148	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. Current Biology, 2021, 31, 3905-3914.e6.	3.9	17
5149	Reactors and active biomass potential as inoculum for nitrogen removal. Bioresource Technology, 2021, 336, 125334.	9.6	4
5150	Analyzing Type 2 Diabetes Associations with the Gut Microbiome in Individuals from Two Ethnic Backgrounds Living in the Same Geographic Area. Nutrients, 2021, 13, 3289.	4.1	17
5151	Soil microbial sensitivity to temperature remains unchanged despite community compositional shifts along geothermal gradients. Global Change Biology, 2021, 27, 6217-6231.	9.5	25
5152	Geographical Relationships between Long-Tailed Goral (Naemorhedus caudatus) Populations Based on Gut Microbiome Analysis. Microorganisms, 2021, 9, 2002.	3.6	3
5153	Agricultural Management Affects the Active Rhizosphere Bacterial Community Composition and Nitrification. MSystems, 2021, 6, e0065121.	3.8	15
5154	The Nasopharyngeal, Ruminal, and Vaginal Microbiota and the Core Taxa Shared across These Microbiomes in Virgin Yearling Heifers Exposed to Divergent In Utero Nutrition during Their First Trimester of Gestation and in Pregnant Beef Heifers in Response to Mineral Supplementation. Microorganisms, 2021, 9, 2011.	3.6	24
5155	Infection with intracellular parasite Amoeboaphelidium protococcarum induces shifts in associated bacterial communities in microalgae cultures. Journal of Applied Phycology, 2021, 33, 2863-2873.	2.8	5
5157	Soil Fungal Community in Grazed Inner Mongolian Grassland Adjacent to Coal-Mining Activity. Frontiers in Microbiology, 2021, 12, 718727.	3.5	2
5161	Monitoring of seven industrial anaerobic digesters supplied with biochar. Biotechnology for Biofuels, 2021, 14, 185.	6.2	17
5162	Compositional Shift of Bacterial, Archaeal, and Fungal Communities Is Dependent on Trophic Lifestyles in Rice Paddy Soil. Frontiers in Microbiology, 2021, 12, 719486.	3.5	5
5163	Improved high throughput protocol for targeting eukaryotic symbionts in metazoan and eDNA samples. Molecular Ecology Resources, 2022, 22, 664-678.	4.8	9
5165	Impact of wastewater on the microbial diversity of periphyton and its tolerance to micropollutants in an engineered flow-through channel system. Water Research, 2021, 203, 117486.	11.3	31

#	Article	IF	CITATIONS
5166	Feeding habits and novel prey of larval fishes in the northern San Francisco Estuary. Environmental DNA, 2021, 3, 1059-1080.	5.8	6
5167	Comparison of the Species Communities of <i>Phytophthora, Pythium </i> , and <i>Phytopythium </i> Associated with Soybean Genotypes in High Disease Environments in Ohio. Phytobiomes Journal, 2021, 5, 288-304.	2.7	7
5168	Partitioning of nutrient removal contribution between granules and flocs in a hybrid granular activated sludge system. Water Research, 2021, 203, 117514.	11.3	18
5169	Periodontitis associates with species-specific gene expression of the oral microbiota. Npj Biofilms and Microbiomes, 2021, 7, 76.	6.4	18
5170	To culture or not to culture: a snapshot of culture-dependent and culture-independent bacterial diversity from peanut rhizosphere. PeerJ, 2021, 9, e12035.	2.0	6
5171	Artificial Rearing of Atlantic Salmon Juveniles for Supportive Breeding Programs Induces Long-Term Effects on Gut Microbiota after Stocking. Microorganisms, 2021, 9, 1932.	3.6	9
5172	Intestinal antiviral signaling is controlled by autophagy gene <i>Epg5</i> independent of the microbiota. Autophagy, 2022, 18, 1062-1077.	9.1	6
5175	Keep your friends close: Host compartmentalisation of microbial communities facilitates decoupling from effects of habitat fragmentation. Ecology Letters, 2021, 24, 2674-2686.	6.4	7
5176	Steering microbiomes by organic amendments towards climate-smart agricultural soils. Biology and Fertility of Soils, 2021, 57, 1053-1074.	4.3	13
5177	Repeated sampling of individuals reveals impact of tropical and temperate habitats on microbiota of a migratory bird. Molecular Ecology, 2021, 30, 5900-5916.	3.9	18
5178	Antigen Presenting Cells Link the Female Genital Tract Microbiome to Mucosal Inflammation, With Hormonal Contraception as an Additional Modulator of Inflammatory Signatures. Frontiers in Cellular and Infection Microbiology, 2021, 11, 733619.	3.9	8
5179	Characterization of gut microbiota in patients with metabolic syndrome candidates for bariatric/metabolic surgery: Preliminary findings of a multi-center prospective study. Diabetes Research and Clinical Practice, 2021, 180, 109079.	2.8	3
5180	Essential Hypertension Is Associated With Changes in Gut Microbial Metabolic Pathways: A Multisite Analysis of Ambulatory Blood Pressure. Hypertension, 2021, 78, 804-815.	2.7	42
5181	Mixedâ€method analysis of undergraduate and graduate student perceptions towards r suggests lecture and selfâ€paced tutorial introductions produce similar outcomes. Journal of Natural Resources and Life Sciences Education, 2021, 50, e20073.	1.5	3
5182	Diversity of Treponema denticola and Other Oral Treponeme Lineages in Subjects with Periodontitis and Gingivitis. Microbiology Spectrum, 2021, 9, e0070121.	3.0	19
5183	Basalt-Hosted Microbial Communities in the Subsurface of the Young Volcanic Island of Surtsey, Iceland. Frontiers in Microbiology, 2021, 12, 728977.	3.5	6
5184	The gut microbiome in konzo. Nature Communications, 2021, 12, 5371.	12.8	8
5185	A Trifecta of New Insights into Ovine Footrot for Infection Drivers, Immune Response, and Host-Pathogen Interactions. Infection and Immunity, 2021, 89, e0027021.	2.2	2

#	Article	IF	Citations
5186	Does Organomineral Fertilizer Combined with Phosphate-Solubilizing Bacteria in Sugarcane Modulate Soil Microbial Community and Functions?. Microbial Ecology, 2022, 84, 539-555.	2.8	13
5187	Occurrence and distribution of microbial pollutants in coastal areas of the Adriatic Sea influenced by river discharge. Environmental Pollution, 2021, 285, 117672.	7.5	18
5188	Pilot Sub-Study of the Effect of Hepatitis C Cure by Glecaprevir/Pibrentasvir on the Gut Microbiome of Patients with Chronic Hepatitis C Genotypes 1 to 6 in the Mythen Study. Pharmaceuticals, 2021, 14, 931.	3.8	5
5189	Low Diversity in Nasal Microbiome Associated With <i>Staphylococcus aureus</i> Bloodstream Infections in Hospitalized Neonates. Open Forum Infectious Diseases, 2021, 8, ofab475.	0.9	6
5190	Non-diphtheriae <i>Corynebacterium</i> species are associated with decreased risk of pneumococcal colonization during infancy. ISME Journal, 2022, 16, 655-665.	9.8	14
5191	Vaginal microbiome topic modeling of laboring Ugandan women with and without fever. Npj Biofilms and Microbiomes, 2021, 7, 75.	6.4	5
5192	Nitric Oxide Impacts Human Gut Microbiota Diversity and Functionalities. MSystems, 2021, 6, e0055821.	3.8	13
5193	Plant biodiversity assessment through pollen DNA metabarcoding in Natura 2000 habitats (Italian) Tj ETQq1 1 (0.78 <u>4</u> 314 r	gBT/Overloc
5194	Temporal Changes in Vaginal Microbiota and Genital Tract Cytokines Among South African Women Treated for Bacterial Vaginosis. Frontiers in Immunology, 2021, 12, 730986.	4.8	25
5195	Exploring how microbiome signatures change across inflammatory bowel disease conditions and disease locations. Scientific Reports, 2021, 11, 18699.	3.3	9
5196	Hydrocarbon substrate richness impacts microbial abundance, microbiome composition, and hydrocarbon loss. Applied Soil Ecology, 2021, 165, 104015.	4.3	3
5197	Standard and non-standard measurements of acidity and the bacterial ecology of northern temperate mineral soils. Soil Biology and Biochemistry, 2021, 160, 108323.	8.8	8
5198	Regulation of host phenotypic plasticity by gut symbiont communities in the eastern subterranean termite (<i>Reticulitermes flavipes</i>). Journal of Experimental Biology, 2021, 224, .	1.7	4
5199	The Skin Microbiome of Patients With Atopic Dermatitis Normalizes Gradually During Treatment. Frontiers in Cellular and Infection Microbiology, 2021, 11, 720674.	3.9	37
5200	Evaluating the Efficiency of DNA Metabarcoding to Analyze the Diet of Hippocampus guttulatus (Teleostea: Syngnathidae). Life, 2021, 11, 998.	2.4	9
5201	Free Faecal Water: Analysis of Horse Faecal Microbiota and the Impact of Faecal Microbial Transplantation on Symptom Severity. Animals, 2021, 11, 2776.	2.3	4
5202	Agricultural Fast Food: Bats Feeding in Banana Monocultures Are Heavier but Have Less Diverse Gut Microbiota. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	5
5203	Ruminant fat intake improves gut microbiota, serum inflammatory parameter and fatty acid profile in tissues of Wistar rats. Scientific Reports, 2021, 11, 18963.	3.3	3

#	Article	IF	CITATIONS
5204	Microbiota-Macroalgal Relationships at a Hawaiian Intertidal Bench Are Influenced by Macroalgal Phyla and Associated Thallus Complexity. MSphere, 2021, 6, e0066521.	2.9	3
5205	Mussel Mass Mortality and the Microbiome: Evidence for Shifts in the Bacterial Microbiome of a Declining Freshwater Bivalve. Microorganisms, 2021, 9, 1976.	3.6	18
5206	Transition and regulation mechanism of bacterial biota in Kishu saba-narezushi (mackerel narezushi) during its fermentation step. Journal of Bioscience and Bioengineering, 2021, 132, 606-612.	2.2	8
5207	Is Toxin-Producing Planktothrix sp. an Emerging Species in Lake Constance?. Toxins, 2021, 13, 666.	3.4	9
5208	Relationship between airway dysbiosis, inflammation and lung function in adults with cystic fibrosis. Journal of Cystic Fibrosis, 2021, 20, 754-760.	0.7	25
5209	Social groups constrain the spatiotemporal dynamics of wild sifaka gut microbiomes. Molecular Ecology, 2021, 30, 6759-6775.	3.9	16
5210	Development of droplet digital Polymerase Chain Reaction assays for the detection of long-finned ($\langle i \rangle$ Anguilla dieffenbachii $\langle i \rangle$) and short-finned ($\langle i \rangle$ Anguilla australis $\langle i \rangle$) eels in environmental samples. PeerJ, 2021, 9, e12157.	2.0	4
5211	Single-colony sequencing reveals microbe-by-microbiome phylosymbiosis between the cyanobacterium Microcystis and its associated bacteria. Microbiome, 2021, 9, 194.	11.1	27
5212	Lactoferrin impact on gut microbiota in preterm infants with late-onset sepsis or necrotising enterocolitis: the MAGPIE mechanisms of action study. Efficacy and Mechanism Evaluation, 2021, 8, 1-88.	0.7	6
5213	Does algae \hat{I}^2 -glucan affect the fecal bacteriome in dairy calves?. PLoS ONE, 2021, 16, e0258069.	2.5	7
5214	Identifying optimal bioinformatics protocols for aerosol microbial community data. PeerJ, 2021, 9, e12065.	2.0	1
5215	Gut microbiome in adolescent depression. Journal of Affective Disorders, 2021, 292, 500-507.	4.1	22
5216	Plant legacies and soil microbial community dynamics control soil respiration. Soil Biology and Biochemistry, 2021, 160, 108350.	8.8	10
5217	Bacterial microbiome of dusky kob Argyrosomus japonicus eggs and rearing water and the bacteriostatic effect of selected disinfectants. Aquaculture, 2021, 542, 736882.	3.5	2
5218	Spatioregional assessment of the gut microbiota in experimental necrotizing pancreatitis. BJS Open, 2021, 5, .	1.7	9
5220	Deciphering the low abundance microbiota of presumed aseptic hip and knee implants. PLoS ONE, 2021, 16, e0257471.	2.5	3
5221	Factors influencing suppressiveness of soils to powdery scab of potato. Australasian Plant Pathology, 2021, 50, 715-728.	1.0	3
5222	Baseline Gut Metagenomic Functional Gene Signature Associated with Variable Weight Loss Responses following a Healthy Lifestyle Intervention in Humans. MSystems, 2021, 6, e0096421.	3.8	19

#	Article	IF	Citations
5223	Comparison of Fecal Collection Methods on Variation in Gut Metagenomics and Untargeted Metabolomics. MSphere, 2021, 6, e0063621.	2.9	12
5224	Microbial diversity and physicochemical characteristics of tropical karst soils in the northeastern Yucatan peninsula, Mexico. Applied Soil Ecology, 2021, 165, 103969.	4.3	6
5225	The importance of environmental microbes for Drosophila melanogaster during seasonal macronutrient variability. Scientific Reports, 2021, 11, 18850.	3.3	5
5226	Multiscale Biology of Cardiovascular Risk in Psoriasis: Protocol for a Case-Control Study. JMIR Research Protocols, 2021, 10, e28669.	1.0	7
5227	Mangrove microbiota along the urban-to-rural gradient of the Cayenne estuary (French Guiana, South) Tj ETQq0 ()	Overlock 10 ⁻
5228	Lower brown adipose tissue activity is associated with non-alcoholic fatty liver disease but not changes in the gut microbiota. Cell Reports Medicine, 2021, 2, 100397.	6.5	35
5229	Temporal patterns of vegetation recovery after wildfire in two obligate seeder ash forests. Forest Ecology and Management, 2021, 496, 119409.	3.2	7
5230	Effects of Rhododendron removal on soil bacterial and fungal communities in southern Appalachian forests. Forest Ecology and Management, 2021, 496, 119398.	3.2	3
5231	The diversity and community structure of symbiotic cyanobacteria in hornworts inferred from longâ€read amplicon sequencing. American Journal of Botany, 2021, 108, 1731-1744.	1.7	26
5232	Gut-associated cGMP mediates colitis and dysbiosis in a mouse model of an activating mutation in <i>GUCY2C</i> . Journal of Experimental Medicine, 2021, 218, .	8.5	14
5233	Upper respiratory tract bacterial-immune interactions during respiratory syncytial virus infection in infancy. Journal of Allergy and Clinical Immunology, 2022, 149, 966-976.	2.9	11
5234	Phosphorus Regulation of Methane Oxidation in Water From Iceâ€Covered Lakes. Journal of Geophysical Research G: Biogeosciences, 2021, 126, e2020JG006190.	3.0	8
5235	Cognate recognition of microbial antigens defines constricted CD4+ TÂcell receptor repertoires in the inflamed colon. Immunity, 2021, 54, 2565-2577.e6.	14.3	8
5236	Composition, Succession, and Source Tracking of Microbial Communities throughout the Traditional Production of a Farmstead Cheese. MSystems, 2021, 6, e0083021.	3.8	16
5237	Changes in the Composition and Function of the Human Salivary Microbiome After Heart Transplantation: A Pilot Study. Transplant Research and Risk Management, 0, Volume 13, 15-21.	0.7	0
5238	Temperature and immigration effects on quorum sensing in the biofilms of anaerobic membrane bioreactors. Journal of Environmental Management, 2021, 293, 112947.	7.8	23
5239	Alteration and the Function of Intestinal Microbiota in High-Fat-Diet- or Genetics-Induced Lipid Accumulation. Frontiers in Microbiology, 2021, 12, 741616.	3.5	4
5240	Synergistic effects of temperature and light affect the relationship between <scp><i>Taonia atomaria</i></scp> and its epibacterial community: a controlled conditions study. Environmental Microbiology, 2021, 23, 6777-6797.	3.8	2

#	Article	IF	CITATIONS
5241	Mild and Severe SARS-CoV-2 Infection Induces Respiratory and Intestinal Microbiome Changes in the K18-hACE2 Transgenic Mouse Model. Microbiology Spectrum, 2021, 9, e0053621.	3.0	21
5242	Resistance and Vulnerability of Honeybee (Apis mellifera) Gut Bacteria to Commonly Used Pesticides. Frontiers in Microbiology, 2021, 12, 717990.	3.5	16
5243	Paleoecological evidence for a multi-trophic regime shift in a perialpine lake (Lake Joux, Switzerland). Anthropocene, 2021, 35, 100301.	3.3	12
5244	Role of Yeasts in the Cranberry Fruit Rot Disease Complex. Plant Disease, 2021, 105, PDIS-11-19-2303.	1.4	3
5245	Dietary whey and egg proteins interact with inulin fiber to modulate energy balance and gut microbiota in obese rats. Journal of Nutritional Biochemistry, 2022, 99, 108860.	4.2	6
5246	Soil fungi are more sensitive than bacteria to short-term plant interactions of Picea asperata and Abies faxoniana. European Journal of Soil Biology, 2021, 106, 103348.	3.2	12
5247	Nutrient Enrichment Predominantly Affects Low Diversity Microbiomes in a Marine Trophic Symbiosis between Algal Farming Fish and Corals. Microorganisms, 2021, 9, 1873.	3.6	7
5248	Social environment drives sex and ageâ€specific variation in <i>Drosophila melanogaster</i> microbiome composition and predicted function. Molecular Ecology, 2021, 30, 5831-5843.	3.9	5
5249	Fungal Spore Richness in School Classrooms is Related to Surrounding Forest in a Season-Dependent Manner. Microbial Ecology, 2022, 84, 351-362.	2.8	1
5250	The decay and fungal succession of apples with bitter rot across a vegetation diversity gradient. Phytobiomes Journal, 0, , .	2.7	1
5251	Profiling the microbial community structure and functional diversity of a damâ€regulated river undergoing gravel bar restoration. Freshwater Biology, 2021, 66, 2170-2184.	2.4	5
5252	Peatland microhabitat heterogeneity drives phototrophic microbes distribution and photosynthetic activity. Environmental Microbiology, 2021, 23, 6811-6827.	3.8	5
5254	Biochar restructures plantâ€soilâ€microbe relationships in a woody cropping system. Soil Science Society of America Journal, 0, , .	2.2	0
5256	Positive Synergistic Effects of Quercetin and Rice Bran on Human Gut Microbiota Reduces Enterobacteriaceae Family Abundance and Elevates Propionate in a Bioreactor Model. Frontiers in Microbiology, 2021, 12, 751225.	3.5	2
5257	Can orchid mycorrhizal fungi be persistently harbored by the plant host?. Fungal Ecology, 2021, 53, 101071.	1.6	10
5258	Janthinobacter additions reduce rotifer grazing of microalga Microchloropsis salina in biotically complex communities. Algal Research, 2021, 58, 102400.	4.6	4
5259	Low-level environmental metal pollution is associated with altered gut microbiota of a wild rodent, the bank vole (Myodes glareolus). Science of the Total Environment, 2021, 790, 148224.	8.0	15
5260	Soil pH has a stronger effect than arsenic content on shaping plastisphere bacterial communities in soil. Environmental Pollution, 2021, 287, 117339.	7.5	35

#	Article	IF	CITATIONS
5261	Microbial interkingdom associations across soil depths reveal network connectivity and keystone taxa linked to soil fine-fraction carbon content. Agriculture, Ecosystems and Environment, 2021, 320, 107559.	5.3	21
5262	Using fecal immunochemical tubes for the analysis of the gut microbiome has the potential to improve colorectal cancer screening. Scientific Reports, 2021, 11, 19603.	3.3	9
5263	Homogeneous selection shapes rare biosphere in rhizosphere of medicinal plant. Ecological Indicators, 2021, 129, 107981.	6.3	14
5264	Effects of fish farm activities on the sponge Weberella bursa, and its associated microbiota. Ecological Indicators, 2021, 129, 107879.	6.3	10
5265	The influence of soil chemistry on branched tetraether lipids in mid- and high latitude soils: Implications for brGDGT- based paleothermometry. Geochimica Et Cosmochimica Acta, 2021, 310, 95-112.	3.9	34
5266	The probiotic Lactobacillus rhamnosus mimics the dark-driven regulation of appetite markers and melatonin receptors' expression in zebrafish (Danio rerio) larvae: Understanding the role of the gut microbiome. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2021, 256, 110634.	1.6	14
5267	Temporal variation of crude and refined oil biodegradation rates and microbial community composition in freshwater systems. Journal of Great Lakes Research, 2021, 47, 1376-1385.	1.9	3
5268	Amplicon metabarcoding data of prokaryotes and eukaryotes present in †Kalamata†table olives packaged under modified atmosphere. Data in Brief, 2021, 38, 107314.	1.0	3
5269	Endophytic PGPB Improves Plant Growth and Quality, and Modulates the Bacterial Community of an Intercropping System. Frontiers in Sustainable Food Systems, 2021, 5, .	3.9	11
5270	Understanding variations in soil properties and microbial communities in bamboo plantation soils along a chromium pollution gradient. Ecotoxicology and Environmental Safety, 2021, 222, 112507.	6.0	28
5271	Fungal community assembly during a high-temperature composting under different pasteurization regimes used to elaborate the Agaricus bisporus substrate. Fungal Biology, 2021, 125, 826-833.	2.5	7
5272	The tombstones at the Monumental Cemetery of Milano select for a specialized microbial community. International Biodeterioration and Biodegradation, 2021, 164, 105298.	3.9	7
5273	Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. Gastroenterology, 2021, 161, 1194-1207.e8.	1.3	28
5274	Tracking de novo protein synthesis in the activated sludge microbiome using BONCAT-FACS. Water Research, 2021, 205, 117696.	11.3	9
5275	Effect of probiotic, prebiotic, and synbiotic on the gut microbiota of autistic children using an in vitro gut microbiome model. Food Research International, 2021, 149, 110657.	6.2	22
5276	A watershed impacted by anthropogenic activities: Microbial community alterations and reservoir of antimicrobial resistance genes. Science of the Total Environment, 2021, 793, 148552.	8.0	4
5277	Metabolite changes of apple Penicillium expansum infection based on a UPLC-Q-TOF metabonomics approach. Postharvest Biology and Technology, 2021, 181, 111646.	6.0	10
5278	Transformation of fish waste protein to Hermetia illucens protein improves the efficacy of poultry by-products in the culture of juvenile barramundi, Lates calcarifer. Science of the Total Environment, 2021, 796, 149045.	8.0	19

#	Article	IF	CITATIONS
5279	Miscanthus x giganteus role in phytodegradation and changes in bacterial community of soil contaminated by petroleum industry. Ecotoxicology and Environmental Safety, 2021, 224, 112630.	6.0	11
5280	Farming systems influence the compositional, structural, and functional characteristics of the sugarcane-associated microbiome. Microbiological Research, 2021, 252, 126866.	5.3	2
5281	Full-fat insect meal in pelleted diets for weaned piglets: Effects on growth performance, nutrient digestibility, gastrointestinal function, and microbiota. Animal Feed Science and Technology, 2021, 281, 115086.	2.2	15
5282	Identification of the phylotypes involved in cis-dichloroethene and 1,4-dioxane biodegradation in soil microcosms. Science of the Total Environment, 2021, 794, 148690.	8.0	9
5283	Adding alfalfa to an annual crop rotation shifts the composition and functional responses of tomato rhizosphere microbial communities. Applied Soil Ecology, 2021, 167, 104102.	4.3	18
5284	Assessment of the fungal community associated with cocoa bean fermentation from two regions in Colombia. Food Research International, 2021, 149, 110670.	6.2	4
5285	Psychobiology of Stress and Adolescent Depression (PSY SAD) Study: Protocol overview for an fMRI-based multi-method investigation. Brain, Behavior, & Immunity - Health, 2021, 17, 100334.	2.5	2
5286	Seasonal variations in soil physicochemical properties and microbial community structure influenced by Spartina alterniflora invasion and Kandelia obovata restoration. Science of the Total Environment, 2021, 797, 149213.	8.0	25
5287	The microbiome affects liver sphingolipids and plasma fatty acids in a murine model of the Western diet based on soybean oil. Journal of Nutritional Biochemistry, 2021, 97, 108808.	4.2	6
5288	New insights in bacterial and eukaryotic diversity of microbial mats inhabiting exploited and abandoned salterns at the Ré Island (France). Microbiological Research, 2021, 252, 126854.	5.3	7
5289	Characterization of tissue-associated bacterial community of two Bathymodiolus species from the adjacent cold seep and hydrothermal vent environments. Science of the Total Environment, 2021, 796, 149046.	8.0	7
5290	Characterizing algal microbiomes using long-read nanopore sequencing. Algal Research, 2021, 59, 102456.	4.6	13
5291	Comparative study of the effects of biocides and metal oxide nanoparticles on microbial community structure in a stream impacted by hydraulic fracturing. Chemosphere, 2021, 284, 131255.	8.2	5
5292	Acylase enzymes disrupting quorum sensing alter the transcriptome and phenotype of Pseudomonas aeruginosa, and the composition of bacterial biofilms from wastewater treatment plants. Science of the Total Environment, 2021, 799, 149401.	8.0	20
5293	Natural attenuation of legacy hydrocarbon spills in pristine soils is feasible despite difficult environmental conditions in the monsoon tropics. Science of the Total Environment, 2021, 799, 149335.	8.0	3
5294	Long-term agricultural management impacts arbuscular mycorrhizal fungi more than short-term experimental drought. Applied Soil Ecology, 2021, 168, 104140.	4.3	17
5295	Anaerobic microbial corrosion of carbon steel under conditions relevant for deep geological repository of nuclear waste. Science of the Total Environment, 2021, 800, 149539.	8.0	21
5296	16S rRNA-based metagenomic profiling of microbes on contact surfaces within shared sanitation facilities. Ecological Genetics and Genomics, 2021, 21, 100095.	0.5	1

#	Article	IF	Citations
5297	Passive exposure to cannabidiol oil does not cause microbiome dysbiosis in larval zebrafish. Current Research in Microbial Sciences, 2021, 2, 100045.	2.3	2
5298	Dynamic variation of endogenous flora in kiwifruit and its association with ripening metabolism in response to ethylene micro-environment. Postharvest Biology and Technology, 2021, 182, 111695.	6.0	8
5299	Bacterial functional prediction tools detect but underestimate metabolic diversity compared to shotgun metagenomics in southwest Florida soils. Applied Soil Ecology, 2021, 168, 104129.	4.3	43
5300	Biochar amendment rapidly shifts microbial community structure with enhanced thermophilic digestion activity. Bioresource Technology, 2021, 341, 125864.	9.6	13
5301	Humic acids enrich the plant microbiota with bacterial candidates for the suppression of pathogens. Applied Soil Ecology, 2021, 168, 104146.	4.3	13
5302	Effect of virgin low density polyethylene microplastic ingestion on intestinal histopathology and microbiota of gilthead sea bream. Aquaculture, 2021, 545, 737245.	3.5	26
5303	Rearranging the sugarcane holobiont via plant growth-promoting bacteria and nitrogen input. Science of the Total Environment, 2021, 800, 149493.	8.0	10
5304	Localized reshaping of the fungal community in response to a forest fungal pathogen reveals resilience of Mediterranean mycobiota. Science of the Total Environment, 2021, 800, 149582.	8.0	7
5305	Effect of operational parameters, environmental conditions, and biotic interactions on bacterial communities present in urban wastewater treatment photobioreactors. Chemosphere, 2021, 284, 131271.	8.2	17
5306	Continuous H2/CO2 fermentation for acetic acid production under transient and continuous sulfide inhibition. Chemosphere, 2021, 285, 131536.	8.2	8
5307	Metagenomic analysis of MWWTP effluent treated via solar photo-Fenton at neutral pH: Effects upon microbial community, priority pathogens, and antibiotic resistance genes. Science of the Total Environment, 2021, 801, 149599.	8.0	13
5308	Effective orthophosphate removal from surface water using hydrogen-oxidizing bacteria: Moving towards applicability. Science of the Total Environment, 2021, 800, 149648.	8.0	5
5309	Fecal bacterial communities of wild black capuchin monkeys (Sapajus nigritus) from the Atlantic Forest biome in Southern Brazil are divergent from those of other non-human primates. Current Research in Microbial Sciences, 2021, 2, 100048.	2.3	6
5310	Soil bacterial diversity related to soil compaction and aggregates sizes in potato cropping systems. Applied Soil Ecology, 2021, 168, 104147.	4.3	7
5311	First proof of concept for full-scale, direct, low-temperature anaerobic treatment of municipal wastewater. Bioresource Technology, 2021, 341, 125786.	9.6	16
5312	Species turnover underpins the effect of elevated CO2 on biofilm communities through early succession. Climate Change Ecology, 2021, 2, 100017.	1.9	1
5313	A multi-omics study on quantifying antimicrobial resistance in European freshwater lakes. Environment International, 2021, 157, 106821.	10.0	9
5314	Green infrastructure influences soil health: Biological divergence one year after installation. Science of the Total Environment, 2021, 801, 149644.	8.0	9

#	Article	IF	CITATIONS
5315	Effects of tank cleaning frequency and sea cucumber co-culture on larval sablefish growth and survival, water quality, and microbial communities. Aquaculture, 2021, 545, 737213.	3.5	3
5316	Delving into the bacterial diversity of spoiled green Manzanilla Spanish-style table olive fermentations. International Journal of Food Microbiology, 2021, 359, 109415.	4.7	4
5317	Microbiota composition and susceptibility to florfenicol and oxytetracycline of bacterial isolates from mussels (Mytilus spp.) reared on different years and distance from salmon farms. Environmental Research, 2022, 204, 112068.	7. 5	8
5318	Squash root microbiome transplants and metagenomic inspection for in situ arid adaptations. Science of the Total Environment, 2022, 805, 150136.	8.0	12
5319	Probiotic yeast Saccharomyces cerevisiae coupled with Lactobacillus casei modulates physiological performance and promotes gut microbiota in juvenile barramundi, Lates calcarifer. Aquaculture, 2022, 546, 737346.	3.5	31
5320	Comparative characterization of microbial communities that inhabit PFAS-rich contaminated sites: A case-control study. Journal of Hazardous Materials, 2022, 423, 126941.	12.4	27
5321	Effect of the natural establishment of two plant species on microbial activity, on the composition of the fungal community, and on the mitigation of potentially toxic elements in an abandoned mine tailing. Science of the Total Environment, 2022, 802, 149788.	8.0	8
5322	Biodegradation of water-accommodated aromatic oil compounds in Arctic seawater at 0°C. Chemosphere, 2022, 286, 131751.	8.2	11
5323	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. Environment International, 2022, 158, 106899.	10.0	40
5324	Combined selective gamma irradiation and pulverized soil inoculation for ecologically relevant soil microfauna studies. Applied Soil Ecology, 2022, 169, 104223.	4.3	5
5325	Livestock microbial landscape patterns: Retail poultry microbiomes significantly vary by region and season. Food Microbiology, 2022, 101, 103878.	4.2	2
5326	Metal(loid)s diffusion pathway triggers distinct microbiota responses in key regions of typical karst non-ferrous smelting assembly. Journal of Hazardous Materials, 2022, 423, 127164.	12.4	12
5327	Gut microbiome alterations in the crustacean Pacifastacus leniusculus exposed to environmental concentrations of antibiotics and effects on susceptibility to bacteria challenges. Developmental and Comparative Immunology, 2022, 126, 104181.	2.3	10
5328	Recovery patterns of soil bacterial and fungal communities in Chinese boreal forests along a fire chronosequence. Science of the Total Environment, 2022, 805, 150372.	8.0	15
5329	Spatiotemporal dynamics of soil health in urban agriculture. Science of the Total Environment, 2022, 805, 150224.	8.0	6
5330	Microbial communities in full-scale woodchip bioreactors treating aquaculture effluents. Journal of Environmental Management, 2022, 301, 113852.	7.8	10
5331	Understanding the host-microbe-environment interactions: Intestinal microbiota and transcriptomes of black tiger shrimp Penaeus monodon at different salinity levels. Aquaculture, 2022, 546, 737371.	3.5	15
5332	Effect of external acetate on lactate-based carboxylate platform: Shifted lactate overloading limit and hydrogen co-production. Science of the Total Environment, 2022, 802, 149885.	8.0	13

#	Article	IF	CITATIONS
5333	Land-use affects soil microbial co-occurrence networks and their putative functions. Applied Soil Ecology, 2022, 169, 104184.	4.3	32
5334	Elevated levels of antibiotic resistance in groundwater during treated wastewater irrigation associated with infiltration and accumulation of antibiotic residues. Journal of Hazardous Materials, 2022, 423, 127155.	12.4	20
5335	Effects of spatially heterogeneous warming on gut microbiota, nutrition and gene flow of a heat-sensitive ungulate population. Science of the Total Environment, 2022, 806, 150537.	8.0	3
5336	Global evaluation of commercial arbuscular mycorrhizal inoculants under greenhouse and field conditions. Applied Soil Ecology, 2022, 169, 104225.	4.3	58
5337	Effect of freeze-dried kombucha culture on microbial composition and assessment of metabolic dynamics during fermentation. Food Microbiology, 2022, 101, 103889.	4.2	14
5338	Does a decrease in microbial biomass alter mycorrhizal attributes and soil quality indicators in coal mining areas under revegetation process?. Science of the Total Environment, 2022, 802, 149843.	8.0	5
5339	Microbial community redundance in biomethanation systems lead to faster recovery of methane production rates after starvation. Science of the Total Environment, 2022, 804, 150073.	8.0	12
5341	Effects of larval rearing substrates on some life-table parameters of Lutzomyia longipalpis sand flies. PLoS Neglected Tropical Diseases, 2021, 15, e0009034.	3.0	3
5342	Investigating the cow skin and teat canal microbiomes of the bovine udder using different sampling and sequencing approaches. Journal of Dairy Science, 2021, 104, 644-661.	3.4	20
5343	Inoculation of <i>Mimosa Pudica</i> with <i>Paraburkholderia phymatum</i> Results in Changes to the Rhizoplane Microbial Community Structure. Microbes and Environments, 2021, 36, n/a.	1.6	5
5344	Temperature and elemental sulfur shape microbial communities in two extremely acidic aquatic volcanic environments. Extremophiles, 2021, 25, 85-99.	2.3	6
5345	A Single Human-Relevant Fast Food Meal Rapidly Reorganizes Metabolomic and Transcriptomic Signatures in a Gut Microbiota-Dependent Manner#. Immunometabolism, 2021, 3, .	1.6	3
5346	Impact of land use on soil function and bacterial community in the Brazilian savanna. Anais Da Academia Brasileira De Ciencias, 2021, 93, e20201906.	0.8	4
5347	Short-term responses to ocean acidification: effects on relative abundance of eukaryotic plankton from the tropical Timor Sea. Marine Ecology - Progress Series, 2021, 658, 59-74.	1.9	3
5348	Illuminating the bacterial microbiome of Australian ticks with 16S and Rickettsia-specific next-generation sequencing. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100037.	1.9	9
5349	Links between gut microbiome composition and fatty liver disease in a large population sample. Gut Microbes, 2021, 13, 1-22.	9.8	41
5351	Morphological identification of ticks and molecular detection of tick-borne pathogens from bare-nosed wombats (Vombatus ursinus). Parasites and Vectors, 2021, 14, 60.	2.5	6
5352	rANOMALY: AmplicoN wOrkflow for Microbial community AnaLYsis. F1000Research, 2021, 10, 7.	1.6	23

#	Article	IF	Citations
5354	Functional plasticity in oyster gut microbiomes along a eutrophication gradient in an urbanized estuary. Animal Microbiome, 2021, 3, 5.	3.8	22
5355	<i>Dechloromonas</i> and close relatives prevail during hydrogenotrophic denitrification in stimulated microcosms with oxic aquifer material. FEMS Microbiology Ecology, 2021, 97, .	2.7	18
5356	Spatial analysis of gut microbiome reveals a distinct ecological niche associated with the mucus layer. Gut Microbes, 2021, 13, 1874815.	9.8	40
5357	Terroir Is the Main Driver of the Epiphytic Bacterial and Fungal Communities of Mango Carposphere in Reunion Island. Frontiers in Microbiology, 2020, 11, 619226.	3.5	5
5358	Root exudates increase soil respiration and alter microbial community structure in alpine permafrost and active layer soils. Environmental Microbiology, 2021, 23, 2152-2168.	3.8	31
5359	Microbial community dynamics of fermented kefir beverages changes over time. International Journal of Dairy Technology, 2021, 74, 324-331.	2.8	21
5360	The Interplay between Campylobacter and the Caecal Microbial Community of Commercial Broiler Chickens over Time. Microorganisms, 2021, 9, 221.	3.6	10
5361	The intestinal microbiota and metabolites in patients with anorexia nervosa. Gut Microbes, 2021, 13, 1-25.	9.8	58
5362	Dinoflagellates alter their carbon and nutrient metabolic strategies across environmental gradients in the central Pacific Ocean. Nature Microbiology, 2021, 6, 173-186.	13.3	45
5363	SARS-CoV-2 infection in nonhuman primates alters the composition and functional activity of the gut microbiota. Gut Microbes, 2021, 13, 1-19.	9.8	75
5364	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. Nature Genetics, 2021, 53, 147-155.	21.4	101
5365	Elevated gut microbiome abundance of <i>Christensenellaceae, Porphyromonadaceae and Rikenellaceae</i> is associated with reduced visceral adipose tissue and healthier metabolic profile in Italian elderly. Gut Microbes, 2021, 13, 1-19.	9.8	127
5366	MZINBVA: variational approximation for multilevel zero-inflated negative-binomial models for association analysis in microbiome surveys. Briefings in Bioinformatics, 2022, 23, .	6.5	2
5367	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, 2021, 13, 1-20.	9.8	9
5368	Parenteral Fish-Oil Containing Lipid Emulsions Limit Initial Lipopolysaccharide-Induced Host Immune Responses in Preterm Pigs. Nutrients, 2021, 13, 205.	4.1	5
5371	Microbial Source Tracking in the Love Creek Watershed, Delaware (USA). Delaware Journal of Public Health, 2021, 7, 22-31.	0.3	0
5373	Identification and Characterization of Metabolic Potential of Different Strains from Genus Rhizobium. Proceedings (mdpi), 2021, 66, .	0.2	0
5374	Changes in Bacterial Community Structure and Enriched Functional Bacteria Associated With Turfgrass Monoculture. Frontiers in Bioengineering and Biotechnology, 2020, 8, 530067.	4.1	3

#	Article	IF	CITATIONS
5375	Temporal Dynamics of Cloacal Microbiota in Adult Laying Chickens With and Without Access to an Outdoor Range. Frontiers in Microbiology, 2020, 11, 626713.	3.5	8
5376	The intestinal microbial composition in Greylag geese differs with steatosis induction mode: spontaneous or induced by overfeeding. Animal Microbiome, 2021, 3, 6.	3.8	1
5377	The starlet sea anemone, <i>Nematostella vectensis</i> , possesses body region-specific bacterial associations with spirochetes dominating the capitulum. FEMS Microbiology Letters, 2021, 368, .	1.8	7
5378	Barrier Housing and Gender Effects on Allergic Airway Disease in a Murine House Dust Mite Model. ImmunoHorizons, 2021, 5, 33-47.	1.8	12
5379	Bacterial diversity and lipid biomarkers in sea ice and sinking particulate organic material during the melt season in the Canadian Arctic. Elementa, 2021, 9, .	3.2	3
5380	Microbiome Signatures in a Fast- and Slow-Progressing Gastric Cancer Murine Model and Their Contribution to Gastric Carcinogenesis. Microorganisms, 2021, 9, 189.	3.6	13
5381	Unravelling the Genetic and Function Diversity of Dominant Bacterial Communities Involved in Co-Composting Bioremediation of Complex Crude Oil Waste Sludge. SSRN Electronic Journal, 0, , .	0.4	0
5382	Parkinson's Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. SSRN Electronic Journal, 0, , .	0.4	0
5383	Gene-Environment-Gut Interactions in Huntington's Disease Mice Are Associated with Environmental Modulation of the Gut Microbiome. SSRN Electronic Journal, 0, , .	0.4	0
5384	Phytophthora Root Rot Modifies the Composition of the Avocado Rhizosphere Microbiome and Increases the Abundance of Opportunistic Fungal Pathogens. Frontiers in Microbiology, 2020, 11, 574110.	3 . 5	40
5385	Grapevine Microbiota Reflect Diversity among Compartments and Complex Interactions within and among Root and Shoot Systems. Microorganisms, 2021, 9, 92.	3.6	29
5386	Dynamics of the Apple Fruit Microbiome after Harvest and Implications for Fruit Quality. Microorganisms, 2021, 9, 272.	3.6	22
5387	Annual phytoplankton dynamics in coastal waters from Fildes Bay, Western Antarctic Peninsula. Scientific Reports, 2021, 11, 1368.	3.3	17
5388	Effects of aging on the skin and gill microbiota of farmed seabass and seabream. Animal Microbiome, 2021, 3, 10.	3.8	23
5389	Relative Influence of Plastic Debris Size and Shape, Chemical Composition and Phytoplankton-Bacteria Interactions in Driving Seawater Plastisphere Abundance, Diversity and Activity. Frontiers in Microbiology, 2020, 11, 610231.	3.5	38
5390	Soil microbial legacies differ following drying-rewetting and freezing-thawing cycles. ISME Journal, 2021, 15, 1207-1221.	9.8	54
5391	Antimicrobial-specific response from resistance gene carriers studied in a natural, highly diverse microbiome. Microbiome, 2021, 9, 29.	11.1	13
5392	Integration of DNA extraction, metabarcoding and an informatics pipeline to underpin a national citizen science honey monitoring scheme. MethodsX, 2021, 8, 101303.	1.6	4

#	Article	IF	Citations
5393	Largeâ€scale eDNA metabarcoding survey reveals marine biogeographic break and transitions over tropical northâ€western Australia. Diversity and Distributions, 2021, 27, 1942-1957.	4.1	45
5395	Trace gas oxidizers are widespread and active members of soil microbial communities. Nature Microbiology, 2021, 6, 246-256.	13.3	97
5397	The Fungal Biome of the Oral Cavity. Methods in Molecular Biology, 2016, 1356, 107-135.	0.9	12
5398	Open Data Science. Lecture Notes in Computer Science, 2018, , 31-39.	1.3	1
5399	Metabarcoding Techniques for Assessing Biodiversity of Marine Animal Forests., 2016, , 1-29.		16
5400	Mentholation triggers brand-specific shifts in the bacterial microbiota of commercial cigarette products. Applied Microbiology and Biotechnology, 2020, 104, 6287-6297.	3.6	11
5401	Characterization of a thermally tolerant Orbicella faveolata reef in Abaco, The Bahamas. Coral Reefs, 2020, 39, 675-685.	2.2	23
5402	Enrichment of endophytic Actinobacteria in roots and rhizomes of Miscanthus × giganteus plants exposed to diclofenac and sulfamethoxazole. Environmental Science and Pollution Research, 2020, 27, 11892-11904.	5. 3	27
5403	Shallow floating treatment wetland capable of sulfate reduction in acid mine drainage impacted waters in a northern climate. Journal of Environmental Management, 2020, 263, 110351.	7.8	10
5404	Homogeneous selection drives antibiotic resistome in two adjacent sub-watersheds, China. Journal of Hazardous Materials, 2020, 398, 122820.	12.4	46
5405	The Surface Microbiome of Clinically Unaffected Skinfolds in Hidradenitis Suppurativa: A Cross-Sectional Culture-Based and 16S rRNA Gene Amplicon Sequencing Study in 60 Patients. Journal of Investigative Dermatology, 2020, 140, 1847-1855.e6.	0.7	38
5406	Particle-attached riverine bacteriome shifts in a pollutant-resistant and pathogenic community during a Mediterranean extreme storm event. Science of the Total Environment, 2020, 732, 139047.	8.0	7
5407	Anaerobic oxidation of methane and associated microbiome in anoxic water of Northwestern Siberian lakes. Science of the Total Environment, 2020, 736, 139588.	8.0	67
5408	Soil N2O emission potential falls along a denitrification phenotype gradient linked to differences in microbiome, rainfall and carbon availability. Soil Biology and Biochemistry, 2020, 150, 108004.	8.8	23
5409	Cryopreservation and fast recovery of enriched syngas-converting microbial communities. Water Research, 2020, 177, 115747.	11.3	11
5410	Surface Stability in Drylands Is Influenced by Dispersal Strategy of Soil Bacteria. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 3403-3418.	3.0	16
5411	Factors influencing bacterial microbiome composition in a wild non-human primate community in TaÃ⁻ National Park, Cà te d'lvoire. ISME Journal, 2018, 12, 2559-2574.	9.8	31
5412	The gut microbiota response to helminth infection depends on host sex and genotype. ISME Journal, 2020, 14, 1141-1153.	9.8	31

#	Article	IF	CITATIONS
5413	Diverse coral reef invertebrates exhibit patterns of phylosymbiosis. ISME Journal, 2020, 14, 2211-2222.	9.8	43
5414	Characteristics of the bacterial microbiome in association with common intestinal parasites in irritable bowel syndrome. Clinical and Translational Gastroenterology, 2018, 9, e161.	2.5	64
5415	Intestinal fungi are causally implicated in microbiome assembly and immune development in mice. Nature Communications, 2020, 11, 2577.	12.8	151
5416	Intergenerational transfer of antibiotic-perturbed microbiota enhances colitis in susceptible mice. Nature Microbiology, 2018, 3, 234-242.	13.3	118
5417	A Common Practice of Widespread Antimicrobial Use in Horse Production Promotes Multi-Drug Resistance. Scientific Reports, 2020, 10, 911.	3.3	30
5418	Next-generation sequencing in the diagnosis of viral encephalitis: sensitivity and clinical limitations. Scientific Reports, 2020, 10, 16173.	3.3	23
5419	Soil microbiomes mediate degradation of vinyl ester-based polymer composites. Communications Materials, 2020, 1 , .	6.9	25
5420	Effects of fecal microbiota transplantation in subjects with irritable bowel syndrome are mirrored by changes in gut microbiome. Gut Microbes, 2020, 12, 1794263.	9.8	31
5421	Changes in IgA-targeted microbiota following fecal transplantation for recurrent <i>Clostridioides difficile</i> infection. Gut Microbes, 2021, 13, 1-12.	9.8	10
5422	Oral microbiome in down syndrome and its implications on oral health. Journal of Oral Microbiology, 2021, 13, 1865690.	2.7	15
5423	Method Validation for Extraction of DNA from Human Stool Samples for Downstream Microbiome Analysis. Biopreservation and Biobanking, 2020, 18, 102-116.	1.0	17
5424	Phylogeny and diversity of alkane-degrading enzyme gene variants in the laurentian great lakes and western atlantic. FEMS Microbiology Letters, 2020, 367, .	1.8	4
5425	Dadasnake, a Snakemake implementation of DADA2 to process amplicon sequencing data for microbial ecology. GigaScience, 2020, 9, .	6.4	39
5426	Minor Changes in the Composition and Function of the Gut Microbiota During a 12-Week Whole Grain Wheat or Refined Wheat Intervention Correlate with Liver Fat in Overweight and Obese Adults. Journal of Nutrition, 2021, 151, 491-502.	2.9	22
5427	Validation of a PNA Clamping Method for Reducing Host DNA Amplification and Increasing Eukaryotic Diversity in Rhizosphere Microbiome Studies. Phytobiomes Journal, 2020, 4, 291-302.	2.7	14
5428	Septic Stability? Gut Microbiota in Young Adult Mice Maintains Overall Stability After Sepsis Compared to Old Adult Mice. Shock, 2021, 55, 519-525.	2.1	12
5429	Defining Microbiome Readiness for Surgery: Dietary Prehabilitation and Stool Biomarkers as Predictive Tools to Improve Outcome. Annals of Surgery, 2022, 276, e361-e369.	4.2	17
5430	Age-related environmental gradients influence invertebrate distribution in the Prince Charles Mountains, East Antarctica. Royal Society Open Science, 2016, 3, 160296.	2.4	10

#	Article	IF	CITATIONS
5431	Genetic diversity of Koala retrovirus env gene subtypes: insights into northern and southern koala populations. Journal of General Virology, 2019, 100, 1328-1339.	2.9	20
5432	Polymicrobial oral biofilm models: simplifying the complex. Journal of Medical Microbiology, 2019, 68, 1573-1584.	1.8	39
5433	Myoviridae phage PDX kills enteroaggregative Escherichia coli without human microbiome dysbiosis. Journal of Medical Microbiology, 2020, 69, 309-323.	1.8	26
5434	Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. Microbial Genomics, 2020, 6, .	2.0	69
5670	Soil microbes of an urban remnant riparian zone have greater potential for N removal than a degraded riparian zone. Environmental Microbiology, 2020, 22, 3302-3314.	3.8	7
5671	Parasitic â€~ <i>Candidatus</i> Aquarickettsia rohweri' is a marker of disease susceptibility in <scp><i>Acropora cervicornis</i></scp> but is lost during thermal stress. Environmental Microbiology, 2020, 22, 5341-5355.	3.8	31
5672	Symbiont community diversity is more variable in corals that respond poorly to stress. Global Change Biology, 2020, 26, 2220-2234.	9.5	34
5673	Seed-Derived Microbial Colonization of Wild Emmer and Domesticated Bread Wheat (<i>Triticum) Tj ETQq1 1 0 and Composition. MBio, 2020, 11, .</i>	.784314 rş 4.1	gBT /Overloc 40
5674	Iron Flocs and the Three Domains: Microbial Interactions in Freshwater Iron Mats. MBio, 2020, 11, .	4.1	5
5675	Robust Archaeal and Bacterial Communities Inhabit Shallow Subsurface Sediments of the Bonneville Salt Flats. MSphere, 2019, 4, .	2.9	22
5676	Dual and Triple Epithelial Coculture Model Systems with Donor-Derived Microbiota and THP-1 Macrophages To Mimic Host-Microbe Interactions in the Human Sinonasal Cavities. MSphere, 2020, 5, .	2.9	14
5677	Randomized Lasso Links Microbial Taxa with Aquatic Functional Groups Inferred from Flow Cytometry. MSystems, 2019, 4, .	3.8	14
5678	The Generalized Matrix Decomposition Biplot and Its Application to Microbiome Data. MSystems, 2019, 4, .	3.8	6
5679	Stability of the Virome in Lab- and Field-Collected Aedes albopictus Mosquitoes across Different Developmental Stages and Possible Core Viruses in the Publicly Available Virome Data of <i>Aedes</i> Mosquitoes. MSystems, 2020, 5, .	3.8	40
5680	Isolation of SAR11 Marine Bacteria from Cryopreserved Seawater. MSystems, 2020, 5, .	3.8	4
5681	Age matters: Submersion period shapes community composition of lake biofilms under glyphosate stress. Facets, 2018, 3, 934-951.	2.4	13
5682	Gut microbiota–dependent modulation of innate immunity and lymph node remodeling affects cardiac allograft outcomes. JCI Insight, 2018, 3, .	5.0	53
5683	Mucosal-associated invariant and $\hat{l}^3\hat{l}^*T$ cell subsets respond to initial Mycobacterium tuberculosis infection. JCI Insight, 2018, 3, .	5.0	59

#	Article	IF	CITATIONS
5684	High dietary salt–induced DC activation underlies microbial dysbiosis-associated hypertension. JCl Insight, 2019, 4, .	5.0	105
5685	Fetal exposure to the maternal microbiota in humans and mice. JCI Insight, 2019, 4, .	5.0	115
5686	Meta-analysis of the gut microbiota in predicting response to cancer immunotherapy in metastatic melanoma. JCI Insight, 2020, 5, .	5.0	85
5687	$\hat{l}^2\text{-Klotho}$ deficiency protects against obesity through a crosstalk between liver, microbiota, and brown adipose tissue. JCl Insight, 2017, 2, .	5.0	41
5688	In situ pilot application of nZVI embedded in activated carbon for remediation of chlorinated ethene-contaminated groundwater: effect on microbial communities. Environmental Sciences Europe, 2020, 32, .	5.5	11
5689	Characterisation of microbiota in saliva, bronchoalveolar lavage fluid, non-malignant, peritumoural and tumour tissue in non-small cell lung cancer patients: a cross-sectional clinical trial. Respiratory Research, 2020, 21, 129.	3.6	32
5690	Lifestyle and the presence of helminths is associated with gut microbiome composition in Cameroonians. Genome Biology, 2020, 21, 122.	8.8	48
5691	Faecal microbiota transplant from aged donor mice affects spatial learning and memory via modulating hippocampal synaptic plasticity- and neurotransmission-related proteins in young recipients. Microbiome, 2020, 8, 140.	11.1	134
5692	Modeling microbial abundances and dysbiosis with beta-binomial regression. Annals of Applied Statistics, 2020, 14, 94-115.	1.1	206
5693	Comparative Analysis of Bacterial Diversity and Community Structure in the Rhizosphere and Root Endosphere of Two Halophytes, <i>Salicornia europaea</i> and <i>Glaux maritima</i> , Collected from Two Brackish Lakes in Japan. Microbes and Environments, 2020, 35, n/a.	1.6	11
5694	Characterization of cellulose-degrading microbiota from the eastern subterranean termite and soil. F1000Research, 0, 6, 2082.	1.6	1
5695	Taxa: An R package implementing data standards and methods for taxonomic data. F1000Research, 2018, 7, 272.	1.6	26
5696	ranacapa: An R package and Shiny web app to explore environmental DNA data with exploratory statistics and interactive visualizations. F1000Research, 2018, 7, 1734.	1.6	132
5697	Microbiota profiling with long amplicons using Nanopore sequencing: full-length 16S rRNA gene and whole rrn operon. F1000Research, 2018, 7, 1755.	1.6	68
5698	Microbiota profiling with long amplicons using Nanopore sequencing: full-length 16S rRNA gene and the 16S-ITS-23S of theÂrrn operon. F1000Research, 2018, 7, 1755.	1.6	67
5699	microbiomeDASim:ÂSimulating longitudinal differential abundance for microbiome data. F1000Research, 2019, 8, 1769.	1.6	3
5700	Staphylococcus aureus nasal carriage and microbiome composition among medical students from Colombia: a cross-sectional study. F1000Research, 2020, 9, 78.	1.6	5
5701	Staphylococcus aureus nasal carriage and microbiome composition among medical students from Colombia: a cross-sectional study. F1000Research, 2020, 9, 78.	1.6	7

#	Article	IF	CITATIONS
5702	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	1.6	11
5703	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. F1000Research, 2016, 5, 1492.	1.6	466
5704	biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. F1000Research, 2016, 5, 2348.	1.6	2
5706	Phylosymbiosis: Relationships and Functional Effects of Microbial Communities across Host Evolutionary History. PLoS Biology, 2016, 14, e2000225.	5.6	475
5707	Metacoder: An R package for visualization and manipulation of community taxonomic diversity data. PLoS Computational Biology, 2017, 13, e1005404.	3.2	526
5708	A joint modeling approach for longitudinal microbiome data improves ability to detect microbiome associations with disease. PLoS Computational Biology, 2020, 16, e1008473.	3.2	7
5709	Bacterial Endophytic Communities in the Grapevine Depend on Pest Management. PLoS ONE, 2014, 9, e112763.	2.5	125
5710	Effects of Vendor and Genetic Background on the Composition of the Fecal Microbiota of Inbred Mice. PLoS ONE, 2015, 10, e0116704.	2.5	268
5711	Estimating Bacterial Diversity for Ecological Studies: Methods, Metrics, and Assumptions. PLoS ONE, 2015, 10, e0125356.	2.5	89
5712	The Gut Microbiota of Wild Mice. PLoS ONE, 2015, 10, e0134643.	2.5	103
5713	Cloacal Microbiome Structure in a Long-Distance Migratory Bird Assessed Using Deep 16sRNA Pyrosequencing. PLoS ONE, 2015, 10, e0137401.	2.5	70
5714	Methanosarcina Play an Important Role in Anaerobic Co-Digestion of the Seaweed Ulva lactuca: Taxonomy and Predicted Metabolism of Functional Microbial Communities. PLoS ONE, 2015, 10, e0142603.	2.5	33
5715	The Metagenome of Utricularia gibba's Traps: Into the Microbial Input to a Carnivorous Plant. PLoS ONE, 2016, 11, e0148979.	2.5	35
5716	Microbial Diversity and Parasitic Load in Tropical Fish of Different Environmental Conditions. PLoS ONE, 2016, 11, e0151594.	2.5	50
5717	Effects of Isoflavone-Enriched Feed on the Rumen Microbiota in Dairy Cows. PLoS ONE, 2016, 11, e0154642.	2.5	43
5718	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.	2.5	60
5719	Investigation into Host Selection of the Cecal Acetogen Population in Rabbits after Weaning. PLoS ONE, 2016, 11, e0158768.	2.5	18
5720	Nutrient Deprivation Affects Salmonella Invasion and Its Interaction with the Gastrointestinal Microbiota. PLoS ONE, 2016, 11, e0159676.	2.5	9

#	Article	IF	Citations
5721	Quantifying the Sensitivity of Soil Microbial Communities to Silver Sulfide Nanoparticles Using Metagenome Sequencing. PLoS ONE, 2016, 11, e0161979.	2.5	41
5722	Urinary Microbiota Associated with Preterm Birth: Results from the Conditions Affecting Neurocognitive Development and Learning in Early Childhood (CANDLE) Study. PLoS ONE, 2016, 11, e0162302.	2.5	18
5723	Taxa of the Nasal Microbiome Are Associated with Influenza-Specific IgA Response to Live Attenuated Influenza Vaccine. PLoS ONE, 2016, 11, e0162803.	2.5	64
5724	Distinctive Feature of Microbial Communities and Bacterial Functional Profiles in Tricholoma matsutake Dominant Soil. PLoS ONE, 2016, 11, e0168573.	2.5	39
5725	Bacterial Communities Associated with Houseflies (Musca domestica L.) Sampled within and between Farms. PLoS ONE, 2017, 12, e0169753.	2.5	69
5726	Diversity and composition of vaginal microbiota of pregnant women at risk for transmitting Group B Streptococcus treated with intrapartum penicillin. PLoS ONE, 2017, 12, e0169916.	2.5	19
5727	Longitudinal assessment of sputum microbiome by sequencing of the 16S rRNA gene in non-cystic fibrosis bronchiectasis patients. PLoS ONE, 2017, 12, e0170622.	2.5	99
5728	Longitudinal sampling of the lung microbiota in individuals with cystic fibrosis. PLoS ONE, 2017, 12, e0172811.	2.5	64
5729	Alterations in airway microbiota in patients with PaO2/FiO2 ratio ≤300 after burn and inhalation injury. PLoS ONE, 2017, 12, e0173848.	2.5	11
5730	Patterns of variation in diversity of the Mississippi river microbiome over 1,300 kilometers. PLoS ONE, 2017, 12, e0174890.	2.5	38
5731	Development of the cutaneous microbiome in the preterm infant: A prospective longitudinal study. PLoS ONE, 2017, 12, e0176669.	2.5	47
5732	Impact of maintenance immunosuppressive therapy on the fecal microbiome of renal transplant recipients: Comparison between an everolimus- and a standard tacrolimus-based regimen. PLoS ONE, 2017, 12, e0178228.	2.5	44
5733	Impact of environmental microbiota on human microbiota of workers in academic mouse research facilities: An observational study. PLoS ONE, 2017, 12, e0180969.	2.5	31
5734	Disruption in the cecal microbiota of chickens challenged with Clostridium perfringens and other factors was alleviated by Bacillus licheniformis supplementation. PLoS ONE, 2017, 12, e0182426.	2.5	74
5735	Active microorganisms thrive among extremely diverse communities in cloud water. PLoS ONE, 2017, 12, e0182869.	2.5	103
5736	A pivotal role for ocean eddies in the distribution of microbial communities across the Antarctic Circumpolar Current. PLoS ONE, 2017, 12, e0183400.	2.5	14
5737	Honey bee foraging ecology: Season but not landscape diversity shapes the amount and diversity of collected pollen. PLoS ONE, 2017, 12, e0183716.	2.5	101
5738	Effects of Eimeria tenella infection on chicken caecal microbiome diversity, exploring variation associated with severity of pathology. PLoS ONE, 2017, 12, e0184890.	2.5	109

#	Article	IF	CITATIONS
5739	Behaviour during transportation predicts stress response and lower airway contamination in horses. PLoS ONE, 2018, 13, e0194272.	2.5	41
5740	Investigation of the seasonal microbiome of Anopheles coluzzii mosquitoes in Mali. PLoS ONE, 2018, 13, e0194899.	2.5	43
5741	In-field bioreactors demonstrate dynamic shifts in microbial communities in response to geochemical perturbations. PLoS ONE, 2020, 15, e0232437.	2.5	5
5742	Defining the sediment prokaryotic communities of the Indian River Lagoon, FL, USA, an Estuary of National Significance. PLoS ONE, 2020, 15, e0236305.	2.5	9
5743	Bone biodeteriorationâ€"The effect of marine and terrestrial depositional environments on early diagenesis and bone bacterial community. PLoS ONE, 2020, 15, e0240512.	2.5	22
5744	Biological invasions alter environmental microbiomes: A meta-analysis. PLoS ONE, 2020, 15, e0240996.	2.5	13
5745	Broiler chickens and early life programming: Microbiome transplant-induced cecal community dynamics and phenotypic effects. PLoS ONE, 2020, 15, e0242108.	2.5	16
5746	Diversity of bacteria populations associated with different thallus regions of the brown alga Laminaria digitata. PLoS ONE, 2020, 15, e0242675.	2.5	23
5747	Response of oat morphologies, root exudates, and rhizosphere fungal communities to amendments in a saline-alkaline environment. PLoS ONE, 2020, 15, e0243301.	2.5	5
5748	The applicability of forensic time since death estimation methods for buried bodies in advanced decomposition stages. PLoS ONE, 2020, 15, e0243395.	2.5	24
5749	MyD88 signaling in dendritic cells and the intestinal epithelium controls immunity against intestinal infection with C. rodentium. PLoS Pathogens, 2017, 13, e1006357.	4.7	31
5750	Loss of CNFY toxin-induced inflammation drives Yersinia pseudotuberculosis into persistency. PLoS Pathogens, 2018, 14, e1006858.	4.7	23
5751	The cervicovaginal mucus barrier to HIV-1 is diminished in bacterial vaginosis. PLoS Pathogens, 2020, 16, e1008236.	4.7	46
5752	Soil microbiome of the postmining areas in polar ecosystems in surroundings of Nadym, Western Siberia, Russia. Open Agriculture, 2019, 4, 684-696.	1.7	13
5753	Serotonin and tryptophan metabolites, autoantibodies and gut microbiome in APECED. Endocrine Connections, 2019, 8, 69-77.	1.9	3
5754	Early genistein exposure of California mice and effects on the gut microbiota–brain axis. Journal of Endocrinology, 2019, 242, 139-157.	2.6	21
5755	Diversity of endophytic fungi in the leaflets and branches of Poincianella pyramidalis, an endemic species of Brazilian tropical dry forest. Acta Botanica Brasilica, 2020, 34, 755-764.	0.8	2
5756	Restoration of soil microbiome in various soil horizons after crown and surface wildfires. Ecological Genetics, 2020, 18, 343-356.	0.5	5

#	Article	IF	CITATIONS
5757	Gut microbiota and metabolite alterations associated with reduced bone mineral density or bone metabolic indexes in postmenopausal osteoporosis. Aging, 2020, 12, 8583-8604.	3.1	130
5758	Gut microbial profile analysis by MiSeq sequencing of pancreatic carcinoma patients in China. Oncotarget, 2017, 8, 95176-95191.	1.8	160
5759	Specific alterations in gut microbiota are associated with prognosis of Budd-Chiari syndrome. Oncotarget, 2018, 9, 3303-3320.	1.8	7
5760	Bacteriome and mycobiome and bacteriome-mycobiome interactions in head and neck squamous cell carcinoma. Oncotarget, 2020, 11, 2375-2386.	1.8	27
5761	MicroRNA-146a constrains multiple parameters of intestinal immunity and increases susceptibility to DSS colitis. Oncotarget, 2015, 6, 28556-28572.	1.8	53
5762	Differential susceptibility to colorectal cancer due to naturally occurring gut microbiota. Oncotarget, 2015, 6, 33689-33704.	1.8	57
5763	 	3.7	6
5765	phylosmith: an R-package for reproducible and efficient microbiome analysis with phyloseq-objects. Journal of Open Source Software, 2019, 4, 1442.	4.6	40
5766	Diet Induces Reproducible Alterations in the Mouse and Human Gut Microbiome. SSRN Electronic Journal, 0, , .	0.4	2
5767	Aims, Study Design, and Enrollment Results From the Assessing Predictors of Infant Respiratory Syncytial Virus Effects and Severity Study. JMIR Research Protocols, 2019, 8, e12907.	1.0	9
5768	Targeting the Infant Gut Microbiota Through a Perinatal Educational Dietary Intervention: Protocol for a Randomized Controlled Trial. JMIR Research Protocols, 2019, 8, e14771.	1.0	11
5769	Impact of winter enclosures on the gut bacterial microbiota of red deer in the Bavarian Forest National Park. Wildlife Biology, 2019, 2019, .	1.4	12
5771	Metagenomic and volatile profiles of ripened cheese obtained from dairy ewes fed a dietary hemp seed supplementation. Journal of Dairy Science, 2020, 103, 5882-5892.	3.4	11
5772	Bacterial community composition of flocculent matter under a salmonid aquaculture site in Newfoundland, Canada. Aquaculture Environment Interactions, 2016, 8, 637-646.	1.8	19
5773	Impact of prawn farming effluent on coral reef water nutrients and microorganisms. Aquaculture Environment Interactions, 2017, 9, 331-346.	1.8	9
5774	Comparing the community structure of Bacteria and micro-Eukarya from the Hawaiian anchialine ecosystem during wet and dry seasons. Aquatic Microbial Ecology, 2018, 82, 87-104.	1.8	6
5775	Bacteria known to induce settlement of larvae of Hydroides elegans are rare in natural inductive biofilm. Aquatic Microbial Ecology, 2020, 84, 31-42.	1.8	8
5776	Nutrient availability and organic matter quality shape bacterial community structure in a lake biofilm. Aquatic Microbial Ecology, 2020, 85, 1-18.	1.8	2

#	Article	IF	CITATIONS
5777	Distinct processes structure bacterioplankton and protist communities across an oceanic front. Aquatic Microbial Ecology, 2020, 85, 19-34.	1.8	9
5778	Microbiome dynamics of two differentially resilient corals. Diseases of Aquatic Organisms, 2018, 131, 213-226.	1.0	7
5779	18S V9 metabarcoding correctly depicts plankton estuarine community drivers. Marine Ecology - Progress Series, 2017, 584, 31-43.	1.9	20
5780	Changes in zooplankton assemblages in northern Monterey Bay, California, during a fall transition. Marine Ecology - Progress Series, 2018, 604, 99-120.	1.9	6
5781	Detecting respiratory bacterial communities of wild dolphins: implications for animal health. Marine Ecology - Progress Series, 2019, 622, 203-217.	1.9	15
5782	Microbiome analyses and presence of cable bacteria in the burrow sediment of Upogebia pugettensis. Marine Ecology - Progress Series, 2020, 648, 79-94.	1.9	14
5783	A Pilot Study of the Effect of Deployment on the Gut Microbiome and Traveler's Diarrhea Susceptibility. Frontiers in Cellular and Infection Microbiology, 2020, 10, 589297.	3.9	5
5784	Hydrological Conditions Influence Soil and Methane-Cycling Microbial Populations in Seasonally Saturated Wetlands. Frontiers in Environmental Science, 2020, 8, .	3.3	12
5785	Exploring Environmental DNA (eDNA) to Assess Biodiversity of Hard Substratum Faunal Communities on the Lucky Strike Vent Field (Mid-Atlantic Ridge) and Investigate Recolonization Dynamics After an Induced Disturbance. Frontiers in Marine Science, 2020, 6, .	2.5	19
5786	Domestication of Local Microbial Consortia for Efficient Recovery of Gold Through Top-Down Selection in Airlift Bioreactors. Frontiers in Microbiology, 2019, 10, 60.	3. 5	7
5787	Schistosomiasis Vector Snails and Their Microbiota Display a Phylosymbiosis Pattern. Frontiers in Microbiology, 2019, 10, 3092.	3.5	28
5788	Bovine Teat Cistern Microbiota Composition and Richness Are Associated With the Immune and Microbial Responses During Transition to Once-Daily Milking. Frontiers in Microbiology, 2020, 11, 602404.	3 . 5	9
5789	Intestinal Epithelial Cell-Derived Extracellular Vesicles Modulate Hepatic Injury via the Gut-Liver Axis During Acute Alcohol Injury. Frontiers in Pharmacology, 2020, 11, 603771.	3.5	17
5790	Shifts in the Active Rhizobiome Paralleling Low Meloidogyne chitwoodi Densities in Fields Under Prolonged Organic Soil Management. Frontiers in Plant Science, 2019, 10, 1697.	3.6	24
5791	Gut Microbiome Composition Remains Stable in Individuals with Diabetes-Related Early to Late Stage Chronic Kidney Disease. Biomedicines, 2021, 9, 19.	3.2	11
5792	Bacterial Composition and Diversity in Deep-Sea Sediments from the Southern Colombian Caribbean Sea. Diversity, 2021, 13, 10.	1.7	11
5793	Growth Performance and Adaptability of European Sea Bass (Dicentrarchus labrax) Gut Microbiota to Alternative Diets Free of Fish Products. Microorganisms, 2020, 8, 1346.	3.6	24
5794	Targeted Next-Generation Sequencing and Informatics as an Effective Tool to Establish the Composition of Bovine Piroplasm Populations in Endemic Regions. Microorganisms, 2021, 9, 21.	3.6	10

#	Article	IF	Citations
5795	Vibrio Colonization Is Highly Dynamic in Early Microplastic-Associated Biofilms as Well as on Field-Collected Microplastics. Microorganisms, 2021, 9, 76.	3.6	48
5796	Effects of a Synbiotic Formula on Functional Bowel Disorders and Gut Microbiota Profile during Long-Term Home Enteral Nutrition (LTHEN): A Pilot Study. Nutrients, 2021, 13, 87.	4.1	3
5797	Diversity and Distribution Patterns of Endolichenic Fungi in Jeju Island, South Korea. Sustainability, 2020, 12, 3769.	3.2	17
5798	In Vivo Entombment of Bacteria and Fungi during Calcium Oxalate, Brushite, and Struvite Urolithiasis. Kidney360, 2021, 2, 298-311.	2.1	14
5799	Secondary metabolites of <i>Bacillus subtilis</i> impact the assembly of soil-derived semisynthetic bacterial communities. Beilstein Journal of Organic Chemistry, 2020, 16, 2983-2998.	2.2	18
5800	Effect of Bifidobacterium infantis NLS super strain in symptomatic coeliac disease patients on long-term gluten-free diet – an exploratory study. Beneficial Microbes, 2020, 11, 527-534.	2.4	16
5801	Characterisation and comparison of the mucosa-associated bacterial communities across the gastrointestinal tract of stranded green turtles, Chelonia mydas . AIMS Microbiology, 2020, 6, 361-378.	2.2	7
5802	The rhizobiome of herbaceous plants in Clovelly and Sterkspruit soils of the Stevenson–Hamilton supersite. Koedoe, 2020, 62, .	0.9	3
5803	The effects of decomposing invasive jellyfish on biogeochemical fluxes and microbial dynamics in an ultra-oligotrophic sea. Biogeosciences, 2020, 17, 5489-5511.	3.3	14
5804	Comparison of Microbial Community of Rhizosphere and Endosphere in Kiwifruit. Plant Pathology Journal, 2019, 35, 705-711.	1.7	8
5807	Convergence between the microcosms of Southeast Asian and North American pitcher plants. ELife, 2018, 7, .	6.0	29
5808	The lost world of Cuatro Ciénegas Basin, a relictual bacterial niche in a desert oasis. ELife, 2018, 7, .	6.0	51
5809	Rarity is a more reliable indicator of land-use impacts on soil invertebrate communities than other diversity metrics. ELife, 2020, 9, .	6.0	20
5810	The skin microbiome facilitates adaptive tetrodotoxin production in poisonous newts. ELife, 2020, 9, .	6.0	51
5811	Rapamycin rejuvenates oral health in aging mice. ELife, 2020, 9, .	6.0	59
5812	Comparing sediment DNA extraction methods for assessing organic enrichment associated with marine aquaculture. PeerJ, 2020, 8, e10231.	2.0	27
5813	Use of next generation sequencing to compare simple habitat and species level differences in the gut microbiota of an invasive and native freshwater fish species. PeerJ, 2020, 8, e10237.	2.0	4
5814	<i>lxodes scapularis</i> microbiome correlates with life stage, not the presence of human pathogens, in ticks submitted for diagnostic testing. PeerJ, 2020, 8, e10424.	2.0	17

#	Article	IF	CITATIONS
5815	Partial restoration of normal intestinal microbiota in morbidly obese women six months after bariatric surgery. PeerJ, 2020, 8, e10442.	2.0	4
5816	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. PeerJ, 2015, 3, e1140.	2.0	222
5817	Environment and host species shape the skin microbiome of captive neotropical bats. PeerJ, 2016, 4, e2430.	2.0	48
5818	Rhea: a transparent and modular R pipeline for microbial profiling based on 16S rRNA gene amplicons. PeerJ, 2017, 5, e2836.	2.0	325
5819	Successive DNA extractions improve characterization of soil microbial communities. PeerJ, 2017, 5, e2915.	2.0	18
5820	Metagenomic identification of active methanogens and methanotrophs in serpentinite springs of the Voltri Massif, Italy. PeerJ, 2017, 5, e2945.	2.0	91
5821	Metabarcoding monitoring analysis: the pros and cons of using co-extracted environmental DNA and RNA data to assess offshore oil production impacts on benthic communities. PeerJ, 2017, 5, e3347.	2.0	101
5822	Using high-throughput sequencing of ITS2 to describe <i>Symbiodinium</i> metacommunities in St. John, US Virgin Islands. PeerJ, 2017, 5, e3472.	2.0	88
5823	Effect of freshwater mussels on the vertical distribution of anaerobic ammonia oxidizers and other nitrogen-transforming microorganisms in upper Mississippi river sediment. PeerJ, 2017, 5, e3536.	2.0	22
5824	A longitudinal study of the diabetic skin and wound microbiome. PeerJ, 2017, 5, e3543.	2.0	93
5825	Microbiome succession during ammonification in eelgrass bed sediments. PeerJ, 2017, 5, e3674.	2.0	24
5826	Canopy soil bacterial communities altered by severing host tree limbs. PeerJ, 2017, 5, e3773.	2.0	9
5827	Microbial community diversity patterns are related to physical and chemical differences among temperate lakes near Beaver Island, MI. PeerJ, 2017, 5, e3937.	2.0	16
5828	5-Fluorouracil and irinotecan (SN-38) have limited impact on colon microbial functionality and composition. PeerJ, 2017, 5, e4017.	2.0	11
5829	A microbial survey of the International Space Station (ISS). PeerJ, 2017, 5, e4029.	2.0	52
5830	A historical legacy of antibiotic utilization on bacterial seed banks in sediments. Peerl, 2018, 6, e4197.	2.0	8
5831	Applying fecal microbiota transplantation (FMT) to treat recurrent <i>Clostridium difficile</i> infections (rCDI) in children. PeerJ, 2018, 6, e4663.	2.0	24
5832	Fine grained compositional analysis of Port Everglades Inlet microbiome using high throughput DNA sequencing. Peerl, 2018, 6, e4671.	2.0	4

#	Article	IF	Citations
5833	Viromes of one year old infants reveal the impact of birth mode on microbiome diversity. PeerJ, 2018, 6, e4694.	2.0	103
5834	Non-biological synthetic spike-in controls and the AMPtk software pipeline improve mycobiome data. PeerJ, 2018, 6, e4925.	2.0	186
5835	Dissemination of antibiotic resistance genes associated with the sporobiota in sediments impacted by wastewater. PeerJ, 2018, 6, e4989.	2.0	12
5836	Marine cyanolichens from different littoral zones are associated with distinct bacterial communities. PeerJ, 2018, 6, e5208.	2.0	31
5837	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.	2.0	26
5838	Effects of agricultural management on phyllosphere fungal diversity in vineyards and the association with adjacent native forests. Peerl, 2018, 6, e5715.	2.0	27
5839	Increased tooth brushing frequency is associated with reduced gingival pocket bacterial diversity in patients with intracranial aneurysms. PeerJ, 2019, 7, e6316.	2.0	11
5840	Disentangling the effect of host-genotype and environment on the microbiome of the coral <i>Acropora tenuis</i>). PeerJ, 2019, 7, e6377.	2.0	60
5841	Evaluation of DESS as a storage medium for microbial community analysis. PeerJ, 2019, 7, e6414.	2.0	18
5842	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.	2.0	85
5843	Circadian disruption and divergent microbiota acquisition under extended photoperiod regimens in chicken. Peerl, 2019, 7, e6592.	2.0	28
5844	Robust and automatic definition of microbiome states. Peerl, 2019, 7, e6657.	2.0	12
5845	A longitudinal study of the faecal microbiome and metabolome of periparturient mares. PeerJ, 2019, 7, e6687.	2.0	14
5846	Ultraviolet disinfection impacts the microbial community composition and function of treated wastewater effluent and the receiving urban river. PeerJ, 2019, 7, e7455.	2.0	17
5847	Diets with and without edible cricket support a similar level of diversity in the gut microbiome of dogs. PeerJ, 2019, 7, e7661.	2.0	30
5848	Effect of radiotherapy on the gut microbiome in pediatric cancer patients: a pilot study. PeerJ, 2019, 7, e7683.	2.0	19
5849	Microbial communities associated with the black morel <i>Morchella sextelata</i> cultivated in greenhouses. Peerl, 2019, 7, e7744.	2.0	50
5850	Stability of the vaginal, oral, and gut microbiota across pregnancy among African American women: the effect of socioeconomic status and antibiotic exposure. PeerJ, 2019, 7, e8004.	2.0	31

#	Article	IF	CITATIONS
5851	The effect of diet on the structure of gut bacterial community of sympatric pair of whitefishes (<i>Coregonus lavaretus</i>): one story more. PeerJ, 2019, 7, e8005.	2.0	18
5852	Different nitrogen sources speed recovery from corallivory and uniquely alter the microbiome of a reef-building coral. Peerl, 2019, 7, e8056.	2.0	20
5853	Acquisition of fungi from the environment modifies ambrosia beetle mycobiome during invasion. PeerJ, 2019, 7, e8103.	2.0	37
5854	Accumulation of di-2-ethylhexyl phthalate from polyvinyl chloride flooring into settled house dust and the effect on the bacterial community. Peerl, 2019, 7, e8147.	2.0	6
5855	Influence of host phylogeny, geographical location and seed harvesting diet on the bacterial community of globally distributed <i> Pheidole</i> ants. PeerJ, 2020, 8, e8492.	2.0	9
5856	Alternative dietary protein and water temperature influence the skin and gut microbial communities of yellowtail kingfish (<i>Seriola lalandi</i>). Peerl, 2020, 8, e8705.	2.0	21
5857	Changes in the gut microbiota during Asian particolored bat (<i>Vespertilio sinensis</i>) development. PeerJ, 2020, 8, e9003.	2.0	10
5858	Effects of biodegradable plastic film mulching on soil microbial communities in two agroecosystems. PeerJ, 2020, 8, e9015.	2.0	62
5859	Population structure and microbial community diversity of two common tetillid sponges in a tropical reef lagoon. PeerJ, 2020, 8, e9017.	2.0	11
5860	Bacterial communities associated with cell phones and shoes. PeerJ, 2020, 8, e9235.	2.0	6
5861	Succession of bacterial communities on carrion is independent of vertebrate scavengers. Peerl, 2020, 8, e9307.	2.0	9
5862	Effects of microbial evolution dominate those of experimental host-mediated indirect selection. PeerJ, 2020, 8, e9350.	2.0	22
5863	Integrating population genetic structure, microbiome, and pathogens presence data in <i>>Dermacentor variabilis</i> >. Peerl, 2020, 8, e9367.	2.0	8
5864	An updated genetic marker for detection of Lake Sinai Virus and metagenetic applications. PeerJ, 2020, 8, e9424.	2.0	6
5865	A comparison of lodgepole and spruce needle chemistry impacts on terrestrial biogeochemical processes during isolated decomposition. PeerJ, 2020, 8, e9538.	2.0	6
5866	Spatial distribution of microbial communities among colonies and genotypes in nursery-reared <i>Acropora cervicornis</i>). Peerl, 2020, 8, e9635.	2.0	18
5867	Microbiome dynamics in the tissue and mucus of acroporid corals differ in relation to host and environmental parameters. PeerJ, 2020, 8, e9644.	2.0	30
5868	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.	2.0	22

#	Article	IF	CITATIONS
5869	Fungal lysozyme leverages the gut microbiota to curb DSS-induced colitis. Gut Microbes, 2021, 13, 1988836.	9.8	29
5870	Diversity and Composition of Microbial Communities in an Eelgrass (<i>Zostera marina</i>) Bed in Tokyo Bay, Japan. Microbes and Environments, 2021, 36, n/a.	1.6	7
5871	Early-life formula feeding is associated with infant gut microbiota alterations and an increased antibiotic resistance load. American Journal of Clinical Nutrition, 2022, 115, 407-421.	4.7	29
5872	Comparison of Primers for Oral Mycobiome Study in Intubated Patients. Journal of Bacteriology and Virology, 2021, 51, 112-119.	0.1	0
5873	A metagenomic approach to assess Neofabraea infection and dynamics on stored apples. Acta Horticulturae, 2021, , 119-126.	0.2	0
5874	Captivity and the co-diversification of great ape microbiomes. Nature Communications, 2021, 12, 5632.	12.8	23
5875	High-Throughput Sequencing for Examining Salmonella Prevalence and Pathogenâ€"Microbiota Relationships in Barn Swallows. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	3
5876	Differential effects of elevated nest temperature and parasitism on the gut microbiota of wild avian hosts. Animal Microbiome, 2021, 3, 67.	3.8	8
5877	Lung microbiome of stable and exacerbated COPD patients in Tshwane, South Africa. Scientific Reports, 2021, 11, 19758.	3.3	11
5878	The East Asian gut microbiome is distinct from colocalized White subjects and connected to metabolic health. ELife, 2021, 10, .	6.0	25
5879	Archaeal community dynamics in biogas fermentation at various temperatures assessed by mcrA amplicon sequencing using different primer pairs. World Journal of Microbiology and Biotechnology, 2021, 37, 188.	3.6	1
5880	Commensal bacteria promote endocrine resistance in prostate cancer through androgen biosynthesis. Science, 2021, 374, 216-224.	12.6	135
5881	Overabundance of <i>Asaia</i> and <i>Serratia</i> Bacteria Is Associated with Deltamethrin Insecticide Susceptibility in <i>Anopheles coluzzii</i> from Agboville, Cà te d'Ivoire. Microbiology Spectrum, 2021, 9, e0015721.	3.0	18
5883	Rapid Increase of Oral Bacteria in Nasopharyngeal Microbiota After Antibiotic Treatment in Children With Invasive Pneumococcal Disease. Frontiers in Cellular and Infection Microbiology, 2021, 11, 744727.	3.9	8
5884	The Mycobiota of High Altitude Pear Orchards Soil in Colombia. Biology, 2021, 10, 1002.	2.8	7
5885	Investigating Chemical and Biological Control Applications for Pythium Root Rot Prevention and Impacts on Creeping Bentgrass Putting Green Rhizosphere Bacterial Communities. Plant Disease, 2022, 106, 641-647.	1.4	2
5886	Tofacitinib-Induced Modulation of Intestinal Adaptive and Innate Immunity and Factors Driving Cellular and Systemic Pharmacokinetics. Cellular and Molecular Gastroenterology and Hepatology, 2022, 13, 383-404.	4.5	11
5887	Reprocessing 16S rRNA Gene Amplicon Sequencing Studies: (Meta)Data Issues, Robustness, and Reproducibility. Frontiers in Cellular and Infection Microbiology, 2021, 11, 720637.	3.9	4

#	Article	IF	CITATIONS
5888	Comparison of PCR versus PCR-Free DNA Library Preparation for Characterising the Human Faecal Virome. Viruses, 2021, 13, 2093.	3.3	9
5890	Arbuscular mycorrhizal fungal communities of a mangrove forest along a salinity gradient on Iriomote Island. Plant and Soil, 2022, 472, 145-159.	3.7	3
5891	A field experiment reveals seasonal variation in the <i>Daphnia</i> gut microbiome. Oikos, 2021, 130, 2191-2201.	2.7	11
5892	Protected Organic Acid and Essential Oils for Broilers Raised Under Field Conditions: Intestinal Health Biomarkers and Cecal Microbiota. Frontiers in Physiology, 2021, 12, 722339.	2.8	7
5893	Bacteria-Oil Microaggregates Are an Important Mechanism for Hydrocarbon Degradation in the Marine Water Column. MSystems, 2021, 6, e0110521.	3.8	5
5896	Airborne Bacterial Community Composition According to Their Origin in Tenerife, Canary Islands. Frontiers in Microbiology, 2021, 12, 732961.	3.5	8
5897	Comprehensive characterization of internal and cuticle surface microbiota of laboratory-reared F1 Anopheles albimanus originating from different sites. Malaria Journal, 2021, 20, 414.	2.3	3
5899	Metatranscriptomics to characterize respiratory virome, microbiome, and host response directly from clinical samples. Cell Reports Methods, 2021, 1, 100091.	2.9	19
5900	High throughput in vitro characterization of pectins for pig(let) nutrition. Animal Microbiome, 2021, 3, 69.	3.8	7
5901	Changes in the Fungal Community Assembly of Apple Fruit Following Postharvest Application of the Yeast Biocontrol Agent Metschnikowia fructicola. Horticulturae, 2021, 7, 360.	2.8	12
5902	Hydrothermal trace metal release and microbial metabolism in the northeastern Lau Basin of the South Pacific Ocean. Biogeosciences, 2021, 18, 5397-5422.	3.3	11
5903	Winter Rye Cover Cropping Changes Squash (<i>Cucurbita pepo</i>) Phyllosphere Microbiota and Reduces <i>Pseudomonas syringae</i>) Symptoms. Phytobiomes Journal, 2022, 6, 3-12.	2.7	2
5904	Evaluation of the Respiratory Microbiome and the Use of Tracheal Lavage as a Diagnostic Tool in Kemp's Ridley Sea Turtles (Lepidochelys kempii). Animals, 2021, 11, 2927.	2.3	0
5905	The soil microbiomics of intact, degraded and partially-restored semi-arid succulent thicket (Albany) Tj ETQq $1\ 1\ C$).784314 r	gBT /Overlo
5906	Metagenomic analysis of Raphidiopsis raciborskii microbiome: beyond the individual. Biodiversity Data Journal, 2021, 9, e72514.	0.8	8
5907	Metagenomic exploration reveals a differential patterning of antibiotic resistance genes in urban and peri-urban stretches of a riverine system. Environmental Science and Pollution Research, 2021, 28, 66477-66484.	5.3	3
5908	A mix of functional amino acids and grape polyphenols promotes the growth of piglets, modulates the gut microbiota in vivo and regulates epithelial homeostasis in intestinal organoids. Amino Acids, 2022, 54, 1357-1369.	2.7	11
5909	Integration of spatio-temporal variations of surface metabolomes and epibacterial communities highlights the importance of copper stress as a major factor shaping host-microbiota interactions within a Mediterranean seaweed holobiont. Microbiome, 2021, 9, 201.	11.1	10

#	Article	IF	CITATIONS
5911	Altered microbiomes of aquatic macroinvertebrates and riparian spiders downstream of municipal wastewater effluents. Science of the Total Environment, 2022, 809, 151156.	8.0	6
5913	The Role of Intestinal Microbiota in Metastatic Colorectal Cancer Patients Treated With Capecitabine. Clinical Colorectal Cancer, 2022, 21, e87-e97.	2.3	6
5914	Mercury, Methylmercury, and Microbial Communities in a Degrading Palsa of the Hudson Bay Lowlands, Far North Ontario. , 2021, , .		1
5915	Transferable Immunoglobulin A–Coated Odoribacter splanchnicus in Responders to Fecal Microbiota Transplantation for Ulcerative Colitis Limits Colonic Inflammation. Gastroenterology, 2022, 162, 166-178.	1.3	60
5916	Biochar dose determines methane uptake and methanotroph abundance in Haplic Luvisol. Science of the Total Environment, 2022, 806, 151259.	8.0	16
5918	The bacterial gut microbiome of probiotic-treated very-preterm infants: changes from admission to discharge. Pediatric Research, 2022, 92, 142-150.	2.3	11
5919	Comparing the gut microbiome along the gastrointestinal tract of three sympatric species of wild rodents. Scientific Reports, 2021, 11, 19929.	3.3	13
5921	Perturbations of the ileal mycobiota by necrotic enteritis in broiler chickens. Journal of Animal Science and Biotechnology, 2021, 12, 107.	5.3	6
5922	16S rRNA Gene Amplicon Sequencing Data of the Iron Quadrangle Ferruginous Caves (Brazil) Shows the Importance of Conserving This Singular and Threatened Geosystem. Diversity, 2021, 13, 494.	1.7	2
5923	Fecal biomarkers of environmental enteric dysfunction and the gut microbiota of rural Malawian children: An observational study. Heliyon, 2021, 7, e08194.	3.2	6
5924	Disturbance alters the forest soil microbiome. Molecular Ecology, 2022, 31, 419-447.	3.9	27
5925	Enhanced pilot bioremediation of oily sludge from petroleum refinery disposal under hot-summer Mediterranean climate. Environmental Technology and Innovation, 2021, 24, 102037.	6.1	7
5927	Analysis of Salivary Mycobiome in a Cohort of Oral Squamous Cell Carcinoma Patients From Sudan Identifies Higher Salivary Carriage of Malassezia as an Independent and Favorable Predictor of Overall Survival. Frontiers in Cellular and Infection Microbiology, 2021, 11, 673465.	3.9	28
5928	Gut microbiome and telomere length in gull hatchlings. Biology Letters, 2021, 17, 20210398.	2.3	7
5929	Baseline Fecal Microbiota in Pediatric Patients With Celiac Disease Is Similar to Controls But Dissimilar After 1 Year on the Gluten-Free Diet. JPGN Reports, 2021, 2, e127.	0.4	2
5932	Bile acid-independent protection against Clostridioides difficile infection. PLoS Pathogens, 2021, 17, e1010015.	4.7	46
5933	Antibiotics accelerate growth at the expense of immunity. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211819.	2.6	9
5934	Wastewater constituents impact biofilm microbial community in receiving streams. Science of the Total Environment, 2022, 807, 151080.	8.0	12

#	Article	IF	CITATIONS
5935	Oceanic heterotrophic flagellates are dominated by a few widespread taxa. Limnology and Oceanography, 2021, 66, 4240-4253.	3.1	20
5936	Microbiome-Specific Statistical Modeling Identifies Interplay Between Gastrointestinal Microbiome and Neurobehavioral Outcomes in Patients With Autism: A Case Control Study. Frontiers in Psychiatry, 2021, 12, 682454.	2.6	10
5938	Longitudinal Analysis of the Intestinal Microbiota in the Obese Mangalica Pig Reveals Alterations in Bacteria and Bacteriophage Populations Associated With Changes in Body Composition and Diet. Frontiers in Cellular and Infection Microbiology, 2021, 11, 698657.	3.9	4
5940	Metabolomic Analysis of Diverse Mice Reveals Hepatic Arginase-1 as Source of Plasma Arginase in Plasmodium chabaudi Infection. MBio, 2021, 12, e0242421.	4.1	7
5942	Effect of the Manufacturing Process on the Microbiota, Organoleptic Properties and Volatilome of Three Salmon-Based Products. Foods, 2021, 10, 2517.	4.3	8
5943	A Comparison of Different Natural Groundwaters from Repository Sitesâ€"Corrosivity, Chemistry and Microbial Community. Corrosion and Materials Degradation, 2021, 2, 603-624.	2.4	3
5944	Revisiting the effect of PCR replication and sequencing depth on biodiversity metrics in environmental DNA metabarcoding. Ecology and Evolution, 2021, 11, 15766-15779.	1.9	35
5945	Yeast \hat{l}^2 -glucan reduces obesity-associated <i>Bilophila</i> abundance and modulates bile acid metabolism in healthy and high-fat diet mouse models. American Journal of Physiology - Renal Physiology, 2021, 321, G639-G655.	3.4	8
5946	Evaluation of Microbial Communities of Bottled Mineral Waters and Preliminary Traceability Analysis Using NGS Microbial Fingerprints. Water (Switzerland), 2021, 13, 2824.	2.7	6
5949	Ambient Air Pollution Shapes Bacterial and Fungal Ivy Leaf Communities. Microorganisms, 2021, 9, 2088.	3.6	9
5950	Microbiome signature and diversity regulates the level of energy production under anaerobic condition. Scientific Reports, 2021, 11, 19777.	3.3	20
5952	Cross-Talk Between Intestinal Microbiota and Host Gene Expression in Gilthead Sea Bream (Sparus) Tj ETQq1 in Physiology, 2021, 12, 748265.	1 0.784314 2.8	rgBT /Overloo 26
5953	Largely invariant communities of bacterial endophytes in the nonphotosynthetic mycoheterotrophic plant <i>Pterospora andromedea</i> . American Journal of Botany, 2021, 108, 2208-2219.	1.7	0
5954	Diet diversity and environment determine the intestinal microbiome and bacterial pathogen load of fire salamanders. Scientific Reports, 2021, 11, 20493.	3.3	7
5955	Diurnal oscillations in gut bacterial load and composition eclipse seasonal and lifetime dynamics in wild meerkats. Nature Communications, 2021, 12, 6017.	12.8	30
5956	Fire impacts bacterial composition in Protea repens (Proteaceae) infructescences. FEMS Microbiology Letters, 2021, 368, .	1.8	1
5957	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. MSystems, 2021, 6, e0038221.	3.8	22
5958	Conditioned soils reveal plant-selected microbial communities that impact plant drought response. Scientific Reports, 2021, 11, 21153.	3.3	13

#	Article	IF	CITATIONS
5959	Parasitism by endoparasitoid wasps alters the internal but not the external microbiome in host caterpillars. Animal Microbiome, 2021, 3, 73.	3.8	12
5960	Bioavailable Nutrients (N and P) and Precipitation Patterns Drive Cyanobacterial Blooms in Missisquoi Bay, Lake Champlain. Microorganisms, 2021, 9, 2097.	3.6	13
5961	The Bioinformatics Virtual Coordination Network: An Open-Source and Interactive Learning Environment. Frontiers in Education, 2021, 6, .	2.1	2
5962	Ewe Vaginal Microbiota: Associations With Pregnancy Outcome and Changes During Gestation. Frontiers in Microbiology, 2021, 12, 745884.	3.5	12
5963	Microbial communities in paddy soil as influenced by nitrogen fertilization and water regimes. Agronomy Journal, 2022, 114, 379-394.	1.8	5
5964	Development of an Amplicon-Based Next-Generation Sequencing Protocol to Identify <i>Leishmania </i> Species and Other Trypanosomatids in Leishmaniasis Endemic Areas. Microbiology Spectrum, 2021, 9, e0065221.	3.0	15
5965	Investigating the Effect of an Oxytetracycline Treatment on the Gut Microbiome and Antimicrobial Resistance Gene Dynamics in Nile Tilapia (Oreochromis niloticus). Antibiotics, 2021, 10, 1213.	3.7	19
5966	Oral Microbiome Alterations and SARS-CoV-2 Saliva Viral Load in Patients with COVID-19. Microbiology Spectrum, 2021, 9, e0005521.	3.0	31
5968	Soil initial bacterial diversity and nutrient availability determine the rate of xenobiotic biodegradation. Microbial Biotechnology, 2022, 15, 318-336.	4.2	6
5969	Microbial Contamination Survey of Environmental Fresh and Saltwater Resources of Upolu Island, Samoa. Environments - MDPI, 2021, 8, 112.	3.3	5
5970	The apple fruit microbiome: influence of orchard management, cultivar, storage time and storage atmosphere. Acta Horticulturae, 2021, , 317-324.	0.2	2
5971	Dimethyl sulfide mediates microbial predator–prey interactions between zooplankton and algae in the ocean. Nature Microbiology, 2021, 6, 1357-1366.	13.3	33
5975	Spatiotemporal dynamics of the resistome and virulome of riverine microbiomes disturbed by a mining mud tsunami. Science of the Total Environment, 2022, 806, 150936.	8.0	6
5976	Characterization and Comparison of Intestinal Bacterial Microbiomes of Euschistus heros and Piezodorus guildinii Collected in Brazil and the United States. Frontiers in Microbiology, 2021, 12, 769965.	3.5	3
5977	Understanding changes in biocrust communities following phosphate mining in the Negev Desert. Environmental Research, 2022, 207, 112200.	7.5	9
5979	Operational and biochemical aspects of co-digestion (co-AD) from sugarcane vinasse, filter cake, and deacetylation liquor. Applied Microbiology and Biotechnology, 2021, 105, 8969-8987.	3.6	14
5981	Broad-Spectrum Inhibitor of Bacterial Polyphosphate Homeostasis Attenuates Virulence Factors and Helps Reveal Novel Physiology of Klebsiella pneumoniae and Acinetobacter baumannii. Frontiers in Microbiology, 2021, 12, 764733.	3.5	9
5982	Understudied, underrepresented, and unknown: Methodological biases that limit detection of early diverging fungi from environmental samples. Molecular Ecology Resources, 2022, 22, 1065-1085.	4.8	14

#	Article	IF	CITATIONS
5983	Apart From the Diet, the Ruminal Microbiota of Lambs Is Modified in Relation to Their Genetic Potential for Feed Efficiency or Feeding Behavior. Frontiers in Microbiology, 2021, 12, 759432.	3.5	10
5984	Mobile Antimicrobial Resistance Genes in Probiotics. Antibiotics, 2021, 10, 1287.	3.7	22
5985	Characterization of the Microbiome of Corals with Stony Coral Tissue Loss Disease along Florida's Coral Reef. Microorganisms, 2021, 9, 2181.	3.6	18
5986	Alterations in Faecal Microbiota and Elevated Levels of Intestinal IgA Following Oral Administration of Lacticaseibacillus casei in mice. Probiotics and Antimicrobial Proteins, 2023, 15, 524-534.	3.9	6
5988	A comprehensive evaluation of single-end sequencing data analyses for environmental microbiome research. Archives of Microbiology, 2021, 203, 6295-6302.	2.2	7
5989	Sheltering Role of Well-Decayed Conifer Logs for Forest Floor Fungi in Long-Term Polluted Boreal Forests. Frontiers in Microbiology, 2021, 12, 729244.	3 . 5	5
5990	Lactobacillus johnsonii N6.2 and Blueberry Phytophenols Affect Lipidome and Gut Microbiota Composition of Rats Under High-Fat Diet. Frontiers in Nutrition, 2021, 8, 757256.	3.7	11
5991	Bacterial community dynamics during embryonic development of the little skate (Leucoraja erinacea). Animal Microbiome, 2021, 3, 72.	3.8	6
5992	Klebsiella oxytoca causes colonization resistance against multidrug-resistant K.Âpneumoniae in the gut via cooperative carbohydrate competition. Cell Host and Microbe, 2021, 29, 1663-1679.e7.	11.0	53
5993	Sulphate-reducing bacterial community structure from produced water of the Periquito and Galo de Campina onshore oilfields in Brazil. Scientific Reports, 2021, 11, 20311.	3.3	11
5994	In vitro Prebiotic Effect of Bread-Making Process in Inflammatory Bowel Disease Microbiome. Frontiers in Microbiology, 2021, 12, 716307.	3.5	3
5995	Impacts of environmental stress on resistance and resilience of algalâ€associated bacterial communities. Ecology and Evolution, 2021, 11, 15004-15019.	1.9	7
5996	Equine grass sickness (a multiple systems neuropathy) is associated with alterations in the gastrointestinal mycobiome. Animal Microbiome, 2021, 3, 70.	3.8	6
5997	Crop host signatures reflected by co-association patterns of keystone Bacteria in the rhizosphere microbiota. Environmental Microbiomes, 2021, 16, 18.	5.0	21
5998	16S rRNA of Mucosal Colon Microbiome and CCL2 Circulating Levels Are Potential Biomarkers in Colorectal Cancer. International Journal of Molecular Sciences, 2021, 22, 10747.	4.1	16
5999	Soil salinization accelerates microbiome stabilization in iterative selections for plant performance. New Phytologist, 2022, 234, 2101-2110.	7.3	14
6000	Arabidopsis assemble distinct root-associated microbiomes through the synthesis of an array of defense metabolites. PLoS ONE, 2021, 16, e0259171.	2.5	25
6002	Plasticity, exudation and microbiome-association of the root system of Pellitory-of-the-wall plants grown in environments impaired in iron availability. Plant Physiology and Biochemistry, 2021, 168, 27-42.	5.8	3

#	ARTICLE	IF	CITATIONS
6003	New region demarcation method for implementing the Joint Prevention and Control of Atmospheric Pollution policy in China. Journal of Cleaner Production, 2021, 325, 129345.	9.3	8
6004	Shaping of soil microbial communities by plants does not translate into specific legacy effects on organic carbon mineralization. Soil Biology and Biochemistry, 2021, 163, 108449.	8.8	12
6005	Plant community legacy effects on nutrient cycling, fungal decomposer communities and decomposition in a temperate grassland. Soil Biology and Biochemistry, 2021, 163, 108450.	8.8	7
6011	biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. F1000Research, 2016, 5, 2348.	1.6	0
6027	Chapter 15 Methodologies for microbiota assessment in infancy and childhood. , 2017, , 283-295.		1
6032	Approaches to in silico analysis of micobiome biodiversity metrics of radionuclide contaminated soils. Bìoresursi ì Prirodokoristuvannâ, 2017, 9, 10-16.	0.2	0
6038	High rates of bacterial vaginosis and Chlamydia in a low-income, high-population-density community in Cape Town. South African Journal of Science and Technology, 2017, 36, .	0.1	0
6040	Hoë voorkomskoers van bakteriële vaginose en Chlamydia in 'n lae-inkomste, hoë-bevolkingsdigtheid gemeenskap in Kaapstad. South African Journal of Science and Technology, 2017, 36, .	0.1	0
6041	Investigation of the response mechanisms of halophilic and mixed culture aerobic granular sludge under hypersaline conditions. Proceedings of the Water Environment Federation, 2018, 2018, 3836-3853.	0.0	0
6051	ShinyDiversity - Understanding Alpha and Beta Diversity through Interactive Visualizations. F1000Research, 0, 7, 479.	1.6	1
6088	Effects of <i>Lactobacillus paracasei</i> K71 on gut microbiota composition and lipid metabolism in <i>ob</i> /i>/ci>ob mice Japanese Journal of Lactic Acid Bacteria, 2018, 29, 152-157.	0.1	0
6090	DETERMINATION OF THE BASIC DIVERSITY METRICS OF RADIONUCLIDE CONTAMINATED SOILS MICROBIOMES. Bìoresursi ì Prirodokoristuvannâ, 2018, 10, .	0.2	1
6103	S100-Alarmins are Crucial Host Factors for the Postnatal Development of Gut Homeostasis. SSRN Electronic Journal, 0 , , .	0.4	0
6115	MicrobiomeR: An R Package for Simplified and Standardized Microbiome Analysis Workflows. Journal of Open Source Software, 2019, 4, 1299.	4.6	6
6132	Within-Lineage Divergence of Avian Haemosporidians: A Case Study to Reveal the Origin of a Widespread Haemoproteus Parasite. Journal of Parasitology, 2019, 105, 414.	0.7	5
6143	Geografiese ligging be \tilde{A} -nvloed vaginale mikrobiese profiele in Suid-Afrikaanse vroue. South African Journal of Science and Technology, 2020, 38, 41-49.	0.1	1
6160	Enhanced biotic degradation of terrestrial POM in an estuarine salinity gradient: interactive effects of organic matter pools and changes of bacterial communities. Aquatic Microbial Ecology, 2019, 83, 147-159.	1.8	5
6196	Making simulation results reproducibleâ€"Survey, guidelines, and examples based on Gradle and Docker. PeerJ Computer Science, 2019, 5, e240.	4.5	4

#	Article	IF	CITATIONS
6202	Comparative Analysis of Fecal Microbiota in Grasscutter (Thryonomys swinderianus) and Other Herbivorous Livestock in Ghana. Microorganisms, 2020, 8, 265.	3.6	5
6204	microbiomeDASim:ÂSimulating longitudinal differential abundance for microbiome data. F1000Research, 2019, 8, 1769.	1.6	5
6223	<p>Gene–Environment Interactions in Major Mental Disorders in the Czech Republic</p> . Neuropsychiatric Disease and Treatment, 2020, Volume 16, 1147-1156.	2.2	0
6224	The Presence of Periodontal Pathogens in Gastric Cancer. Exploratory Research and Hypothesis in Medicine, 2020, 000, 1-10.	0.4	2
6227	Alterations in the sap-associated microbiota of Carica papaya in response to drought stress. Symbiosis, 2020, 81, 93-100.	2.3	0
6236	Microbial community analysis in the gills of abalones suggested possible dominance of epsilonproteobacterium in <i>Haliotis gigantea</i>). PeerJ, 2020, 8, e9326.	2.0	5
6242	Spontaneous onset of TNFαâ€ŧriggered colonic inflammation depends on functional T lymphocytes, <scp>S100A8</scp> / <scp>A9</scp> alarmins, and <scp>MHC</scp> Hâ€2 haplotype. Journal of Pathology, 2020, 251, 388-399.	4.5	5
6270	Precipitation Controls on Soil Biogeochemical and Microbial Community Composition in Rainfed Agricultural Systems in Tropical Drylands. Sustainability, 2021, 13, 11848.	3.2	0
6271	Dysbiosis and structural disruption of the respiratory microbiota in COVID-19 patients with severe and fatal outcomes. Scientific Reports, 2021, 11, 21297.	3.3	48
6272	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. Nature Communications, 2021, 12, 6243.	12.8	42
6274	Diversity Profiling of Seed Associated Endophytic Microbiome in Important Species of Caricaceae Family. Microbiology Research, 2021, 12, 779-792.	1.9	2
6275	Choices on sampling, sequencing, and analyzing DNA influence the estimation of community composition of plant fungal symbionts. Applications in Plant Sciences, 2021, 9, e11449.	2.1	2
6278	Altered gut ecosystems plus the microbiota's potential for rapid evolution: A recipe for inevitable change with unknown consequences. Computational and Structural Biotechnology Journal, 2021, 19, 5969-5977.	4.1	2
6279	Does Physical Inactivity Induce Significant Changes in Human Gut Microbiota? New Answers Using the Dry Immersion Hypoactivity Model. Nutrients, 2021, 13, 3865.	4.1	12
6280	Fungal Metagenome of Chernevaya Taiga Soils: Taxonomic Composition, Differential Abundance and Factors Related to Plant Gigantism. Journal of Fungi (Basel, Switzerland), 2021, 7, 908.	3.5	4
6281	Fecal Microbiota Transplantation Increases Colonic IL-25 and Dampens Tissue Inflammation in Patients with Recurrent Clostridioides difficile. MSphere, 2021, 6, e0066921.	2.9	9
6282	Climate-assisted persistence of tropical fish vagrants in temperate marine ecosystems. Communications Biology, 2021, 4, 1231.	4.4	5
6283	Performance of 16S Metagenomic Profiling in Formalin-Fixed Paraffin-Embedded versus Fresh-Frozen Colorectal Cancer Tissues. Cancers, 2021, 13, 5421.	3.7	11

#	Article	IF	CITATIONS
6284	Beyond Archaea: The Table Salt Bacteriome. Frontiers in Microbiology, 2021, 12, 714110.	3.5	13
6286	Associations Between the Gut Microbiota and Internalizing Behaviors in Preschool Children. Psychosomatic Medicine, 2022, 84, 159-169.	2.0	9
6288	Technical challenges regarding the use of formalin-fixed paraffin embedded (FFPE) tissue specimens for the detection of bacterial alterations in colorectal cancer. BMC Microbiology, 2021, 21, 297.	3.3	11
6289	Sargassum Differentially Shapes the Microbiota Composition and Diversity at Coastal Tide Sites and Inland Storage Sites on Caribbean Islands. Frontiers in Microbiology, 2021, 12, 701155.	3.5	13
6290	Exploring the nasopharyngeal microbiota composition in infants with whooping cough: A test-negative case-control study. PLoS ONE, 2021, 16, e0259318.	2.5	3
6291	The treasure inside barley seeds: microbial diversity and plant beneficial bacteria. Environmental Microbiomes, 2021, 16, 20.	5.0	37
6292	Sea Ice Dynamics Drive Benthic Microbial Communities in McMurdo Sound, Antarctica. Frontiers in Microbiology, 2021, 12, 745915.	3.5	7
6293	Gut microbiome signatures distinguish type 2 diabetes mellitus from non-alcoholic fatty liver disease. Computational and Structural Biotechnology Journal, 2021, 19, 5920-5930.	4.1	17
6294	Defining gut mycobiota for wild animals: a need for caution in assigning authentic resident fungal taxa. Animal Microbiome, 2021, 3, 75.	3.8	15
6295	Perinatal Administration of C-Phycocyanin Protects Against Atherosclerosis in apoE-Deficient Mice by Modulating Cholesterol and Trimethylamine-N-Oxide Metabolisms. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, e512-e523.	2.4	3
6296	Wild gut microbiomes reveal individuals, species, and location as drivers of variation in two critically endangered Hawaiian honeycreepers. PeerJ, 2021, 9, e12291.	2.0	7
6297	In vitro metabolic capacity of carbohydrate degradation by intestinal microbiota of adults and pre-frail elderly. ISME Communications, 2021, 1 , .	4.2	6
6298	Geobiology of Andean Microbial Ecosystems Discovered in Salar de Atacama, Chile. Frontiers in Microbiology, 2021, 12, 762076.	3.5	6
6299	Changes in the Gut Microbiome and Predicted Functional Metabolic Effects in an Australian Parkinson's Disease Cohort. Frontiers in Neuroscience, 2021, 15, 756951.	2.8	15
6300	Dissolved organic matter production from herder application and in-situ burning of crude oil at high latitudes: Bioavailable molecular composition patterns and microbial community diversity effects. Journal of Hazardous Materials, 2022, 424, 127598.	12.4	7
6301	A combined culture-independent and simulation reactor approach to assess the microbial community	2.7	1
6302	Phenology-dependent root bacteria enhance yield of Brassica napus. Soil Biology and Biochemistry, 2022, 166, 108468.	8.8	10
6303	Short Communication: Obesity Intervention Resulting in Significant Changes in the Human Gut Viral Composition. Applied Sciences (Switzerland), 2021, 11, 10039.	2.5	4

#	Article	IF	CITATIONS
6304	Is the gut microbiota associated with suicidality? Non-significant finding among a large cohort of psychiatrically hospitalized individuals with serious mental illness. Journal of Affective Disorders Reports, 2021, 6, 100266.	1.7	1
6305	Predicting measures of soil health using the microbiome and supervised machine learning. Soil Biology and Biochemistry, 2022, 164, 108472.	8.8	55
6307	Longâ€ŧerm warming effects on the microbiome and <i>nifH < /i>gene abundance of a common moss species in subâ€Arctic tundra. New Phytologist, 2022, 234, 2044-2056.</i>	7.3	23
6310	Metagenomic Analysis of Biocide-Treated Neotropical Oil Reservoir Water Unveils Microdiversity of Thermophile Tepidiphilus. Frontiers in Microbiology, 2021, 12, 741555.	3.5	4
6311	Diversity and Biogeography of Bathyal and Abyssal Seafloor Bacteria and Archaea Along a Mediterranean—Atlantic Gradient. Frontiers in Microbiology, 2021, 12, 702016.	3.5	2
6312	Aquaculture production of hatchling Hawaiian Bobtail Squid (Euprymna scolopes) is negatively impacted by decreasing environmental microbiome diversity. Journal of Applied Microbiology, 2022, 132, 1724-1737.	3.1	3
6313	Circular alternatives to peat in growing media: A microbiome perspective. Journal of Cleaner Production, 2021, 327, 129375.	9.3	15
6314	Utilization of low-molecular-weight organic compounds by the filterable fraction of a lotic microbiome. FEMS Microbiology Ecology, 2021, 97, .	2.7	0
6317	Microbial Community Response to Carbon-Nitrogen Ratio Manipulation in Biofloc Culture. Philippine Journal of Fisheries, 2020, , 193-207.	0.3	4
6319	Nasal Tissue Extraction Is Essential for Characterization of the Murine Upper Respiratory Tract Microbiota. MSphere, 2020, 5, .	2.9	5
6320	Role of Metagenomics in Plant Disease Management. Environmental and Microbial Biotechnology, 2021, , 203-220.	0.7	0
6323	Rock Surface Fungi in Deep Continental Biosphereâ€"Exploration of Microbial Community Formation with Subsurface In Situ Biofilm Trap. Microorganisms, 2021, 9, 64.	3.6	11
6324	Anaerobic Carbon Monoxide Uptake by Microbial Communities in Volcanic Deposits at Different Stages of Successional Development on O-yama Volcano, Miyake-jima, Japan. Microorganisms, 2021, 9, 12.	3.6	6
6328	Efficient Monitoring of Adult and Immature Mosquitoes Through Metabarcoding of Bulk Samples: A Case Study for Non-Model Culicids With Unique Ecologies. Journal of Medical Entomology, 2021, 58, 1210-1218.	1.8	5
6330	Analysis of Microbial Water Contamination, Soil Microbial Community Structure, and Soil Respiration in a Collaborative First-Year Students as Scholars Program (SAS). Frontiers in Microbiology, 2020, 11, 590035.	3.5	1
6331	Agroindustrial by-products from tomato, grape and myrtle given at low dosage to lactating dairy ewes: effects on rumen parameters and microbiota. Italian Journal of Animal Science, 2020, 19, 1462-1462.	1.9	9
6333	Uncovering host-microbiome interactions in global systems with collaborative programming: a novel approach integrating social and data sciences. F1000Research, 0, 9, 1478.	1.6	0
6334	Temperature management potentially affects carbon mineralization capacity and microbial community composition of a shallow aquifer. FEMS Microbiology Ecology, 2021, 97, .	2.7	6

#	Article	IF	CITATIONS
6335	Microbiome of the Healthy External Auditory Canal. Otology and Neurotology, 2020, Publish Ahead of Print, e609-e614.	1.3	9
6336	External ear canal mycobiome of some rabbit breeds. Medical Mycology, 2021, 59, 683-693.	0.7	3
6337	New Insights into the Ecology and Physiology of Methanomassilicoccales from Terrestrial and Aquatic Environments. Microorganisms, 2021, 9, 30.	3.6	23
6340	Consistent patterns in 16S and 18S microbial diversity from the shells of the common and widespread red-eared slider turtle (Trachemys scripta). PLoS ONE, 2020, 15, e0244489.	2.5	6
6341	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. PLoS ONE, 2020, 15, e0243609.	2.5	6
6343	Statistical Methods for Analyzing Tree-Structured Microbiome Data. Frontiers in Probability and the Statistical Sciences, 2021, , 193-220.	0.1	1
6344	Belowground mechanisms for oak regeneration: Interactions among fire, soil microbes, and plant community alter oak seedling growth. Forest Ecology and Management, 2022, 503, 119774.	3.2	8
6345	Diverse crop rotations influence the bacterial and fungal communities in root, rhizosphere and soil and impact soil microbial processes. Applied Soil Ecology, 2022, 169, 104241.	4.3	17
6346	Effect of the passive natural ventilation on the bioaerosol in a small room. Building and Environment, 2022, 207, 108438.	6.9	14
6347	A baseline of Arbutus unedo L. microbiome for future research: In vitro versus ex vitro. Scientia Horticulturae, 2022, 292, 110657.	3.6	3
6348	Pesticide effects on nitrogen cycle related microbial functions and community composition. Science of the Total Environment, 2022, 807, 150734.	8.0	25
6349	Towards understanding microbial degradation of chloroquine in large saltwater systems. Science of the Total Environment, 2022, 807, 150532.	8.0	4
6350	Bioremediation of an oxyfluorfen-polluted soil using biostimulants obtained by fermentation processes: Effect on biological properties. Applied Soil Ecology, 2022, 170, 104270.	4.3	7
6352	Incorporating concentration-dependent sediment microbial activity into methylmercury production kinetics modeling. Environmental Sciences: Processes and Impacts, 2022, 24, 1392-1405.	3.5	1
6353	Gut microbiota of adults with asthma is broadly similar to non-asthmatics in a large population with varied ethnic origins. Gut Microbes, 2021, 13, 1995279.	9.8	6
6356	Composition and Diversity of Soil Bacterial Communities along an Environmental Gradient in the Sudano-Sahelian Region of Senegal. Open Journal of Soil Science, 2020, 10, 58-89.	0.8	1
6359	Influence of associative bacterial strains on the structure of the microbiocenosis of the rhizosphere of Triticum aestivum L E3S Web of Conferences, 2020, 224, 04002.	0.5	0
6360	Diversity and Structure of the Prokaryotic Communities Indigenous to Two Volcanic Lakes: Nyos and Monoun in Cameroon. Open Journal of Ecology, 2020, 10, 632-650.	1.0	4

#	Article	IF	Citations
6362	State of microbiocenosis of southern chernozem under the no-till system. E3S Web of Conferences, 2020, 224, 04009.	0.5	2
6392	Biological H ₂ and CO oxidation activities are sensitive to compositional change of soil microbial communities. Canadian Journal of Microbiology, 2020, 66, 263-273.	1.7	4
6394	Dysbiosis of Gut Microbiota Promotes Hepatocellular Carcinoma Progression by Regulating the Immune Response. Journal of Immunology Research, 2021, 2021, 1-13.	2.2	12
6396	Legacy Effects of Intercropping and Nitrogen Fertilization on Soil N Cycling, Nitrous Oxide Emissions, and the Soil Microbial Community in Tropical Maize Production. Frontiers in Soil Science, 2021, 1, .	2.2	6
6397	Microbial Diversity in Cultivated and Feral Vanilla Vanilla planifolia Orchids Affected by Stem and Rot Disease. Microbial Ecology, 2022, 84, 821-833.	2.8	8
6400	Correlating Biodegradation Kinetics of 2,4-Dichlorophenoxyacetic Acid (2,4-D) and 2,4,5-Trichlorophenoxyacetic Acid (2,4,5-T) to the Dynamics of Microbial Communities Originating From Soil in Vietnam Contaminated With Herbicides. Frontiers in Sustainable Cities, 2021, 3, .	2.4	8
6401	Phage-delivered CRISPR-Cas9 for strain-specific depletion and genomic deletions in the gut microbiome. Cell Reports, 2021, 37, 109930.	6.4	68
6402	Utilizing a reductionist model to study host-microbe interactions in intestinal inflammation. Microbiome, 2021, 9, 215.	11.1	8
6405	Transmission of Escherichia coli from Manure to Root Zones of Field-Grown Lettuce and Leek Plants. Microorganisms, 2021, 9, 2289.	3.6	7
6406	An insight into tropical milk microbiome: Bacterial community composition of cattle milk produced in Sri Lanka. International Dairy Journal, 2022, 126, 105266.	3.0	2
6407	Invasive Amphibian Gut Microbiota and Functions Shift Differentially in an Expanding Population but Remain Conserved Across Established Populations. Microbial Ecology, 2022, 84, 1042-1054.	2.8	4
6408	Sea ice presence is linked to higher carbon export and vertical microbial connectivity in the Eurasian Arctic Ocean. Communications Biology, 2021, 4, 1255.	4.4	21
6410	Dysbiosis of Gut Microbiome Is Associated With Rupture of Cerebral Aneurysms. Stroke, 2022, 53, 895-903.	2.0	27
6411	Candida albicans Isolates 529L and CHN1 Exhibit Stable Colonization of the Murine Gastrointestinal Tract. MBio, 2021, 12, e0287821.	4.1	21
6412	Spatial and temporal comparisons of salt marsh soil fungal communities following the deepwater horizon spill. Wetlands Ecology and Management, 0, , 1.	1.5	0
6413	Antibiotic resistance genes of emerging concern in municipal and hospital wastewater from a major Swedish city. Science of the Total Environment, 2022, 812, 151433.	8.0	28
6414	Long-term dynamics of the human oral microbiome during clinical disease progression. BMC Biology, 2021, 19, 240.	3.8	10
6415	Tick virome diversity in Hubei Province, China, and the influence of host ecology. Virus Evolution, 2021, 7, veab089.	4.9	24

#	Article	IF	Citations
6416	Stochastic processes regulate belowground community assembly in alpine grasslands on the Tibetan Plateau. Environmental Microbiology, 2022, 24, 179-194.	3.8	28
6417	Characterization of the endometrial, cervicovaginal and anorectal microbiota in post-menopausal women with endometrioid and serous endometrial cancers. PLoS ONE, 2021, 16, e0259188.	2.5	6
6420	Land use influences stream bacterial communities in lowland tropical watersheds. Scientific Reports, 2021, 11, 21752.	3.3	10
6421	The Eco-Evo Mandala: Simplifying Bacterioplankton Complexity into Ecohealth Signatures. Entropy, 2021, 23, 1471.	2.2	6
6422	Microbial Surface Biofilm Responds to the Growth-Reproduction-Senescence Cycle of the Dominant Coral Reef Macroalgae Sargassum spp Life, 2021, 11, 1199.	2.4	0
6423	Terrestrial-type nitrogen-fixing symbiosis between seagrass and a marine bacterium. Nature, 2021, 600, 105-109.	27.8	48
6424	Horsenettle (<i>Solanum carolinense</i>) fruit bacterial communities are not variable across fine spatial scales. PeerJ, 2021, 9, e12359.	2.0	0
6426	Dietary calcium phosphate strongly impacts gut microbiome changes elicited by inulin and galacto-oligosaccharides consumption. Microbiome, 2021, 9, 218.	11.1	32
6427	Spatial and temporal dynamics of SAR11 marine bacteria across a nearshore to offshore transect in the tropical Pacific Ocean. PeerJ, 2021, 9, e12274.	2.0	4
6428	Distinct methane-dependent biogeochemical states in Arctic seafloor gas hydrate mounds. Nature Communications, 2021, 12, 6296.	12.8	9
6429	Variability of Microbial Communities in Two Long-Term Ice-Covered Freshwater Lakes in the Subarctic Region of Yakutia, Russia. Microbial Ecology, 2022, 84, 958-973.	2.8	5
6430	Linking gut microbiome with the feeding behavior of the Arunachal macaque (Macaca munzala). Scientific Reports, 2021, 11, 21926.	3.3	1
6431	Longitudinal assessment of taurine and amino acid concentrations in dogs fed a green lentil diet. Journal of Animal Science, 2021, 99, .	0.5	5
6432	Evidence of MHC class I and II influencing viral and helminth infection via the microbiome in a non-human primate. PLoS Pathogens, 2021, 17, e1009675.	4.7	22
6433	Dataset complexity impacts both MOTU delimitation and biodiversity estimates in eukaryotic 18S rRNA metabarcoding studies. Environmental DNA, 2022, 4, 363-384.	5.8	7
6435	eDNA captures depth partitioning in a kelp forest ecosystem. PLoS ONE, 2021, 16, e0253104.	2.5	30
6481	A glimpse of antimicrobial resistance gene diversity in kefir and yoghurt. Scientific Reports, 2020, 10, 22458.	3.3	27
6496	The difference between cellulolytic  culturomes' and microbiomes inhabiting two contrasting soil types. PLoS ONE, 2020, 15, e0242060.	2.5	6

#	ARTICLE	IF	CITATIONS
6498	Goats fed with non-protein nitrogen: ruminal bacterial community and ruminal fermentation, intake, digestibility and nitrogen balance. Journal of Agricultural Science, 2020, 158, 781-790.	1.3	4
6499	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 183-94.	0.7	12
6500	Distinct Ecological Niche of Anal, Oral, and Cervical Mucosal Microbiomes in Adolescent Women. Yale Journal of Biology and Medicine, 2016, 89, 277-284.	0.2	11
6501	16S rRNA deep sequencing for the characterization of healthy human pharyngeal microbiome. Hippokratia, 2018, 22, 29-36.	0.3	3
6502	OUP accepted manuscript. FEMS Microbiology Ecology, 2021, , .	2.7	7
6503	Taxonomic and functional characterization of the rumen microbiome of Japanese Black cattle revealed by 16S rRNA gene amplicon and metagenome shotgun sequencing. FEMS Microbiology Ecology, 2021, 97, .	2.7	9
6505	Developmental Stage, Solid Food Introduction, and Suckling Cessation Differentially Influence the Comaturation of the Gut Microbiota and Intestinal Epithelium in Rabbits. Journal of Nutrition, 2022, 152, 723-736.	2.9	5
6506	Feeding ecology and microbiome of the pteropod Limacina helicina antarctica. Aquatic Microbial Ecology, 2022, 88, 19-24.	1.8	5
6507	MAIT cell activation is reduced by direct and microbiota-mediated exposure to bisphenols. Environment International, 2022, 158, 106985.	10.0	10
6508	Assessing the efficacy of antibiotic treatment to produce earthworms with a suppressed microbiome. European Journal of Soil Biology, 2022, 108, 103366.	3.2	2
6509	Coupling ecological network analysis with high-throughput sequencing-based surveys: Lessons from the next-generation biomonitoring project. Advances in Ecological Research, 2021, 65, 367-430.	2.7	5
6510	Forest landscapes increase diversity of honeybee diets in the tropics. Forest Ecology and Management, 2022, 504, 119869.	3.2	6
6511	Mucosal microbiome associates with progression to gastric cancer. Theranostics, 2022, 12, 48-58.	10.0	17
6512	Carbon dioxide to bio-oil in a bioelectrochemical system-assisted microalgae biorefinery process. Sustainable Energy and Fuels, 2021, 6, 150-161.	4.9	22
6513	Impact of anoxic conditions, uranium(VI) and organic phosphate substrate on the biogeochemical potential of the indigenous bacterial community of bentonite. Applied Clay Science, 2022, 216, 106331.	5.2	11
6514	Role of rhizosphere microbiome during phytoremediation of heavy metals., 2022,, 263-291.		5
6515	Biodiversity of the intestinal microbiota of black tiger prawn, Penaeus monodon, increases with age and is only transiently impacted by major ingredient replacement in the diet. Aquaculture Reports, 2022, 22, 100948.	1.7	0
6516	The nitrification inhibitor nitrapyrin has non-target effects on the soil microbial community structure, composition, and functions. Applied Soil Ecology, 2022, 171, 104350.	4.3	9

#	Article	IF	CITATIONS
6517	Deciphering the Fusarium-wilt control effect and succession driver of microbial communities managed under low-temperature conditions. Applied Soil Ecology, 2022, 171, 104334.	4.3	8
6518	Proximity to subsurface drip irrigation emitters altered soil microbial communities in two commercial processing tomato fields. Applied Soil Ecology, 2022, 171, 104315.	4.3	2
6519	Predicting soil farming system and attributes based on soil bacterial community. Applied Soil Ecology, 2022, 171, 104335.	4.3	5
6520	Evaluating DNA metabarcoding to analyze diet composition of wild long-snouted seahorse Hippocampus guttulatus., 2021,,.		1
6521	Classification and prediction of Mycobacterium Avium subsp. Paratuberculosis (MAP) shedding severity in cattle based on young stock heifer faecal microbiota composition using random forest algorithms. Animal Microbiome, 2021, 3, 78.	3.8	2
6522	Nonstarter Bacterial Communities in Aged Cheddar Cheese: Patterns on Two Timescales. Applied and Environmental Microbiology, 2022, 88, AEM0193921.	3.1	3
6523	Residential bacteria and fungi identified by high-throughput sequencing and childhood respiratory health. Environmental Research, 2022, 204, 112377.	7.5	6
6525	Unravelling the contribution of nitrifying and methanotrophic bacteria to micropollutant co-metabolism in rapid sand filters. Journal of Hazardous Materials, 2022, 424, 127760.	12.4	14
6526	Giant sulfur bacteria (Beggiatoaceae) from sediments underlying the Benguela upwelling system host diverse microbiomes. PLoS ONE, 2021, 16, e0258124.	2.5	8
6527	Insights into the Oral Bacterial Microbiota of Sows. Microorganisms, 2021, 9, 2314.	3.6	2
6528	Distinct microbiome profiles and biofilms in Leishmania donovani-driven cutaneous leishmaniasis wounds. Scientific Reports, 2021, 11, 23181.	3.3	10
6529	Distinctive roles between rumen epimural and content bacterial communities on beef cattle feed efficiency: A combined analysis. Current Research in Microbial Sciences, 2021, 2, 100085.	2.3	5
6531	Contrasting Community Assembly Forces Drive Microbial Structural and Potential Functional Responses to Precipitation in an Incipient Soil System. Frontiers in Microbiology, 2021, 12, 754698.	3 . 5	4
6532	The Spanish gut microbiome reveals links between microorganisms and Mediterranean diet. Scientific Reports, 2021, 11, 21602.	3.3	12
6533	Monitoring fish communities through environmental DNA metabarcoding in the fish pass system of the second largest hydropower plant in the world. Scientific Reports, 2021, 11, 23167.	3.3	5
6534	The meta-gut: community coalescence of animal gut and environmental microbiomes. Scientific Reports, 2021, 11, 23117.	3 . 3	17
6535	Evidence for host–microbiome coâ€evolution in apple. New Phytologist, 2022, 234, 2088-2100.	7.3	40
6536	Metabarcoding, direct stomach observation and stable isotope analysis reveal a highly diverse diet for the invasive green crab in Atlantic Patagonia. Biological Invasions, 2022, 24, 505-526.	2.4	9

#	Article	IF	CITATIONS
6537	Profiling Branchial Bacteria of Atlantic Salmon (Salmo salar L.) Following Exposure to Antimicrobial Agents. Frontiers in Animal Science, 2021, 2, .	1.9	4
6538	Decay by ectomycorrhizal fungi couples soil organic matter to nitrogen availability. Ecology Letters, 2022, 25, 391-404.	6.4	32
6539	Circadian dynamics of the teleost skin immune-microbiome interface. Microbiome, 2021, 9, 222.	11.1	20
6540	Geographic and position-based variations in phyllospheric bacterial communities present on flue-cured tobacco. Applied Microbiology and Biotechnology, 2021, 105, 9297-9308.	3.6	5
6541	Tetrabromobisphenol A (TBBPA) biodegradation in acidogenic systems: One step further on where and who. Science of the Total Environment, 2022, 808, 152016.	8.0	6
6542	A Faithful Gut: Core Features of Gastrointestinal Microbiota of Long-Distance Migratory Bats Remain Stable despite Dietary Shifts Driving Differences in Specific Bacterial Taxa. Microbiology Spectrum, 2021, 9, e0152521.	3.0	3
6543	Activated sludge microbial communities influencing the performance of a full-scale wastewater treatment plant treating optoelectronic wastewater. Journal of Environmental Chemical Engineering, 2021, 10, 106833.	6.7	3
6545	Influence of timing of maternal antibiotic administration during caesarean section on infant microbial colonisation: a randomised controlled trial. Gut, 2022, 71, 1803-1811.	12.1	19
6546	Microbial Response to Fungal Infection in a Fungus-Growing Termite, Odontotermes formosanus (Shiraki). Frontiers in Microbiology, 2021, 12, 723508.	3.5	2
6547	Metabarcoding Reveals Lacustrine Picocyanobacteria Respond to Environmental Change Through Adaptive Community Structuring. Frontiers in Microbiology, 2021, 12, 757929.	3.5	8
6548	Bacterial Communities in the Embryo of Maize Landraces: Relation with Susceptibility to Fusarium Ear Rot. Microorganisms, 2021, 9, 2388.	3.6	7
6549	Enhancing diversity analysis by repeatedly rarefying next generation sequencing data describing microbial communities. Scientific Reports, 2021, 11, 22302.	3.3	80
6550	Photoheterotrophy by aerobic anoxygenic bacteria modulates carbon fluxes in a freshwater lake. ISME Journal, 2022, 16, 1046-1054.	9.8	15
6551	Unveiling Ecological and Genetic Novelty within Lytic and Lysogenic Viral Communities of Hot Spring Phototrophic Microbial Mats. Microbiology Spectrum, 2021, , e0069421.	3.0	4
6552	Bacterial response to spatial gradients of algal-derived nutrients in a porous microplate. ISME Journal, 2022, 16, 1036-1045.	9.8	21
6553	Insights into the nutritional properties and microbiome diversity in sweet and sour yogurt manufactured in Bangladesh. Scientific Reports, 2021, 11, 22667.	3.3	5
6554	Nasopharyngeal bacterial and fungal microbiota in normal horses and horses with nasopharyngeal cicatrix syndrome. Journal of Veterinary Internal Medicine, 2021, 35, 2897.	1.6	4
6555	Bacterial Abundance, Diversity and Activity During Long-Term Colonization of Non-biodegradable and Biodegradable Plastics in Seawater. Frontiers in Microbiology, 2021, 12, 734782.	3.5	35

#	Article	IF	CITATIONS
6556	The Gut Microbiota of an Individual Varies With Intercontinental Four-Month Stay Between Italy and Nigeria: A Pilot Study. Frontiers in Cellular and Infection Microbiology, 2021, 11, 725769.	3.9	2
6557	Improved quantitative microbiome profiling for environmental antibiotic resistance surveillance. Environmental Microbiomes, 2021, 16, 21.	5.0	4
6558	Emergent bacterial community properties induce enhanced drought tolerance in Arabidopsis. Npj Biofilms and Microbiomes, 2021, 7, 82.	6.4	45
6560	Non-Specific Interactions of Rhizospheric Microbial Communities Support the Establishment of Mimosa acutistipula var. ferrea in an Amazon Rehabilitating Mineland. Processes, 2021, 9, 2079.	2.8	12
6561	Sustaining low pressure drop and homogeneous flow by adopting a fluidized bed biofilter treating gaseous toluene. Chemosphere, 2021, 291, 132951.	8.2	3
6562	Modulation of Gilthead Sea Bream Gut Microbiota by a Bioactive Egg White Hydrolysate: Interactions Between Bacteria and Host Lipid Metabolism. Frontiers in Marine Science, 2021, 8, .	2.5	9
6563	Effects of Resistant Starch on Symptoms, Fecal Markers, and Gut Microbiota in Parkinson's Disease — The RESISTA-PD Trial. Genomics, Proteomics and Bioinformatics, 2022, 20, 274-287.	6.9	26
6564	Soil chemistry, temperature and bacterial community composition drive brGDGT distributions along a subarctic elevation gradient. Organic Geochemistry, 2022, 163, 104346.	1.8	11
6565	Comparison of gastrointestinal microbiota in golden snub-nosed monkey (Rhinopithecus roxellanae), green monkey (Chlorocebus aethiops sabaeus), and ring-tailed lemur (Lemur catta) by high throughput sequencing. Global Ecology and Conservation, 2022, 33, e01946.	2.1	3
6566	Bacterial Diversity in House Dust: Characterization of a Core Indoor Microbiome. Frontiers in Environmental Science, 2021, 9, .	3.3	7
6567	The Use of Ascophyllum nodosum and Bacillus subtilis C-3102 in the Management of Canine Chronic Inflammatory Enteropathy: A Pilot Study. Animals, 2021, 11, 3417.	2.3	5
6568	Polar Cryoconite Associated Microbiota Is Dominated by Hemispheric Specialist Genera. Frontiers in Microbiology, 2021, 12, 738451.	3.5	4
6569	Identifying prognostic pairwise relationships among bacterial species in microbiome studies. PLoS Computational Biology, 2021, 17, e1009501.	3.2	0
6570	Molecular Characterization of Distinct Fungal Communities in the Soil of a Rare Earth Mining Area. Microbial Ecology, 2022, 84, 1212-1223.	2.8	8
6571	Biodiversity of Soil Bacterial Communities from the Sasso Fratino Integral Nature Reserve. Microbiology Research, 2021, 12, 862-877.	1.9	4
6572	Diversity of Oral Microbiome of Women From Urban and Rural Areas of Indonesia: A Pilot Study. Frontiers in Oral Health, 2021, 2, 738306.	3.0	5
6573	Bacterial community dynamics of tomato hydroponic greenhouses infested with hairy root disease. FEMS Microbiology Ecology, 2021, 97, .	2.7	5
6574	An Insight into Vaginal Microbiome Techniques. Life, 2021, 11, 1229.	2.4	9

#	Article	IF	CITATIONS
6575	Impact of Oropharyngeal Administration of Colostrum in Preterm Newborns' Oral Microbiome. Nutrients, 2021, 13, 4224.	4.1	13
6576	Antibiotic Resistance Genes and Potentially Pathogenic Bacteria in the Central Adriatic Sea: Are They Connected to Urban Wastewater Inputs?. Water (Switzerland), 2021, 13, 3335.	2.7	12
6577	Preservation methods of honey bee-collected pollen are not a source of bias in ITS2 metabarcoding. Environmental Monitoring and Assessment, 2021, 193, 785.	2.7	5
6578	Association between Parkinson's disease and the faecal eukaryotic microbiota. Npj Parkinson's Disease, 2021, 7, 101.	5.3	7
6579	Micronutrient supplements can promote disruptive protozoan and fungal communities in the developing infant gut. Nature Communications, 2021, 12, 6729.	12.8	17
6580	Effects of Early, Small-Scale Nitrogen Addition on Germination and Early Growth of Scots Pine (Pinus) Tj ETQq1 1 12, 1589.	0.784314 2.1	rgBT /Overl
6581	Organic Amendments and Sampling Date Influences on Soil Bacterial Community Composition and Their Predictive Functional Profiles in an Olive Grove Ecosystem. Agriculture (Switzerland), 2021, 11, 1178.	3.1	4
6582	Deterministic processes drive the microbial assembly during the recovery of an anaerobic digester after a severe ammonia shock. Bioresource Technology, 2022, 347, 126432.	9.6	3
6583	The effect of low-pH concrete on microbial community development in bentonite suspensions as a model for microbial activity prediction in future nuclear waste repository. Science of the Total Environment, 2022, 808, 151861.	8.0	11
6584	Commensal Bifidobacterium Strains Enhance the Efficacy of Neo-Epitope Based Cancer Vaccines. Vaccines, 2021, 9, 1356.	4.4	10
6585	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. Nature Communications, 2021, 12, 6740.	12.8	89
6586	Baseline Data of the Fungal Phytobiome of Three Sorghum (Sorghum bicolor) Cultivars in South Africa using Targeted Environmental Sequencing. Journal of Fungi (Basel, Switzerland), 2021, 7, 978.	3.5	4
6588	Comparison of fecal sample collection methods for microbial analysis embedded within colorectal cancer screening programs. Cancer Epidemiology Biomarkers and Prevention, 2021, , cebp.0188.2021.	2.5	10
6589	Cross-feeding between intestinal pathobionts promotes their overgrowth during undernutrition. Nature Communications, 2021, 12, 6860.	12.8	17
6590	Mycorrhizal symbiosis balances rootstock-mediated growth-defence tradeoffs. Biology and Fertility of Soils, 2022, 58, 17-34.	4.3	19
6591	An examination of the use of antibiotics as a method to experimentally perturb the microbiota of suspensionâ€feeding bivalves. Invertebrate Biology, 2021, 140, .	0.9	2
6592	Effects of Orally Administered Cannabidiol on Neuroinflammation and Intestinal Inflammation in the Attenuation of Experimental Autoimmune Encephalomyelitis. Journal of NeuroImmune Pharmacology, 2022, 17, 15-32.	4.1	21
6593	Effects of Alcohol Binge Drinking and Oleoylethanolamide Pretreatment in the Gut Microbiota. Frontiers in Cellular and Infection Microbiology, 2021, 11, 731910.	3.9	9

#	Article	IF	Citations
6594	Inconsistent Patterns of Microbial Diversity and Composition Between Highly Similar Sequencing Protocols: A Case Study With Reef-Building Corals. Frontiers in Microbiology, 2021, 12, 740932.	3.5	8
6595	Assessing the microbiota of recycled bedding sand on a Wisconsin dairy farm. Journal of Animal Science and Biotechnology, 2021, 12, 114.	5. 3	4
6598	Diversity Indices of Plant Communities and Their Rhizosphere Microbiomes: An Attempt to Find the Connection. Microorganisms, 2021, 9, 2339.	3.6	12
6599	The gut microbiome of extremely preterm infants randomized to the early progression of enteral feeding. Pediatric Research, 2022, 92, 799-804.	2.3	5
6600	Comprehensive Compositional Analysis of the Slit Lamp Bacteriota. Frontiers in Cellular and Infection Microbiology, 2021, 11, 745653.	3.9	0
6601	The influence of the Doce River mouth on the microbiome of nearby coastal areas three years after the Fundão Dam failure, Brazil. Science of the Total Environment, 2022, 807, 151777.	8.0	7
6602	An integrated host-microbiome response to atrazine exposure mediates toxicity in Drosophila. Communications Biology, 2021, 4, 1324.	4.4	10
6603	Broad Dissemination of Plasmids across Groundwater-Fed Rapid Sand Filter Microbiomes. MBio, 2021, 12, e0306821.	4.1	6
6604	Oral microbiome associated with lymph node metastasis in oral squamous cell carcinoma. Scientific Reports, 2021, 11, 23176.	3.3	26
6605	Assessment of the Effects of Dietary Vitamin D Levels on Olanzapine-Induced Metabolic Side Effects: Focus on the Endocannabinoidome-Gut Microbiome Axis. International Journal of Molecular Sciences, 2021, 22, 12361.	4.1	4
6606	Next- and Third-Generation Sequencing Outperforms Culture-Based Methods in the Diagnosis of Ascitic Fluid Bacterial Infections of ICU Patients. Cells, 2021, 10, 3226.	4.1	10
6607	Size-Resolved Community Structure of Bacteria and Fungi Transported by Dust in the Middle East. Frontiers in Microbiology, 2021, 12, 744117.	3.5	12
6608	Eubacterium coprostanoligenes and Methanoculleus identified as potential producers of metabolites that contribute to swine manure foaming. Journal of Applied Microbiology, 2022, 132, 2906-2924.	3.1	5
6609	Metabarcoding hyperdiverse kelp holdfast communities on temperate reefs: An experimental approach to inform future studies. Environmental DNA, 2022, 4, 492-509.	5.8	1
6610	Multivariable association discovery in population-scale meta-omics studies. PLoS Computational Biology, 2021, 17, e1009442.	3.2	691
6611	Seasonal Dynamics of Bathyarchaeota-Dominated Benthic Archaeal Communities Associated with Seagrass (Zostera japonica) Meadows. Journal of Marine Science and Engineering, 2021, 9, 1304.	2.6	6
6612	Oil and Gas Wastewater Components Alter Streambed Microbial Community Structure and Function. Frontiers in Microbiology, 2021, 12, 752947.	3.5	4
6613	Effects of Fusarium metabolites beauvericin and enniatins alone or in mixture with deoxynivalenol on weaning piglets. Food and Chemical Toxicology, 2021, 158, 112719.	3.6	10

#	Article	IF	CITATIONS
6614	Applications of the indole-alkaloid gramine modulate the assembly of individual members of the barley rhizosphere microbiota. PeerJ, 2021, 9, e12498.	2.0	12
6615	Weaning Age and Its Effect on the Development of the Swine Gut Microbiome and Resistome. MSystems, 2021, 6, e0068221.	3.8	26
6616	Microbiome composition of Anna's hummingbirds differs among regions of the gastrointestinal tract. Journal of Avian Biology, 2022, 2022, .	1.2	3
6617	Spatial and Temporal Constraints on the Composition of Microbial Communities in Subsurface Boreholes of the Edgar Experimental Mine. Microbiology Spectrum, 2021, 9, e0063121.	3.0	2
6618	Revealing the composition of the eukaryotic microbiome of oyster spat by CRISPR-Cas Selective Amplicon Sequencing (CCSAS). Microbiome, 2021, 9, 230.	11.1	6
6619	A systematic meta-analysis reveals enrichment of Actinobacteria and Firmicutes in the fish gut in response to black soldier fly (Hermetica illucens) meal-based diets. Aquaculture, 2022, 549, 737760.	3 . 5	17
6620	Effect of voluntary exercise upon the metabolic syndrome and gut microbiome composition in mice. Physiological Reports, 2021, 9, e15068.	1.7	2
6621	Multispecies Populations of Methanotrophic <i>Methyloprofundus</i> and Cultivation of a Likely Dominant Species from the Iheya North Deep-Sea Hydrothermal Field. Applied and Environmental Microbiology, 2022, 88, AEM0075821.	3.1	12
6622	Use of universal primers for the 18S ribosomal RNA gene and whole soil DNAs to reveal the taxonomic structures of soil nematodes by high-throughput amplicon sequencing. PLoS ONE, 2021, 16, e0259842.	2.5	3
6624	Between Interactions and Aggregates: The PolyQ Balance. Genome Biology and Evolution, 2021, 13, .	2.5	9
6625	Effect of fiber source and crude protein level on nursery pig performance and fecal microbial communities. Journal of Animal Science, 2021, 99, .	0.5	3
6626	Impact of Electrolyzed Water on the Microbial Spoilage Profile of Piedmontese Steak Tartare. Microbiology Spectrum, 2021, 9, e0175121.	3.0	4
6628	Larval sites of the mosquito <i>Aedes aegypti formosus</i> in forest and domestic habitats in Africa and the potential association with oviposition evolution. Ecology and Evolution, 2021, 11, 16327-16343.	1.9	16
6629	Winter diet of Japanese macaques from Chubu Sangaku National Park, Japan incorporates freshwater biota. Scientific Reports, 2021, 11, 23091.	3.3	5
6630	From DNA sequences to microbial ecology: Wrangling NEON soil microbe data with the neonMicrobe R package. Ecosphere, 2021, 12, e03842.	2.2	3
6631	Soil microbial community response to winter climate change is phylogenetically conserved and highly resilient in a cool-temperate forest. Soil Biology and Biochemistry, 2022, 165, 108499.	8.8	15
6632	Gut microbiome and metabolome in a non-human primate model of chronic excessive alcohol drinking. Translational Psychiatry, 2021, 11, 609.	4.8	12
6633	Intestinal microbiota modulation and improved growth in pigs with post-weaning antibiotic and ZnO supplementation but only subtle microbiota effects with Bacillus altitudinis. Scientific Reports, 2021, 11, 23304.	3.3	4

#	Article	IF	Citations
6634	Heat stress reduces the contribution of diazotrophs to coral holobiont nitrogen cycling. ISME Journal, 2022, 16, 1110-1118.	9.8	21
6635	Engineering living and regenerative fungal–bacterial biocomposite structures. Nature Materials, 2022, 21, 471-478.	27.5	47
6636	Feed and Host Genetics Drive Microbiome Diversity with Resultant Consequences for Production Traits in Mass-Reared Black Soldier Fly (Hermetia illucens) Larvae. Insects, 2021, 12, 1082.	2.2	15
6637	N-Cycling Microbiome Recruitment Differences Between Modern andÂWild <i>Zea mays</i> Phytobiomes Journal, 2022, 6, 151-160.	2.7	5
6638	The restructuring of grape berry waxes by calcium changes the surface microbiota. Food Research International, 2021, 150, 110812.	6.2	6
6639	Host species identity shapes the diversity and structure of insect microbiota. Molecular Ecology, 2022, 31, 723-735.	3.9	21
6640	Bacterial, archaeal, and fungal community structure and interrelationships of deep-sea shrimp intestine and the surrounding sediment. Environmental Research, 2022, 205, 112461.	7. 5	5
6641	Structure of the manure resistome and the associated mobilome for assessing the risk of antimicrobial resistance transmission to crops. Science of the Total Environment, 2022, 808, 152144.	8.0	13
6642	Time-restricted feeding induces Lactobacillus- and Akkermansia-specific functional changes in the rat fecal microbiota. Npj Biofilms and Microbiomes, 2021, 7, 85.	6.4	14
6643	Antigen-presenting innate lymphoid cells orchestrate neuroinflammation. Nature, 2021, 600, 707-712.	27.8	35
6644	Effect of Geography and Captivity on Scat Bacterial Communities in the Imperiled Channel Island Fox. Frontiers in Microbiology, 2021, 12, 748323.	3.5	3
6646	Dental caries and its association with the oral microbiomes and HIV in young childrenâ€"Nigeria (DOMHaIN): a cohort study. BMC Oral Health, 2021, 21, 620.	2.3	9
6647	Exploring the Microbiome Analysis and Visualization Landscape. Frontiers in Bioinformatics, 2021, 1, .	2.1	4
6648	Dysbiosis and relapse-related microbiome in inflammatory bowel disease: A shotgun metagenomic approach. Computational and Structural Biotechnology Journal, 2021, 19, 6481-6489.	4.1	21
6649	Wheat Genotype-Specific Recruitment of Rhizosphere Bacterial Microbiota Under Controlled Environments. Frontiers in Plant Science, 2021, 12, 718264.	3.6	7
6650	An ancient antimicrobial protein co-opted by a fungal plant pathogen for in planta mycobiome manipulation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	45
6651	Analyzing gut microbiota composition in individual Anopheles mosquitoes after experimental treatment. IScience, 2021, 24, 103416.	4.1	4
6653	Factors Influencing the Fungal Diversity on Audio–Visual Materials. Microorganisms, 2021, 9, 2497.	3.6	8

#	Article	IF	CITATIONS
6654	Tracking Bacterial Pollution at a Marine Wastewater Outfall Site $\hat{a} \in \hat{a}$ a Case Study from Norway. SSRN Electronic Journal, $0, , .$	0.4	0
6655	Microbial processes and community structure as influenced by cover crop residue type and placement during repeated dry-wet cycles. Applied Soil Ecology, 2022, 172, 104349.	4.3	4
6656	Microbial community responses to phosphorus and nitrogen inputs in the organic soil horizons of two contrasting temperate beech forests. Applied Soil Ecology, 2022, 172, 104357.	4.3	7
6657	PIMBA: A Pipeline for MetaBarcoding Analysis. Lecture Notes in Computer Science, 2021, , 106-116.	1.3	3
6658	Plant Root Exudates and Rhizosphere Bacterial Communities Shift with Competitive Neighbor. SSRN Electronic Journal, 0, , .	0.4	0
6659	Polyploidy and Microbiome Associations Mediate Distinct Plant Responses to Pathogens. SSRN Electronic Journal, 0, , .	0.4	0
6660	Tracking Spoilage Bacteria in the Tuna Necrobiome. SSRN Electronic Journal, 0, , .	0.4	0
6661	Multivariate associative patterns between the gut microbiota and large-scale brain network connectivity. Gut Microbes, 2021, 13, 2006586.	9.8	14
6663	Contrasting Effects of Local Environmental and Biogeographic Factors on the Composition and Structure of Bacterial Communities in Arid Monospecific Mangrove Soils. Microbiology Spectrum, 2022, 10, e0090321.	3.0	11
6664	Riparian Cottonwood Trees and Adjacent River Sediments Have Different Microbial Communities and Produce Methane With Contrasting Carbon Isotope Compositions. Journal of Geophysical Research G: Biogeosciences, 2022, 127, .	3.0	4
6665	Intra―and interâ€annual variability of nitrification in the rhizosphere of fieldâ€grown bioenergy sorghum. GCB Bioenergy, 2022, 14, 393-410.	5.6	6
6666	Exploring the universal healthy human gut microbiota around the World. Computational and Structural Biotechnology Journal, 2022, 20, 421-433.	4.1	14
6667	Anaerobic Digestion of Kraft Pulp Mill Foul Condensate Under Thermophilic and Mesophilic Conditions. Environmental Engineering Science, 2022, 39, 573-583.	1.6	3
6668	Maternal regulation of biliary disease in neonates via gut microbial metabolites. Nature Communications, 2022, 13, 18.	12.8	13
6669	From Surface to Subsurface: Diversity, Composition, and Abundance of Sessile and Endolithic Bacterial, Archaeal, and Eukaryotic Communities in Sand, Clay and Rock Substrates in the Laurentians (Quebec, Canada). Microorganisms, 2022, 10, 129.	3.6	6
6670	Intestinal Taxa Abundance and Diversity in Inflammatory Bowel Disease Patients: An Analysis including Covariates and Confounders. Nutrients, 2022, 14, 260.	4.1	21
6671	Comparative Microbiomes of the Respiratory Tract and Joints of Feedlot Cattle Mortalities. Microorganisms, 2022, 10, 134.	3.6	5
6672	Seasonality drives microbiome composition and nitrogen cycling in soil below biocrusts. Soil Biology and Biochemistry, 2022, 166, 108551.	8.8	14

#	Article	IF	CITATIONS
6673	Distinct gut microbiomes in two polar bear subpopulations inhabiting different sea ice ecoregions. Scientific Reports, 2022, 12, 522.	3.3	4
6676	Eukaryotic Parasites Are Integral to a Productive Microbial Food Web in Oxygen-Depleted Waters. Frontiers in Microbiology, 2021, 12, 764605.	3.5	11
6678	Structure and functional capacity of a benzene-mineralizing, nitrate-reducing microbial community. Journal of Applied Microbiology, 2022, 132, 2795-2811.	3.1	6
6680	Size-Fractionated Microbiome Structure in Subarctic Rivers and a Coastal Plume Across DOC and Salinity Gradients. Frontiers in Microbiology, 2021, 12, 760282.	3.5	9
6681	Characterization of captive and wild 13 -lined ground squirrel cecal microbiotas using Illumina-based sequencing. Animal Microbiome, 2022, 4, 1.	3.8	6
6682	Combined Histo-endoscopic Remission but not Endoscopic Healing Alone in Ulcerative Colitis is Associated with a Mucosal Transcriptional Profile Resembling Healthy Mucosa. Journal of Crohn's and Colitis, 2022, 16, 1020-1029.	1.3	5
6683	Presence of bacteria capable of PCB biotransformation in stormwater bioretention cells. FEMS Microbiology Ecology, 2022, , .	2.7	4
6684	Implications of taxonomic and numerical resolution on DNA metabarcoding-based inference of benthic macroinvertebrate responses to river restoration. Ecological Indicators, 2022, 135, 108508.	6. 3	3
6685	Natural forest chronosequence maintains better soil fertility indicators and assemblage of total belowground soil biota than Chinese fir monoculture in subtropical ecosystem. Journal of Cleaner Production, 2022, 334, 130228.	9.3	11
6686	Microbiota of Crassostrea virginica larvae during a hatchery crash and under normal production: Amplicon sequence data. Data in Brief, 2022, 40, 107755.	1.0	1
6687	Predicting the occurrence of monooxygenases and their associated phylotypes in soil microcosms. Journal of Microbiological Methods, 2022, 193, 106401.	1.6	5
6688	Response of growth performance, serum metabolites, intestinal tight junction structure and bacterial microbiomes to the long-term intervention of aflatoxin B1 in Lateolabrax maculatus diets. Aquaculture Reports, 2022, 22, 101005.	1.7	2
6689	Tracking the impacts of nutrient inputs on estuary ecosystem function. Science of the Total Environment, 2022, 811, 152405.	8.0	6
6690	Effects of sterilization and maturity of compost on soil bacterial and fungal communities and wheat growth. Geoderma, 2022, 409, 115598.	5.1	22
6691	A bacterial index to estimate lake trophic level: National scale validation. Science of the Total Environment, 2022, 812, 152385.	8.0	7
6692	Use of metagenomic microbial source tracking to investigate the source of a foodborne outbreak of cryptosporidiosis. Food and Waterborne Parasitology, 2022, 26, e00142.	2.7	6
6693	Quantifying the immediate response of the soil microbial community to different grazing intensities on irrigated pastures. Agriculture, Ecosystems and Environment, 2022, 326, 107805.	5. 3	13
6694	Exploring the relationship between the gut microbiome and mental health outcomes in a posttraumatic stress disorder cohort relative to trauma-exposed controls. European Neuropsychopharmacology, 2022, 56, 24-38.	0.7	26

#	Article	IF	CITATIONS
6695	Microbiota composition is moderately associated with greenspace composition in a UK cohort of twins. Science of the Total Environment, 2022, 813, 152321.	8.0	7
6696	Microbiome response to foam fractionation and ozonation in RAS. Aquaculture, 2022, 550, 737846.	3.5	9
6697	Alteration of bacterial communities and co-occurrence networks as a legacy effect upon exposure to polyethylene residues under field environment. Journal of Hazardous Materials, 2022, 426, 128126.	12.4	11
6698	Fructans from Agave enhance probiotic yoghurt by modulating gut microbiota on children with overweight or obesity. Food Bioscience, 2022, 46, 101516.	4.4	5
6700	Decoupled richness of generalist anaerobes and sulphateâ€reducing bacteria is driven by <scp>pH</scp> across land uses in temperate soils. European Journal of Soil Science, 2021, 72, 2445-2456.	3.9	4
6702	Effect of mare's milk prebiotic supplementation on the gut microbiome and the immune system following antibiotic therapy. Biodiversitas, 2020, 21, .	0.6	O
6703	Gut Microbiota Is Linked to Physical Health Improvements Resulting from Energy-Restricted Diet and Exercise: A Randomized Controlled Trial in Healthy Adults. , 2020, 61, .		1
6705	Long-Term Organic Fertilization Promotes the Resilience of Soil Multifunctionality Driven by Bacterial Communities. SSRN Electronic Journal, 0, , .	0.4	O
6706	Productive effects of a colostrum-oriented amino acid dietary supply for sows in transition from gestation to lactation. Italian Journal of Animal Science, 2021, 20, 1837-1850.	1.9	3
6707	Pilot-Scale VOC Treatment Process Combining Absorption in Silicone Oil and Biological Regeneration in a Two-Phase Partitioning Bioreactor (TPPB) by Activated Sludge. SSRN Electronic Journal, 0, , .	0.4	O
6709	Characterization of bacterial strains from bacterial culture collection of rice sheath in Burundi highlights an Alcaligenes species strain with antibacterial activity against Pseudomonas fuscovaginae rice pathogen. African Journal of Microbiology Research, 2021, 15, 497-511.	0.4	6
6710	Characterization of the consensus mucosal microbiome of colorectal cancer. NAR Cancer, 2021, 3, zcab049.	3.1	9
6711	Influence of pneumococcal conjugate vaccine 13 on upper respiratory tract microbial biodiversity in infants. Biodiversitas, 2021, 22, .	0.6	0
6712	Fungal Patterns from Soils in Madagascar: an Insight from Maromizaha Forest (Evergreen Humid) Tj ETQq1 1 ().784314 rgB ⁻ 2.8	T <u>{</u> Overlock
6713	Antibiotic Exposure, Not Alloreactivity, Is the Major Driver of Microbiome Changes in Hematopoietic Cell Transplantation. Transplantation and Cellular Therapy, 2022, 28, 135-144.	1.2	11
6714	Microbial Community Response to Polysaccharide Amendment in Anoxic Hydrothermal Sediments of the Guaymas Basin. Frontiers in Microbiology, 2021, 12, 763971.	3.5	2
6715	Comparison of Female Genital Tract Cytokine and Microbiota Signatures Induced by Initiation of Intramuscular DMPA and NET-EN Hormonal Contraceptives - a Prospective Cohort Analysis. Frontiers in Immunology, 2021, 12, 760504.	4.8	5
6716	Physical Activity and Dietary Composition Relate to Differences in Gut Microbial Patterns in a Multi-Ethnic Cohortâ€"The HELIUS Study. Metabolites, 2021, 11, 858.	2.9	6

#	Article	IF	CITATIONS
6717	The P4 Study: Postpartum Maternal and Infant Faecal Microbiome 6 Months After Hypertensive Versus Normotensive Pregnancy. Frontiers in Cellular and Infection Microbiology, 2022, 12, 646165.	3.9	3
6719	Maple and hickory leaf litter fungal communities reflect pre-senescent leaf communities. PeerJ, 2022, 10, e12701.	2.0	5
6721	Microbiome differential abundance methods produce different results across 38 datasets. Nature Communications, 2022, 13, 342.	12.8	286
6722	Antibiotics Alter Pocillopora Coral-Symbiodiniaceae-Bacteria Interactions and Cause Microbial Dysbiosis During Heat Stress. Frontiers in Marine Science, 2022, 8, .	2.5	8
6723	Irritable bowel syndrome therapy in Vietnam with probiotic enterococci. Eksperimental'naya I Klinicheskaya Gastroenterologiya, 2022, , 35-43.	0.4	2
6724	Pilot Study on Poultry Meat from Antibiotic Free and Conventional Farms: Can Metagenomics Detect Any Difference?. Foods, 2022, 11, 249.	4.3	13
6727	Effects of activated sludge and UV disinfection processes on the bacterial community and antibiotic resistance profile in a municipal wastewater treatment plant. Environmental Science and Pollution Research, 2022, 29, 36088-36099.	5.3	4
6729	Roux-En-Y Gastric Bypass (RYGB) Surgery during High Liquid Sucrose Diet Leads to Gut Microbiota-Related Systematic Alterations. International Journal of Molecular Sciences, 2022, 23, 1126.	4.1	7
6730	Effects of altitude on soil properties in coastal fog ecosystems in Morro Moreno National Park, Antofagasta, Chile. European Journal of Soil Science, 2022, 73, .	3.9	4
6731	Nipponaclerda Biwakoensis Infestation of Phragmites australis in the Mississippi River Delta, USA: Do Fungal Microbiomes Play a Role?. Wetlands, 2022, 42, 1.	1.5	2
6732	Antibiotics reduce bacterial load in Exaiptasia diaphana, but biofilms hinder its development as a gnotobiotic coral model. Access Microbiology, 2022, 4, 000314.	0.5	4
6733	Elevated atmospheric CO2 alters the microbial community composition and metabolic potential to mineralize organic phosphorus in the rhizosphere of wheat. Microbiome, 2022, 10, 12.	11.1	24
6735	To culture or not to culture: careful assessment of metabarcoding data is necessary when evaluating the microbiota of a modified-atmosphere-packaged vegetarian meat alternative throughout its shelf-life period. BMC Microbiology, 2022, 22, 34.	3.3	8
6736	A Microcosm Model for the Study of Microbial Community Shift and Carbon Emission from Landfills. Indian Journal of Microbiology, 2022, 62, 195-203.	2.7	5
6737	On the origin of feces: Fungal diversity, distribution, and conservation implications from feces of small mammals. Environmental DNA, 2022, 4, 608-626.	5.8	5
6738	Mink (<i>Neovison vison</i>) fecal microbiomes are influenced by sex, temperature, and time postdefecation. Journal of Mammalogy, 2022, 103, 316-327.	1.3	4
6739	Gut microbiota of the threatened takahē: biogeographic patterns and conservation implications. Animal Microbiome, 2022, 4, 11.	3.8	6
6740	Unlocking the Changes of Phyllosphere Fungal Communities of Fishscale Bamboo (Phyllachora) Tj ETQq1 1 0.784	1314 rgBT 2.1	Overlock 1

#	Article	IF	CITATIONS
6741	Microbiome composition indicate dysbiosis and lower richness in tumor breast tissues compared to healthy adjacent paired tissue, within the same women. BMC Cancer, 2022, 22, 30.	2.6	23
6742	Performance of distinct microbial based solutions in a Campylobacter infection challenge model in poultry. Animal Microbiome, 2022, 4, 2.	3.8	8
6743	Hydrocarbon biodegradation potential of microbial communities from high Arctic beaches in Canada's Northwest Passage. Marine Pollution Bulletin, 2022, 174, 113288.	5.0	13
6744	Microbiome profiling reveals that <i>Pseudomonas</i> antagonises parasitic nodule colonisation of cheater rhizobia in <i>Lotus</i> New Phytologist, 2022, 234, 242-255.	7.3	16
6745	Meconium Microbiome of Very Preterm Infants across Germany. MSphere, 2022, 7, e0080821.	2.9	15
6746	Positive Effect of Lactobacillus acidophilus EG004 on Cognitive Ability of Healthy Mice by Fecal Microbiome Analysis Using Full-Length 16S-23S rRNA Metagenome Sequencing. Microbiology Spectrum, 2022, 10, e0181521.	3.0	8
6747	Rhizosphere impacts bacterial community structure in the tea (Camellia sinensis (L.) O . Kuntze .) estates of Darjeeling, India. Environmental Microbiology, 2021, , .	3.8	3
6748	Structural and functional changes in the fungal community of plant detritus in an invaded Atlantic Forest. BMC Microbiology, 2022, 22, 10.	3.3	3
6749	Longitudinal variability in the urinary microbiota of healthy premenopausal women and the relation to neighboring microbial communities: A pilot study. PLoS ONE, 2022, 17, e0262095.	2.5	6
6750	Pomegranate Extract Improves Colitis in ILâ€10 Knockout Mice Fed a High Fat High Sucrose Diet. Molecular Nutrition and Food Research, 2022, 66, e2100730.	3.3	5
6751	Alterations and Prediction of Functional Profiles of Gut Microbiota After Fecal Microbiota Transplantation for Iranian Recurrent Clostridioides difficile Infection with Underlying Inflammatory Bowel Disease: A Pilot Study. Journal of Inflammation Research, 2022, Volume 15, 105-116.	3.5	12
6752	IncHI1A plasmids potentially facilitate horizontal flow of antibiotic resistance genes to pathogens in microbial communities of urban residential sewage. Molecular Ecology, 2022, 31, 1595-1608.	3.9	14
6754	NLRP6 Inflammasome Modulates Disease Progression in a Chronic-Plus-Binge Mouse Model of Alcoholic Liver Disease. Cells, 2022, 11, 182.	4.1	12
6755	Domestication Impacts the Wheat-Associated Microbiota and the Rhizosphere Colonization by Seedand Soil-Originated Microbiomes, Across Different Fields. Frontiers in Plant Science, 2021, 12, 806915.	3.6	16
6756	Specific gut bacterial responses to natural diets of tropical birds. Scientific Reports, 2022, 12, 713.	3.3	18
6757	Fungal diversity on brewery filling hall surfaces and quality control samples. Yeast, 2022, 39, 141-155.	1.7	7
6759	Composition of Seagrass Root Associated Bacterial Communities Are Linked to Nutrients and Heavy Metal Concentrations in an Anthropogenically Influenced Estuary. Frontiers in Marine Science, 2022, 8, .	2.5	11
6760	Human Beta Defensin 2 Ameliorated Alcohol-Associated Liver Disease in Mice. Frontiers in Physiology, 2021, 12, 812882.	2.8	8

#	Article	lF	CITATIONS
6761	Host phenotype and microbiome vary with infection status, parasite genotype, and parasite microbiome composition. Molecular Ecology, 2022, 31, 1577-1594.	3.9	22
6762	Prokaryotic diversity across a pH gradient in the "El Chichón―crater-lake: a naturally thermo-acidic environment. Extremophiles, 2022, 26, 8.	2.3	2
6763	Sediment-associated microbial community profiling: sample pre-processing through sequential membrane filtration for 16S rRNA amplicon sequencing. BMC Microbiology, 2022, 22, 33.	3.3	3
6764	Gut microbial trimethylamine is elevated in alcohol-associated hepatitis and contributes to ethanol-induced liver injury in mice. ELife, 2022, 11 , .	6.0	21
6765	Diversity of soil fungi in the vineyards of Changli region in China. Canadian Journal of Microbiology, 2022, 68, 341-352.	1.7	5
6766	Contrasting effects of genotype and root size on the fungal and bacterial communities associated with apple rootstocks. Horticulture Research, 2022, 9, .	6.3	7
6767	Bacterial community of reindeer lichens differs between northern and southern lichen woodlands. Canadian Journal of Forest Research, 0, , .	1.7	5
6768	Reef environments shape microbial partners in a highly connected coral population. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212459.	2.6	9
6769	The gut microbiota of chickens in a commercial farm treated with a Salmonella phage cocktail. Scientific Reports, 2022, 12, 991.	3.3	15
6770	Total nitrogen influence bacterial community structure of active layer permafrost across summer and winter seasons in Ny-Älesund, Svalbard. World Journal of Microbiology and Biotechnology, 2022, 38, 28.	3.6	8
6771	Caecal microbiota in horses with trigeminalâ€mediated headshaking. Veterinary Medicine and Science, 2022, 8, 1049-1055.	1.6	3
6772	Effects of wilting during a cloudy day and storage temperature on the fermentation quality and microbial community of Napier grass silage. Journal of the Science of Food and Agriculture, 2022, , .	3.5	3
6773	A randomized clinical trial to investigate the effect of dietary protein sources on periodontal health. Journal of Clinical Periodontology, 2022, 49, 388-400.	4.9	11
6774	Geochemically Defined Space-for-Time Transects Successfully Capture Microbial Dynamics Along Lacustrine Chronosequences in a Polar Desert. Frontiers in Microbiology, 2021, 12, 783767.	3 . 5	5
6775	Fruit fly phylogeny imprints bacterial gut microbiota. Evolutionary Applications, 2022, 15, 1621-1638.	3.1	5
6776	The Influence of Kerosene on Microbiomes of Diverse Soils. Life, 2022, 12, 221.	2.4	9
6777	Effects of Periodontal Treatment in Patients with Periodontitis and Kidney Failure: A Pilot Study. International Journal of Environmental Research and Public Health, 2022, 19, 1533.	2.6	2
6778	Microbiome Structuring Within a Coral Colony and Along a Sedimentation Gradient. Frontiers in Marine Science, 2022, 8, .	2.5	11

#	Article	IF	CITATIONS
6779	Gut-Microbiome Composition in Response to Phenylketonuria Depends on Dietary Phenylalanine in BTBR Pahenu2 Mice. Frontiers in Nutrition, 2021, 8, 735366.	3.7	4
6780	The Role of Photobionts as Drivers of Diversification in an Island Radiation of Lichen-Forming Fungi. Frontiers in Microbiology, 2021, 12, 784182.	3.5	9
6781	The dynamic gut microbiota of zoophilic members of the Anopheles gambiae complex (Diptera:) Tj ETQq0 0 0 rgl	BT /Qverlo	ck ₃ 10 Tf 50 6
6782	Bacterioplankton Diversity and Distribution in Relation to Phytoplankton Community Structure in the Ross Sea Surface Waters. Frontiers in Microbiology, 2022, 13, 722900.	3.5	8
6783	Phytoplankton prey of an abundant estuarine copepod identified <i>in situ </i> using DNA metabarcoding. Journal of Plankton Research, 2022, 44, 316-332.	1.8	1
6784	The structure of the microbiome of the southern chernozem of rhizosphere of winter wheat under the conditions of the use of associative strains of microorganisms. Bulletin of the State Nikita Botanical Gardens, 2022, , 120-129.	0.1	0
6785	Analysis of soil bacterial communities and physicochemical properties associated with Fusarium wilt disease of banana in Malaysia. Scientific Reports, 2022, 12, 999.	3.3	9
6786	Co-toxicity of Endotoxin and Indoxyl Sulfate, Gut-Derived Bacterial Metabolites, to Vascular Endothelial Cells in Coronary Arterial Disease Accompanied by Gut Dysbiosis. Nutrients, 2022, 14, 424.	4.1	11
6787	Metagenomic community composition and resistome analysis in a full-scale cold climate wastewater treatment plant. Environmental Microbiomes, 2022, 17, 3.	5.0	16
6788	Associations of Childhood and Perinatal Blood Metals with Children's Gut Microbiomes in a Canadian Gestation Cohort. Environmental Health Perspectives, 2022, 130, 17007.	6.0	13
6789	Variability in Host Specificity and Functional Potential of Antarctic Sponge-Associated Bacterial Communities. Frontiers in Microbiology, 2021, 12, 771589.	3.5	8
6790	Human Milk Oligosaccharides Reduce Murine Group B <i>Streptococcus</i> Vaginal Colonization with Minimal Impact on the Vaginal Microbiota. MSphere, 2022, 7, e0088521.	2.9	14
6791	Torula yeast in the diet of Atlantic salmon Salmo salar and the impact on growth performance and gut microbiome. Scientific Reports, 2022, 12, 567.	3.3	12
6792	Monitoring of honey bee floral resources with pollen DNA metabarcoding as a complementary tool to vegetation surveys. Ecological Solutions and Evidence, 2022, 3, .	2.0	13
6793	Enteric virome negatively affects seroconversion following oral rotavirus vaccination in a longitudinally sampled cohort of Ghanaian infants. Cell Host and Microbe, 2022, 30, 110-123.e5.	11.0	23
6794	Whole-Genome Duplication and Host Genotype Affect Rhizosphere Microbial Communities. MSystems, 2022, 7, e0097321.	3.8	6
6795	Taqman qPCR Quantification and Fusarium Community Analysis to Evaluate Toxigenic Fungi in Cereals. Toxins, 2022, 14, 45.	3.4	5
6796	Deepâ€sea wooden shipwrecks influence sediment microbiome diversity. Limnology and Oceanography, 2022, 67, 482-497.	3.1	7

#	Article	IF	CITATIONS
6797	A biogeographic 16S rRNA survey of bacterial communities of ureolytic biomineralization from California public restrooms. PLoS ONE, 2022, 17, e0262425.	2.5	1
6798	Impacts of Shade Trees on the Adjacent Cacao Rhizosphere in a Young Diversified Agroforestry System. Agronomy, 2022, 12, 195.	3.0	6
6799	ZIP8-Mediated Intestinal Dysbiosis Impairs Pulmonary Host Defense against Bacterial Pneumonia. International Journal of Molecular Sciences, 2022, 23, 1022.	4.1	8
6800	The ecological assembly of bacterial communities in Antarctic wetlands varies across levels of phylogenetic resolution. Environmental Microbiology, 2022, , .	3.8	1
6801	Role of Subterranean Microbiota in the Carbon Cycle and Greenhouse Gas Dynamics. SSRN Electronic Journal, 0, , .	0.4	0
6802	Pyrolysis-Aided Microbial Biodegradation of High-Density Polyethylene Plastic by Environmental Inocula Enrichment Cultures. ACS Sustainable Chemistry and Engineering, 2022, 10, 2022-2033.	6.7	17
6803	Parkinson's Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. MSystems, 2022, 7, e0119121.	3.8	13
6805	Microbiota of the prostate tumor environment investigated by whole-transcriptome profiling. Genome Medicine, 2022, 14, 9.	8.2	14
6806	Intestinal microbiota profiles in a genetic model of colon tumorigenesis correlates with colon cancer biomarkers. Scientific Reports, 2022, 12, 1432.	3.3	9
6807	Assessment of marine benthic diatom communities: insights from a combined morphological–metabarcoding approach in Mediterranean shallow coastal waters. Marine Pollution Bulletin, 2022, 174, 113183.	5.0	13
6808	Associations between Gut Microbiota and Intestinal Inflammation, Permeability and Damage in Young Malawian Children. Journal of Tropical Pediatrics, 2022, 68, .	1.5	5
6809	Effects of lactic acid-producing bacteria as direct-fed microbials on the ruminal microbiome. Journal of Dairy Science, 2022, 105, 2242-2255.	3.4	14
6810	The Dark Side of Microbial Processes: Accumulation of Nitrate During Storage of Surface Water in the Dark and the Underlying Mechanism. Microbiology Spectrum, 2022, 10, e0223221.	3.0	0
6811	Fresh Rumen Liquid Inoculant Enhances the Rumen Microbial Community Establishment in Pre-weaned Dairy Calves. Frontiers in Microbiology, 2021, 12, 758395.	3.5	8
6812	Lesion Material From Treponema-Associated Hoof Disease of Wild Elk Induces Disease Pathology in the Sheep Digital Dermatitis Model. Frontiers in Veterinary Science, 2021, 8, 782149.	2.2	4
6813	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. Nature Communications, 2022, 13, 117.	12.8	17
6814	Biological composition analysis of a natural medicine, Faeces Vespertilionis, with complex sources using DNA metabarcoding. Scientific Reports, 2022, 12, 375.	3.3	3
6815	Innate lymphoid cell characterization in the rat and their correlation to gut commensal microbes. European Journal of Immunology, 2022, 52, 717-729.	2.9	2

#	Article	IF	CITATIONS
6817	Dominance of Fructose-Associated Fructobacillus in the Gut Microbiome of Bumblebees (Bombus) Tj ETQq0 0 0	rgBT/Over	lock 10 Tf 50
6818	Microbiome Development of Seawater-Incubated Pre-production Plastic Pellets Reveals Distinct and Predictive Community Compositions. Frontiers in Marine Science, 2022, 8, .	2.5	10
6819	Modulation of Atlantic salmon (Salmo salar) gut microbiota composition and predicted metabolic capacity by feeding diets with processed black soldier fly (Hermetia illucens) larvae meals and fractions. Animal Microbiome, 2022, 4, 9.	3.8	20
6820	Therapeutic Potential of Metabolites from Lactobacillus rhamnosus and Mare's Milk in the Treatment of Dysbiosis. BioMed Research International, 2022, 2022, 1-8.	1.9	2
6821	A field indicator for rhizosphere effect monitoring in arable soils. Plant and Soil, $0, 1$.	3.7	1
6822	Does revegetation cause soil microbiota recovery? Evidence from revisiting a revegetation chronosequence 6 years after initial sampling. Restoration Ecology, 2022, 30, .	2.9	8
6823	Genomic characterization of the dominating Beta, V2Âvariant carrying vaccinated (Oxfordâ^'AstraZeneca) and nonvaccinated COVIDâ€19 patient samples in Bangladesh: A metagenomics and wholeâ€genome approach. Journal of Medical Virology, 2022, 94, 1670-1688.	5.0	6
6824	Living in a bottle: Bacteria from sedimentâ€essociated Mediterranean waste and potential growth on polyethylene terephthalate. MicrobiologyOpen, 2022, 11, e1259.	3.0	13
6825	Ectomycorrhizal Fungi Dominated the Root and Rhizosphere Microbial Communities of Two Willow Cultivars Grown for Six-Years in a Mixed-Contaminated Environment. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /	/O væ5 lock∶	104Tf 50 417
6826	Short-Term Effects of Reclamation of Aquaculture Ponds to Paddy Fields on Soil Chemical Properties and Bacterial Communities in Eastern China Coastal Zone. Sustainability, 2022, 14, 1613.	3.2	0
6827	Unveiling biogeographical patterns of the ichthyofauna in the Tuichi basin, a biodiversity hotspot in the Bolivian Amazon, using environmental DNA. PLoS ONE, 2022, 17, e0262357.	2.5	2
6828	Fecal microbiome profiles of neonatal dairy calves with varying severities of gastrointestinal disease. PLoS ONE, 2022, 17, e0262317.	2.5	17
6829	Bovine Rumen Microbiome: Impact of DNA Extraction Methods and Comparison of Non-Invasive Sampling Sites. Ruminants, 2022, 2, 112-132.	1,1	4
6830	Phytoplankton diversity and ecology through the lens of high throughput sequencing technologies., 2022,, 353-413.		8
6831	Integrative analyses of probiotics, pathogenic infections and host immune response highlight the importance of gut microbiota in understanding disease recovery in rainbow trout (Oncorhynchus) Tj ETQq0 0 0 r	gBI.1Over	oala 10 Tf 50
6833	molBV reveals immune landscape of bacterial vaginosis and predicts human papillomavirus infection natural history. Nature Communications, 2022, 13, 233.	12.8	20
6834	Diversity and Distribution of Microbial Communities Associated with Reef Corals of the Malay Peninsula. Microbial Ecology, 2023, 85, 37-48.	2.8	7
6835	Peppermint oil effects on the gut microbiome in children with functional abdominal pain. Clinical and Translational Science, 2022, 15, 1036-1049.	3.1	6

#	Article	IF	CITATIONS
6839	Skin Microbiome in Patients with Hand Eczema and Healthy Controls: A Three-week Prospective Study. Acta Dermato-Venereologica, 2021, 102, adv00633.	1.3	3
6840	Viral dysbiosis in children with new-onset celiac disease. PLoS ONE, 2022, 17, e0262108.	2.5	12
6841	Construction of Aerobic/Anaerobic-Substrate-Induced Gene Expression Procedure for Exploration of Metagenomes From Subseafloor Sediments. Frontiers in Microbiology, 2021, 12, 726024.	3.5	0
6842	Intratumor Microbiome Analysis Identifies Positive Association Between Megasphaera and Survival of Chinese Patients With Pancreatic Ductal Adenocarcinomas. Frontiers in Immunology, 2022, 13, 785422.	4.8	25
6843	Microbiota of the Digestive Glands and Extrapallial Fluids of Clams Evolve Differently Over Time Depending on the Intertidal Position. Microbial Ecology, 2023, 85, 288-297.	2.8	4
6844	DNA Metabarcoding from Microbial Communities Recovered from Stream and Its Potential for Bioremediation Processes. Current Microbiology, 2022, 79, 70.	2.2	3
6846	Tipping the Balance: Vitamin D Inadequacy in Children Impacts the Major Gut Bacterial Phyla. Biomedicines, 2022, 10, 278.	3.2	7
6847	Dispersed Crude Oil Induces Dysbiosis in the Red Snapper <i>Lutjanus campechanus</i> External Microbiota. Microbiology Spectrum, 2022, 10, e0058721.	3.0	6
6848	Genotypic variation in floral volatiles influences floral microbiome more strongly than interactions with herbivores and mycorrhizae in strawberries. Horticulture Research, 2022, 9, .	6.3	13
6849	Aquatic Macrophytes Are Associated With Variation in Biogeochemistry and Bacterial Assemblages of Mountain Lakes. Frontiers in Microbiology, 2021, 12, 777084.	3.5	6
6850	Substitution of Refined Conventional Wheat Flour with Wheat High in Resistant Starch Modulates the Intestinal Microbiota and Fecal Metabolites in Healthy Adults: A Randomized, Controlled Trial. Journal of Nutrition, 2022, 152, 1426-1437.	2.9	13
6851	Characterizing the oral and distal gut microbiota of the threatened southern sea otter (<i>Enhydra) Tj ETQq1 1</i>	. 0.784314 r 2.0	gBT /Overlo
6852	The mosquito microbiome includes habitat-specific but rare symbionts. Computational and Structural Biotechnology Journal, 2022, 20, 410-420.	4.1	13
6854	Elasmobranch diversity across a remote coral reef atoll revealed through environmental DNA metabarcoding. Zoological Journal of the Linnean Society, 2022, 196, 593-607.	2.3	13
6855	A multi-omics approach unravels metagenomic and metabolic alterations of a probiotic and synbiotic additive in rainbow trout (Oncorhynchus mykiss). Microbiome, 2022, 10, 21.	11.1	25
6856	Cambios en la microbiota intestinal de pacientes crÃticos con sepsis una semana después del ingreso a la Unidad de Cuidados Intensivos. Acta Colombiana De Cuidado Intensivo, 2022, , .	0.2	0
6857	Binary Toxin Expression by <i>Clostridioides difficile</i> Is Associated With Worse Disease. Open Forum Infectious Diseases, 2022, 9, ofac001.	0.9	16
6860	Hen raising helps chicks establish gut microbiota in their early life and improve microbiota stability after H9N2 challenge. Microbiome, 2022, 10, 14.	11.1	17

#	ARTICLE	IF	CITATIONS
6861	Consistent changes in the intestinal microbiota of Atlantic salmon fed insect meal diets. Animal Microbiome, 2022, 4, 8.	3.8	9
6862	Dysbiotic microbes and how to find them: a review of microbiome profiling in prostate cancer. Journal of Experimental and Clinical Cancer Research, 2022, 41, 31.	8.6	8
6863	Mechanism of Intermittent Deep Tillage and Different Depths Improving Crop Growth From the Perspective of Rhizosphere Soil Nutrients, Root System Architectures, Bacterial Communities, and Functional Profiles. Frontiers in Microbiology, 2021, 12, 759374.	3.5	8
6864	Fate of influent microbial populations during medium chain carboxylic acid recovery from brewery and pre-fermented food waste streams. Environmental Science: Water Research and Technology, 2022, 8, 257-269.	2.4	6
6865	Accumulation of Nylon Microplastics and Polybrominated Diphenyl Ethers and Effects on Gut Microbial Community OfÂChironomus Sancticaroli. SSRN Electronic Journal, 0, , .	0.4	0
6866	Sex Differences in Fish Oil and Olanzapine Effects on Gut Microbiota in Diet-Induced Obese Mice. Nutrients, 2022, 14, 349.	4.1	2
6867	Bacterial Indicators Are Ubiquitous Members of Pelagic Microbiome in Anthropogenically Impacted Coastal Ecosystem. Frontiers in Microbiology, 2021, 12, 765091.	3.5	16
6868	Prolonged oral antimicrobial administration prevents doxorubicin-induced loss of active intestinal stem cells. Gut Microbes, 2022, 14, 2018898.	9.8	5
6869	Non-destructive extraction of DNA from preserved tissues in medical collections. BioTechniques, 2022, 72, 60-64.	1.8	4
6870	Predicted functional genes for the biodegradation of xenobiotics in groundwater and sediment at two contaminated naval sites. Applied Microbiology and Biotechnology, 2022, 106, 835-853.	3.6	13
6871	Endoscopic ultrasound-guided fine-needle biopsy as a tool for studying the intra-tumoral microbiome in pancreatic ductal adenocarcinoma: a pilot study. Scientific Reports, 2022, 12, 107.	3.3	4
6872	A Bacteriophage Cocktail Significantly Reduces Listeria monocytogenes without Deleterious Impact on the Commensal Gut Microbiota under Simulated Gastrointestinal Conditions. Viruses, 2022, 14, 190.	3.3	13
6873	Metagenomic insights into the environmental adaptation and metabolism of <i>Candidatus</i> Haloplasmatales, one archaeal order thriving in saline lakes. Environmental Microbiology, 2022, 24, 2239-2258.	3.8	9
6874	Do aphids in Dutch sweet pepper greenhouses carry heritable elements that protect them against biocontrol parasitoids?. Evolutionary Applications, 2022, 15, 1580-1593.	3.1	10
6875	Impact of Dietary Sodium Butyrate and Salinomycin on Performance and Intestinal Microbiota in a Broiler Gut Leakage Model. Animals, 2022, 12, 111.	2.3	7
6876	A Detection Assay to Identify Alternative Food Sources of the Two-Spotted Stink Bug, <i>Bathycoelia distincta</i> (Hemiptera: Pentatomidae). Journal of Economic Entomology, 2022, 115, 519-525.	1.8	2
6877	Climate-induced forest dieback drives compositional changes in insect communities that are more pronounced for rare species. Communications Biology, 2022, 5, 57.	4.4	9
6878	Characterization of the Microbiota Associated With 12-Week-Old Bovine Fetuses Exposed to Divergent in utero Nutrition. Frontiers in Microbiology, 2021, 12, 771832.	3.5	16

#	ARTICLE	IF	CITATIONS
6880	Rare genera differentiate urban green space soil bacterial communities in three cities across the world. Access Microbiology, 2022, 4, 000320.	0.5	2
6882	Gene-environment-gut interactions in Huntington's disease mice are associated with environmental modulation of the gut microbiome. IScience, 2022, 25, 103687.	4.1	20
6883	Alterations of the Gut Microbiome Associated to Methane Metabolism in Mexican Children with Obesity. Children, 2022, 9, 148.	1.5	7
6884	Microbiological Characteristics of Some Stations of Moscow Subway. Biology, 2022, 11, 170.	2.8	3
6885	Comparison of the Effects of Microbial Inoculants on Fermentation Quality and Microbiota in Napier Grass (Pennisetum purpureum) and Corn (Zea mays L.) Silage. Frontiers in Microbiology, 2021, 12, 784535.	3.5	8
6886	Differences in gut microbiome by insulin sensitivity status in Black and White women of the National Growth and Health Study (NGHS): A pilot study. PLoS ONE, 2022, 17, e0259889.	2.5	5
6888	Richness estimation in microbiome data obtained from denoising pipelines. Computational and Structural Biotechnology Journal, 2022, 20, 508-520.	4.1	18
6889	Mapping the Green-Lipped Mussel (Perna canaliculus) Microbiome: A Multi-Tissue Analysis of Bacterial and Fungal Diversity. Current Microbiology, 2022, 79, 76.	2.2	10
6890	Screening and Application of Ligninolytic Microbial Consortia to Enhance Aerobic Degradation of Solid Digestate. Microorganisms, 2022, 10, 277.	3.6	2
6891	Inulin Improves Diet-Induced Hepatic Steatosis and Increases Intestinal Akkermansia Genus Level. International Journal of Molecular Sciences, 2022, 23, 991.	4.1	17
6892	Organic matter and metal loadings influence the spatial gradient of the benthic bacterial community in a temperate estuary. Marine and Freshwater Research, 2022, 73, 428-440.	1.3	5
6893	Effectiveness of Multistrain Probiotic Formulation on Common Infectious Disease Symptoms and Gut Microbiota Modulation in Flu-Vaccinated Healthy Elderly Subjects. BioMed Research International, 2022, 2022, 1-16.	1.9	9
6895	Host-specific epibiomes of distinct Acropora cervicornis genotypes persist after field transplantation. Coral Reefs, 2022, 41, 265-276.	2.2	8
6898	Women with type 1 diabetes exhibit a progressive increase in gut Saccharomyces cerevisiae in pregnancy associated with evidence of gut inflammation. Diabetes Research and Clinical Practice, 2022, 184, 109189.	2.8	6
6899	DNA metabarcoding reveals host-specific communities of arthropods residing in fungal fruit bodies. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212622.	2.6	6
6900	Prairie Strips Impact on Transport of Antimicrobial Resistance Indicators in Poultry Litter. Journal of Environmental Quality, 2022, , .	2.0	4
6901	Gene expression plasticity and frontloading promote thermotolerance in Pocillopora corals., 0, 2, .		9
6902	Genotypic and phenotypic characterization of hydrogenotrophic denitrifiers. Environmental Microbiology, 2022, 24, 1887-1901.	3.8	7

#	ARTICLE	IF	CITATIONS
6903	Determining the Composition of Resident and Transient Members of the Oyster Microbiome. Frontiers in Microbiology, 2021, 12, 828692.	3.5	10
6904	Diets Containing Egg or Whey Protein and Inulin Fiber Improve Energy Balance and Modulate Gut Microbiota in Exercising Obese Rats. Molecular Nutrition and Food Research, 2022, 66, e2100653.	3.3	4
6905	Beeâ€associated fungi mediate effects of fungicides on bumble bees. Ecological Entomology, 2022, 47, 411-422.	2.2	6
6907	Epiphytic fungal communities vary by substrate type and at submetre spatial scales. Molecular Ecology, 2022, 31, 1879-1891.	3.9	7
6908	Characterizing the Ectomycorrhizal Fungal Community of Whitebark Pine in Interior British Columbia: Mature Trees, Natural Regeneration and Planted Seedlings. Frontiers in Forests and Global Change, 2022, 4, .	2.3	1
6909	Increased Yield and High Resilience of Microbiota Representatives With Organic Soil Amendments in Smallholder Farms of Uganda. Frontiers in Plant Science, 2021, 12, 815377.	3.6	0
6911	Changes in the skin microbiome associated with squamous cell carcinoma in transplant recipients. ISME Communications, 2022, 2, .	4.2	6
6912	Intestinal Microbiota Remodeling Protects Mice from Western Diet-Induced Brain Inflammation and Cognitive Decline. Cells, 2022, 11, 504.	4.1	11
6914	Longitudinal 16S rRNA gut microbiota data of infant triplets show partial susceptibility to host genetics. IScience, 2022, 25, 103861.	4.1	5
6915	Exploring microbiome engineering as a strategy for improved thermal tolerance in <i>Exaiptasia diaphana</i> . Journal of Applied Microbiology, 2022, 132, 2940-2956.	3.1	14
6916	Diatom Biogeography, Temporal Dynamics, and Links to Bacterioplankton across Seven Oceanographic Time-Series Sites Spanning the Australian Continent. Microorganisms, 2022, 10, 338.	3.6	5
6917	Adaptations of microbial communities and dissolved organics to seasonal pressures in a mesotrophic coastal Mediterranean lake. Environmental Microbiology, 2022, 24, 2282-2298.	3.8	9
6918	Microbial Nitrogen Transformation Potential in Sediments of Two Contrasting Lakes Is Spatially Structured but Seasonally Stable. MSphere, 2022, 7, e0101321.	2.9	10
6919	Feeding an acetate-based oral electrolyte reduces the ex vivo Escherichia coli growth potential in the abomasum of calves fed oral electrolytes alone or 30 minutes following a milk feeding compared with feeding a bicarbonate-based oral electrolyte. Journal of Dairy Science, 2022, 105, 1542-1554.	3.4	O
6920	Changes in the rodent gut microbiome following chronic restraint stress and low-intensity rTMS. Neurobiology of Stress, 2022, 17, 100430.	4.0	15
6921	The application of the skin virome for human identification. Forensic Science International: Genetics, 2022, 57, 102662.	3.1	8
6922	Deciphering the fate of sulfate in one- and two-chamber bioelectrochemical systems. Electrochimica Acta, 2022, 408, 139942.	5.2	12
6923	Kaempferol acts on bile acid signaling and gut microbiota to attenuate the tumor burden in ApcMin/+ mice. European Journal of Pharmacology, 2022, 918, 174773.	3.5	18

#	Article	IF	CITATIONS
6924	Unravelling biogeochemical drivers of methylmercury production in an Arctic fen soil and a bog soil. Environmental Pollution, 2022, 299, 118878.	7. 5	8
6925	Selective pressure on microbial communities in a drinking water aquifer – Geochemical parameters vs. micropollutants. Environmental Pollution, 2022, 299, 118807.	7.5	7
6926	Influence of reductive soil disinfestation on the chemical and microbial characteristics of a greenhouse soil infested with Fusarium oxysporum. Physiological and Molecular Plant Pathology, 2022, 118, 101805.	2.5	9
6927	Wanted not, wasted not: Searching for non-target taxa in environmental DNA metabarcoding by-catch. Environmental Advances, 2022, 7, 100169.	4.8	6
6928	Spartina alterniflora invasion has a greater impact than non-native species, Phragmites australis and Kandelia obovata, on the bacterial community assemblages in an estuarine wetland. Science of the Total Environment, 2022, 822, 153517.	8.0	10
6929	Anaerobes and methanogens dominate the microbial communities in water harvesting ponds used by Kenyan rural smallholder farmers. Science of the Total Environment, 2022, 819, 153040.	8.0	5
6930	Soil microbiomes in three farming systems more affected by depth than farming system. Applied Soil Ecology, 2022, 173, 104396.	4.3	4
6931	Improved drinking water quality after adding advanced oxidation for organic micropollutant removal to pretreatment of river water undergoing dune infiltration near The Hague, Netherlands. Journal of Hazardous Materials, 2022, 429, 128346.	12.4	12
6932	The biological sink of atmospheric H2 is more sensitive to spatial variation of microbial diversity than N2O and CO2 emissions in a winter cover crop field trial. Science of the Total Environment, 2022, 821, 153420.	8.0	2
6933	Vertical stratification of microbial communities and isotope geochemistry tie groundwater denitrification to sampling location within a nitrate-contaminated aquifer. Science of the Total Environment, 2022, 820, 153092.	8.0	8
6934	Intercolony Comparisons of Gut Microbiome Composition From Lab Reared Eastern Subterranean Termites (Blattodea: Rhinotermitidae). Journal of Insect Science, 2022, 22, .	1.5	2
6935	Phosphate enrichment induces increased dominance of the parasite <i>Aquarickettsia</i> in the coral <i>Acropora cervicornis</i> . FEMS Microbiology Ecology, 2022, 98, .	2.7	13
6936	Energetic Return on Investment Determines Overall Soil Microbial Activity. SSRN Electronic Journal, 0, , .	0.4	0
6937	Impact of long-term dietary habits on the human gut resistome in the Dutch population. Scientific Reports, 2022, 12, 1892.	3.3	12
6938	Associations and recovery dynamics of the nasopharyngeal microbiota during influenza-like illness in the aging population. Scientific Reports, 2022, 12, 1915.	3.3	5
6939	Refining a Protocol for Faecal Microbiota Engraftment in Animal Models After Successful Antibiotic-Induced Gut Decontamination. Frontiers in Medicine, 2022, 9, 770017.	2.6	7
6940	Degradation of soil arbuscular mycorrhizal fungal diversity and functionality accompanied by the aggravation of pepper <i>Phytophthora</i> blight in a facility shed in Southwest China. Land Degradation and Development, 2022, 33, 1337-1346.	3.9	5
6941	Machine Learning Predicts Biogeochemistry from Microbial Community Structure in a Complex Model System. Microbiology Spectrum, 2022, 10, e0190921.	3.0	7

#	Article	IF	CITATIONS
6942	Similar Gut Bacterial Composition Between Patients With Ulcerative Colitis and Healthy Controls in a High Incidence Population: A Cross-sectional Study of the Faroe Islands IBD Cohort. Inflammatory Bowel Diseases, 2022, 28, 1081-1089.	1.9	5
6943	Effects of freshwater salinization on a saltâ€naÃ⁻ve planktonic eukaryote community. Limnology and Oceanography Letters, 2023, 8, 38-47.	3.9	16
6944	The role of predicted chemotactic and hydrocarbon degrading taxa in natural source zone depletion at a legacy petroleum hydrocarbon site. Journal of Hazardous Materials, 2022, 430, 128482.	12.4	8
6945	Human Stool Preservation Impacts Taxonomic Profiles in 16S Metagenomics Studies. Frontiers in Cellular and Infection Microbiology, 2022, 12, 722886.	3.9	5
6947	Desulfurivibrio spp. mediate sulfur-oxidation coupled to Sb(V) reduction, a novel biogeochemical process. ISME Journal, 2022, 16, 1547-1556.	9.8	48
6948	Seasonal airway microbiome and transcriptome interactions promote childhood asthma exacerbations. Journal of Allergy and Clinical Immunology, 2022, 150, 204-213.	2.9	31
6949	Human Gut Microbes Associated with Systolic Blood Pressure. International Journal of Hypertension, 2022, 2022, 1-12.	1.3	1
6950	APOE genetics influence murine gut microbiome. Scientific Reports, 2022, 12, 1906.	3.3	17
6951	Axillary Microbiota Is Associated with Cognitive Impairment in Parkinson's Disease Patients. Microbiology Spectrum, 2022, 10, e0235821.	3.0	3
6952	Distinct microbiota composition and fermentation products indicate functional compartmentalization in the hindgut of a marine herbivorous fish. Molecular Ecology, 2022, 31, 2494-2509.	3.9	19
6953	Phyllosphere-associated microbiota in built environment: Do they have the potential to antagonize human pathogens?. Journal of Advanced Research, 2023, 43, 109-121.	9.5	9
6954	Constructing Micro-Landscapes: Management and Selection Practices on Microbial Communities in a Traditional Fermented Beverage. Frontiers in Ecology and Evolution, 2022, 10, .	2.2	3
6955	Predominance of Staphylococcus Correlates with Wound Burden and Disease Activity in Dystrophic Epidermolysis Bullosa: A Prospective Case-Control Study. Journal of Investigative Dermatology, 2022, 142, 2117-2127.e8.	0.7	10
6956	Critically ill patients with COVID-19 show lung fungal dysbiosis with reduced microbial diversity in patients colonized with Candida spp International Journal of Infectious Diseases, 2022, 117, 233-240.	3.3	11
6957	Additional Resistant Starch from One Potato Side Dish per Day Alters the Gut Microbiota but Not Fecal Short-Chain Fatty Acid Concentrations. Nutrients, 2022, 14, 721.	4.1	7
6958	Gut Mucosal Microbiome Signatures of Colorectal Cancer Differ According to BMI Status. Frontiers in Medicine, 2021, 8, 800566.	2.6	4
6959	Organic matter removal in a simultaneous nitrification–denitrification process using fixed-film system. Scientific Reports, 2022, 12, 1882.	3.3	3
6960	Patterns of Relative Bacterial Richness and Community Composition in Seawater and Marine Sediment Are Robust for Both Operational Taxonomic Units and Amplicon Sequence Variants. Frontiers in Microbiology, 2022, 13, 796758.	3.5	6

#	Article	IF	CITATIONS
6961	A specific microbiota signature is associated to various degrees of ulcerative colitis as assessed by a machine learning approach. Gut Microbes, 2022, 14, 2028366.	9.8	26
6962	Influence of 16S rRNA reference databases in amplicon-based environmental microbiome research. Biotechnology Letters, 2022, 44, 523-533.	2.2	8
6963	Nonâ€invasive monitoring of multiple wildlife health factors by fecal microbiome analysis. Ecology and Evolution, 2022, 12, e8564.	1.9	16
6965	Diversity, activity, and abundance of benthic microbes in the Southeastern Mediterranean Sea. FEMS Microbiology Ecology, 2022, 98, .	2.7	13
6966	Effects of viremia and CD4 recovery on gut "microbiome-immunity―axis in treatment-naïve HIV-1-infected patients undergoing antiretroviral therapy. World Journal of Gastroenterology, 2022, 28, 635-652.	3.3	6
6967	Larval habitat determines the bacterial and fungal microbiota of the mosquito vector <i>Aedes aegypti</i> . FEMS Microbiology Ecology, 2022, 98, .	2.7	17
6968	Microbial and Chemical Profiles of Commercial Kombucha Products. Nutrients, 2022, 14, 670.	4.1	21
6969	High-throughput qPCR and 16S rRNA gene amplicon sequencing as complementary methods for the investigation of the cheese microbiota. BMC Microbiology, 2022, 22, 48.	3.3	21
6970	Variation in rhizosphere microbial communities and its association with the nodulation ability of peanut. Archives of Agronomy and Soil Science, 2023, 69, 759-770.	2.6	4
6971	Inhaled diesel exhaust particles result in microbiome-related systemic inflammation and altered cardiovascular disease biomarkers in C57Bl/6 male mice. Particle and Fibre Toxicology, 2022, 19, 10.	6.2	5
6972	Monthly Succession of Biofouling Communities and Corresponding Inter-Taxa Associations in the North- and South-West of the Arabian Gulf. Frontiers in Marine Science, 2022, 8, .	2.5	2
6973	Compensatory intestinal antibody response against pro-inflammatory microbiota after bariatric surgery. Gut Microbes, 2022, 14, 2031696.	9.8	13
6975	Seaweeds influence oyster microbiota and disease susceptibility. Journal of Animal Ecology, 2022, 91, 805-818.	2.8	4
6976	Daily feeding rhythm linked to microbiome composition in two zooplankton species. PLoS ONE, 2022, 17, e0263538.	2.5	6
6977	Mycorrhizal Fungi Associated With Juniper and Oak Seedlings Along a Disturbance Gradient in Central Mexico. Frontiers in Forests and Global Change, 2022, 5, .	2.3	2
6978	Evaluation of Different Phyllosphere Sample Types for Parallel Metabarcoding of Fungi and Oomycetes in <i>Vitis vinifera</i> . Phytobiomes Journal, 2022, 6, 207-213.	2.7	6
6979	Unravelling the genetic and functional diversity of dominant bacterial communities involved in manure co-composting bioremediation of complex crude oil waste sludge. Heliyon, 2022, 8, e08945.	3.2	11
6980	Homeostatic interferon-lambda response to bacterial microbiota stimulates preemptive antiviral defense within discrete pockets of intestinal epithelium. ELife, 2022, 11 , .	6.0	25

#	Article	IF	CITATIONS
6981	Soil fauna drives vertical redistribution of soil organic carbon in a longâ€term irrigated dry pine forest. Global Change Biology, 2022, 28, 3145-3160.	9.5	12
6982	Stratification of the Gut Microbiota Composition Landscape across the Alzheimer's Disease Continuum in a Turkish Cohort. MSystems, 2022, 7, e0000422.	3.8	20
6983	Solea senegalensis Bacterial Intestinal Microbiota Is Affected by Low Dietary Inclusion of Ulva ohnoi. Frontiers in Microbiology, 2021, 12, 801744.	3.5	5
6984	Sources of protein diet differentially stimulate the gut and water microbiota under freshwater crayfish, marron (<i>Cherax cainii</i> , Austin 2002) culture. Environmental Microbiology Reports, 2022, 14, 286-298.	2.4	6
6985	A Comprehensive Profile of Antibiotic Resistance Genes in the Water Column of a Shallow-Sea Hydrothermal Vent Ecosystem. Sustainability, 2022, 14, 1776.	3.2	3
6987	Alterations in the Stool Microbiome in Newborns Undergoing Mild Therapeutic Hypothermia after Hypoxic-Ischemic Encephalopathy. Developmental Neuroscience, 2022, 44, 373-383.	2.0	2
6988	Different stochastic processes regulate bacterial and fungal community assembly in estuarine wetland soils. Soil Biology and Biochemistry, 2022, 167, 108586.	8.8	41
6989	Sediment and their bacterial communities in an industrialized estuary after Hurricane Harvey. Marine Pollution Bulletin, 2022, 175, 113359.	5.0	2
6991	Fungal mycobiome drives IL-33 secretion and type 2 immunity in pancreatic cancer. Cancer Cell, 2022, 40, 153-167.e11.	16.8	118
6992	Comparison of microbial communities in replicated woodchip bioreactors. Journal of Environmental Quality, 2021, , .	2.0	4
6993	Influence of Physical-Chemical Soil Parameters on Microbiota Composition and Diversity in a Deep Hyperarid Core of the Atacama Desert. Frontiers in Microbiology, 2021, 12, 794743.	3.5	11
6994	Linkage analysis identifies novel genetic modifiers of microbiome traits in families with inflammatory bowel disease. Gut Microbes, 2022, 14, 2024415.	9.8	5
6996	Circulating microbiome in patients with portal hypertension. Gut Microbes, 2022, 14, 2029674.	9.8	22
6997	Influence of Geographical Location on Maternal-Infant Microbiota: Study in Two Populations From Asia and Europe. Frontiers in Cellular and Infection Microbiology, 2021, 11, 663513.	3.9	6
6999	Environmental structure impacts microbial composition and secondary metabolism. ISME Communications, 2022, 2, .	4.2	19
7000	The gut virome in two indigenous populations from Malaysia. Scientific Reports, 2022, 12, 1824.	3.3	8
7001	Single-cell genomics for resolution of conserved bacterial genes and mobile genetic elements of the human intestinal microbiota using flow cytometry. Gut Microbes, 2022, 14, 2029673.	9.8	5
7002	Dynamic Responses of Endosymbiotic Microbial Communities Within Microcystis Colonies in North American Lakes to Altered Nitrogen, Phosphorus, and Temperature Levels. Frontiers in Microbiology, 2021, 12, 781500.	3.5	3

#	Article	IF	CITATIONS
7003	Isolation of DiNP-Degrading Microbes from the Mouse Colon and the Influence DiNP Exposure Has on the Microbiota, Intestinal Integrity, and Immune Status of the Colon. Toxics, 2022, 10, 75.	3.7	4
7004	Sodium molybdate does not inhibit sulfate-reducing bacteria but increases shell growth in the Pacific oyster Magallana gigas. PLoS ONE, 2022, 17, e0262939.	2.5	2
7005	Profiling of the Bacterial Microbiota along the Murine Alimentary Tract. International Journal of Molecular Sciences, 2022, 23, 1783.	4.1	6
7006	Local Habitat Filtering Shapes Microbial Community Structure in Four Closely Spaced Lakes in the High Arctic. Frontiers in Microbiology, 2022, 13, 779505.	3.5	4
7007	Methane production and microbial community acclimation of five manure inocula during psychrophilic anaerobic digestion of swine manure. Journal of Cleaner Production, 2022, 340, 130772.	9.3	17
7008	Ammonia-oxidizing bacteria and fungal denitrifier diversity are associated with N2O production in tropical soils. Soil Biology and Biochemistry, 2022, 166, 108563.	8.8	28
7009	The Effects of Non-Fiber Carbohydrate Content and Forage Type on Rumen Microbiome of Dairy Cows. Animals, 2021, 11, 3519.	2.3	16
7010	Intestinal Microbiota in Postmenopausal Breast Cancer Patients and Controls. Cancers, 2021, 13, 6200.	3.7	16
7012	Assessing Gut Microbiota in an Infant with Congenital Propionic Acidemia before and after Probiotic Supplementation. Microorganisms, 2021, 9, 2599.	3.6	5
7013	Efficacy of Phototherapy With 308-nm Excimer Light for Skin Microbiome Dysbiosis and Skin Barrier Dysfunction in Canine Atopic Dermatitis. Frontiers in Veterinary Science, 2021, 8, 762961.	2.2	5
7014	Relationships among Indicators of Metabolism, Mammary Health and the Microbiomes of Periparturient Holstein Cows. Animals, 2022, 12, 3.	2.3	3
7015	Anaerobic Dynamic Membrane Bioreactor Development to Facilitate Organic Waste Conversion to Medium-Chain Carboxylic Acids and Their Downstream Recovery. ACS ES&T Engineering, 2022, 2, 169-180.	7.6	11
7016	Alpha-diversity and microbial community structure of the male urinary microbiota depend on urine sampling method. Scientific Reports, 2021, 11, 23758.	3.3	9
7017	Honey Bee Larval and Adult Microbiome Life Stages Are Effectively Decoupled with Vertical Transmission Overcoming Early Life Perturbations. MBio, 2021, 12, e0296621.	4.1	19
7018	Gut microbiome composition, not alpha diversity, is associated with survival in a natural vertebrate population. Animal Microbiome, 2021, 3, 84.	3.8	28
7019	Contrasting patterns of carbon cycling and dissolved organic matter processing in two phytoplankton–bacteria communities. Biogeosciences, 2021, 18, 6589-6616.	3.3	5
7020	Successful strategies for human microbiome data generation, storage and analyses. Journal of Biosciences, 2019, 44, .	1.1	0
7021	Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of prakriti. Journal of Biosciences, 2019, 44, .	1.1	6

#	Article	IF	Citations
7022	Microbiome and imputed metagenome study of crude and refined petroleum-oil-contaminated soils: Potential for hydrocarbon degradation and plant-growth promotion. Journal of Biosciences, 2019, 44, .	1.1	7
7023	Microbiome data science. Journal of Biosciences, 2019, 44, .	1.1	8
7024	Visual exploration of microbiome data. Journal of Biosciences, 2019, 44, .	1.1	1
7025	Improved Drinking Water Quality after Adding Advanced Oxidation for Organic Micropollutant Removal to Pretreatment of River Water Undergoing Dune Infiltration Near the Hague, Netherlands. SSRN Electronic Journal, 0, , .	0.4	0
7026	The Gut Microbiome. , 2022, , .		0
7027	The G Protein-Coupled Receptor, VPAC1, Mediates Vasoactive Intestinal Peptide-Dependent Functional Homeostasis of the Gut Microbiota., 2022, 1, 253-264.		2
7028	Solar Photo-Fenton Mediated by Alternative Oxidants for Mwwtp Effluent Quality Improvement: Impact on Microbial Community, Priority Pathogens and Removal of Antibiotic-Resistant Genes. SSRN Electronic Journal, 0, , .	0.4	0
7029	Dynamics of Gut Microbiome, IgA Response and Plasma Metabolome in Development of Pediatric Celiac Disease. SSRN Electronic Journal, 0, , .	0.4	0
7031	Functional Variability in Specific Root Respiration Translates to Autotrophic Differences in Soil Respiration in a Temperate Deciduous Forest. SSRN Electronic Journal, 0, , .	0.4	0
7032	Assessing the Long-Term Impact of Urease and Nitrification Inhibitor Use on Microbial Community Composition, Diversity and Function in Grassland Soil. SSRN Electronic Journal, 0, , .	0.4	0
7033	Pot-pollen supplementation reduces fasting glucose and modulates the gut microbiota in high-fat/high-sucrose fed C57BL/6 mice. Food and Function, 2022, 13, 3982-3992.	4.6	2
7034	Minimizing Tillage Modifies Fungal Denitrifier Communities, Increases Denitrification Rates and Enhances the Genetic Potential for Fungal Relative to Bacterial Denitrification. SSRN Electronic Journal, 0, , .	0.4	0
7035	Responses of Microbial Communities from Forest Soils of Differing Tree Species Diversity to Drying-Rewetting Cycles. SSRN Electronic Journal, 0, , .	0.4	1
7036	Stream Bacterial Diversity Peaks at Intermediate Freshwater Salinity and Varies by Salt Type. SSRN Electronic Journal, 0, , .	0.4	0
7037	Analysis methods for the gut microbiome in neuropsychiatric and neurodegenerative disorders. Computational and Structural Biotechnology Journal, 2022, 20, 1097-1110.	4.1	5
7038	Impact of Norway Spruce Pre-Degradation Stages Induced by G. Trabeum on Fungal and Bacterial Communities. SSRN Electronic Journal, 0, , .	0.4	0
7039	Endolichenic Fungal Community Analysis by Pure Culture Isolation and Metabarcoding: A Case Study of <i>Parmotrema tinctorum</i> . Mycobiology, 2022, 50, 55-65.	1.7	8
7040	Succession of founding microbiota in an anaerobic baffled bioreactor treating low-temperature raw domestic wastewater. Environmental Science: Water Research and Technology, 2022, 8, 792-806.	2.4	1

#	Article	IF	CITATIONS
7041	The Role of Soil Communities on the Germination of a Pioneer Tree Species in the Atlantic Rainforest. SSRN Electronic Journal, 0 , , .	0.4	0
7042	The Combined Enhancement of Rl, Nzvi and Aqds on the Microbial Anaerobic-Aerobic Degradation of Pahs in Soil. SSRN Electronic Journal, 0, , .	0.4	O
7043	Bacteriome in Ticks Collected from Domestic Livestock in Kenya. Advances in Microbiology, 2022, 12, 67-82.	0.6	1
7044	Is the Intestinal Bacterial Community in the Australian Rabbitfish Siganus fuscescens Influenced by Seaweed Supplementation or Geography?. Microorganisms, 2022, 10, 497.	3. 6	1
7046	Global <scp>16S rRNA</scp> diversity of provannid snail endosymbionts from <scp>Indoâ€Pacific</scp> deepâ€sea hydrothermal vents. Environmental Microbiology Reports, 2022, 14, 299-307.	2.4	8
7048	Combination of High-Pressure Treatment at 500 MPa and Biopreservation with a Lactococcus lactis Strain for Lowering the Bacterial Growth during Storage of Diced Cooked Ham with Reduced Nitrite Salt. Microorganisms, 2022, 10, 456.	3.6	3
7049	Microbial diversity of sub-bottom sediment cores from a tropical reef system. Coral Reefs, 2022, 41, 397-403.	2.2	1
7050	Dominant remodelling of cattle rumen microbiome by Schedonorus arundinaceus (tall fescue) KY-31 carrying a fungal endophyte. Access Microbiology, 2022, 4, 000322.	0.5	2
7051	Defining the <i>Sphagnum</i> Core Microbiome across the North American Continent Reveals a Central Role for Diazotrophic Methanotrophs in the Nitrogen and Carbon Cycles of Boreal Peatland Ecosystems. MBio, 2022, 13, .	4.1	18
7052	Changes in Fungal and Oomycete Community Composition Following Irrigation Reductions Aimed at Increasing Water Use Efficiency in a Containerized Nursery Crop. Phytobiomes Journal, 2022, 6, 247-260.	2.7	1
7053	Methanogen Productivity and Microbial Community Composition Varies With Iron Oxide Mineralogy. Frontiers in Microbiology, 2021, 12, 705501.	3. 5	8
7054	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. Frontiers in Bioinformatics, 2022, 2, .	2.1	10
7055	Microbial-driven preterm labour involves crosstalk between the innate and adaptive immune response. Nature Communications, 2022, 13, 975.	12.8	38
7057	Amplicon sequencing of <i>Fusarium</i> translation elongation factor $1\hat{1}\pm$ reveals that soil communities of <i>Fusarium</i> species are resilient to disturbances caused by crop and tillage practices. Phytobiomes Journal, 0, , .	2.7	1
7058	Gut microbiota differences between paired intestinal wall and digesta samples in three small species of fish. PeerJ, 2022, 10, e12992.	2.0	6
7059	Generation and Characterization of a Zebrafish IL-2Rγc SCID Model. International Journal of Molecular Sciences, 2022, 23, 2385.	4.1	13
7060	Effect of water management on microbial diversity and composition in an Italian rice field system. FEMS Microbiology Ecology, 2022, 98, .	2.7	11
7061	Bacterial communities in carnivorous pitcher plants colonize and persist in inquiline mosquitoes. Animal Microbiome, 2022, 4, 13.	3.8	3

#	Article	IF	CITATIONS
7063	Altered Gut Microbiome and Fecal Immune Phenotype in Early Preterm Infants With Leaky Gut. Frontiers in Immunology, 2022, 13, 815046.	4.8	10
7064	Culturable fungal endophyte communities of primary successional plants on Mount St. Helens, WA, USA. Bmc Ecology and Evolution, 2022, 22, 18.	1.6	3
7065	Collateral Damage in the Human Gut Microbiome - Blastocystis Is Significantly Less Prevalent in an Antibiotic-Treated Adult Population Compared to Non-Antibiotic Treated Controls. Frontiers in Cellular and Infection Microbiology, 2022, 12, 822475.	3.9	3
7066	Bioleaching of Heavy Metals from Printed Circuit Boards with an Acidophilic Iron-Oxidizing Microbial Consortium in Stirred Tank Reactors. Bioengineering, 2022, 9, 79.	3.5	8
7067	Biodiversity and Metabolic Potential of Bacteria in Bulk Soil from the Peri-Root Zone of Black Alder (Alnus glutinosa), Silver Birch (Betula pendula) and Scots Pine (Pinus sylvestris). International Journal of Molecular Sciences, 2022, 23, 2633.	4.1	7
7068	Investigation and characterization of human gut phageome in advanced liver cirrhosis of defined etiologies. Gut Pathogens, 2022, 14, 9.	3.4	1
7069	Microbial biogeography of the wombat gastrointestinal tract. PeerJ, 2022, 10, e12982.	2.0	2
7070	Oxidation to Control Cyanobacteria and Cyanotoxins in Drinking Water Treatment Plants: Challenges at the Laboratory and Full-Scale Plants. Water (Switzerland), 2022, 14, 537.	2.7	3
7073	Mesopelagic microbial community dynamics in response to increasing oil and Corexit 9500 concentrations. PLoS ONE, 2022, 17, e0263420.	2.5	3
7074	Impact of the Ileal Microbiota on Surgical Site Infections in Crohn's Disease: A Nationwide Prospective Cohort. Journal of Crohn's and Colitis, 2022, , .	1.3	3
7076	Mycobiome-Host Coevolution? The Mycobiome of Ancestral Human Populations Seems to Be Different and Less Diverse Than Those of Extant Native and Urban-Industrialized Populations. Microorganisms, 2022, 10, 459.	3.6	3
7077	Early life inter-kingdom interactions shape the immunological environment of the airways. Microbiome, 2022, 10, 34.	11.1	16
7078	Dysbiosis of Oral and Gut Microbiomes in SARS-CoV-2 Infected Patients in Bangladesh: Elucidating the Role of Opportunistic Gut Microbes. Frontiers in Medicine, 2022, 9, 821777.	2.6	33
7079	Bermudagrass Cultivars with Different Tolerance to Nematode Damage Are Characterized by Distinct Fungal but Similar Bacterial and Archaeal Microbiomes. Microorganisms, 2022, 10, 457.	3.6	2
7080	Biofilms in Water Hoses of a Meat Processing Environment Harbor Complex Microbial Communities. Frontiers in Microbiology, 2022, 13, 832213.	3.5	7
7081	Membrane Bioreactor Pretreatment of High-Salinity O& GProduced Water. ACS ES&T Water, 2022, 2, 484-494.	4.6	9
7082	Manipulating the microbiome alters regenerative outcomes in <i>Xenopus laevis</i> tadpoles via lipopolysaccharide signalling. Wound Repair and Regeneration, 2022, 30, 636-651.	3.0	3
7083	Integrated analysis of microbe-host interactions in Crohn's disease reveals potential mechanisms of microbial proteins on host gene expression. IScience, 2022, 25, 103963.	4.1	7

#	Article	IF	CITATIONS
7084	Gut microbiota and BMI throughout childhood: the role of firmicutes, bacteroidetes, and short-chain fatty acid producers. Scientific Reports, 2022, 12, 3140.	3.3	65
7085	Ranking the biases: The choice of OTUs vs. ASVs in 16S rRNA amplicon data analysis has stronger effects on diversity measures than rarefaction and OTU identity threshold. PLoS ONE, 2022, 17, e0264443.	2.5	49
7087	Microbial Biomass, Composition, and Functions Are Responsible for the Differential Removal of Trace Organic Chemicals in Biofiltration Systems: A Batch Study. Frontiers in Water, 2022, 4, .	2.3	4
7088	Metabolic Diversity and Aero-Tolerance in Anammox Bacteria from Geochemically Distinct Aquifers. MSystems, 2022, 7, e0125521.	3.8	13
7089	Plant Genotype Shapes the Bacterial Microbiome of Fruits, Leaves, and Soil in Olive Plants. Plants, 2022, 11, 613.	3.5	16
7090	Vertical Microbial Profiling of Arabian Sea Oxygen Minimal Zone Reveals Complex Bacterial Communities and Distinct Functional Implications. Microbial Ecology, 2023, 85, 357-371.	2.8	1
7091	Selective targeting of skin pathobionts and inflammation with topically applied lactobacilli. Cell Reports Medicine, 2022, 3, 100521.	6.5	20
7092	Microbial Community Structure and Functional Potential of Deep-Sea Sediments on Low Activity Hydrothermal Area in the Central Indian Ridge. Frontiers in Marine Science, 2022, 9, .	2.5	6
7093	A Parallel Tracking of Salivary and Gut Microbiota Profiles Can Reveal Maturation and Interplay of Early Life Microbial Communities in Healthy Infants. Microorganisms, 2022, 10, 468.	3.6	4
7094	Effects of Escherichia coli Nissle 1917 on the Porcine Gut Microbiota, Intestinal Epithelium and Immune System in Early Life. Frontiers in Microbiology, 2022, 13, 842437.	3.5	8
7095	Uncovering the mycorrhizal community of two Habenaria orchids in South Africa. South African Journal of Botany, 2022, 146, 856-863.	2.5	1
7096	Impacts of UV-C Irradiation on Marine Biofilm Community Succession. Applied and Environmental Microbiology, 2022, 88, aem0229821.	3.1	3
7097	The shifts in the structure of the prokaryotic community of mountain-grassland soil under the influence of artificial larch plantations. PLoS ONE, 2022, 17, e0263135.	2.5	0
7098	The Role of Environmental Processes and Geographic Distance in Regulating Local and Regionally Abundant and Rare Bacterioplankton in Lakes. Frontiers in Microbiology, 2021, 12, 793441.	3.5	4
7099	Dysbiosis of skin microbiome and gut microbiome in melanoma progression. BMC Microbiology, 2022, 22, 63.	3.3	27
7100	Characterization of the Endophytic Mycobiome in Cowpea (Vigna unguiculata) from a Single Location Using Illumina Sequencing. Agriculture (Switzerland), 2022, 12, 333.	3.1	1
7101	Disentangling bias for non-destructive insect metabarcoding. PeerJ, 2022, 10, e12981.	2.0	18
7102	Bacterial composition in the toheroa (Paphies ventricosa), a threatened surf clam from Aotearoa (New Zealand). Marine Biology, 2022, 169, 1.	1.5	1

#	Article	IF	CITATIONS
7104	Association between host genetics of sheep and the rumen microbial composition. Tropical Animal Health and Production, 2022, 54, 109.	1.4	1
7105	Host Plant Species Influences the Composition of Milkweed and Monarch Microbiomes. Frontiers in Microbiology, 2022, 13, 840078.	3.5	5
7106	Does the Amniotic Fluid of Mice Contain a Viable Microbiota?. Frontiers in Immunology, 2022, 13, 820366.	4.8	12
7107	Age-Dependent Reduction in Asthmatic Pathology through Reprogramming of Postviral Inflammatory Responses. Journal of Immunology, 2022, 208, 1467-1482.	0.8	6
7108	Soil Nitrogen Treatment Alters Microbiome Networks Across Farm Niches. Frontiers in Microbiology, 2021, 12, 786156.	3.5	3
7109	Intratumoral Microbiome of Human Primary Liver Cancer. Hepatology Communications, 2022, 6, 1741-1752.	4.3	18
7110	Changes in root microbiome during wheat evolution. BMC Microbiology, 2022, 22, 64.	3.3	12
7111	Electronic Cigarette Use Promotes a Unique Periodontal Microbiome. MBio, 2022, 13, e0007522.	4.1	8
7112	Biannual Administrations of Azithromycin and the Gastrointestinal Microbiome of Malawian Children: A Nested Cohort Study Within a Randomized Controlled Trial. Frontiers in Public Health, 2022, 10, 756318.	2.7	1
7113	Biosolids for safe land application: does wastewater treatment plant size matters when considering antibiotics, pollutants, microbiome, mobile genetic elements and associated resistance genes?. Environmental Microbiology, 2022, 24, 1573-1589.	3.8	14
7115	Enrichment of Anaerobic Microbial Communities from Midgut and Hindgut of Sun Beetle Larvae (Pachnoda marginata) on Wheat Straw: Effect of Inoculum Preparation. Microorganisms, 2022, 10, 761.	3.6	11
7116	Maltodextrin Consumption Impairs the Intestinal Mucus Barrier and Accelerates Colitis Through Direct Actions on the Epithelium. Frontiers in Immunology, 2022, 13, 841188.	4.8	13
7117	Network-Based Differences in the Vaginal and Bladder Microbial Communities Between Women With and Without Urgency Urinary Incontinence. Frontiers in Cellular and Infection Microbiology, 2022, 12, 759156.	3.9	12
7118	Compositions of gut microbiota before and shortly after hepatitis C viral eradication by direct antiviral agents. Scientific Reports, 2022, 12, 5481.	3.3	8
7119	Aerobic Methoxydotrophy: Growth on Methoxylated Aromatic Compounds by Methylobacteriaceae. Frontiers in Microbiology, 2022, 13, 849573.	3.5	4
7121	Comparison of the Respiratory Resistomes and Microbiota in Children Receiving Short versus Standard Course Treatment for Community-Acquired Pneumonia. MBio, 2022, 13, e0019522.	4.1	16
7122	Changes in the composition of soil microbial communities and their carbonâ€cycle genes following the conversion of primary broadleaf forests to plantations and secondary forests. Land Degradation and Development, 2022, 33, 974-985.	3.9	5
7123	The Stickland Reaction Precursor <i>trans</i> -4-Hydroxy- <scp> </scp> -Proline Differentially Impacts the Metabolism of Clostridioides difficile and Commensal <i>Clostridia</i> MSphere, 2022, 7, e0092621.	2.9	8

#	Article	IF	CITATIONS
7124	The primate gut mycobiome-bacteriome interface is impacted by environmental and subsistence factors. Npj Biofilms and Microbiomes, 2022, 8, 12.	6.4	13
7126	Microbiome structure in large pelagic sharks with distinct feeding ecologies. Animal Microbiome, 2022, 4, 17.	3.8	11
7127	Cervicovaginal DNA Virome Alterations Are Associated with Genital Inflammation and Microbiota Composition. MSystems, 2022, 7, e0006422.	3.8	14
7128	Rumen and lower gut microbiomes relationship with feed efficiency and production traits throughout the lactation of Holstein dairy cows. Scientific Reports, 2022, 12, 4904.	3.3	20
7129	Integrated Omics Approaches Revealed the Osmotic Stress-Responsive Genes and Microbiota in Gill of Marine Medaka. MSystems, 2022, 7, e0004722.	3.8	10
7130	Microbiomes of Hadal Fishes across Trench Habitats Contain Similar Taxa and Known Piezophiles. MSphere, 2022, 7, e0003222.	2.9	2
7131	Cysteine dependence of Lactobacillus iners is a potential therapeutic target for vaginal microbiota modulation. Nature Microbiology, 2022, 7, 434-450.	13.3	32
7132	Temporal and Spatial Changes in the Microbiome Following Pediatric Severe Traumatic Brain Injury. Pediatric Critical Care Medicine, 2022, 23, 425-434.	0.5	8
7133	Deep-Rooted Plant Species Recruit Distinct Bacterial Communities in the Subsoil. Phytobiomes Journal, 2022, 6, 236-246.	2.7	0
7134	Resilience of a microphytobenthos community from the Severn Estuary, UK, to chlorination: A mesocosm approach. Marine Pollution Bulletin, 2022, 176, 113443.	5.0	0
7135	Long-Term, Simultaneous Impact of Antimicrobials on the Efficiency of Anaerobic Digestion of Sewage Sludge and Changes in the Microbial Community. Energies, 2022, 15, 1826.	3.1	3
7136	Faecal DNA metabarcoding reveals novel bacterial community patterns of critically endangered Southern River Terrapin, <i>Batagur affinis</i> . PeerJ, 2022, 10, e12970.	2.0	2
7137	Modulation of Gut Microbiota Metabolism in Obesity-Related Type 2 Diabetes Reduces Osteomyelitis Severity. Microbiology Spectrum, 2022, 10, e0017022.	3.0	13
7138	Temporal dynamics of the soil bacterial community following Bacillus invasion. IScience, 2022, 25, 104185.	4.1	9
7139	Microbiome network traits in the rumen predict average daily gain in beef cattle under different backgrounding systems. Animal Microbiome, 2022, 4, 25.	3.8	10
7140	Intestinal permeability before and after albendazole treatment in low and high socioeconomic status schoolchildren in Makassar, Indonesia. Scientific Reports, 2022, 12, 3394.	3.3	2
7141	Recirculation of H ₂ , CO ₂ , and Ethylene Improves Carbon Fixation and Carboxylate Yields in Anaerobic Fermentation. ACS Sustainable Chemistry and Engineering, 2022, 10, 4073-4081.	6.7	9
7142	Persistent Circulation of Enterohemorrhagic Escherichia coli (EHEC) O157:H7 in Cattle Farms: Characterization of Enterohemorrhagic Escherichia coli O157:H7 Strains and Fecal Microbial Communities of Bovine Shedders and Non-shedders. Frontiers in Veterinary Science, 2022, 9, 852475.	2.2	4

#	Article	IF	CITATIONS
7143	Heat-Killed <i>Lactiplantibacillus plantarum</i> LRCC5314 Mitigates the Effects of Stress-Related Type 2 Diabetes in Mice via Gut Microbiome Modulation. Journal of Microbiology and Biotechnology, 2022, 32, 324-332.	2.1	12
7144	Soil Bacterial Community Along an Altitudinal Gradient in the Sumaco, a Stratovolcano in the Amazon Region. Frontiers in Forests and Global Change, 2022, 5, .	2.3	3
7145	DNA Metabarcoding Enables High-Throughput Detection of Spotted Wing Drosophila (Drosophila) Tj ETQq0 0 0 r	gBT/Over	logk 10 Tf 50
7146	Lactate and Ethanol Chain Elongation in the Presence of Lactose: Insight into Product Selectivity and Microbiome Composition. ACS Sustainable Chemistry and Engineering, 2022, 10, 3407-3416.	6.7	8
7147	Intestinal Microbial Diversity of Free-Range and Captive Yak in Qinghai Province. Microorganisms, 2022, 10, 754.	3.6	4
7149	Mucospheres produced by a mixotrophic protist impact ocean carbon cycling. Nature Communications, 2022, 13, 1301.	12.8	27
7150	Population Differences and Host Species Predict Variation in the Diversity of Host-Associated Microbes in Hydra. Frontiers in Microbiology, 2022, 13, 799333.	3.5	5
7151	A carvacrol-based product reduces Campylobacter jejuni load and alters microbiota composition in the caeca of chickens. Journal of Applied Microbiology, 2022, 132, 4501-4516.	3.1	4
7152	Assessment of the effectiveness of muck-digesting bacterial pellets. Lake and Reservoir Management, 0, , 1-15.	1.3	0
7153	The Oral and Fecal Microbiota in a Canadian Cohort of Alzheimer's Disease. Journal of Alzheimer's Disease, 2022, 87, 247-258.	2.6	17
7154	Extensive sampling of <i>Saccharomyces cerevisiae</i> in Taiwan reveals ecology and evolution of predomesticated lineages. Genome Research, 2022, , .	5.5	13
7155	High Salt Levels Reduced Dissimilarities in Root-Associated Microbiomes of Two Barley Genotypes. Molecular Plant-Microbe Interactions, 2022, 35, 592-603.	2.6	3
7156	Machine learning-assisted identification of bioindicators predicts medium-chain carboxylate production performance of an anaerobic mixed culture. Microbiome, 2022, 10, 48.	11.1	14
7157	Effects of operational taxonomic unit inference methods on soil microeukaryote community analysis using longâ€read metabarcoding. Ecology and Evolution, 2022, 12, e8676.	1.9	3
7158	Biomineralization of lithium nanoparticles by Li-resistant Pseudomonas rodhesiae isolated from the Atacama salt flat. Biological Research, 2022, 55, 12.	3.4	6
7159	Protocatechuic Acid, a Gut Bacterial Metabolite of Black Raspberries, Inhibits Adenoma Development and Alters Gut Microbiome Profiles in <i>Apc</i> ^{Min/+} Mice. Journal of Cancer Prevention, 2022, 27, 50-57.	2.0	9
7160	Temporal variations of Microsporidia diversity and discovery of new host–parasite interactions in a lake ecosystem. Environmental Microbiology, 2022, 24, 1672-1686.	3.8	11
7161	Microbial community characterization in advanced water reclamation for potable reuse. Applied Microbiology and Biotechnology, 2022, 106, 2763-2773.	3.6	3

#	Article	IF	CITATIONS
7162	Age-Related Changes in the Nasopharyngeal Microbiome Are Associated With Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection and Symptoms Among Children, Adolescents, and Young Adults. Clinical Infectious Diseases, 2022, 75, e928-e937.	5.8	22
7163	Reef Location and Client Diversity Influence the Skin Microbiome of the Caribbean Cleaner Goby Elacatinus evelynae. Microbial Ecology, 2023, 85, 372-382.	2.8	2
7164	Global Grassland Diazotrophic Communities Are Structured by Combined Abiotic, Biotic, and Spatial Distance Factors but Resilient to Fertilization. Frontiers in Microbiology, 2022, 13, 821030.	3.5	1
7166	Fungal and Bacterial Diversity in the Tuber magnatum Ecosystem and Microbiome. Microbial Ecology, 2022, , 1.	2.8	4
7167	Seed microbiota revealed by a largeâ€scale metaâ€analysis including 50 plant species. New Phytologist, 2022, 234, 1448-1463.	7.3	59
7168	The Diverse Indigenous Bacterial Community in the Rudna Mine Does Not Cause Dissolution of Copper from Kupferschiefer in Oxic Conditions. Minerals (Basel, Switzerland), 2022, 12, 366.	2.0	3
7169	Tree Species Diversity and Forest Edge Density Jointly Shape the Gut Microbiota Composition in Juvenile Great Tits (Parus major). Frontiers in Microbiology, 2022, 13, 790189.	3.5	5
7170	Cryptic Methane-Cycling by Methanogens During Multi-Year Incubation of Estuarine Sediment. Frontiers in Microbiology, 2022, 13, 847563.	3.5	3
7171	Effect of Long-Term Agricultural Management on the Soil Microbiota Influenced by the Time of Soil Sampling. Frontiers in Soil Science, 2022, 2, .	2.2	10
7172	Microbial Identification Using rRNA Operon Region: Database and Tool for Metataxonomics with Long-Read Sequence. Microbiology Spectrum, 2022, 10, e0201721.	3.0	11
7173	Immunogenetic variation shapes the gut microbiome in a natural vertebrate population. Microbiome, 2022, 10, 41.	11.1	12
7174	The core root microbiome of Spartina alterniflora is predominated by sulfur-oxidizing and sulfate-reducing bacteria in Georgia salt marshes, USA. Microbiome, 2022, 10, 37.	11.1	22
7175	Starvation causes changes in the intestinal transcriptome and microbiome that are reversed upon refeeding. BMC Genomics, 2022, 23, 225.	2.8	10
7176	Mild chronic exposure to pesticides alters physiological markers of honey bee health without perturbing the core gut microbiota. Scientific Reports, 2022, 12, 4281.	3.3	30
7177	Fecal transplantation can alleviate tic severity in a Tourette syndrome mouse model by modulating intestinal flora and promoting serotonin secretion. Chinese Medical Journal, 2022, 135, 707-713.	2.3	9
7179	Differential Response of Wheat Rhizosphere Bacterial Community to Plant Variety and Fertilization. International Journal of Molecular Sciences, 2022, 23, 3616.	4.1	7
7181	Dynamics of Bacterial Root Endophytes of Malus domestica Plants Grown in Field Soils Affected by Apple Replant Disease. Frontiers in Microbiology, 2022, 13, 841558.	3.5	5
7182	Fungal Communities of Spring Barley from Seedling Emergence to Harvest During a Severe Puccinia hordei Epidemic. Microbial Ecology, 2023, 85, 617-627.	2.8	4

#	Article	IF	CITATIONS
7183	Genetic and phenotypic diversity of fecal Candida albicans strains in irritable bowel syndrome. Scientific Reports, 2022, 12, 5391.	3.3	8
7184	Classic Hoarding Cages Increase Gut Bacterial Abundance and Reduce the Individual Immune Response of Honey Bee (<i>Apis mellifera</i>) Workers. Journal of Insect Science, 2022, 22, .	1.5	1
7185	Postmortem Skeletal Microbial Community Composition and Function in Buried Human Remains. MSystems, 2022, 7, e0004122.	3.8	9
7187	Geographical and Seasonal Analysis of the Honeybee Microbiome. Microbial Ecology, 2023, 85, 765-778.	2.8	8
7188	Interaction of bacterial genera associated with therapeutic response to immune checkpoint PD-1 blockade in a United States cohort. Genome Medicine, 2022, 14, 35.	8.2	29
7189	Variation in diet composition and its relation to gut microbiota in a passerine bird. Scientific Reports, 2022, 12, 3787.	3.3	8
7190	Upregulation of antimicrobial peptide expression in slc26a3-/- mice with colonic dysbiosis and barrier defect. Gut Microbes, 2022, 14, 2041943.	9.8	7
7191	Exogenous Microorganisms Promote Moss Biocrust Growth by Regulating the Microbial Metabolic Pathway in Artificial Laboratory Cultivation. Frontiers in Microbiology, 2022, 13, 819888.	3.5	5
7192	Linkages Among Dissolved Organic Matter Export, Dissolved Metabolites, and Associated Microbial Community Structure Response in the Northwestern Sargasso Sea on a Seasonal Scale. Frontiers in Microbiology, 2022, 13, 833252.	3.5	10
7193	Skin Microbiota Variation Among Bat Species in China and Their Potential Defense Against Pathogens. Frontiers in Microbiology, 2022, 13, 808788.	3.5	5
7194	Formalin-Fixed Paraffin-Embedded (FFPE) samples are not a beneficial replacement for frozen tissues in fetal membrane microbiota research. PLoS ONE, 2022, 17, e0265441.	2.5	4
7196	Epilithic Microbial Community Functionality in Deep Oligotrophic Continental Bedrock. Frontiers in Microbiology, 2022, 13, 826048.	3.5	10
7197	Host Traits and Phylogeny Contribute to Shaping Coral-Bacterial Symbioses. MSystems, 2022, 7, e0004422.	3.8	22
7198	Soil microbial communities following 20Âyears of fertilization and crop rotation practices in the Czech Republic. Environmental Microbiomes, 2022, 17, 13.	5.0	7
7200	Contribution of Ruminal Bacteriome to the Individual Variation of Nitrogen Utilization Efficiency of Dairy Cows. Frontiers in Microbiology, 2022, 13, 815225.	3.5	5
7201	Association of secretor status and recent norovirus infection with gut microbiome diversity metrics in a Veterans Affairs population. Open Forum Infectious Diseases, 2022, 9, ofac125.	0.9	0
7202	Microbiome Analysis via OTU and ASV-Based Pipelinesâ€"A Comparative Interpretation of Ecological Data in WWTP Systems. Bioengineering, 2022, 9, 146.	3.5	13
7204	Succession of the wheat seed-associated microbiome as affected by soil fertility level and introduction of <i>Penicillium </i> Bacillus Inoculants in the field. FEMS Microbiology Ecology, 2022, 98, .	2.7	5

#	Article	IF	CITATIONS
7206	Sex differences associate with late microbiome alterations after murine surgical sepsis. Journal of Trauma and Acute Care Surgery, 2022, 93, 137-146.	2.1	8
7207	Compatibility of Diatom Valve Records With Sedimentary Ancient DNA Amplicon Data: A Case Study in a Brackish, Alkaline Tibetan Lake. Frontiers in Earth Science, 2022, 10, .	1.8	8
7208	No Guts About It: Captivity, But Not Neophobia Phenotype, Influences the Cloacal Microbiome of House Sparrows (<i>Passer domesticus</i>). Integrative Organismal Biology, 2022, 4, obac010.	1.8	6
7209	Changes in Soil Quality of an Urban Wetland as a Result of Anthropogenic Disturbance. Land, 2022, 11, 394.	2.9	1
7210	Effects of Plastic Shed Cultivation System on the Properties of Red Paddy Soil and Its Management by Reductive Soil Disinfestation. Horticulturae, 2022, 8, 279.	2.8	5
7211	Linking photoacclimation responses and microbiome shifts between depth-segregated sibling species of reef corals. Royal Society Open Science, 2022, 9, 211591.	2.4	3
7212	Original Leaf Colonisers Shape Fungal Decomposer Communities of Phragmites australis in Intermittent Habitats. Journal of Fungi (Basel, Switzerland), 2022, 8, 284.	3.5	6
7213	The Prebiotic Potential of Geraniin and Geraniin-Enriched Extract against High-Fat-Diet-Induced Metabolic Syndrome in Sprague Dawley Rats. Antioxidants, 2022, 11, 632.	5.1	4
7214	Microbial community succession of submerged bones in an aquatic habitat. Journal of Forensic Sciences, 2022, , .	1.6	5
7215	Squalene epoxidase drives cancer cell proliferation and promotes gut dysbiosis to accelerate colorectal carcinogenesis. Gut, 2022, 71, 2253-2265.	12.1	54
7217	Computational Tools for the Analysis of Uncultivated Phage Genomes. Microbiology and Molecular Biology Reviews, 2022, 86, e0000421.	6.6	13
7218	Reduced Growth, Altered Gut Microbiome and Metabolite Profile, and Increased Chronic Kidney Disease Risk in Young Pigs Consuming a Diet Containing Highly Resistant Protein. Frontiers in Nutrition, 2022, 9, 816749.	3.7	7
7219	Diversity and Effect of Increasing Temperature on the Activity of Methanotrophs in Sediments of Fildes Peninsula Freshwater Lakes, King George Island, Antarctica. Frontiers in Microbiology, 2022, 13, 822552.	3.5	12
7220	Antimetabolite Drugs Exhibit Distinctive Immunomodulatory Mechanisms and Effects on the Intestinal Microbiota in Experimental Autoimmune Uveitis., 2022, 63, 30.		6
7221	Spatial and Interannual Patterns of Epipelagic Summer Mesozooplankton Community Structures in the Western Arctic Ocean in 2016–2020. Journal of Geophysical Research: Oceans, 2022, 127, .	2.6	3
7223	Microbial Dispersal, Including Bison Dung Vectored Dispersal, Increases Soil Microbial Diversity in a Grassland Ecosystem. Frontiers in Microbiology, 2022, 13, 825193.	3.5	4
7224	Multi-omics reveals microbiome, host gene expression, and immune landscape in gastric carcinogenesis. IScience, 2022, 25, 103956.	4.1	19
7225	Reduced methane emissions in former permafrost soils driven by vegetation and microbial changes following drainage. Global Change Biology, 2022, 28, 3411-3425.	9.5	6

#	Article	IF	CITATIONS
7226	Multiomic Analysis of the Gut Microbiome in Psoriasis Reveals Distinct Hostâ€'Microbe Associations. JID Innovations, 2022, 2, 100115.	2.4	8
7227	Developmental microbiome of the small carpenter bee, <i>Ceratina calcarata</i> . Environmental DNA, 2022, 4, 808-819.	5. 8	7
7228	Long-Term Analysis of Resilience of the Oral Microbiome in Allogeneic Stem Cell Transplant Recipients. Microorganisms, 2022, 10, 734.	3.6	8
7229	Sputum Bacterial Metacommunities in Distinguishing Heterogeneity in Respiratory Health and Disease. Frontiers in Microbiology, 2022, 13, 719541.	3.5	2
7231	Comparative Fecal Microbiota Analysis of Infants With Acute Bronchiolitis Caused or Not Caused by Respiratory Syncytial Virus. Frontiers in Cellular and Infection Microbiology, 2022, 12, 815715.	3.9	2
7232	Reactive nitrogen restructures and weakens microbial controls of soil N2O emissions. Communications Biology, 2022, 5, 273.	4.4	11
7233	The gut microbiome of exudivorous marmosets in the wild and captivity. Scientific Reports, 2022, 12, 5049.	3.3	11
7234	Roux-en-Y gastric bypass and sleeve gastrectomy induce substantial and persistent changes in microbial communities and metabolic pathways. Gut Microbes, 2022, 14, 2050636.	9.8	16
7235	Biogeography of reef water microbes from within-reef to global scales. Aquatic Microbial Ecology, 2022, 88, 81-94.	1.8	2
7236	Habitatâ€edapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. New Phytologist, 2022, 234, 2111-2125.	7.3	18
7237	Alterations in common marmoset gut microbiome associated with duodenal strictures. Scientific Reports, 2022, 12, 5277.	3.3	8
7238	Small rain events during drought alter sediment dissolved organic carbon leaching and respiration in intermittent stream sediments. Biogeochemistry, 2022, 159, 159-178.	3.5	6
7239	Functional properties of miscanthus fiber and prebiotic blends in extruded canine diets. Journal of Animal Science, 2022, 100, .	0.5	4
7240	Biological Soil Crust From Mesic Forests Promote a Specific Bacteria Community. Frontiers in Microbiology, 2022, 13, 769767.	3.5	8
7241	The Biogeochemical Legacy of Arctic Subglacial Sediments Exposed by Glacier Retreat. Global Biogeochemical Cycles, 2022, 36, .	4.9	14
7243	Effects of Fermented Vegetable Consumption on Human Gut Microbiome Diversityâ€"A Pilot Study. Fermentation, 2022, 8, 118.	3.0	4
7244	Skin microbiota diversity among genetically unrelated individuals of Indian origin. PeerJ, 2022, 10, e13075.	2.0	2
7245	Alternations in the gut microbiota and metabolome with newly diagnosed unstable angina. Journal of Genetics and Genomics, 2022, 49, 240-248.	3.9	3

#	Article	IF	Citations
7246	Antarctic Glacial Meltwater Impacts the Diversity of Fungal Parasites Associated With Benthic Diatoms in Shallow Coastal Zones. Frontiers in Microbiology, 2022, 13, 805694.	3.5	7
7247	Loss of gut microbial diversity in the cultured, agastric fish, Mexican pike silverside (<i>Chirostoma) Tj ETQq1</i>	1 0.78431	4 rgBJT /Overloo
7248	Freeze-drying can replace cold-chains for transport and storage of fecal microbiome samples. PeerJ, 2022, 10, e13095.	2.0	3
7249	Bacterial communities associated with wood rot fungi that use distinct decomposition mechanisms. ISME Communications, 2022, 2, .	4.2	13
7250	Prophylactic Addition of Glucose Suppresses Cyanobacterial Abundance in Lake Water. Life, 2022, 12, 385.	2.4	2
7253	The gut commensal bacterium <scp><i>Enterococcus faecalis</i> LX10</scp> contributes to defending against <scp><i>Nosema bombycis</i> cli></scp> infection in <scp><i>Bombyx mori</i> cli></scp> . Pest Management Science, 2022, 78, 2215-2227.	3.4	11
7254	The Effect of Topical Anesthetics on 16S Ribosomal Ribonucleic Acid Amplicon Sequencing Results in Ocular Surface Microbiome Research. Translational Vision Science and Technology, 2022, 11, 2.	2.2	9
7255	Changes in the gut microbiota of Nigerian infants within the first year of life. PLoS ONE, 2022, 17, e0265123.	2.5	11
7256	Salivary Microbiota and Host-Inflammatory Responses in Periodontitis Affected Individuals With and Without Rheumatoid Arthritis. Frontiers in Cellular and Infection Microbiology, 2022, 12, 841139.	3.9	11
7257	Using palaeolimnology to guide rehabilitation of a culturally significant lake in New Zealand. Aquatic Conservation: Marine and Freshwater Ecosystems, 2022, 32, 931-950.	2.0	7
7258	Host genotype interacts with aerial spore communities and influences the needle mycobiome of Norway spruce. Environmental Microbiology, 2022, 24, 3640-3654.	3.8	7
7259	Alterations in the Gut Fungal Community in a Mouse Model of Huntington's Disease. Microbiology Spectrum, 2022, 10, e0219221.	3.0	11
7260	Heart Failure Severity Closely Correlates with Intestinal Dysbiosis and Subsequent Metabolomic Alterations. Biomedicines, 2022, 10, 809.	3.2	13
7261	The Power of Microbiome Studies: Some Considerations on Which Alpha and Beta Metrics to Use and How to Report Results. Frontiers in Microbiology, 2021, 12, 796025.	3.5	44
7262	Co-Occurrence of L. monocytogenes with Other Bacterial Genera and Bacterial Diversity on Cleaned Conveyor Surfaces in a Swine Slaughterhouse. Microorganisms, 2022, 10, 613.	3.6	4
7263	Exome and Tissue-Associated Microbiota as Predictive Markers of Response to Neoadjuvant Treatment in Locally Advanced Rectal Cancer. Frontiers in Oncology, 2022, 12, 809441.	2.8	2
7264	Antimicrobial resistance determinants in silage. Scientific Reports, 2022, 12, 5243.	3.3	2
7265	Oral and Stool Microbiome Coalescence and Its Association With Antibiotic Exposure in Acute Leukemia Patients. Frontiers in Cellular and Infection Microbiology, 2022, 12, 848580.	3.9	2

#	Article	IF	CITATIONS
7266	Insights from shotgun metagenomics into bacterial species and metabolic pathways associated with NAFLD in obese youth. Hepatology Communications, 2022, 6, 1962-1974.	4.3	20
7267	Salinity as a key control on the diazotrophic community composition in the southern Baltic Sea. Ocean Science, 2022, 18, 401-417.	3.4	4
7268	The Effects of Commonly Consumed Dietary Fibres on the Gut Microbiome and Its Fibre Fermentative Capacity in Adults with Inflammatory Bowel Disease in Remission. Nutrients, 2022, 14, 1053.	4.1	14
7269	A Two-Time Point Analysis of Gut Microbiota in the General Population of Buenos Aires and Its Variation Due to Preventive and Compulsory Social Isolation During the COVID-19 Pandemic. Frontiers in Microbiology, 2022, 13, 803121.	3.5	8
7270	Functional feeds marginally alter immune expression and microbiota of Atlantic salmon (Salmo salar) gut, gill, and skin mucosa though evidence of tissue-specific signatures and host–microbe coadaptation remain. Animal Microbiome, 2022, 4, 20.	3.8	15
7271	Gastrointestinal Microbiome Disruption and Antibiotic-Associated Diarrhea in Children Receiving Antibiotic Therapy for Community-Acquired Pneumonia. Journal of Infectious Diseases, 2022, 226, 1109-1119.	4.0	6
7272	Pairing litter decomposition with microbial community structures using the Tea Bag Index (TBI). Soil, 2022, 8, 163-176.	4.9	10
7273	Dietary manipulation of the gut microbiome in inflammatory bowel disease patients: Pilot study. Gut Microbes, 2022, 14, 2046244.	9.8	29
7274	Towards standardized and reproducible research in skin microbiomes. Environmental Microbiology, 2022, 24, 3840-3860.	3.8	5
7275	Can gut microbiota throughout the first 10 years of life predict executive functioning in childhood?. Developmental Psychobiology, 2022, 64, e22226.	1.6	4
7276	Adaptive changes of sediment microbial communities associated with cleanup of oil spills in Nigerian mangrove forests. Marine Pollution Bulletin, 2022, 176, 113406.	5.0	10
7277	Urbanization comprehensively impairs biological rhythms in coral holobionts. Global Change Biology, 2022, 28, 3349-3364.	9.5	14
7278	Effect of Long-Term Supplementation With Silkworm Pupae Oil on the Methane Yield, Ruminal Protozoa, and Archaea Community in Sheep. Frontiers in Microbiology, 2022, 13, 780073.	3.5	6
7279	Mycobiome detection from a single subterranean gametophyte using metabarcoding techniques. Applications in Plant Sciences, 2022, 10, e11461.	2.1	6
7281	Airborne environmental DNA metabarcoding for the monitoring of terrestrial insects—A proof of concept from the field. Environmental DNA, 2022, 4, 790-807.	5.8	45
7282	Ubiquity of dominant cyanobacterial taxa along glacier retreat in the Antarctic Peninsula. FEMS Microbiology Ecology, 2022, 98, .	2.7	2
7283	Temporally Selective Modification of the Tomato Rhizosphere and Root Microbiome by Volcanic Ash Fertilizer Containing Micronutrients. Applied and Environmental Microbiology, 2022, 88, e0004922.	3.1	4
7284	Reproducible Propagation of Species-Rich Soil Bacterial Communities Suggests Robust Underlying Deterministic Principles of Community Formation. MSystems, 2022, 7, e0016022.	3.8	10

#	Article	IF	CITATIONS
7285	Analysis of gut microbiome profiles in common marmosets (Callithrix jacchus) in health and intestinal disease. Scientific Reports, 2022, 12, 4430.	3.3	9
7286	Metabolome and microbiome multi-omics integration from a murine lung inflammation model of bronchopulmonary dysplasia. Pediatric Research, 2022, 92, 1580-1589.	2.3	5
7288	Stem traits, compartments and tree species affect fungal communities on decaying wood. Environmental Microbiology, 2022, 24, 3625-3639.	3.8	4
7289	Fecal Filobasidium Is Associated with Clinical Remission and Endoscopic Response following Fecal Microbiota Transplantation in Mild-to-Moderate Ulcerative Colitis. Microorganisms, 2022, 10, 737.	3.6	7
7290	Diversity and distribution of sediment bacteria across an ecological and trophic gradient. PLoS ONE, 2022, 17, e0258079.	2.5	3
7291	Digital Therapeutics Care Utilizing Genetic and Gut Microbiome Signals for the Management of Functional Gastrointestinal Disorders: Results From a Preliminary Retrospective Study. Frontiers in Microbiology, 2022, 13, 826916.	3.5	9
7292	Dietary proanthocyanidins promote localized antioxidant responses in porcine pulmonary and gastrointestinal tissues during ⟨i⟩Ascaris suum⟨/i⟩ â€induced type 2 inflammation. FASEB Journal, 2022, 36, e22256.	0.5	7
7293	Diverse Bathyarchaeotal Lineages Dominate Archaeal Communities in the Acidic Dajiuhu Peatland, Central China. Microbial Ecology, 2023, 85, 557-571.	2.8	4
7294	Persistent, Asymptomatic Colonization with <i>Candida</i> is Associated with Elevated Frequencies of Highly Activated Cervical Th17-Like Cells and Related Cytokines in the Reproductive Tract of South African Adolescents. Microbiology Spectrum, 2022, 10, e0162621.	3.0	2
7295	Fecal microbiota of adolescent and young adult cancer survivors and metabolic syndrome: an exploratory study. Pediatric Hematology and Oncology, 2022, 39, 629-643.	0.8	1
7297	Soil Aggregation Shaped the Distribution and Interaction of Bacterial-Fungal Community Based on a 38-Year Fertilization Experiment in China. Frontiers in Microbiology, 2022, 13, 824681.	3.5	3
7298	Rocks support a distinctive and consistent mycobiome across contrasting dry regions of Earth. FEMS Microbiology Ecology, 2022, 98, .	2.7	2
7299	Role of adherent and invasive <i>Escherichia coli </i> in Crohn's disease: lessons from the postoperative recurrence model. Gut, 2023, 72, 39-48.	12.1	22
7300	The microbiome of common bedding materials before and after use on commercial dairy farms. Animal Microbiome, 2022, 4, 18.	3.8	8
7301	Protocol to assess the impact of early-life antibiotic exposure on murine longevity. STAR Protocols, 2022, 3, 101220.	1.2	1
7302	IL10 Secretion Endows Intestinal Human iNKT Cells with Regulatory Functions Towards Pathogenic T Lymphocytes. Journal of Crohn's and Colitis, 2022, 16, 1461-1474.	1.3	8
7303	Long Term Influence of Fertility and Rotation on Soil Nitrification Potential and Nitrifier Communities. Frontiers in Soil Science, 2022, 2, .	2.2	4
7304	A mouse model of occult intestinal colonization demonstrating antibiotic-induced outgrowth of carbapenem-resistant Enterobacteriaceae. Microbiome, 2022, 10, 43.	11.1	8

#	Article	IF	CITATIONS
7305	The polyâ€extreme tolerant black yeasts are prevalent under high ultraviolet light and climatic seasonality across soils of global biomes. Environmental Microbiology, 2022, 24, 1988-1999.	3.8	2
7306	Rhizosheath–root system changes exopolysaccharide content but stabilizes bacterial community across contrasting seasons in a desert environment. Environmental Microbiomes, 2022, 17, 14.	5.0	13
7307	Biogeography, succession, and origin of the chicken intestinal mycobiome. Microbiome, 2022, 10, 55.	11.1	17
7308	Vertical transmission of attaching and invasive E. coli from the dam to neonatal mice predisposes to more severe colitis following exposure to a colitic insult later in life. PLoS ONE, 2022, 17, e0266005.	2.5	3
7309	Involvement of microbiota and short-chain fatty acids on non-alcoholic steatohepatitis when induced by feeding a hypercaloric diet rich in saturated fat and fructose. Gut Microbiome, 0, , 1-33.	3.2	2
7310	Legacies of invertebrate exclusion and tree secondary metabolites control fungal communities in dead wood. Molecular Ecology, 2022, 31, 3241-3253.	3.9	6
7311	Significant effects of host dietary guild and phylogeny in wild lemur gut microbiomes. ISME Communications, 2022, 2, .	4.2	4
7312	Newly designed foraminifera primers identify habitatâ€specific lineages through metabarcoding analyses. Journal of Eukaryotic Microbiology, 2022, 69, e12913.	1.7	0
7313	Assessing the effects of experimental bacterial challenge with Pasteurella multocida and ampicillin on the respiratory microbiota of pre-weaned Holstein calves. Veterinary Microbiology, 2022, 269, 109428.	1.9	0
7314	MicrobioSee: A Web-Based Visualization Toolkit for Multi-Omics of Microbiology. Frontiers in Genetics, 2022, 13, 853612.	2.3	2
7315	A Single Application of Compost Can Leave Lasting Impacts on Soil Microbial Community Structure and Alter Cross-Domain Interaction Networks. Frontiers in Soil Science, 2022, 2, .	2.2	15
7317	Efficacy and Safety of Lactobacillus reuteri CCFM1040 in Allergic Rhinitis and Asthma: A Randomized, Placebo-Controlled Trial. Frontiers in Nutrition, 2022, 9, 862934.	3.7	5
7318	Abiotic Treatment to Common Bean Plants Results in an Altered Endophytic Seed Microbiome. Microbiology Spectrum, 2022, 10, e0021021.	3.0	12
7319	Short-term exposure to the mycotoxins zearalenone or fumonisins affects rumen fermentation and microbiota, and health variables in cattle. Food and Chemical Toxicology, 2022, 162, 112900.	3.6	16
7320	The human milk microbiome aligns with lactation stage and not birth mode. Scientific Reports, 2022, 12, 5598.	3.3	16
7321	Pharmacologically induced weight loss is associated with distinct gut microbiome changes in obese rats. BMC Microbiology, 2022, 22, 91.	3.3	4
7322	Development of an eDNAâ€based survey method for urban fish markets. Methods in Ecology and Evolution, 2022, 13, 1568-1580.	5.2	3
7323	Protist Predation Influences the Temperature Response of Bacterial Communities. Frontiers in Microbiology, 2022, 13, 847964.	3.5	11

#	ARTICLE	IF	CITATIONS
7324	Cophylogeny and convergence shape holobiont evolution in sponge–microbe symbioses. Nature Ecology and Evolution, 2022, 6, 750-762.	7.8	21
7325	Ride the dust: linking dust dispersal and spatial distribution of microorganisms across an arid landscape. Environmental Microbiology, 2022, 24, 4094-4107.	3.8	7
7326	The relationship between dietary trophic level, parasites and the microbiome of Pacific walrus () Tj ETQq0 0 0 rgB 289, 20220079.	Γ /Overlocl 2.6	k 10 Tf 50 6 3
7327	Temporal dynamics of Campylobacter and Arcobacter in a freshwater lake that receives fecal inputs from migratory geese. Water Research, 2022, 217, 118397.	11.3	7
7328	Salinity significantly affects intestinal microbiota and gene expression in striped catfish juveniles. Applied Microbiology and Biotechnology, 2022, 106, 3245-3264.	3.6	14
7329	Soil environment reshapes microbiota of laboratory-maintained Collembola during host development. Environmental Microbiomes, 2022, 17, 16.	5.0	1
7330	Obesity influences composition of salivary and fecal microbiota and impacts the interactions between bacterial taxa. Physiological Reports, 2022, 10, e15254.	1.7	14
7331	The bacteriology of pleural infection (TORPIDS): an exploratory metagenomics analysis through next generation sequencing. Lancet Microbe, The, 2022, 3, e294-e302.	7.3	22
7332	Longitudinal Characterization of the Fungal Skin Microbiota in Healthy Subjects Over the Period of One Year. Journal of Investigative Dermatology, 2022, , .	0.7	1
7333	Contrasting resistance and resilience to light variation of the coupled oxic and anoxic components of an experimental microbial ecosystem. Ecology and Evolution, 2022, 12, e8793.	1.9	1
7334	<i>Sarracenia</i> pitcher plantâ€essociated microbial communities differ primarily by host species across a longitudinal gradient. Environmental Microbiology, 2022, 24, 3500-3516.	3.8	2
7335	A Pilot Study Exploring the Association of Entacapone, Gut Microbiota, and the Subsequent Side Effects in Patients With Parkinson's Disease. Frontiers in Cellular and Infection Microbiology, 2022, 12, 837019.	3.9	6
7337	Human land use impacts viral diversity and abundance in a New Zealand river. Virus Evolution, 2022, 8, veac032.	4.9	13
7338	Not all permafrost microbiomes are created equal: Influence of permafrost thaw on the soil microbiome in a laboratory incubation study. Soil Biology and Biochemistry, 2022, 167, 108605.	8.8	7
7339	Environment and Co-occurring Native Mussel Species, but Not Host Genetics, Impact the Microbiome of a Freshwater Invasive Species (Corbicula fluminea). Frontiers in Microbiology, 2022, 13, 800061.	3.5	10
7341	Marine Vertebrates Impact the Bacterial Community Composition and Food Webs of Antarctic Microbial Mats. Frontiers in Microbiology, 2022, 13, 841175.	3.5	6
7342	Can seagrass modify the effects of ocean acidification on oysters?. Marine Pollution Bulletin, 2022, 177, 113438.	5.0	7
7344	Accumulation of nylon microplastics and polybrominated diphenyl ethers and effects on gut microbial community of Chironomus sancticaroli. Science of the Total Environment, 2022, 832, 155089.	8.0	17

#	Article	IF	CITATIONS
7345	Vaginal Microbiota Diversity in Response to Lipopolysaccharide in Gilts Housed Under Three Housing Systems. Frontiers in Genetics, 2022, 13, 836962.	2.3	2
7346	Deep-rooted perennial crops differ in capacity to stabilize C inputs in deep soil layers. Scientific Reports, 2022, 12, 5952.	3.3	20
7347	Salinity and host drive ⟨i⟩Ulva⟨ i⟩â€associated bacterial communities across the Atlantic–Baltic Sea gradient. Molecular Ecology, 2023, 32, 6260-6277.	3.9	6
7348	Influence of Chlorella vulgaris on growth, digestibility and gut morphology and microbiota of weaned piglet. Scientific Reports, 2022, 12, 6012.	3.3	13
7349	Genomics and Informatics, Conjoined Tools Vital for Understanding and Protecting Plant Health. Phytopathology, 2022, 112, 981-995.	2.2	2
7350	Spirulina platensis biomass enhances the proliferation rate of Lactobacillus acidophilus 5 (La-5) and combined with La-5 impact the gut microbiota of medium-age healthy individuals through an in vitro gut microbiome model. Food Research International, 2022, 154, 110880.	6.2	9
7351	MTD: a unique pipeline for host and meta-transcriptome joint and integrative analyses of RNA-seq data. Briefings in Bioinformatics, 2022, 23, .	6.5	1
7352	The Right Place at the Right Time: Seasonal Variation of Bacterial Communities in Arid Avicennia marina Soils in the Red Sea Is Specific to Its Position in the Intertidal. Frontiers in Ecology and Evolution, 2022, 10, .	2.2	3
7353	Increasing transparency and reproducibility in stroke-microbiota research: A toolbox for microbiota analysis. Science, 2022, 25, 103998.	4.1	3
7354	Effects of caloric restriction on the gut microbiome are linked with immune senescence. Microbiome, 2022, 10, 57.	11.1	38
7355	Association of Gut Microbiota with Dietary-dependent Childhood Obesity. Archives of Medical Research, 2022, 53, 407-415.	3.3	5
7356	Characterization of the skin microbiota in bullous pemphigoid patients and controls reveals novel microbial indicators of disease. Journal of Advanced Research, 2023, 44, 71-79.	9.5	9
7357	Ectomycorrhizal diversity on the roots of Pitch pine (<i>Pinus rigida </i> Mill.) saplings as influenced by remediation and soil metal content. Restoration Ecology, 0, , .	2.9	0
7358	Microbial communities in sandy beaches from the three domains of life differ by microhabitat and intertidal location. Molecular Ecology, 2022, 31, 3210-3227.	3.9	6
7359	Community composition of bacteria isolated from Swiss banknotes varies depending on collection environment. Molecular Ecology, 2023, 32, 2619-2632.	3.9	2
7360	Susceptibility to epilepsy after traumatic brain injury is associated with preexistent gut microbiome profile. Epilepsia, 2022, 63, 1835-1848.	5.1	13
7361	Correlating the above- and belowground genotype of Pinus pinaster trees and rhizosphere bacterial communities under drought conditions. Science of the Total Environment, 2022, 832, 155007.	8.0	6
7362	Next generation restoration metrics: Using soil eDNA bacterial community data to measure trajectories towards rehabilitation targets. Journal of Environmental Management, 2022, 310, 114748.	7.8	14

#	Article	IF	CITATIONS
7363	The nature of gas production patterns associated with methanol degradation in natural aquifer sediments: A microcosm study. Journal of Contaminant Hydrology, 2022, 247, 103988.	3.3	0
7364	Brine salt concentration reduction and inoculation with autochthonous consortia: Impact on Protected Designation of Origin Nyons black table olive fermentations. Food Research International, 2022, 155, 111069.	6.2	8
7365	Potential pathobionts in vaginal microbiota are affected by fish oil and/or probiotics intervention in overweight and obese pregnant women. Biomedicine and Pharmacotherapy, 2022, 149, 112841.	5.6	9
7366	Adolescent exposure to a solid high-fat, high-sugar †cafeteria†diet leads to more pronounced changes in metabolic measures and gut microbiome composition than liquid sugar in female rats. Appetite, 2022, 172, 105973.	3.7	5
7367	Blooms of the harmful algae Margalefidinium polykrikoides and Alexandrium monilatum alter the York River Estuary microbiome. Harmful Algae, 2022, 114, 102216.	4.8	3
7368	Colitis-associated microbiota drives changes in behaviour in male mice in the absence of inflammation. Brain, Behavior, and Immunity, 2022, 102, 266-278.	4.1	19
7369	The role of plant input physical-chemical properties, and microbial and soil chemical diversity on the formation of particulate and mineral-associated organic matter. Soil Biology and Biochemistry, 2022, 168, 108648.	8.8	59
7370	Free-living marine bacterioplankton composition and diversity along the Kuroshio region. Deep-Sea Research Part I: Oceanographic Research Papers, 2022, 183, 103741.	1.4	0
7371	Cold seeps alter the near-bottom biogeochemistry in the ultraoligotrophic Southeastern Mediterranean Sea. Deep-Sea Research Part I: Oceanographic Research Papers, 2022, 183, 103744.	1.4	9
7372	Metabarcoding analysis of microbiome dynamics during a Phaeocystis globosa bloom in the Beibu Gulf, China. Harmful Algae, 2022, 114, 102217.	4.8	3
7373	Linking soil microbial community structure to potential carbon mineralization: A continental scale assessment of reduced tillage. Soil Biology and Biochemistry, 2022, 168, 108618.	8.8	17
7374	Effects of sampling and storage procedures on 16S rDNA amplicon sequencing results of kelp microbiomes. Marine Genomics, 2022, 63, 100944.	1.1	6
7375	Muskoxen homogenise soil microbial communities and affect the abundance of methanogens and methanotrophs. Science of the Total Environment, 2022, 827, 153877.	8.0	2
7376	A new insight into spacing patterns of soil bacterial microbiome induced by root rot of Carya cathayensis. Applied Soil Ecology, 2022, 174, 104416.	4.3	6
7377	Land use and roles of soil bacterial community in the dissipation of atrazine. Science of the Total Environment, 2022, 827, 154239.	8.0	15
7378	Metataxonomic signature of beef burger perishability depends on the meat origin prior grinding. Food Research International, 2022, 156, 111103.	6.2	6
7379	Metagenomics analysis of probable transmission of determinants of antibiotic resistance from wastewater to the environment $\hat{a} \in A$ case study. Science of the Total Environment, 2022, 827, 154354.	8.0	16
7380	A reciprocal transplant experiment sheds new light on a classic marine seagrass-algal symbiosis and suggests influence of epiphytic symbiont on seagrass microbiota. Aquatic Botany, 2022, 179, 103511.	1.6	7

#	Article	IF	Citations
7381	Fecal microbiota in pediatric depression and its relation to bowel habits. Journal of Psychiatric Research, 2022, 150, 113-121.	3.1	10
7382	The level and distribution of methyl-esters influence the impact of pectin on intestinal T cells, microbiota, and Ahr activation. Carbohydrate Polymers, 2022, 286, 119280.	10.2	13
7383	Enrichment in biodiversity and maturation of the soil food web under conservation agriculture is associated with suppression of rice-parasitic nematodes. Agriculture, Ecosystems and Environment, 2022, 331, 107913.	5.3	13
7384	Structural shifts in sea ice prokaryotic communities across a salinity gradient in the subarctic. Science of the Total Environment, 2022, 827, 154286.	8.0	4
7385	Bacterial metataxonomic analysis of industrial Spanish-style green table olive fermentations. Food Control, 2022, 137, 108969.	5.5	4
7386	Zeolite mediated processing of nitrogenous waste in the rearing environment influences gut and sediment microbial community in freshwater crayfish (Cherax cainii) culture. Chemosphere, 2022, 298, 134276.	8.2	5
7387	Secondary succession and parent material drive soil bacterial community composition in terraced abandoned olive groves from a Mediterranean hyper-humid mountainous area. Agriculture, Ecosystems and Environment, 2022, 332, 107932.	5. 3	8
7388	Temporal variation of management effects on soil microbial communities. Geoderma, 2022, 418, 115828.	5.1	6
7389	Comparing resistome profiles from anthropogenically impacted and non-impacted areas of two South Shetland Islands $\hat{a} \in Maritime$ Antarctica. Environmental Pollution, 2022, 304, 119219.	7.5	10
7390	Tracking bacterial pollution at a marine wastewater outfall site – A case study from Norway. Science of the Total Environment, 2022, 829, 154257.	8.0	5
7391	Climate change impact on fungi in the atmospheric microbiome. Science of the Total Environment, 2022, 830, 154491.	8.0	15
7392	Evidence for saponin diversity–mycobiome links and conservatism of plant–fungi interaction patterns across Holarctic disjunct Panax species. Science of the Total Environment, 2022, 830, 154583.	8.0	9
7393	Role of subterranean microbiota in the carbon cycle and greenhouse gas dynamics. Science of the Total Environment, 2022, 831, 154921.	8.0	19
7394	Cyanotoxin-encoding genes as powerful predictors of cyanotoxin production during harmful cyanobacterial blooms in an inland freshwater lake: Evaluating a novel early-warning system. Science of the Total Environment, 2022, 830, 154568.	8.0	10
7395	Microbial DNA in human nucleic acid extracts: Recoverability of the microbiome in DNA extracts stored frozen long-term and its potential and ethical implications for forensic investigation. Forensic Science International: Genetics, 2022, 59, 102686.	3.1	8
7396	Cattle manure application triggers short-term dominance of Acinetobacter in soil microbial communities. Applied Soil Ecology, 2022, 176, 104466.	4.3	6
7397	Tracking the diversity and interaction of methanogens in the energy recovery process of a full-scale wastewater treatment plant. Environmental Research, 2022, 211, 113010.	7.5	2
7398	Arbuscular mycorrhizal fungi community linkages to soil nutrient availability across contrasting agroecosystems. Applied Soil Ecology, 2022, 176, 104464.	4.3	12

#	Article	IF	CITATIONS
7399	Solar photo-Fenton mediated by alternative oxidants for MWWTP effluent quality improvement: Impact on microbial community, priority pathogens and removal of antibiotic-resistant genes. Chemical Engineering Journal, 2022, 441, 136060.	12.7	10
7400	Effects of in situ experimental selenium exposure on finescale dace (Phoxinus neogaeus) gut microbiome. Environmental Research, 2022, 212, 113151.	7.5	5
7401	Key Factors Governing Microbial Community in Extremely Acidic Mine Drainage (pH <3). Frontiers in Microbiology, 2021, 12, 761579.	3.5	12
7402	Composite microbialites: Thrombolite, dendrolite, and stromatolite associations in a modern environment, Pozo Bravo lake, Salar de Antofalla, Catamarca Puna, Argentina. Journal of Sedimentary Research, 2021, 91, 1305-1330.	1.6	4
7403	Culture-Independent Survey of Thermophilic Microbial Communities of the North Caucasus. Biology, 2021, 10, 1352.	2.8	13
7404	Zooplankton diversity monitoring strategy for the urban coastal region using metabarcoding analysis. Scientific Reports, 2021, 11, 24339.	3.3	7
7405	Robust bacterial co-occurence community structures are independent of r- and K-selection history. Scientific Reports, 2021, 11, 23497.	3.3	3
7406	Recovered microbiome of an oviparous lizard differs across gut and reproductive tissues, cloacal swabs, and faeces. Molecular Ecology Resources, 2022, 22, 1693-1705.	4.8	10
7407	Life History Traits in Two Drosophila Species Differently Affected by Microbiota Diversity under Lead Exposure. Insects, 2021, 12, 1122.	2.2	4
7410	Systematic molecular evolution enables robust biomolecule discovery. Nature Methods, 2022, 19, 55-64.	19.0	34
7412	Fiber mixture-specific effect on distal colonic fermentation and metabolic health in lean but not in prediabetic men. Gut Microbes, 2022, 14, 2009297.	9.8	15
7413	Gut Microbiota Linked with Reduced Fear of Humans in Red Junglefowl Has Implications for Early Domestication. Genetics & Genomics Next, 2021, 2, .	1.5	7
7414	Assessing the impact of storage time on the stability of stool microbiota richness, diversity, and composition. Gut Pathogens, 2021, 13, 75.	3.4	14
7416	Nitrogen Fertiliser Immobilisation and Uptake in the Rhizospheres of Wheat and Canola. Agronomy, 2021, 11, 2507.	3.0	0
7417	Gut Microbiota and Serum Metabolic Signatures of High-Fat-Induced Bone Loss in Mice. Frontiers in Cellular and Infection Microbiology, 2021, 11, 788576.	3.9	19
7418	Host Factors Affect the Gut Microbiome More Significantly than Diet Shift. Microorganisms, 2021, 9, 2520.	3.6	11
7419	Heat-killed <i>Lactiplantibacillus plantarum</i> LRCC5314 mitigates the effects of stress-related type 2 diabetes in mice via gut microbiome modulation. Journal of Microbiology and Biotechnology, 2021, 32, .	2.1	5
7420	Yeast and Filamentous Fungi Microbial Communities in Organic Red Grape Juice: Effect of Vintage, Maturity Stage, SO2, and Bioprotection. Frontiers in Microbiology, 2021, 12, 748416.	3.5	12

#	Article	IF	CITATIONS
7421	eDNA metabarcoding for diet analyses of green sea turtles (Chelonia mydas). Marine Biology, 2022, 169, 1.	1.5	14
7422	The effects of Levilactobacillus brevis on the physiological parameters and gut microbiota composition of rats subjected to desynchronosis. Microbial Cell Factories, 2021, 20, 226.	4.0	5
7423	Combined metagenomic and archaeobotanical analyses on human dental calculus: A cross-section of lifestyle conditions in a Copper Age population of central Italy. Quaternary International, 2023, 653-654, 69-81.	1.5	6
7424	Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. Genome Biology, 2021, 22, 336.	8.8	18
7425	A Volatile and Dynamic Longitudinal Microbiome Is Associated With Less Reduction in Lung Function in Adolescents With Cystic Fibrosis. Frontiers in Cellular and Infection Microbiology, 2021, 11, 763121.	3.9	5
7426	Cancer Induces a Stress Ileopathy Depending on \hat{l}^2 -Adrenergic Receptors and Promoting Dysbiosis that Contributes to Carcinogenesis. Cancer Discovery, 2022, 12, 1128-1151.	9.4	44
7428	The Meta-Organism Response of the Environmental Generalist Pocillopora damicornis Exposed to Differential Accumulation of Heat Stress. Frontiers in Marine Science, 2021, 8, .	2.5	6
7429	Phytoplankton settling quality has a subtle but significant effect on sediment microeukaryotic and bacterial communities. Scientific Reports, 2021, 11, 24033.	3.3	2
7430	Depth dependence of climatic controls on soil microbial community activity and composition. ISME Communications, 2021, 1, .	4.2	16
7431	Characterization of External Mucosal Microbiomes of Nile Tilapia and Grey Mullet Co-cultured in Semi-Intensive Pond Systems. Frontiers in Microbiology, 2021, 12, 773860.	3.5	9
7432	Variation and transmission of the human gut microbiota across multiple familial generations. Nature Microbiology, 2022, 7, 87-96.	13.3	32
7433	The polar night shift: seasonal dynamics and drivers of Arctic Ocean microbiomes revealed by autonomous sampling. ISME Communications, 2021, 1, .	4.2	27
7434	Interplay between microbial community composition and chemodiversity of dissolved organic matter throughout the Black Sea water column redox gradient. Limnology and Oceanography, 2022, 67, 329-347.	3.1	8
7435	Mycobiome in the Middle Ear Cavity with and Without Otitis Media with Effusion. Turkish Archives of Otorhinolaryngology, 2021, 59, 261-270.	0.5	1
7437	Dynamic changes in antibiotic resistance genes and gut microbiota after <i>Helicobacter pylori</i> eradication therapies. Helicobacter, 2022, 27, e12871.	3.5	8
7438	Large-scale characterisation of the pregnancy vaginal microbiome and sialidase activity in a low-risk Chinese population. Npj Biofilms and Microbiomes, 2021, 7, 89.	6.4	10
7441	Bacterial Succession during Vermicomposting of Silver Wattle (Acacia dealbata Link). Microorganisms, 2022, 10, 65.	3.6	9
7442	Human-provisioned foods reduce gut microbiome diversity in American black bears (<i>Ursus) Tj ETQq1 1 0.7843</i>	14.rgBT /C	Overlock 10 T

#	Article	IF	Citations
7443	Sputum microbiota profiles of treatment-na \tilde{A} -ve TB patients in Uganda before and during first-line therapy. Scientific Reports, 2021, 11, 24486.	3.3	5
7444	Characterization of the Gut Microbiota in Individuals with Overweight or Obesity during a Real-World Weight Loss Dietary Program: A Focus on the Bacteroides 2 Enterotype. Biomedicines, 2022, 10, 16.	3.2	8
7445	The Relationship between Gut Microbiome and Cognition in Older Australians. Nutrients, 2022, 14, 64.	4.1	8
7446	Effects of Dietary Supplementation with Mushroom or Vitamin D2-Enriched Mushroom Powders on Gastrointestinal Health Parameters in the Weaned Pig. Animals, 2021, 11, 3603.	2.3	9
7447	Gut microbiota features associated with Clostridioides difficileÂcolonization in dairy calves. PLoS ONE, 2021, 16, e0251999.	2.5	7
7448	An Interplay between Viruses and Bacteria Associated with the White Sea Sponges Revealed by Metagenomics. Life, 2022, 12, 25.	2.4	3
7449	Microbiota-dependent increase in \hat{l} -valerobetaine alters neuronal function and is responsible for age-related cognitive decline. Nature Aging, 2021, 1, 1127-1136.	11.6	20
7452	Analysis of Biodeteriogens on Architectural Heritage. An Approach of Applied Botany on a Gothic Building in Southern Italy. Sustainability, 2022, 14, 34.	3.2	5
7453	<i>Enterococcus</i> Intestinal Domination Is Associated With Increased Mortality in the Acute Leukemia Chemotherapy Population. Clinical Infectious Diseases, 2024, 78, 414-422.	5.8	8
7454	Cold Acclimation in Brachypodium Is Accompanied by Changes in Above-Ground Bacterial and Fungal Communities. Plants, 2021, 10, 2824.	3.5	7
7456	Secreted osteopontin from CD4+ TÂcells limits acute graft-versus-host disease. Cell Reports, 2021, 37, 110170.	6.4	7
7457	Soil Fungal Diversity of the Aguarongo Andean Forest (Ecuador). Biology, 2021, 10, 1289.	2.8	6
7458	Comparison of the airway microbiota in children with chronic suppurative lung disease. BMJ Open Respiratory Research, 2021, 8, e001106.	3.0	3
7459	Streptozotocin-induced hyperglycemia alters the cecal metabolome and exacerbates antibiotic-induced dysbiosis. Cell Reports, 2021, 37, 110113.	6.4	11
7460	Plant diets of land snail community members are similar in composition but differ in richness. Journal of Molluscan Studies, 2021, 87, .	1,2	0
7461	Amsterdam urban canals contain novel niches for methaneâ€cycling microorganisms. Environmental Microbiology, 2022, 24, 82-97.	3.8	8
7462	Ileal microbial shifts after Roux-en-Y gastric bypass orchestrate changes in glucose metabolism through modulation of bile acids and L-cell adaptation. Scientific Reports, 2021, 11, 23813.	3.3	10
7464	Assembly and potential transmission of the <i>Lens culinaris</i> seed microbiome. FEMS Microbiology Ecology, 2022, 97, .	2.7	6

#	Article	IF	CITATIONS
7465	Archaeal and Bacterial Diversity and Distribution Patterns in Mediterranean-Climate Vernal Pools of Mexico and the Western USA. Microbial Ecology, 2023, 85, 24-36.	2.8	4
7467	Population study of the gut microbiome: associations with diet, lifestyle, and cardiometabolic disease. Genome Medicine, 2021, 13, 188.	8.2	27
7468	Resilience of cold-water coral holobionts to thermal stress. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20212117.	2.6	9
7470	You are more than what you eat: potentially adaptive enrichment of microbiome functions across bat dietary niches. Animal Microbiome, 2021, 3, 82.	3.8	15
7471	EcoPLOT: dynamic analysis of biogeochemical data. Bioinformatics, 2022, 38, 1480-1482.	4.1	0
7472	Molecular phylogeny of heritable symbionts and microbiota diversity analysis in phlebotominae sand flies and Culex nigripalpus from Colombia. PLoS Neglected Tropical Diseases, 2021, 15, e0009942.	3.0	5
7473	The microbial gbu gene cluster links cardiovascular disease risk associated with red meat consumption to microbiota l-carnitine catabolism. Nature Microbiology, 2022, 7, 73-86.	13.3	36
7474	Mining wastes of the Russian North-West: microbiological prerequisites of reclamation. IOP Conference Series: Earth and Environmental Science, 2021, 938, 012015.	0.3	0
7475	Secondary metabolite biosynthetic diversity in Arctic Ocean metagenomes. Microbial Genomics, 2021, 7,	2.0	4
7477	Flooding and ecological restoration promote wetland microbial communities and soil functions on former cranberry farmland. PLoS ONE, 2021, 16, e0260933.	2.5	1
7478	Microbial Composition in Larval Water Enhances Aedes aegypti Development but Reduces Transmissibility of Zika Virus. MSphere, 2021, 6, e0068721.	2.9	5
7479	Performance of Conventional Urine Culture Compared to 16S rRNA Gene Amplicon Sequencing in Children with Suspected Urinary Tract Infection. Microbiology Spectrum, 2021, 9, e0186121.	3.0	10
7480	Impact of intensive lifestyle intervention on gut microbiota composition in type 2 diabetes: a <i>post-hoc</i> analysis of a randomized clinical trial. Gut Microbes, 2022, 14, 2005407.	9.8	10
7481	A Round Trip to the Desert: In situ Nanopore Sequencing Informs Targeted Bioprospecting. Frontiers in Microbiology, 2021, 12, 768240.	3.5	10
7482	Associations of physical activity with gut microbiota in pre-adolescent children. Physical Activity and Nutrition, 2021, 25, 24-37.	0.8	6
7483	Characterization of soils conducive and non-conducive to Prunus replant disease. PLoS ONE, 2021, 16, e0260394.	2.5	3
7485	The Association Between Breast Density and Gut Microbiota Composition at 2 Years Post-Menarche: A Cross-Sectional Study of Adolescents in Santiago, Chile. Frontiers in Cellular and Infection Microbiology, 2021, 11, 794610.	3.9	3
7486	Taxonomic structure of the southern chernozem under application of biological preparations and different farming systems. IOP Conference Series: Earth and Environmental Science, 2021, 937, 032011.	0.3	0

#	Article	IF	CITATIONS
7487	Mammalian gut metabolomes mirror microbiome composition and host phylogeny. ISME Journal, 2022, 16, 1262-1274.	9.8	12
7488	Effects of Malted Rice Amazake on Constipation Symptoms and Gut Microbiota in Children and Adults with Severe Motor and Intellectual Disabilities: A Pilot Study. Nutrients, 2021, 13, 4466.	4.1	7
7489	Lack of Effect of Gluten Challenge on Fecal Microbiome in Patients With Celiac Disease and Non-Celiac Gluten Sensitivity. Clinical and Translational Gastroenterology, 2021, 12, e00441.	2.5	4
7490	Aging-Associated Changes in the Adult Human Skin Microbiome and the Host Factors that Affect Skin Microbiome Composition. Journal of Investigative Dermatology, 2022, 142, 1934-1946.e21.	0.7	29
7492	Djulis Hull Improves Insulin Resistance and Modulates the Gut Microbiota in High-Fat Diet (HFD)-Induced Hyperglycaemia. Antioxidants, 2022, 11, 45.	5.1	8
7493	Long-Term Effects of a Web-Based Low-FODMAP Diet Versus Probiotic Treatment for Irritable Bowel Syndrome, Including Shotgun Analyses of Microbiota: Randomized, Double-Crossover Clinical Trial. Journal of Medical Internet Research, 2021, 23, e30291.	4.3	15
7494	The Bacterial Microbiome of the Tomato Fruit Is Highly Dependent on the Cultivation Approach and Correlates With Flavor Chemistry. Frontiers in Plant Science, 2021, 12, 775722.	3.6	5
7495	Above―and belowâ€ground biodiversity responses to the prolonged flood pulse in centralâ€western Amazonia, Brazil. Environmental DNA, 2022, 4, 533-548.	5. 8	1
7496	Impacts of Enriched Human Milk Cells on Fecal Metabolome and Gut Microbiome of Premature Infants with Stage I Necrotizing Enterocolitis: A Pilot Study. Molecular Nutrition and Food Research, 2022, 66, e2100342.	3.3	4
7498	Impact of wood species on microbial community composition, beer chemistry and sensory characteristics during barrelâ€ageing of beer. International Journal of Food Science and Technology, 2022, 57, 1122-1136.	2.7	6
7499	Understanding host-microbiota interactions in the commercial piglet around weaning. Scientific Reports, 2021, 11, 23488.	3.3	17
7500	Early life skin microbial trajectory as a function of vertical and environmental transmission in Bornean foam-nesting frogs. Animal Microbiome, 2021, 3, 83.	3.8	10
7501	Long-Term Effects of Amendment with Olive Mill Wastewater on Soil Chemical Properties, Microbial Community, and Olive Tree Vegetative and Productive Activities. Agronomy, 2021, 11, 2562.	3.0	6
7502	Effect of inactivated natureâ€derived microbial composition on mouse immune system. Immunity, Inflammation and Disease, 2022, 10, .	2.7	6
7503	Drought legacy in rhizosphere bacterial communities alters subsequent plant performance. Plant and Soil, 2022, 471, 443-461.	3.7	9
7505	Clinical health issues, reproductive hormones, and metabolic hormones associated with gut microbiome structure in African and Asian elephants. Animal Microbiome, 2021, 3, 85.	3.8	19
7506	Pelagic <scp>N₂</scp> fixation dominated by sediment diazotrophic communities in a shallow temperate estuary. Limnology and Oceanography, 2022, 67, 364-378.	3.1	9
7508	The Influence of Foureye Butterflyfish (Chaetodon capistratus) and Symbiodiniaceae on the Transmission of Stony Coral Tissue Loss Disease. Frontiers in Marine Science, 2022, 9, .	2.5	5

#	Article	IF	CITATIONS
7510	Marker Genes (16S and ITS) Protocol for Plant Microbiome Analyses. Bio-protocol, 2022, 12, .	0.4	0
7511	Lactoferrin modulates gut microbiota and Toll-like receptors (TLRs) in mice with dysbiosis induced by antibiotics. Food and Function, 2022, 13, 5854-5869.	4.6	14
7512	Rumen bacteria and feed efficiency of beef cattle fed diets with different protein content. Animal Production Science, 2022, , .	1.3	2
7513	Physical and Dietary Intervention with Opuntia ficus-indica (Nopal) in Women with Obesity Improves Health Condition through Gut Microbiota Adjustment. Nutrients, 2022, 14, 1008.	4.1	7
7514	Inhibitory Bacterial Diversity and Mucosome Function Differentiate Susceptibility of Appalachian Salamanders to Chytrid Fungal Infection. Applied and Environmental Microbiology, 2022, 88, e0181821.	3.1	19
7515	Fecal DNA Virome Is Associated with the Development of Colorectal Neoplasia in a Murine Model of Colorectal Cancer. Pathogens, 2022, 11, 457.	2.8	7
7516	Phylogenetic relatedness of food plants reveals highest insect herbivore specialization at intermediate temperatures along a broad climatic gradient. Global Change Biology, 2022, 28, 4027-4040.	9 . 5	5
7517	Flavin-Containing Monooxygenase 3 (FMO3) Is Critical for Dioxin-Induced Reorganization of the Gut Microbiome and Host Insulin Sensitivity. Metabolites, 2022, 12, 364.	2.9	6
7518	The Impact of Local Estrogen on the Urogenital Microbiome in Genitourinary Syndrome of Menopause: A Randomized-Controlled Trial. Female Pelvic Medicine and Reconstructive Surgery, 2022, 28, e157-e162.	1.1	8
7519	Contrasting controls on seasonal and spatial distribution of marine cable bacteria (<i>Candidatus) Tj ETQq1 1 0 Oceanography, 2022, 67, 1357-1373.</i>	.784314 rg 3.1	gBT /Overlock 9
7520	Evaluation of Host Depletion and Extraction Methods for Shotgun Metagenomic Analysis of Bovine Vaginal Samples. Microbiology Spectrum, 2022, 10, e0041221.	3.0	2
7521	Best practices in metabarcoding of fungi: From experimental design to results. Molecular Ecology, 2022, 31, 2769-2795.	3.9	87
7522	The validation of the existence of the entero-mammary pathway and the assessment of the differences of the pathway between first and third parity sows. Translational Animal Science, 2022, 6, .	1.1	4
7523	Enhancing Metabolic Efficiency through Optimizing Metabolizable Protein Profile in a Time Progressive Manner with Weaned Goats as a Model: Involvement of Gut Microbiota. Microbiology Spectrum, 2022, 10, e0254521.	3.0	5
7524	Marginal lands and fungi – linking the type of soil contamination with fungal community composition. Environmental Microbiology, 2022, 24, 3809-3825.	3.8	2
7526	The Chronic Wound Phageome: Phage Diversity and Associations with Wounds and Healing Outcomes. Microbiology Spectrum, 2022, 10, e0277721.	3.0	14
7528	Lichen holobionts show compositional structure along elevation. Molecular Ecology, 2023, 32, 6619-6630.	3.9	12
7529	Dynamics of the infant gut microbiota in the first 18 months of life: the impact of maternal HIV infection and breastfeeding. Microbiome, 2022, 10, 61.	11.1	11

#	Article	IF	Citations
7530	Differential Modulation of the European Sea Bass Gut Microbiota by Distinct Insect Meals. Frontiers in Microbiology, 2022, 13, 831034.	3.5	17
7531	The Effects of High Fiber Rye, Compared to Refined Wheat, on Gut Microbiota Composition, Plasma Short Chain Fatty Acids, and Implications for Weight Loss and Metabolic Risk Factors (the RyeWeight) Tj ETQq1 1	97 84314	⊦ в g BT /Ον <mark>er</mark>
7532	Keystone taxa and functional analysis in arsenic and antimony co-contaminated rice terraces. Environmental Science and Pollution Research, 2022, 29, 61236-61246.	5. 3	3
7534	Metformin-induced reductions in tumor growth involves modulation of the gut microbiome. Molecular Metabolism, 2022, 61, 101498.	6.5	21
7535	Metabarcoding the Antarctic Peninsula biodiversity using a multi-gene approach. ISME Communications, 2022, 2, .	4.2	8
7536	Bacterial colonisation of plastic in the Rockall Trough, North-East Atlantic: An improved understanding of the deep-sea plastisphere. Environmental Pollution, 2022, 305, 119314.	7.5	8
7537	Community Assembly and Stability in the Root Microbiota During Early Plant Development. Frontiers in Microbiology, 2022, $13,826521$.	3.5	7
7538	DNA sequence and taxonomic gap analyses to quantify the coverage of aquatic cyanobacteria and eukaryotic microalgae in reference databases: Results of a survey in the Alpine region. Science of the Total Environment, 2022, 834, 155175.	8.0	18
7539	High-Resolution Screening for Marine Prokaryotes and Eukaryotes With Selective Preference for Polyethylene and Polyethylene Terephthalate Surfaces. Frontiers in Microbiology, 2022, 13, 845144.	3.5	6
7540	Nitrogen services provided by interseeded cover crops in organic corn systems. Agronomy Journal, 2022, 114, 2458-2472.	1.8	3
7541	An engineered live biotherapeutic for the prevention of antibiotic-induced dysbiosis. Nature Biomedical Engineering, 2022, 6, 910-921.	22.5	36
7542	Effects of a Low-Carbohydrate, High-Protein Diet on Gut Microbiome Composition in Insulin-Resistant Individuals With Chronic Spinal Cord Injury: Preliminary Results From a Randomized Controlled Trial. Archives of Physical Medicine and Rehabilitation, 2022, 103, 1269-1278.	0.9	6
7543	Impact of HLA-B27 and Disease Status on the Gut Microbiome of the Offspring of Ankylosing Spondylitis Patients. Children, 2022, 9, 569.	1.5	8
7544	The travelling particles: community dynamics of biofilms on microplastics transferred along a salinity gradient. ISME Communications, 2022, 2, .	4.2	15
7545	Skin microbiome alters attractiveness to Anopheles mosquitoes. BMC Microbiology, 2022, 22, 98.	3.3	9
7546	Oral Immune Priming Treatment Alters Microbiome Composition in the Red Flour Beetle Tribolium castaneum. Frontiers in Microbiology, 2022, 13, 793143.	3.5	5
7547	Dried Plum's Polyphenolic Compounds and Carbohydrates Contribute to Its Osteoprotective Effects and Exhibit Prebiotic Activity in Estrogen Deficient C57BL/6 Mice. Nutrients, 2022, 14, 1685.	4.1	2
7548	Farm-scale differentiation of active microbial colonizers. ISME Communications, 2022, 2, .	4.2	1

#	ARTICLE	IF	CITATIONS
7549	Comparative Analysis of the Rhizospheric Bacterial Communities of Flue-Cured Tobacco Affected by Granville Wilt. PhytoFrontiers, 0 , , .	1.6	0
7550	Murine Gut Microbiome Meta-analysis Reveals Alterations in Carbohydrate Metabolism in Response to Aging. MSystems, 2022, 7, e0124821.	3.8	5
7551	Symbiont Community Composition in <i>Rimicaris kairei</i> Shrimps from Indian Ocean Vents with Notes on Mineralogy. Applied and Environmental Microbiology, 2022, 88, e0018522.	3.1	5
7552	INFLUENCE OF FLG LOSS-OF-FUNCTION MUTATIONS IN HOST–MICROBE INTERACTIONS DURING ATOPIC SKIN INFLAMMATION. Journal of Dermatological Science, 2022, , .	1.9	O
7554	Delineating the Drivers and Functionality of Methanogenic Niches within an Arid Landfill. Applied and Environmental Microbiology, 2022, 88, e0243821.	3.1	3
7555	Molecular signature of postmortem lung tissue from COVID-19 patients suggests distinct trajectories driving mortality. DMM Disease Models and Mechanisms, 2022, 15, .	2.4	14
7556	Menopause Is Associated with an Altered Gut Microbiome and Estrobolome, with Implications for Adverse Cardiometabolic Risk in the Hispanic Community Health Study/Study of Latinos. MSystems, 2022, 7, .	3.8	16
7557	Dominance of coniferous and broadleaved trees drives bacterial associations with boreal feather mosses. Environmental Microbiology, 2022, 24, 3517-3528.	3.8	7
7558	Bacterial Dynamics and Their Influence on the Biogeochemical Cycles in a Subtropical Hypereutrophic Lake During the Rainy Season. Frontiers in Microbiology, 2022, 13, 832477.	3.5	7
7559	Complex impacts of hydraulic fracturing return fluids on soil microbial community respiration, structure and functional potentials. Environmental Microbiology, 2022, 24, 4108-4123.	3.8	2
7560	Novel symbionts and potential human pathogens excavated from argasid tick microbiomes that are shaped by dual or single symbiosis. Computational and Structural Biotechnology Journal, 2022, 20, 1979-1992.	4.1	4
7562	Drinking water chlorination has minor effects on the intestinal flora and resistomes of Bangladeshi children. Nature Microbiology, 2022, 7, 620-629.	13.3	9
7565	Diversity and structure of sparids external microbiota (Teleostei) and its link with monogenean ectoparasites. Animal Microbiome, 2022, 4, 27.	3.8	6
7566	A Study in Blue: Secondary Copperâ€Rich Minerals and Their Associated Bacterial Diversity in Icelandic Lava Tubes. Earth and Space Science, 2022, 9, .	2.6	2
7567	Megathyrsus maximus and Brachiaria decumbens improve soil characteristics and select promising rhizobacteria during rhizoremediation of petroleum hydrocarbons. Rhizosphere, 2022, 22, 100517.	3.0	5
7568	Choice of 16S Ribosomal RNA Primers Impacts Male Urinary Microbiota Profiling. Frontiers in Cellular and Infection Microbiology, 2022, 12, 862338.	3.9	11
7569	Organic management enhances soil quality and drives microbial community diversity in cocoa production systems. Science of the Total Environment, 2022, 834, 155223.	8.0	17
7570	Catestatin selects for colonization of antimicrobial-resistant gut bacterial communities. ISME Journal, 2022, 16, 1873-1882.	9.8	3

#	Article	IF	Citations
7571	Distinct Cecal and Fecal Microbiome Responses to Stress Are Accompanied by Sex- and Diet-Dependent Changes in Behavior and Gut Serotonin. Frontiers in Neuroscience, 2022, 16, 827343.	2.8	7
7572	Clinical significance and intestinal microbiota composition in immunocompromised children with norovirus gastroenteritis. PLoS ONE, 2022, 17, e0266876.	2.5	2
7573	Anti-allergic effects of two potential probiotic strains isolated from infant feces in China. Journal of Functional Foods, 2022, 92, 105070.	3.4	6
7574	Fungal endophyte effects on invasive Phragmites australis performance in field and growth chamber environments. Fungal Ecology, 2022, 57-58, 101153.	1.6	1
7575	Contrasting community responses of root and soil dwelling fungi to extreme drought in a temperate grassland. Soil Biology and Biochemistry, 2022, 169, 108670.	8.8	11
7576	Condensed tannins protect against aflatoxin B1-induced toxicity in Lateolabrax maculatus by restoring intestinal integrity and regulating bacterial microbiota. Aquaculture, 2022, 555, 738255.	3.5	5
7577	Comparative analysis of diversity and environmental niches of soil bacterial, archaeal, fungal and protist communities reveal niche divergences along environmental gradients in the Alps. Soil Biology and Biochemistry, 2022, 169, 108674.	8.8	17
7578	Recycled concrete aggregates are an economic form of urban riparian erosion management with limited impacts on freshwater chemistry and microbial diversity. Journal of Hazardous Materials, 2022, 434, 128934.	12.4	2
7579	Ammonia volatilization and Sporosarcina genus abundance in an Oxisol enriched with urea, compost and biochar. Applied Soil Ecology, 2022, 176, 104494.	4.3	5
8941	Effect of Chronic Exposure to Sublethal Doses of Imidacloprid and Nosema ceranae on Immunity, Gut Microbiota, and Survival of Africanized Honey Bees. Microbial Ecology, 2023, 85, 1485-1497.	2.8	6
8942	The gut fungal and bacterial microbiota in pediatric patients with inflammatory bowel disease introduced to treatment with anti-tumor necrosis factor-α. Scientific Reports, 2022, 12, 6654.	3.3	5
8943	Characterisation of the symbionts in the Mediterranean fruit fly gut. Microbial Genomics, 2022, 8, .	2.0	3
8944	Microbial community origin and fate through a rural wastewater treatment plant. Environmental Microbiology, 2022, 24, 2516-2542.	3.8	4
8945	Asymmetric belowground carbon transfer in a diverse tree community. Molecular Ecology, 2022, 31, 3481-3495.	3.9	9
8946	The Australian dingo is an early offshoot of modern breed dogs. Science Advances, 2022, 8, eabm5944.	10.3	14
8947	Can the Salivary Microbiome Predict Cardiovascular Diseases? Lessons Learned From the Qatari Population. Frontiers in Microbiology, 2021, 12, 772736.	3.5	5
8948	Decreased diversity of salivary microbiome in patients with stable decompensated cirrhosis Hippokratia, 2020, 24, 157-165.	0.3	0
8950	Stabilization of swine faecal samples influences taxonomic and functional results in microbiome analyses. MethodsX, 2022, 9, 101716.	1.6	0

#	Article	IF	CITATIONS
8951	Bacterial Assemblage in Mediterranean Salt Marshes: Disentangling the Relative Importance of Seasonality, Zonation and Halophytes. SSRN Electronic Journal, 0, , .	0.4	0
8952	<i>Eucommiae cortex</i> polysaccharides mitigate obesogenic diet-induced cognitive and social dysfunction via modulation of gut microbiota and tryptophan metabolism. Theranostics, 2022, 12, 3637-3655.	10.0	25
8953	Effect of sodium silicate on drinking water biofilm development. Environmental Science: Water Research and Technology, 2022, 8, 1300-1311.	2.4	2
8954	Exploration of Mycobiota in <i>Cypripedium japonicum</i> , an Endangered Species. Mycobiology, 2022, 50, 142-149.	1.7	O
8956	Gut Microbiome Characteristics in Mothers and Infants According to the Presence of Atopic Dermatitis. BioMed Research International, 2022, 2022, 1-12.	1.9	5
8957	Longitudinal and Comparative Analysis of Gut Microbiota of Tunisian Newborns According to Delivery Mode. Frontiers in Microbiology, 2022, 13, 780568.	3.5	4
8958	Diversity of Microfungi in a High Radon Cave Ecosystem. Frontiers in Microbiology, 2022, 13, 869661.	3.5	9
8959	Probiotic Mixture Containing Lactobacillus helveticus, Bifidobacterium longum and Lactiplantibacillus plantarum Affects Brain Responses Toward an Emotional Task in Healthy Subjects: A Randomized Clinical Trial. Frontiers in Nutrition, 2022, 9, 827182.	3.7	9
8960	Metagenomic Analysis of the Gastrointestinal Microbiota of Gadus morhua callarias L. Originating from a Chemical Munition Dump Site. Toxics, 2022, 10, 206.	3.7	3
8961	Suppressive Effect of Soil Microbiomes Associated with Tropical Fruit Trees on Meloidogyne enterolobii. Microorganisms, 2022, 10, 894.	3.6	2
8962	Insights into the microbiome assembly during different growth stages and storage of strawberry plants. Environmental Microbiomes, 2022, 17, 21.	5.0	18
8963	Host-Associated Bacterial Communities Vary Between Daphnia galeata Genotypes but Not by Host Genetic Distance. Microbial Ecology, 2023, 85, 1578-1589.	2.8	6
8964	Influence of Aging, Macronutrient Composition and Time-Restricted Feeding on the Fischer 344 x Brown Norway Rat Gut Microbiota. Nutrients, 2022, 14, 1758.	4.1	8
8965	Changes to the gut microbiota of a wild juvenile passerine in a multidimensional urban mosaic. Scientific Reports, 2022, 12, 6872.	3.3	9
8967	Recent Differentiation of Aquatic Bacterial Communities in a Hydrological System in the Cuatro Ciénegas Basin, After a Natural Perturbation. Frontiers in Microbiology, 2022, 13, 825167.	3.5	4
8968	Synchronous Seasonality in the Gut Microbiota of Wild Mouse Populations. Frontiers in Microbiology, 2022, 13, 809735.	3.5	14
8969	Soil fungal communities in young Norway spruce-dominant stands: footprints of former land use and selective thinning. European Journal of Forest Research, 2022, 141, 503-516.	2.5	8
8970	The car tank lid bacteriome: a reservoir of bacteria with potential in bioremediation of fuel. Npj Biofilms and Microbiomes, 2022, 8, 32.	6.4	6

#	Article	IF	CITATIONS
8971	Soil <scp>DNA</scp> chronosequence analysis shows bacterial community reâ€assembly following postâ€mining forest rehabilitation. Restoration Ecology, 2023, 31, .	2.9	3
8972	Optimisation and Application of a Novel Method to Identify Bacteriophages in Maternal Milk and Infant Stool Identifies Host-Phage Communities Within Preterm Infant Gut. Frontiers in Pediatrics, 2022, 10, 856520.	1.9	2
8973	Health Status of Mytilus chilensis from Intensive Culture Areas in Chile Assessed by Molecular, Microbiological, and Histological Analyses. Pathogens, 2022, 11, 494.	2.8	0
8974	Characterization of the Upper Respiratory Bacterial Microbiome in Critically III COVID-19 Patients. Biomedicines, 2022, 10, 982.	3.2	8
8975	Short- term effect of probiotic <i>Lactobacillus reuteri</i> profile of subjects undergoing orthodontic treatment with fixed appliances. Journal of Oral Microbiology, 2022, 14, 2067103.	2.7	3
8976	Effect of Two Soybean Varieties Treated with Different Heat Intensities on Ileal and Caecal Microbiota in Broiler Chickens. Animals, 2022, 12, 1109.	2.3	2
8977	Differences in the Composition of the Rumen Microbiota of Finishing Beef Cattle Divergently Ranked for Residual Methane Emissions. Frontiers in Microbiology, 2022, 13, 855565.	3.5	8
8978	Monitoring Bacterial Community Dynamics in a Drinking Water Treatment Plant: An Integrative Approach Using Metabarcoding and Microbial Indicators in Large Water Volumes. Water (Switzerland), 2022, 14, 1435.	2.7	6
8979	Identification of vaginal microbiome associated with IVF pregnancy. Scientific Reports, 2022, 12, 6807.	3.3	4
8980	Patients with Primary and Secondary Bile Duct Stones Harbor Distinct Biliary Microbial Composition and Metabolic Potential. Frontiers in Cellular and Infection Microbiology, 2022, 12, 881489.	3.9	7
8981	Faecal Microbiota Divergence in Allopatric Populations of Podarcis lilfordi and P. pityusensis, Two Lizard Species Endemic to the Balearic Islands. Microbial Ecology, 2023, 85, 1564-1577.	2.8	9
8982	Not All Liver Abscesses Are Created Equal: The Impact of Tylosin and Antibiotic Alternatives on Bovine Liver Abscess Microbial Communities and a First Look at Bacteroidetes-Dominated Communities. Frontiers in Microbiology, 2022, 13, 882419.	3.5	13
8983	Fluid flow stimulates chemoautotrophy in hydrothermally influenced coastal sediments. Communications Earth & Environment, 2022, 3, .	6.8	2
8984	Dietary carbohydrate-to-protein ratio influences growth performance, hepatic health and dynamic of gut microbiota in atlantic salmon (Salmo salar). Animal Nutrition, 2022, 10, 261-279.	5.1	19
8985	Bladder Microbiota Are Associated with Clinical Conditions That Extend beyond the Urinary Tract. Microorganisms, 2022, 10, 874.	3.6	3
8986	The Chemo-Gut Pilot Study: Associations between Gut Microbiota, Gastrointestinal Symptoms, and Psychosocial Health Outcomes in a Cross-Sectional Sample of Young Adult Cancer Survivors. Current Oncology, 2022, 29, 2973-2994.	2.2	11
8987	Fecal microbiota transfer between young and aged mice reverses hallmarks of the aging gut, eye, and brain. Microbiome, 2022, 10, 68.	11.1	107
8988	Streptozotocin-Induced Hyperglycemia Is Associated with Unique Microbiome Metabolomic Signatures in Response to Ciprofloxacin Treatment. Antibiotics, 2022, 11, 585.	3.7	O

#	Article	IF	CITATIONS
8989	Litter Management Strategies and Their Impact on the Environmental and Respiratory Microbiome Might Influence Health in Poultry. Microorganisms, 2022, 10, 878.	3.6	1
8992	Altered Salivary Microbiota Following Bifidobacterium animalis Subsp. Lactis BL-11 Supplementation Are Associated with Anthropometric Growth and Social Behavior Severity in Individuals with Prader-Willi Syndrome. Probiotics and Antimicrobial Proteins, 2022, , 1.	3.9	0
8993	Biochar accelerates soil organic carbon mineralization via rhizodeposit-activated Actinobacteria. Biology and Fertility of Soils, 2022, 58, 565-577.	4.3	22
8994	The Biodiversity of Grapevine Bacterial Endophytes of Vitis amurensis Rupr Plants, 2022, 11, 1128.	3.5	7
8995	Type VI secretion systems of pathogenic and commensal bacteria mediate niche occupancy in the gut. Cell Reports, 2022, 39, 110731.	6.4	24
8998	Gut Microbial Composition of Pacific Salmonids Differs across Oregon River Basins and Hatchery Ancestry. Microorganisms, 2022, 10, 933.	3.6	2
8999	Biomonitoring via DNA metabarcoding and light microscopy of bee pollen in rainforest transformation landscapes of Sumatra. Bmc Ecology and Evolution, 2022, 22, 51.	1.6	6
9000	Brassica napus Bacterial Assembly Processes Vary with Plant Compartment and Growth Stage but Not between Lines. Applied and Environmental Microbiology, 2022, 88, e0027322.	3.1	10
9002	Gut microbiota alterations in critically ill older patients: a multicenter study. BMC Geriatrics, 2022, 22, 373.	2.7	12
9003	Long-Term Heat Selection of the Coral Endosymbiont Cladocopium C1acro (Symbiodiniaceae) Stabilizes Associated Bacterial Communities. International Journal of Molecular Sciences, 2022, 23, 4913.	4.1	15
9004	Sputum Metabolites Associated with Nontuberculous Mycobacterial Infection in Cystic Fibrosis. MSphere, 2022, 7, e0010422.	2.9	2
9005	Deploying an <i>In Vitro </i> Gut Model to Assay the Impact of the Mannan-Oligosaccharide Prebiotic Bio-Mos on the Atlantic Salmon (<i>Salmo salar </i>) Gut Microbiome. Microbiology Spectrum, 2022, 10, e0195321.	3.0	3
9006	Direct and indirect effects of fire on microbial communities in a pyrodiverse dryâ€sclerophyll forest. Journal of Ecology, 2022, 110, 1687-1703.	4.0	9
9007	Multiple Groups of Methanotrophic Bacteria Mediate Methane Oxidation in Anoxic Lake Sediments. Frontiers in Microbiology, 2022, 13, .	3.5	4
9008	Sugars dominate the seagrass rhizosphere. Nature Ecology and Evolution, 2022, 6, 866-877.	7.8	27
9009	Short Chain Fatty Acids and Bacterial Taxa Associated with Reduced Salmonella enterica serovar I 4,[5],12:i:- Shedding in Swine Fed a Diet Supplemented with Resistant Potato Starch. Microbiology Spectrum, 2022, 10, e0220221.	3.0	10
9010	The Active Microbiota of the Eggs and the Nauplii of the Pacific Blue Shrimp Litopenaeus stylirostris Partially Shaped by a Potential Vertical Transmission. Frontiers in Microbiology, 2022, 13, .	3 . 5	7
9011	Do amino and fatty acid profiles of pollen provisions correlate with bacterial microbiomes in the mason bee <i>Osmia bicornis</i> Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20210171.	4.0	14

#	ARTICLE	IF	CITATIONS
9012	Microbiome "Inception†an Intestinal Cestode Shapes a Hierarchy of Microbial Communities Nested within the Host. MBio, 2022, 13, e0067922.	4.1	8
9013	DNA metabarcoding quantifies the relative biomass of arthropod taxa in songbird diets: Validation with cameraâ€recorded diets. Ecology and Evolution, 2022, 12, e8881.	1.9	19
9014	Unique Geothermal Chemistry Shapes Microbial Communities on Mt. Erebus, Antarctica. Frontiers in Microbiology, 2022, 13, 836943.	3 . 5	3
9015	Unsalable Vegetables Ensiled With Sorghum Promote Heterofermentative Lactic Acid Bacteria and Improve in vitro Rumen Fermentation. Frontiers in Microbiology, 2022, 13, .	3 . 5	2
9017	Agricultural Management Drive Bacterial Community Assembly in Different Compartments of Soybean Soil-Plant Continuum. Frontiers in Microbiology, 2022, 13, .	3 . 5	3
9018	Transitions of foliar mycobiota community and transcriptome in response to pathogenic conifer needle interactions. Scientific Reports, 2022, 12, 7832.	3.3	3
9019	Mating Leads to a Decline in the Diversity of Symbiotic Microbiomes and Promiscuity Increased Pathogen Abundance in a Moth. Frontiers in Microbiology, 2022, 13, .	3.5	5
9020	Assessing the long-term impact of urease and nitrification inhibitor use on microbial community composition, diversity and function in grassland soil. Soil Biology and Biochemistry, 2022, 170, 108709.	8.8	17
9021	Effect of commercial slow-release urea product on in vitro rumen fermentation and ruminal microbial community using RUSITEC technique. Journal of Animal Science and Biotechnology, 2022, 13, 56.	5.3	9
9022	Associations between microbial communities and key chemical constituents in U.S. domestic moist snuff. PLoS ONE, 2022, 17, e0267104.	2.5	2
9024	Supplementation with a probiotic mixture accelerates gut microbiome maturation and reduces intestinal inflammation in extremely preterm infants. Cell Host and Microbe, 2022, 30, 696-711.e5.	11.0	63
9025	The influence of maternal unhealthy diet on maturation of offspring gut microbiota in rat. Animal Microbiome, 2022, 4, 31.	3.8	4
9026	Uncovering the genetic diversity of Giardia intestinalis in isolates from outbreaks in New Zealand. Infectious Diseases of Poverty, 2022, 11, 49.	3.7	4
9027	<scp>eDNA</scp> metabarcoding of log hollow sediments and soils highlights the importance of substrate type, frequency of sampling and animal size, for vertebrate species detection. Environmental DNA, 2022, 4, 940-953.	5.8	15
9028	Potential effect of two <i>Bacillus</i> probiotic strains on performance and fecal microbiota of breeding sows and their piglets. Journal of Animal Science, 2022, 100, .	0.5	6
9029	Rumen sampling methods bias bacterial communities observed. PLoS ONE, 2022, 17, e0258176.	2.5	12
9030	The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. Science, 2022, 376, eabl4896.	12.6	289
9031	Unraveling global and diazotrophic bacteriomes of boreal forest floor feather mosses and their environmental drivers at the ecosystem and at the plant scale in North America. Science of the Total Environment, 2022, 837, 155761.	8.0	11

#	ARTICLE	IF	CITATIONS
9032	Heterogeneity in statin responses explained by variation in the human gut microbiome. Med, 2022, 3, 388-405.e6.	4.4	21
9033	Metatranscriptomic profiling reveals diverse tickâ€borne bacteria, protozoans and viruses in ticks and wildlife from Australia. Transboundary and Emerging Diseases, 2022, 69, .	3.0	9
9035	An extensive description of the microbiological effects of silver diamine fluoride on dental biofilms using an oral in situ model. Scientific Reports, 2022, 12, 7435.	3.3	3
9036	Lignocellulose Fermentation Products Generated by Giant Panda Gut Microbiomes Depend Ultimately on pH Rather than Portion of Bamboo: A Preliminary Study. Microorganisms, 2022, 10, 978.	3.6	0
9038	Preferential associations of soil fungal taxa under mixed compositions of eastern American tree species. FEMS Microbiology Ecology, 2022, 98, .	2.7	0
9039	Holistic Impact Evaluation of Human Activities on the Coastal Fish Biodiversity in the Chinese Coastal Environment. Environmental Science & Environment. Environmental Science & Environmental Science	10.0	8
9040	Gut microbial similarity in twins is driven by shared environment and aging. EBioMedicine, 2022, 79, 104011.	6.1	7
9041	The effects of fish meal substitution by clam meal on the growth and health of Florida pompano (Trachinotus carolinus). Scientific Reports, 2022, 12, 7696.	3.3	3
9042	Long-term antibiotic exposure promotes mortality after systemic fungal infection by driving lymphocyte dysfunction and systemic escape of commensal bacteria. Cell Host and Microbe, 2022, 30, 1020-1033.e6.	11.0	37
9043	Biodiversity screening of gut microbiome during the allogeneic hematopoietic stem cell transplantation: data from the real-life clinical practice. International Journal of Transgender Health, 2022, 15, 547-554.	2.3	1
9044	Black Soldier Fly Larvae Influence Internal and Substrate Bacterial Community Composition Depending on Substrate Type and Larval Density. Applied and Environmental Microbiology, 2022, 88, e0008422.	3.1	10
9045	DivCom: A Tool for Systematic Partition of Groups of Microbial Profiles Into Intrinsic Subclusters and Distance-Based Subgroup Comparisons. Frontiers in Bioinformatics, 2022, 2, .	2.1	2
9046	A randomization-based causal inference framework for uncovering environmental exposure effects on human gut microbiota. PLoS Computational Biology, 2022, 18, e1010044.	3.2	8
9047	A 4-Week Diet Low or High in Advanced Glycation Endproducts Has Limited Impact on Gut Microbial Composition in Abdominally Obese Individuals: The deAGEing Trial. International Journal of Molecular Sciences, 2022, 23, 5328.	4.1	13
9048	Dancing with Douglasâ€fir: Determinism dominates fungal community assembly processes. Journal of Ecology, 2022, 110, 1857-1870.	4.0	6
9050	Composition, Structure and Diversity of Soil Bacterial Communities before, during and after Transit through the Gut of the Earthworm Aporrectodea caliginosa. Microorganisms, 2022, 10, 1025.	3.6	12
9051	Oral dysbiosis and its linkage with SARS-CoV-2 infection. Microbiological Research, 2022, 261, 127055.	5.3	21
9052	Dynamic change in an ocean desert: Microbial diversity and trophic transfer along the 110 °E meridional in the Indian Ocean. Deep-Sea Research Part II: Topical Studies in Oceanography, 2022, 201, 105097.	1.4	6

#	Article	IF	CITATIONS
9053	Elevational Gradients Impose Dispersal Limitation on Streptomyces. Frontiers in Microbiology, 2022, 13, 856263.	3.5	1
9054	Exploring the Causal Effect of Constipation on Parkinson's Disease Through Mediation Analysis of Microbial Data. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	3.9	10
9055	Ultraviolet light alters experimental aquarium water microbial communities. Zoo Biology, 2022, , .	1.2	0
9056	Evaluating Spatial and Temporal Dynamics of Riverâ€Floodplain Surface Water Connectivity Using Hydrometric, Geochemical and Microbial Indicators. Water Resources Research, 2022, 58, .	4.2	5
9057	Bacterial Colonisation: From Airborne Dispersal to Integration Within the Soil Community. Frontiers in Microbiology, 2022, 13, .	3.5	6
9058	The Microbial Community of the Respiratory Tract of Commercial Chickens and Turkeys. Microorganisms, 2022, 10, 987.	3.6	5
9059	Large-herbivore nemabiomes: patterns of parasite diversity and sharing. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212702.	2.6	6
9060	The gut microbiota prime systemic antiviral immunity via the cGAS-STING-IFN-I axis. Immunity, 2022, 55, 847-861.e10.	14.3	125
9061	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. Frontiers in Microbiology, 2022, 13, .	3.5	3
9062	DNA metabarcoding reveals high relative abundance of trunk disease fungi in grapevines from Marlborough, New Zealand. BMC Microbiology, 2022, 22, 126.	3.3	6
9063	Catching change in microbial diversity indicators under different soil organic matter managements: Higher taxonomic resolution, better discrimination?. Ecological Indicators, 2022, 139, 108897.	6.3	2
9064	Methotrexate promotes recovery of arthritis-induced alveolar bone loss and modifies the composition of the oral-gut microbiota. Anaerobe, 2022, 75, 102577.	2.1	6
9065	Uterine microbiota plasticity during the menstrual cycle: Differences between healthy controls and patients with recurrent miscarriage or implantation failure. Journal of Reproductive Immunology, 2022, 151, 103634.	1.9	14
9066	Crown closure affects endophytic leaf mycobiome compositional dynamics over time in Pseudotsuga menziesii var. menziesii. Fungal Ecology, 2022, 57-58, 101155.	1.6	O
9067	Microbial pioneers of plastic colonisation in coastal seawaters. Marine Pollution Bulletin, 2022, 179, 113701.	5.0	31
9068	Ex vivo folate production by fecal bacteria does not predict human blood folate status: Associations between dietary patterns, gut microbiota, and folate metabolism. Food Research International, 2022, 156, 111290.	6.2	11
9069	Variation in blood microbial lipopolysaccharide (LPS) contributes to immune reconstitution in response to suppressive antiretroviral therapy in HIV. EBioMedicine, 2022, 80, 104037.	6.1	13
9070	Revealing the microbial heritage of traditional Brazilian cheeses through metagenomics. Food Research International, 2022, 157, 111265.	6.2	12

#	Article	IF	CITATIONS
9071	Bait input altered microbial community structure and increased greenhouse gases production in coastal wetland sediment. Water Research, 2022, 218, 118520.	11.3	58
9072	Nitrous oxide emissions and microbial communities during the transition to conservation agriculture using N-enhanced efficiency fertilisers in a semiarid climate. Soil Biology and Biochemistry, 2022, 170, 108687.	8.8	7
9073	Neonatal immune challenge influences the microbiota and behaviour in a sexually dimorphic manner. Brain, Behavior, and Immunity, 2022, 103, 232-242.	4.1	5
9074	FoodMicrobionet v4: A large, integrated, open and transparent database for food bacterial communities. International Journal of Food Microbiology, 2022, 372, 109696.	4.7	7
9075	Eucalypt species drive rhizosphere bacterial and fungal community assembly but soil phosphorus availability rearranges the microbiome. Science of the Total Environment, 2022, 836, 155667.	8.0	7
9076	Bacterial biofilms on medical masks disposed in the marine environment: a hotspot of biological and functional diversity. Science of the Total Environment, 2022, 837, 155731.	8.0	19
9077	Influence of cyclonic and anticyclonic eddies on plankton in the southeastern Mediterranean Sea during late summertime. Ocean Science, 2022, 18, 693-715.	3.4	12
9078	Structural analysis of microbiomes from salt caverns used for underground gas storage. International Journal of Hydrogen Energy, 2022, 47, 20684-20694.	7.1	21
9079	Temporal changes in skin and gill microbiomes of Atlantic salmon in a recirculating aquaculture system – Why do they matter?. Aquaculture, 2022, 558, 738352.	3.5	10
9080	Adaptation of gut microbiome and host metabolic systems to lignocellulosic degradation in bamboo rats. ISME Journal, 2022, 16, 1980-1992.	9.8	14
9081	Effects of Harmful Algal Blooms on Fish and Shellfish Species: A Case Study of New Zealand in a Changing Environment. Toxins, 2022, 14, 341.	3.4	19
9082	Microbiome assembly predictably shapes diversity across a range of disturbance frequencies in experimental microcosms. Npj Biofilms and Microbiomes, 2022, 8, 41.	6.4	9
9083	Optimisation of a bead-beating procedure for simultaneous extraction of bacterial and fungal DNA from pig faeces and liquid feed for 16S and ITS2 rDNA amplicon sequencing., 2022, 1, 100012.		4
9084	Seasonal phytoplankton and geochemical shifts in the subsurface chlorophyll maximum layer of a dimictic ferruginous lake. MicrobiologyOpen, 2022, 11 , .	3.0	O
9085	Home is where the hollow is: Revealing vertebrate tree hollow user biodiversity with <scp>eDNA</scp> metabarcoding. Environmental DNA, 2022, 4, 1078-1091.	5.8	9
9086	Minimizing tillage modifies fungal denitrifier communities, increases denitrification rates and enhances the genetic potential for fungal, relative to bacterial, denitrification. Soil Biology and Biochemistry, 2022, 170, 108718.	8.8	6
9087	Spatiotemporal Heterogeneity and Intragenus Variability in Rhizobacterial Associations with <i>Brassica rapa</i>	3.8	3
9088	Seasonal variation of microbiota composition in <i>Anopheles gambiae</i> and <i>Anopheles coluzzii</i> in two different ecoâ€geographical localities in Cameroon. Medical and Veterinary Entomology, 2022, 36, 269-282.	1.5	14

#	ARTICLE	IF	CITATIONS
9089	Diets maintained in a changing world: Does landâ€use intensification alter wild bee communities by selecting for flexible generalists?. Ecology and Evolution, 2022, 12, .	1.9	15
9090	Tree Size Drives Diversity and Community Structure of Microbial Communities on the Bark of Beech (Fagus sylvatica). Frontiers in Forests and Global Change, 2022, 5, .	2.3	O
9091	Diversity of Microbial Eukaryotes Along the West Antarctic Peninsula in Austral Spring. Frontiers in Microbiology, 2022, 13, .	3.5	2
9092	Breaking Barriers with Bread: Using the Sourdough Starter Microbiome to Teach High-Throughput Sequencing Techniques. Journal of Microbiology and Biology Education, 2022, 23, .	1.0	2
9093	Gut Microbial Stability is Associated with Greater Endurance Performance in Athletes Undertaking Dietary Periodization. MSystems, 2022, 7, e0012922.	3.8	12
9094	Machine Learning Based Microbiome Signature to Predict Inflammatory Bowel Disease Subtypes. Frontiers in Microbiology, 2022, 13, .	3.5	7
9095	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, .	0.5	7
9096	Meter-scale variation within a single transect demands attention to taxon accumulation curves in riverine microbiome studies. Frontiers of Environmental Science and Engineering, 2022, 16, .	6.0	1
9097	Altered Vaginal Microbiota Composition Correlates With Human Papillomavirus and Mucosal Immune Responses in Women With Symptomatic Cervical Ectopy. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	3.9	10
9098	Intergenerational Transfer of Persistent Bacterial Communities in Female Nile Tilapia. Frontiers in Microbiology, 2022, 13, .	3.5	4
9099	Cultured and uncultured microbial community associated with biogas production in anaerobic digestion processes. Archives of Microbiology, 2022, 204, 340.	2.2	8
9100	Consistency and Variation in the Kelp Microbiota: Patterns of Bacterial Community Structure Across Spatial Scales. Microbial Ecology, 2023, 85, 1265-1275.	2.8	8
9101	Intestinal microbiota composition of children with infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and multisystem inflammatory syndrome (MIS-C). European Journal of Pediatrics, 2022, 181, 3175-3191.	2.7	20
9102	A high-fibre personalised dietary advice given via a web tool reduces constipation complaints in adults. Journal of Nutritional Science, 2022, 11, e31.	1.9	1
9103	Altered serum bile acid profile in fibromyalgia is associated with specific gut microbiome changes and symptom severity. Pain, 2023, 164, e66-e76.	4.2	9
9104	Variations of microbial communities and substrate regimes in the eastern Fram Strait between summer and fall. Environmental Microbiology, 2022, 24, 4124-4136.	3.8	9
9105	Rootstock–scion combination contributes to shape diversity and composition of microbial communities associated with grapevine root system. Environmental Microbiology, 2022, 24, 3791-3808.	3.8	12
9106	<i>Brassicaceae</i> host plants mask the feedback from the previous year's soil history on bacterial communities, except when they experience drought. Environmental Microbiology, 2022, 24, 3529-3548.	3.8	5

#	Article	IF	CITATIONS
9107	Contextâ€dependent role of abiotic and biotic factors structuring nematode communities along two environmental gradients. Molecular Ecology, 2022, 31, 3903-3916.	3.9	5
9108	Acquisition of a complex root microbiome reshapes the transcriptomes of rice plants. New Phytologist, 2022, 235, 2008-2021.	7.3	8
9109	Acacia Fiber Protects the Gut from Extended-Spectrum Beta-Lactamase (ESBL)-Producing Escherichia coli Colonization Enabled by Antibiotics. MSphere, 2022, 7, e0007122.	2.9	2
9110	Prophylactic Delivery of a Bacteriophage Cocktail in Feed Significantly Reduces Salmonella Colonization in Pigs. Microbiology Spectrum, 2022, 10, e0042222.	3.0	19
9111	Microbiomes of the Sydney Rock Oyster are acquired through both vertical and horizontal transmission. Animal Microbiome, 2022, 4, 32.	3.8	11
9112	Human Gut Microbiome Across Different Lifestyles: From Hunter-Gatherers to Urban Populations. Frontiers in Microbiology, 2022, 13, 843170.	3.5	19
9113	The effect of gestational weight gain on serum total oxidative stress, total antioxidant capacity and gut microbiota. Bioscience of Microbiota, Food and Health, 2022, 41, 160-167.	1.8	4
9114	Changes in the gut microbiome associated with liver stiffness improvement in nonalcoholic steatohepatitis. Therapeutic Advances in Gastroenterology, 2022, 15, 175628482210982.	3.2	2
9119	Oil Absorbent Polypropylene Particles Stimulate Biodegradation of Crude Oil by Microbial Consortia. Frontiers in Microbiology, 2022, 13, .	3.5	1
9120	MIntO: A Modular and Scalable Pipeline For Microbiome Metagenomic and Metatranscriptomic Data Integration. Frontiers in Bioinformatics, 2022, 2, .	2.1	5
9121	Dominance of Ciliophora and Chlorophyta Among Phyllosphere Protists of Solanaceous Plants. Phytobiomes Journal, 2023, 7, 270-280.	2.7	4
9122	The Vaginal Microbiome is Associated with Endometrial Cancer Grade and Histology. Cancer Research Communications, 2022, 2, 447-455.	1.7	8
9123	Gut Microbiota and Associated Mucosal Immune Response in Eosinophilic Granulomatosis with Polyangiitis (EGPA). Biomedicines, 2022, 10, 1227.	3.2	4
9124	A Nine-Strain Bacterial Consortium Improves Portal Hypertension and Insulin Signaling and Delays NAFLD Progression In Vivo. Biomedicines, 2022, 10, 1191.	3.2	2
9126	Microbiomes of microscopic marine invertebrates do not reveal signatures of phylosymbiosis. Nature Microbiology, 2022, 7, 810-819.	13.3	26
9127	Bacteroidetes and Firmicutes Drive Differing Microbial Diversity and Community Composition Among Micro-Environments in the Bovine Rumen. Frontiers in Veterinary Science, 2022, 9, .	2.2	12
9128	Microbial Community Analysis and Food Safety Practice Survey-Based Hazard Identification and Risk Assessment for Controlled Environment Hydroponic/Aquaponic Farming Systems. Frontiers in Microbiology, 2022, 13, .	3.5	4
9129	Time-course full profiling of circulating miRNAs in neurologically deceased organ donors: a proof of concept study to understand the onset of the cytokine storm. Epigenetics, 2022, 17, 1546-1561.	2.7	0

#	Article	IF	CITATIONS
9130	Differences in composition of interdigital skin microbiota predict sheep and feet that develop footrot. Scientific Reports, 2022, 12, .	3.3	5
9131	Shifts in gut microbiome across five decades of repeated guppy translocations in Trinidadian streams. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	2.6	4
9132	Effects of Gut Microbiota Alterations on Motor, Gastrointestinal, and Behavioral Phenotype in a Mouse Model of Parkinson's Disease. Journal of Parkinson's Disease, 2022, 12, 1479-1495.	2.8	2
9134	Thermal Stress Has Minimal Effects on Bacterial Communities of Thermotolerant Symbiodinium Cultures. Frontiers in Ecology and Evolution, 2022, 10, .	2.2	5
9135	A 16S rRNA Gene-Based Metabarcoding of Phosphate-Rich Deposits in Muierilor Cave, South-Western Carpathians. Frontiers in Microbiology, 2022, 13, .	3.5	1
9136	Changes in the Bacterial Community Associated With Experimental Symbiont Loss in the Mucus Layer of Cassiopea xamachana Jellyfish. Frontiers in Marine Science, 2022, 9, .	2.5	1
9137	Application of Dual Metabarcoding Platforms for the Meso- and Macrozooplankton Taxa in the Ross Sea. Genes, 2022, 13, 922.	2.4	1
9138	Metagenomic nextâ f generation sequencing (mNGS) data reveals the phyllosphere microbiome of wheat plants infected by the fungal pathogen Zymoseptoria tritici. Phytobiomes Journal, 0, , .	2.7	4
9139	Global landscape of gut microbiome diversity and antibiotic resistomes across vertebrates. Science of the Total Environment, 2022, 838, 156178.	8.0	10
9140	Egg microbiota is the starting point of hatchling gut microbiota in the endangered yellowâ€spotted Amazon river turtle. Molecular Ecology, 2022, 31, 3917-3933.	3.9	4
9141	Exploring microbial communities of Spanish-style green table olives of Conservolea and Halkidiki cultivars during modified atmosphere packaging in multi-layered pouches through culture-dependent techniques and metataxonomic analysis. Food Microbiology, 2022, 107, 104063.	4.2	5
9144	Lentils and Yeast Fibers: A New Strategy to Mitigate Enterotoxigenic Escherichia coli (ETEC) Strain H10407 Virulence?. Nutrients, 2022, 14, 2146.	4.1	0
9145	Plasma Levels of Endocannabinoids and Their Analogues Are Related to Specific Fecal Bacterial Genera in Young Adults: Role in Gut Barrier Integrity. Nutrients, 2022, 14, 2143.	4.1	4
9146	Microbial Communities in Underground Gas Reservoirs Offer Promising Biotechnological Potential. Fermentation, 2022, 8, 251.	3.0	6
9147	DNA/RNA Preservation in Glacial Snow and Ice Samples. Frontiers in Microbiology, 2022, 13, .	3.5	4
9148	Multimodal Data Integration Reveals Mode of Delivery and Snack Consumption Outrank Salivary Microbiome in Association With Caries Outcome in Thai Children. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	3.9	6
9149	A Comparison of Microbial Communities of Mango and Orange Residues for Bioprospecting of Biosurfactant Producers. Ecologies, 2022, 3, 120-130.	1.6	2
9150	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. Communications Earth & Environment, 2022, 3, .	6.8	13

#	Article	IF	CITATIONS
9151	Field response of N2O emissions, microbial communities, soil biochemical processes and winter barley growth to the addition of conventional and biodegradable microplastics. Agriculture, Ecosystems and Environment, 2022, 336, 108023.	5.3	26
9152	Cover crop composition drives changes in the abundance and diversity of nitrifiers and denitrifiers in citrus orchards with critical effects on N2O emissions. Geoderma, 2022, 422, 115952.	5.1	7
9153	Environmental selection dominates over dispersal limitation in shaping bacterial biogeographical patterns across different soil horizons of the Qinghai-Tibet Plateau. Science of the Total Environment, 2022, 838, 156177.	8.0	7
9154	A novel fish meal-free diet formulation supports proper growth and does not impair intestinal parasite susceptibility in gilthead sea bream (Sparus aurata) with a reshape of gut microbiota and tissue-specific gene expression patterns. Aquaculture, 2022, 558, 738362.	3.5	11
9155	Acidogenic Fermentation of Grape Marc with Sewage Sludge to Produce Volatile Fatty Acids. SSRN Electronic Journal, 0, , .	0.4	0
9156	Reactive Iron, Not Fungal Community, Drives Organic Carbon Oxidation Potential in Floodplain Soils. SSRN Electronic Journal, 0, , .	0.4	1
9157	Implications of Parkinson's Disease-Associated Alterations in the Oral and Gut Microbiome on Vitamin B ₁₂ Biosynthesis and Levodopa Bioavailability. SSRN Electronic Journal, 0, , .	0.4	0
9158	Harmful Cyanobacterial Aerosolization Dynamics in the Airshed of a Eutrophic Estuary. SSRN Electronic Journal, 0, , .	0.4	0
9159	Microbiome Diversity Analysis of the Bacterial Community in Idah River, Kogi State, Nigeria. Advances in Microbiology, 2022, 12, 343-362.	0.6	3
9160	Assessing the Tsetse Fly Microbiome Composition and the Potential Association of Some Bacteria Taxa with Trypanosome Establishment. Microorganisms, 2022, 10, 1141.	3.6	3
9161	Humanization of wildlife gut microbiota in urban environments. ELife, 0, 11, .	6.0	18
9162	The Impact of Probiotic Supplementation on Cognitive, Pathological and Metabolic Markers in a Transgenic Mouse Model of Alzheimer's Disease. Frontiers in Neuroscience, 2022, 16, .	2.8	13
9163	Anaerobic digester microbiome dynamics in response to moderate and failure-inducing shock loads of fats, oils and greases. Bioresource Technology, 2022, 359, 127400.	9.6	1
9164	Metabarcoding Approaches in Amphibian Disease Ecology: Disentangling the Functional Contributions of Skin Bacteria on Disease Outcome. Integrative and Comparative Biology, 2022, 62, 252-261.	2.0	3
9165	Polyploidy and microbiome associations mediate similar responses to pathogens in Arabidopsis. Current Biology, 2022, 32, 2719-2729.e5.	3.9	12
9166	Bacterial colonisation dynamics of household plastics in a coastal environment. Science of the Total Environment, 2022, 838, 156199.	8.0	12
9167	Gut microbiota transplantation drives the adoptive transfer of colonic genotype-phenotype characteristics between mice lacking catestatin and their wild type counterparts. Gut Microbes, 2022, 14, .	9.8	2
9169	Effect of cryopreservation medium conditions on growth and isolation of gut anaerobes from human faecal samples. Microbiome, 2022, 10, .	11.1	6

#	Article	IF	CITATIONS
9170	High diversity of lysisâ€resistant cells upon the application of targeted physical and chemical lysis to environmental samples originating from three different water bodies. Environmental DNA, 0, , .	5.8	1
9171	Cloaca―and feather―ssociated bacteria communities in common waxbills <i>Estrilda astrild</i> Journal of Avian Biology, 2022, 2022, .	1.2	1
9172	A Two-Stage Biogas Desulfurization Process Using Cellular Concrete Filtration and an Anoxic Biotrickling Filter. Energies, 2022, 15, 3762.	3.1	5
9173	Clinical evaluation and microbiota analysis in 9 dogs with antibioticâ€responsive enteropathy: A prospective comparison study. Journal of Veterinary Internal Medicine, 2022, 36, 1220-1228.	1.6	5
9174	Similar Carcass Surface Microbiota Observed Following Primary Processing of Different Pig Batches. Frontiers in Microbiology, 2022, 13, .	3 . 5	4
9175	Expanding the temporal and spatial scales of environmental DNA research with autonomous sampling. Environmental DNA, 2022, 4, 972-984.	5 . 8	18
9176	Nitrogen Removal Capacity of Microbial Communities Developing in Compost- and Woodchip-Based Multipurpose Reactive Barriers for Aquifer Recharge With Wastewater. Frontiers in Microbiology, 2022, 13, .	3.5	7
9178	Biodiversity of mycobial communities in health and onychomycosis. Scientific Reports, 2022, 12, .	3.3	3
9179	Phylogenetic, Microbiome, and Diet Characterisation of Wall Lizards in the Columbretes Archipelago (Spain): Clues for Their Conservation. Diversity, 2022, 14, 408.	1.7	1
9180	Complex and unexpected outcomes of antibiotic therapy against a polymicrobial infection. ISME Journal, 2022, 16, 2065-2075.	9.8	11
9181	Integrated Microbiome and Host Transcriptome Profiles Link Parkinson's Disease to Blautia Genus: Evidence From Feces, Blood, and Brain. Frontiers in Microbiology, 2022, 13, .	3 . 5	6
9182	Response of Prokaryotic Communities to Freshwater Salinization. Applied Microbiology, 2022, 2, 330-346.	1.6	2
9183	Unearthing Shifts in Microbial Communities Across a Soil Disturbance Gradient. Frontiers in Microbiology, 2022, 13, .	3.5	3
9184	Reductive Soil Disinfestation Enhances Microbial Network Complexity and Function in Intensively Cropped Greenhouse Soil. Horticulturae, 2022, 8, 476.	2.8	7
9185	Barley Rhizosphere Microbiome Transplantation – A Strategy to Decrease Susceptibility of Barley Grown in Soils With Low Microbial Diversity to Powdery Mildew. Frontiers in Microbiology, 2022, 13, .	3.5	8
9186	A synbiotics, long chain polyunsaturated fatty acids, and milk fat globule membranes supplemented formula modulates microbiota maturation and neurodevelopment. Clinical Nutrition, 2022, 41, 1697-1711.	5.0	9
9187	Enhancing biomarkers with co-abundance. Nature Computational Science, 2022, 2, 290-291.	8.0	1
9188	Host genomic influence on bacterial composition in the switchgrass rhizosphere. Molecular Ecology, 2022, 31, 3934-3950.	3.9	13

#	Article	IF	CITATIONS
9189	Gut microbiota composition does not associate with <i>toxoplasma</i> infection in rats. Molecular Ecology, 2022, 31, 3963-3970.	3.9	5
9191	Organic Amendment Types Influence Soil Properties, the Soil Bacterial Microbiome, and Tomato Growth. Agronomy, 2022, 12, 1236.	3.0	7
9192	Clay chips and beads capture <i>in situ</i> barley root microbiota and facilitate <i>in vitro</i> long-term preservation of microbial strains. FEMS Microbiology Ecology, 0, , .	2.7	3
9193	Enhanced Fermentative Hydrogen Production from Food Waste in Continuous Reactor after Butyric Acid Treatment. Energies, 2022, 15, 4048.	3.1	4
9194	Planktonic protist diversity across contrasting Subtropical and Subantarctic waters of the southwest Pacific. Progress in Oceanography, 2022, 206, 102809.	3.2	11
9195	Effects of a Moderate or Aggressive Implant Strategy on the Rumen Microbiome and Metabolome in Steers. Frontiers in Animal Science, 0, 3, .	1.9	0
9197	Synthetic community improves crop performance and alters rhizosphere microbial communities., 2022, 1, 118-131.		18
9198	Toxin tolerance across landscapes: Ecological exposure not a prerequisite. Functional Ecology, 2022, 36, 2119-2131.	3.6	4
9199	Analysis of microbiome in gastrointestinal stromal tumors: Looking for different players in tumorigenesis and novel therapeutic options. Cancer Science, 2022, 113, 2590-2599.	3.9	4
9200	Using microbiome information to understand and improve animal performance. Italian Journal of Animal Science, 2022, 21, 899-913.	1.9	4
9201	The bacterial hitchhiker's guide to COI: Universal primer-based COI capture probes fail to exclude bacterial DNA, but 16S capture leaves metazoa behind. Metabarcoding and Metagenomics, 0, 6, .	0.0	1
9202	Responses of Soil Microbiota to Different Control Methods of the Spartina alterniflora in the Yellow River Delta. Microorganisms, 2022, 10, 1122.	3. 6	2
9204	First-Void Urine Microbiome in Women with Chlamydia trachomatis Infection. International Journal of Molecular Sciences, 2022, 23, 5625.	4.1	1
9205	Response of Poplar and Associated Fungal Endophytic Communities to a PAH Contamination Gradient. International Journal of Molecular Sciences, 2022, 23, 5909.	4.1	4
9209	Effects of Microbial-Mineral Interactions on Organic Carbon Stabilization in a Ponderosa Pine Root Zone: A Micro-Scale Approach. Frontiers in Earth Science, 2022, 10, .	1.8	1
9210	Fecal microbiota and bile acids in IBD patients undergoing screening for colorectal cancer. Gut Microbes, 2022, 14, .	9.8	20
9211	The Effect of Syringic Acid and Phenoxy Herbicide 4-chloro-2-methylphenoxyacetic acid (MCPA) on Soil, Rhizosphere, and Plant Endosphere Microbiome. Frontiers in Plant Science, 2022, 13, .	3.6	2
9212	Longitudinal Sampling of the Rainbow Trout (Oncorhynchus mykiss) Microbiome Reveals Effects of Dietary Cecropin A and Yersinia ruckeri Infection. Frontiers in Marine Science, 2022, 9, .	2.5	2

#	Article	IF	CITATIONS
9213	Fecal Microbiota Signatures Are Not Consistently Related to Symptom Severity in Irritable Bowel Syndrome. Digestive Diseases and Sciences, 2022, 67, 5137-5148.	2.3	10
9215	Intestinal inflammation alters the antigen-specific immune response to a skin commensal. Cell Reports, 2022, 39, 110891.	6.4	8
9216	Impact of a 7-day homogeneous diet on interpersonal variation in human gut microbiomes and metabolomes. Cell Host and Microbe, 2022, 30, 863-874.e4.	11.0	16
9217	Metagenomic assembled plasmids of the human microbiome vary across disease cohorts. Scientific Reports, 2022, 12, .	3.3	7
9218	Water quality drives the distribution of freshwater cable bacteria. Science of the Total Environment, 2022, 841, 156468.	8.0	6
9219	Enrichment of sulphate-reducers and depletion of butyrate-producers may be hyperglycaemia signatures in the diabetic oral microbiome. Journal of Oral Microbiology, 2022, 14, .	2.7	4
9220	Early life microbial exposures shape the Crassostrea gigas immune system for lifelong and intergenerational disease protection. Microbiome, 2022, 10, .	11.1	24
9221	Minority report: small-scale metagenomic analysis of the non-bacterial kitchen sponge microbiota. Archives of Microbiology, 2022, 204, .	2.2	1
9222	Gut microbiota differs between treatment outcomes early after fecal microbiota transplantation against recurrent <i>Clostridioides difficile</i> infection. Gut Microbes, 2022, 14, .	9.8	16
9223	Shared Microbial Taxa Respond Predictably to Cyclic Time-Varying Oxygen Limitation in Two Disparate Soils. Frontiers in Microbiology, 2022, 13, .	3.5	1
9224	Propionigenium and Vibrio species identified as possible component causes of shrimp white feces syndrome (WFS) associated with the microsporidian Enterocytozoon hepatopenaei. Journal of Invertebrate Pathology, 2022, 192, 107784.	3.2	11
9225	Gastrointestinal symbiont diversity in wild gorilla: A comparison of bacterial and strongylid communities across multiple localities. Molecular Ecology, 2022, 31, 4127-4145.	3.9	2
9226	Microbial community diversity changes during voltage reversal repair in a 12-unit microbial fuel cell. Chemical Engineering Journal, 2022, 446, 137334.	12.7	9
9227	Patterns of Microbiome Composition Vary Across Spatial Scales in a Specialist Insect. Frontiers in Microbiology, 2022, 13, .	3.5	3
9228	The sanitary indoor environment—a potential source for intact human-associated anaerobes. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	5
9231	Prenatal exposure to Hurricane Maria is associated with an altered infant nasal microbiome. , 2022, 1, 128-137.		2
9232	Organic matter availability drives the spatial variation in the community composition and activity of Antarctic marine bacterioplankton. Environmental Microbiology, 2022, 24, 4030-4048.	3.8	4
9233	Composition and Functional Potential of the Human Mammary Microbiota Prior to and Following Breast Tumor Diagnosis. MSystems, 2022, 7, .	3.8	10

#	Article	IF	Citations
9234	Functional Insights into the Kelp Microbiome from Metagenome-Assembled Genomes. MSystems, 2022, 7 , .	3.8	26
9235	Microbial Turnover and Dispersal Events Occur in Synchrony with Plant Phenology in the Perennial Evergreen Tree Crop < i > Citrus sinensis < l i > . MBio, 2022, 13, .	4.1	6
9236	Effect of antimicrobial administration on fecal microbiota of critically ill dogs: dynamics of antimicrobial resistance over time. Animal Microbiome, 2022, 4, .	3.8	6
9237	Evolution of pesticide tolerance and associated changes in the microbiome in the water flea Daphnia magna. Ecotoxicology and Environmental Safety, 2022, 240, 113697.	6.0	6
9238	Rice protein concentrate as a fish meal substitute in Oreochromis niloticus: Effects on immune response, intestinal cytokines, Aeromonas veronii resistance, and gut microbiota composition. Fish and Shellfish Immunology, 2022, 126, 237-250.	3.6	28
9239	Invasive earthworms alter forest soil microbiomes and nitrogen cycling. Soil Biology and Biochemistry, 2022, 171, 108724.	8.8	11
9240	Interspecies and seasonal variations in macroalgae from the Nordic region: Chemical composition and impacts on rumen fermentation and microbiome assembly. Journal of Cleaner Production, 2022, 363, 132456.	9.3	16
9241	Relationships between pond water and tilapia skin microbiomes in aquaculture ponds in Malawi. Aquaculture, 2022, 558, 738367.	3.5	9
9242	Effects of probiotic consortia on plant metabolites are associated with soil indigenous microbiota and fertilization regimes. Industrial Crops and Products, 2022, 185, 115138.	5.2	6
9249	Exploring the patient-microbiome interaction patterns for pan-cancer. Computational and Structural Biotechnology Journal, 2022, 20, 3068-3079.	4.1	4
9251	Bacterial, Fungal, and Mycorrhizal Communities in the Soil Differ between Clearcuts and Insect Outbreaks in the Boreal Forest 50 Years after Disturbance. SSRN Electronic Journal, 0, , .	0.4	1
9253	The relative abundances of yeasts attractive to Drosophila suzukii differ between fruit types and are greatest on raspberries. Scientific Reports, 2022, 12, .	3.3	6
9254	Applying Modified VP53A Recombinant Protein as an Anti-White Spot Syndrome Virus Biological Agent in Litopenaeus vannamei Farming. Viruses, 2022, 14, 1353.	3.3	1
9255	Does Exposure of Broodstock to Dietary Soybean Meal Affect Its Utilization in the Offspring of Zebrafish (Danio rerio)?. Animals, 2022, 12, 1475.	2.3	0
9256	Phyllosphere bacterial and fungal communities vary with host species identity, plant traits and seasonality in a subtropical forest. Environmental Microbiomes, 2022, 17, .	5.0	12
9257	Artificial sandpit lake as a habitat of brackish diatom species. Botany Letters, 2022, 169, 360-369.	1.4	3
9258	Dynamic metabolic interactions and trophic roles of human gut microbes identified using a minimal microbiome exhibiting ecological properties. ISME Journal, 2022, 16, 2144-2159.	9.8	16
9259	Nasopulmonary mites (Acari: Halarachnidae) as potential vectors of bacterial pathogens, including Streptococcus phocae, in marine mammals. PLoS ONE, 2022, 17, e0270009.	2.5	3

#	Article	IF	CITATIONS
9260	Multi-Omic Analyses Reveal Bifidogenic Effect and Metabolomic Shifts in Healthy Human Cohort Supplemented With a Prebiotic Dietary Fiber Blend. Frontiers in Nutrition, 0, 9, .	3.7	6
9261	Landscape Composition and Soil Physical–Chemical Properties Drive the Assemblages of Bacteria and Fungi in Conventional Vegetable Fields. Microorganisms, 2022, 10, 1202.	3.6	14
9262	The role of soil communities on the germination of a pioneer tree species in the Atlantic rainforest. Soil Biology and Biochemistry, 2022, 172, 108762.	8.8	2
9264	Diversity assessment of photosynthesizers: comparative analysis of pre-cultivated and natural microbiome of sediments from Cerrado biome in Maranhão, Brazil. Environmental Science and Pollution Research, 0, , .	5. 3	O
9265	phyloMDA: an R package for phylogeny-aware microbiome data analysis. BMC Bioinformatics, 2022, 23, .	2.6	0
9266	Impacts of Host Genotype and Grafting on Root, Rhizosphere, and Core Microbiomes in Theobroma cacao Seedlings. Phytobiomes Journal, 0, , .	2.7	0
9267	Gut dysbiosis and the clinical spectrum in anti-Ro positive mothers of children with neonatal lupus. Gut Microbes, 2022, 14, .	9.8	6
9268	How Microbiome Composition Correlates with Biochemical Changes during Sauerkraut Fermentation: a Focus on Neglected Bacterial Players and Functionalities. Microbiology Spectrum, 2022, 10, .	3.0	14
9269	A High-Carbohydrate Diet Prolongs Dysbiosis and Clostridioides difficile Carriage and Increases Delayed Mortality in a Hamster Model of Infection. Microbiology Spectrum, 2022, 10, .	3.0	4
9270	Saponification with calcium enhanced methane yield in anaerobic digestion of fat, oil, and grease: The essential role of calcium. Renewable Energy, 2022, 195, 1103-1112.	8.9	3
9271	Bacterial, Phytoplankton, and Viral Distributions and Their Biogeochemical Contexts in Meromictic Lake Cadagno Offer Insights into the Proterozoic Ocean Microbial Loop. MBio, 2022, 13, .	4.1	8
9272	Dysbiosis of skin microbiota with increased fungal diversity is associated with severity of disease in atopic dermatitis. Journal of the European Academy of Dermatology and Venereology, 2022, 36, 1811-1819.	2.4	11
9273	Diversity of an uncommon elastic hypersaline microbial mat along a small-scale transect. PeerJ, 0, 10, e13579.	2.0	10
9275	Salivary microbiota composition may discriminate between patients with eosinophilic oesophagitis (<scp>EoE</scp> and <scp>nonâ€EoE</scp> subjects. Alimentary Pharmacology and Therapeutics, 2022, 56, 450-462.	3.7	8
9276	Endotracheal tube microbiome in hospitalized patients defined largely by hospital environment. Respiratory Research, 2022, 23, .	3.6	5
9277	Metagenomic analysis of the microbiome of the upper reproductive tract: combating ovarian cancer through predictive, preventive, and personalized medicine. EPMA Journal, 2022, 13, 487-498.	6.1	4
9278	Changes of the Freshwater Microbial Community Structure and Assembly Processes during Different Sample Storage Conditions. Microorganisms, 2022, 10, 1176.	3.6	4
9280	Trypanosomatid Richness Among Rats, Opossums, and Dogs in the Caatinga Biome, Northeast Brazil, a Former Endemic Area of Chagas Disease. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	5

#	ARTICLE	IF	CITATIONS
9282	Exploring the microbiome, antibiotic resistance genes, mobile genetic element, and potential resistant pathogens in municipal wastewater treatment plants in Brazil. Science of the Total Environment, 2022, 842, 156773.	8.0	8
9283	TEMPORARY REMOVAL: PCB exposure is associated with reduction of endosymbionts in riparian spider microbiomes. Science of the Total Environment, 2022, , 156726.	8.0	O
9284	Effect of sainfoin (<i>Onobrychis viciifolia</i>) on cyathostomin eggs excretion, larval development, larval community structure and efficacy of ivermectin treatment in horses. Parasitology, 2022, 149, 1439-1449.	1.5	7
9285	Donor-dependent fecal microbiota transplantation efficacy against necrotizing enterocolitis in preterm pigs. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	8
9286	Ammonium sensitivity of biological nitrogen fixation by anaerobic diazotrophs in cultures and benthic marine sediments. Journal of Geophysical Research G: Biogeosciences, 0, , .	3.0	1
9287	Bacterial Community Assembly, Succession, and Metabolic Function during Outdoor Cultivation of <i>Microchloropsis salina</i>	2.9	5
9288	The influence of bioclimate on soil microbial communities of cork oak. BMC Microbiology, 2022, 22, .	3.3	10
9289	Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. Science, 2022, 376, 1220-1223.	12.6	63
9290	Seq' and <scp>ARMS</scp> shall find: <scp>DNA</scp> (meta)barcoding of Autonomous Reef Monitoring Structures across the tree of life uncovers hidden cryptobiome of tropical urban coral reefs. Molecular Ecology, 2023, 32, 6223-6242.	3.9	11
9291	Spatio-temporal variation in the root-associated microbiota of orchard-grown apple trees. Environmental Microbiomes, 2022, 17, .	5.0	7
9293	Removal of a Mixture of Seven Volatile Organic Compounds (VOCs) Using an Industrial Pilot-Scale Process Combining Absorption in Silicone Oil and Biological Regeneration in a Two-Phase Partitioning Bioreactor (TPPB). Energies, 2022, 15, 4576.	3.1	3
9294	More persistent bacterial than fungal associations in the microbiota of a pest insect. Journal of Pest Science, 2023, 96, 785-796.	3.7	2
9296	What will polyethylene film mulching bring to the root-associated microbial community of Paeonia ostii?. Applied Microbiology and Biotechnology, 0, , .	3.6	1
9297	Microbial Communities in Saltpan Sediments Show Tolerance to Mars Analog Conditions, but Susceptibility to Chloride and Perchlorate Toxicity. Astrobiology, 0, , .	3.0	O
9298	Specific Plant Mycorrhizal Responses Are Linked to Mycorrhizal Fungal Species Interactions. Frontiers in Plant Science, 0, 13, .	3.6	8
9299	Correlations Between the Metabolome and the Endophytic Fungal Metagenome Suggests Importance of Various Metabolite Classes in Community Assembly in Horseradish (Armoracia rusticana,) Tj ETQq1 1 0.78431	4 gB T /Ov	rei s ock 10 Tf
9300	Gut virome profiling identifies a widespread bacteriophage family associated with metabolic syndrome. Nature Communications, 2022, 13, .	12.8	32
9302	Culturable Bacterial Diversity from the Basaltic Subsurface of the Young Volcanic Island of Surtsey, Iceland. Microorganisms, 2022, 10, 1177.	3.6	1

#	Article	IF	CITATIONS
9303	Glyphosate-based herbicide exposure: effects on gill microbiota of rainbow trout (<i>Oncorhynchus) Tj ETQq0 0 0</i>	O rgBT /Ov	erlock 10 Tf 5
9304	High Serum Vitamin D Concentrations, Induced via Diet, Trigger Immune and Intestinal Microbiota Alterations Leading to Type 1 Diabetes Protection in NOD Mice. Frontiers in Immunology, 0, 13, .	4.8	6
9305	Human gut microbiota composition and its predicted functional properties in people with western and healthy dietary patterns. European Journal of Nutrition, 2022, 61, 3887-3903.	3.9	8
9306	Nitrogen fixation by diverse diazotrophic communities can support population growth of arboreal ants. BMC Biology, 2022, 20, .	3.8	2
9307	Geographically driven differences in microbiomes of <i>Acropora cervicornis</i> originating from different regions of Florida's Coral Reef. PeerJ, 0, 10, e13574.	2.0	13
9308	Disentangling the genetic basis of rhizosphere microbiome assembly in tomato. Nature Communications, 2022, 13, .	12.8	53
9309	Hurricane Harvey Impacts on Water Quality and Microbial Communities in Houston, TX Waterbodies. Frontiers in Microbiology, 0, 13 , .	3.5	2
9310	Microbial Interactions — Underexplored Links Between Public Health Relevant Bacteria and Protozoa in Coastal Environments. Frontiers in Microbiology, 0, 13, .	3.5	5
9311	Cow Farmers' Homes Host More Diverse Airborne Bacterial Communities Than Pig Farmers' Homes and Suburban Homes. Frontiers in Microbiology, 0, 13, .	3.5	6
9312	Microbial Communities in Biocrusts Are Recruited From the Neighboring Sand at Coastal Dunes Along the Baltic Sea. Frontiers in Microbiology, 0, 13 , .	3.5	5
9313	Bee pollen in zebrafish diet affects intestinal microbiota composition and skin cutaneous melanoma development. Scientific Reports, 2022, 12, .	3.3	5
9314	Microbiome composition of disturbed soils from sandy-gravel mining complexes with different reclamation approaches. One Ecosystem, 0, 7, .	0.0	0
9315	Optimization and Evaluation of the 30S-S11 rRNA Gene for Taxonomic Profiling of Oral Streptococci. Applied and Environmental Microbiology, 2022, 88, .	3.1	7
9316	The gut metabolite indole-3 propionate promotes nerve regeneration and repair. Nature, 2022, 607, 585-592.	27.8	93
9317	Frankia diversity in sympatrically occurring red alder (Alnus rubra) and Sitka alder (Alnus viridis) trees in an early successional environment. Trees - Structure and Function, 2022, 36, 1665-1675.	1.9	4
9318	Metatranscriptomic Comparison of Viromes in Endemic and Introduced Passerines in New Zealand. Viruses, 2022, 14, 1364.	3.3	9
9319	Alterations in rumen microbiota via oral fiber administration during early life in dairy cows. Scientific Reports, 2022, 12, .	3.3	4
9320	Microbial Forensics: A Present to Future Perspective on Genomic Targets, Bioinformatic Challenges, and Applications. Forensic Genomics, 2022, 2, 42-64.	0.5	3

#	Article	IF	CITATIONS
9321	Intestinal Microbes in Patients With Schizophrenia Undergoing Short-Term Treatment: Core Species Identification Based on Co-Occurrence Networks and Regression Analysis. Frontiers in Microbiology, 0, 13, .	3.5	3
9323	Following the flow—Microbial ecology in surface―and groundwaters in the glacial forefield of a rapidly retreating glacier in Iceland. Environmental Microbiology, 2022, 24, 5840-5858.	3.8	3
9324	Modulation of Gut Microbiota and Neuroprotective Effect of a Yeast-Enriched Beer. Nutrients, 2022, 14, 2380.	4.1	11
9325	Traits and tradeoffs among nonâ€native ectomycorrhizal fungal symbionts affect pine seedling establishment in a Hawaiian coâ€invasion landscape. Molecular Ecology, 0, , .	3.9	1
9326	Adherence to Gluten-Free Diet Restores Alpha Diversity in Celiac People but the Microbiome Composition Is Different to Healthy People. Nutrients, 2022, 14, 2452.	4.1	10
9327	Subsurface microbial communities as a tool for characterizing regional-scale groundwater flow. Science of the Total Environment, 2022, 842, 156768.	8.0	13
9328	Interpretation of gut microbiota data in the â€eye of the beholder': A commentary and reâ€evaluation of data from â€Impacts of radiation exposure on the bacterial and fungal microbiome of small mammals in the Chernobyl Exclusion Zone'. Journal of Animal Ecology, 2022, 91, 1535-1545.	2.8	4
9329	COI amplicon sequence data of environmental DNA collected from the Bronx River Estuary, New York City. Metabarcoding and Metagenomics, 0, 6, .	0.0	2
9330	Study of the variation of the Malassezia load in the interdigital fold of dogs with pododermatitis. Veterinary Research Communications, 0, , .	1.6	0
9331	A high-throughput DNA sequencing study of fecal bacteria of seven Mexican horse breeds. Archives of Microbiology, 2022, 204, .	2.2	1
9332	Species- and site-specific circulating bacterial DNA in Subantarctic sentinel mussels Aulacomya atra and Mytilus platensis. Scientific Reports, 2022, 12, .	3.3	2
9335	All Set before Flowering: A 16S Gene Amplicon-Based Analysis of the Root Microbiome Recruited by Common Bean (Phaseolus vulgaris) in Its Centre of Domestication. Plants, 2022, 11, 1631.	3.5	3
9336	Effects of short-interval reburns in the boreal forest on soil bacterial communities compared to long-interval reburns. FEMS Microbiology Ecology, 2022, 98, .	2.7	3
9337	Geological activity shapes the microbiome in deep-subsurface aquifers by advection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
9338	Microbiome Restructuring: Dominant Coral Bacterium <i>Endozoicomonas</i> Species Respond Differentially to Environmental Changes. MSystems, 2022, 7, .	3.8	11
9339	Bacterial and fungal communities in tracheal aspirates of intubated COVID-19 patients: a pilot study. Scientific Reports, 2022, 12, .	3.3	2
9340	Gut microbial characteristics in poor appetite and undernutrition: a cohort of older adults and microbiota transfer in germâ€free mice. Journal of Cachexia, Sarcopenia and Muscle, 2022, 13, 2188-2201.	7.3	8
9341	Metabarcoding analysis of marine zooplankton confirms the ecological role of a sheltered bight along an exposed continental shelf. Molecular Ecology, 2023, 32, 6210-6222.	3.9	5

#	Article	IF	CITATIONS
9342	Turnover in Life-Strategies Recapitulates Marine Microbial Succession Colonizing Model Particles. Frontiers in Microbiology, $0,13,1$	3.5	5
9343	Metagenetic characterization of bacterial communities associated with ready-to-eat leafy vegetables and study of temperature effect on their composition during storage. Food Research International, 2022, 158, 111563.	6.2	7
9344	Soil microbial diversity and community composition during conversion from conventional to organic agriculture. Molecular Ecology, 2022, 31, 4017-4030.	3.9	11
9345	Why Does Doxycycline Pose a Relatively Low Risk for Promotion of Clostridioides difficile Infection?. Pathogens and Immunity, 2022, 7, 81-94.	3.1	7
9349	Lactococcus lactis NCDO2118 exerts visceral antinociceptive properties in rat via GABA production in the gastro-intestinal tract. ELife, 0, 11 , .	6.0	12
9350	Transitory Shifts in Skin Microbiota Composition and Reductions in Bacterial Load and Psoriasin following Ethanol Perturbation. MSphere, 2022, 7, .	2.9	1
9351	Identification of coronaviruses in farmed wild animals reveals their evolutionary origins in Guangdong, southern China. Virus Evolution, 2022, 8, .	4.9	6
9352	Phototrophic sponge productivity may not be enhanced in a high <scp>CO₂</scp> world. Global Change Biology, 2022, 28, 4900-4911.	9.5	3
9354	Cecal Microbial Hydrogen Cycling Potential Is Linked to Feed Efficiency Phenotypes in Chickens. Frontiers in Veterinary Science, 0, 9, .	2.2	2
9355	Eco-Plastics in the Sea: Succession of Micro- and Macro-Fouling on a Biodegradable Polymer Augmented With Oyster Shell. Frontiers in Marine Science, 0, 9, .	2.5	5
9356	Anthropogenic Disturbance Impacts Gut Microbiome Homeostasis in a Malagasy Primate. Frontiers in Microbiology, $0,13,.$	3.5	7
9357	Unravelling Stratified Microbial Assemblages in Australia's Only Deep Anchialine System, The Bundera Sinkhole. Frontiers in Marine Science, 0, 9, .	2.5	10
9358	Antibiotic-Induced Treatments Reveal Stress-Responsive Gene Expression in the Endangered Lichen LobariaÂpulmonaria. Journal of Fungi (Basel, Switzerland), 2022, 8, 625.	3 . 5	2
9359	Impact of the Gram-Negative-Selective Inhibitor MAC13243 on In Vitro Simulated Gut Microbiota. Pharmaceuticals, 2022, 15, 731.	3.8	1
9360	Highly Specialized Carbohydrate Metabolism Capability in <i>Bifidobacterium</i> Strains Associated with Intestinal Barrier Maturation in Early Preterm Infants. MBio, 2022, 13, .	4.1	10
9361	Predicting the effects of multiple global change drivers on microbial communities remains challenging. Global Change Biology, 2022, 28, 5575-5586.	9.5	9
9362	Shifts in Pseudomonas species diversity influence adaptation of brown planthopper to changing climates and geographical locations. IScience, 2022, 25, 104550.	4.1	7
9363	The seasonal investigation of Symbiodiniaceae in broadcast spawning, <i>Acropora humilis</i> brooding, <i>Pocillopora</i> cf. <i>damicornis</i> corals. Peerl, 0, 10, e13114.	2.0	2

#	Article	IF	CITATIONS
9364	Feeding a Saccharomyces cerevisiae Fermentation Product (Olimond BB) Does Not Alter the Fecal Microbiota of Thoroughbred Racehorses. Animals, 2022, 12, 1496.	2.3	4
9365	Reclamation of nutrients, carbon, and metals from compromised surface waters fated to the Salton Sea: Biomass production and ecosystem services using an attached periphytic algae flow-way. Algal Research, 2022, 66, 102757.	4.6	1
9366	Diet Quality and the Gut Microbiota in Women Living in Alabama. American Journal of Preventive Medicine, 2022, 63, S37-S46.	3.0	4
9367	The supplementation of a prebiotic improves the microbial community in the gut and the skin of Atlantic salmon (Salmo salar). Aquaculture Reports, 2022, 25, 101204.	1.7	7
9368	Diversity of rumen microbiota using metagenome sequencing and methane yield in Indian sheep fed on straw and concentrate diet. Saudi Journal of Biological Sciences, 2022, 29, 103345.	3.8	4
9369	Plant root exudates and rhizosphere bacterial communities shift with neighbor context. Soil Biology and Biochemistry, 2022, 172, 108753.	8.8	47
9370	From the bacterial citrus microbiome to the selection of potentially host-beneficial microbes. New Biotechnology, 2022, 70, 116-128.	4.4	7
9371	Resilience in soil bacterial communities of the boreal forest from one to five years after wildfire across a severity gradient. Soil Biology and Biochemistry, 2022, 172, 108755.	8.8	8
9372	Stream bacterial diversity peaks at intermediate freshwater salinity and varies by salt type. Science of the Total Environment, 2022, 840, 156690.	8.0	6
9373	Competing drivers of soil microbial community assembly in a cold arid zone and their implications on constraints of n-alkane proxies. Chemical Geology, 2022, 606, 120985.	3.3	1
9374	Large-scale sampling of the freshwater microbiome suggests pollution-driven ecosystem changes. Environmental Pollution, 2022, 308, 119627.	7. 5	7
9375	Soil macrofauna and microbial communities respond in similar ways to management drivers in an irrigated maize system of Colorado (USA). Applied Soil Ecology, 2022, 178, 104562.	4.3	3
9376	Changes in the prokaryotic diversity in response to hydrochemical variations during an acid mine drainage passive treatment. Science of the Total Environment, 2022, 842, 156629.	8.0	3
9377	Fungal biodiversity in commercial table olive packages. Food Microbiology, 2022, 107, 104082.	4.2	4
9378	Microbial diversity and antimicrobial susceptibility in endotracheal tube biofilms recovered from mechanically ventilated COVID-19 patients. Biofilm, 2022, 4, 100079.	3.8	9
9379	Microbial Communities Mediating Net Methylmercury Formation Along a Trophic Gradient in a Peatland Chronosequence. SSRN Electronic Journal, 0, , .	0.4	0
9380	Functional Variability in Specific Root Respiration Translates to Autotrophic Differences in Soil Respiration in a Temperate Decicuous Forest. SSRN Electronic Journal, 0, , .	0.4	0
9381	Pinpointing the Distinctive Impacts of Ten Cover Crop Species on the Resident and Active Fractions of the Soil Microbiome. SSRN Electronic Journal, 0, , .	0.4	O

#	Article	IF	CITATIONS
9383	Thermal and Latitudinal Patterns in Pace-of-Life Traits are Partly Mediated by the Gut Microbiome. SSRN Electronic Journal, 0, , .	0.4	0
9384	Sediment Metagenomics Reveals the Impacts of Poultry Industry Wastewater on Antibiotic Resistance and Nitrogen Cycling Genes in Tidal Creek Ecosystems. SSRN Electronic Journal, 0, , .	0.4	0
9385	Plutonium Mobilization from Contaminated Estuary Sediments, Esk Estuary (UK). SSRN Electronic Journal, $0, , .$	0.4	0
9388	Host Age Prediction from Fecal Microbiota Composition in Male C57BL/6J Mice. Microbiology Spectrum, 2022, 10, .	3.0	7
9390	Integrated Analysis of the Alterations in Gut Microbiota and Metabolites of Mice Induced After Long-Term Intervention With Different Antibiotics. Frontiers in Microbiology, 0, 13, .	3.5	4
9391	Landscape Topography and Regional Drought Alters Dust Microbiomes in the Sierra Nevada of California. Frontiers in Microbiology, $0,13,.$	3.5	1
9392	Gut microbiota differs in composition between adults with type 1 diabetes with or without depression and healthy control participants: a case-control study. BMC Microbiology, 2022, 22, .	3.3	7
9393	Early Introduction of Plant Polysaccharides Drives the Establishment of Rabbit Gut Bacterial Ecosystems and the Acquisition of Microbial Functions. MSystems, 2022, 7, .	3.8	2
9394	An Infancy-Onset 20-Year Dietary Counselling Intervention and Gut Microbiota Composition in Adulthood. Nutrients, 2022, 14, 2667.	4.1	2
9395	Patients with Infections of The Central Nervous System Have Lowered Gut Microbiota Alpha Diversity. Current Issues in Molecular Biology, 2022, 44, 2903-2914.	2.4	4
9396	Genetic disruption of <i>Arabidopsis</i> secondary metabolite synthesis leads to microbiome-mediated modulation of nematode invasion. ISME Journal, 2022, 16, 2230-2241.	9.8	9
9397	Microbiomes of bloom-forming <i>Phaeocystis</i> both symbiotic and opportunistic modes. ISME Journal, 2022, 16, 2255-2264.	9.8	19
9398	Gut Commensal Parabacteroides goldsteinii MTS01 Alters Gut Microbiota Composition and Reduces Cholesterol to Mitigate Helicobacter pylori-Induced Pathogenesis. Frontiers in Immunology, 0, 13, .	4.8	11
9399	Bacterial Endophytes Contribute to Rice Seedling Establishment Under Submergence. Frontiers in Plant Science, 0, 13, .	3.6	5
9400	Divergent gut microbiota in two closely related house mouse subspecies under common garden conditions. FEMS Microbiology Ecology, 2022, 98, .	2.7	5
9401	Roux-en-Y gastric bypass with a long versus a short biliopancreatic limb improves weight loss and glycemic control in obese mice. Surgery for Obesity and Related Diseases, 2022, 18, 1286-1297.	1.2	1
9402	Benthic Biofilms in Glacier-Fed Streams from Scandinavia to the Himalayas Host Distinct Bacterial Communities Compared with the Streamwater. Applied and Environmental Microbiology, 2022, 88, .	3.1	12
9403	Features of the gut prokaryotic virome of Japanese patients with Crohn's disease. Journal of Gastroenterology, 2022, 57, 559-570.	5.1	10

#	Article	IF	Citations
9404	Postbiotic heat-killed lactobacilli modulates on body weight associated with gut microbiota in a pig model. AMB Express, 2022, 12 , .	3.0	8
9405	microbiomeMarker: an R/Bioconductor package for microbiome marker identification and visualization. Bioinformatics, 2022, 38, 4027-4029.	4.1	87
9406	Niche partitioning between planktivorous fish in the pelagic Baltic Sea assessed by DNA metabarcoding, qPCR and microscopy. Scientific Reports, 2022, 12, .	3.3	3
9407	Fusarium oxysporum Disrupts Microbiome-Metabolome Networks in Arabidopsis thaliana Roots. Microbiology Spectrum, 2022, 10, .	3.0	8
9408	Organohalide respiration potential in marine sediments from Aarhus Bay. FEMS Microbiology Ecology, 2022, 98, .	2.7	6
9409	Climate dictates microbial community composition and diversity in Australian biological soil crusts (biocrusts). Environmental Microbiology, 2022, 24, 5467-5482.	3.8	6
9410	Cross-feeding niches among commensal leaf bacteria are shaped by the interaction of strain-level diversity and resource availability. ISME Journal, 2022, 16, 2280-2289.	9.8	14
9411	Gut Microbiome 16S rRNA Gene Amplicon Taxonomic Profiling of Hospitalized Moroccan COVID-19 Patients. Microbiology Resource Announcements, 2022, 11, .	0.6	2
9413	Mixed-Mode Bacterial Transmission via Eggshells in an Oviparous Reptile Without Parental Care. Frontiers in Microbiology, 0, 13 , .	3.5	2
9414	Gut Microbiome Changes Occurring with Norovirus Infection and Recovery in Infants Enrolled in a Longitudinal Birth Cohort in Leon, Nicaragua. Viruses, 2022, 14, 1395.	3.3	3
9415	Vaginal Microbiota Is Stable and Mainly Dominated by Lactobacillus at Third Trimester of Pregnancy and Active Childbirth: A Longitudinal Study of Ten Mexican Women. Current Microbiology, 2022, 79, .	2.2	4
9416	Rhizosphere 16S-ITS Metabarcoding Profiles in Banana Crops Are Affected by Nematodes, Cultivation, and Local Climatic Variations. Frontiers in Microbiology, 0, 13, .	3.5	4
9417	Milk microbiomes of three great ape species vary among host species and over time. Scientific Reports, 2022, 12, .	3.3	3
9418	Dysbiosis of fish gut microbiota is associated with helminths parasitism rather than exposure to PAHs at environmentally relevant concentrations. Scientific Reports, 2022, 12, .	3.3	3
9419	The Microbiome of the †Williams' Pear Variety Grown in the Organic Orchard and Antifungal Activity by the Autochthonous Bacterial and Yeast Isolates. Microorganisms, 2022, 10, 1282.	3.6	6
9421	Microbiome Differentiation Among Coexisting Nematode Species in Estuarine Microhabitats: A Metagenetic Analysis. Frontiers in Marine Science, 0, 9, .	2.5	1
9422	Dynamics of Small Non-coding RNA Profiles and the Intestinal Microbiome of High and Low Weight Chickens. Frontiers in Microbiology, 0, 13 , .	3.5	3
9423	Schoolyard Biodiversity Determines Short-Term Recovery of Disturbed Skin Microbiota in Children. Microbial Ecology, 2023, 86, 658-669.	2.8	5

#	Article	IF	CITATIONS
9426	Biogeographic Variation and Functional Pathways of the Gut Microbiota in Celiac Disease. Gastroenterology, 2022, 163, 1351-1363.e15.	1.3	15
9427	Intracellular nitrate storage by diatoms can be an important nitrogen pool in freshwater and marine ecosystems. Communications Earth & Environment, 2022, 3, .	6.8	11
9429	Imbalanced gut microbiota fuels hepatocellular carcinoma development by shaping the hepatic inflammatory microenvironment. Nature Communications, 2022, 13, .	12.8	68
9430	Microbial Community Compositional Stability in Agricultural Soils During Freeze-Thaw and Fertilizer Stress. Frontiers in Environmental Science, $0,10,10$	3.3	3
9431	Persisting Microbiota and Neuronal Imbalance Following T. gondii Infection Reliant on the Infection Route. Frontiers in Immunology, 0, 13, .	4.8	6
9432	Analysis of Microbiota Persistence in Quebec's Terroir Cheese Using a Metabarcoding Approach. Microorganisms, 2022, 10, 1381.	3.6	3
9433	Prebiotic potential of apple pomace and pectins from different apple varieties: Modulatory effects on key target commensal microbial populations. Food Hydrocolloids, 2022, 133, 107958.	10.7	18
9434	Effects of the Lipid Profile, Type 2 Diabetes and Medication on the Metabolic Syndrome—Associated Gut Microbiome. International Journal of Molecular Sciences, 2022, 23, 7509.	4.1	11
9435	Relationships between Sphaerulina musiva Infection and the <i>Populus</i> Microbiome and Metabolome. MSystems, 2022, 7, .	3.8	2
9436	Altered Composition of the Oral Microbiota in Depression Among Cigarette Smokers: A Pilot Study. Frontiers in Psychiatry, 0, 13 , .	2.6	5
9437	Conjunctival Intraepithelial Lymphocytes, Lacrimal Cytokines and Ocular Commensal Microbiota: Analysis of the Three Main Players in Allergic Conjunctivitis. Frontiers in Immunology, 0, 13, .	4.8	10
9438	An efficient earlyâ€pooling protocol for environmental <scp>DNA</scp> metabarcoding. Environmental DNA, 2022, 4, 1212-1228.	5.8	9
9439	Environmental Stress and the Primate Microbiome: Glucocorticoids Contribute to Structure Gut Bacterial Communities of Black Howler Monkeys in Anthropogenically Disturbed Forest Fragments. Frontiers in Ecology and Evolution, 0, 10, .	2.2	1
9440	Vertical distribution of bacterial community diversity in the Greater Khingan Mountain permafrost region. Ecology and Evolution, 2022, 12, .	1.9	3
9441	Transplantation of bacteriophages from ulcerative colitis patients shifts the gut bacteriome and exacerbates the severity of DSS colitis. Microbiome, 2022, 10, .	11.1	23
9442	Diversity of <i>Fusarium</i> community assembly shapes mycotoxin accumulation of diseased wheat heads. Molecular Ecology, 2023, 32, 2504-2518.	3.9	7
9443	Impact of COVID-19 Lockdown on the Nasopharyngeal Microbiota of Children and Adults Self-Confined at Home. Viruses, 2022, 14, 1521.	3.3	10
9444	Microbial community shifts correspond with suppression of decomposition 25 years after liming of acidic forest soils. Global Change Biology, 2022, 28, 5399-5415.	9.5	11

#	Article	IF	CITATIONS
9445	Withinâ€community variation of interspecific divergence patterns in passerine gut microbiota. Ecology and Evolution, 2022, 12, .	1.9	2
9446	Microbiome Heritability and Its Role in Adaptation of Hosts to Novel Resources. Frontiers in Microbiology, 0, 13, .	3.5	3
9447	Fecal microbiota and their association with heat stress in Bos taurus. BMC Microbiology, 2022, 22, .	3.3	7
9449	A plant-based diet supplemented with Hermetia illucens alone or in combination with poultry by-product meal: one step closer to sustainable aquafeeds for European seabass. Journal of Animal Science and Biotechnology, 2022, 13, .	5.3	4
9450	Differential Overlap in Human and Animal Fecal Microbiomes and Resistomes in Rural versus Urban Bangladesh. Applied and Environmental Microbiology, 2022, 88, .	3.1	3
9451	Oral and gut dysbiosis leads to functional alterations in Parkinson's disease. Npj Parkinson's Disease, 2022, 8, .	5.3	15
9452	Inoculum Concentration and Mineral Fertilization: Effects on the Endophytic Microbiome of Soybean. Frontiers in Microbiology, $0,13,.$	3.5	6
9453	Auxiliary Metabolic Gene Functions in Pelagic and Benthic Viruses of the Baltic Sea. Frontiers in Microbiology, $0,13,.$	3.5	21
9456	Impact of Putative Probiotics on Growth, Behavior, and the Gut Microbiome of Farmed Arctic Char (Salvelinus alpinus). Frontiers in Microbiology, 0, 13, .	3.5	5
9457	Nasal microbiota evolution within the congregate setting imposed by military training. Scientific Reports, 2022, 12, .	3.3	5
9458	High resolution parallel sequencing reveals multistrain Campylobacter in broiler chicken flocks testing â€~negative' by conventional culture methods: implications for control of Campylobacter infection. Poultry Science, 2022, 101, 102048.	3.4	0
9459	The Many Ages of Microbiome–Gut–Brain Axis. Nutrients, 2022, 14, 2937.	4.1	10
9460	Watershedâ€scale liming reveals the short―and longâ€term effects of <scp>pH < /scp>on the forest soil microbiome and carbon cycling. Environmental Microbiology, 2022, 24, 6184-6199.</scp>	3.8	10
9462	Environmental Selection Shapes Bacterial Community Composition in Traditionally Fermented Maize-Based Foods from Benin, Tanzania and Zambia. Microorganisms, 2022, 10, 1354.	3.6	2
9463	International shipping as a potent vector for spreading marine parasites. Diversity and Distributions, 2022, 28, 1922-1933.	4.1	6
9464	Seasonal Variation of the Atmospheric Bacterial Community in the Greenlandic High Arctic Is Influenced by Weather Events and Local and Distant Sources. Frontiers in Microbiology, 0, 13, .	3.5	6
9465	Updating Urinary Microbiome Analyses to Enhance Biologic Interpretation. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	4
9466	Habitat and Host Species Drive the Structure of Bacterial Communities of Two Neotropical Trap-Jaw Odontomachus Ants. Microbial Ecology, 0, , .	2.8	1

#	Article	IF	CITATIONS
9467	Characterization and manipulation of the bacterial community in the midgut of Ixodes ricinus. Parasites and Vectors, 2022, 15 , .	2.5	8
9468	Controlled natural selection of soil microbiome through plant-soil feedback confers resistance to a foliar pathogen. Plant and Soil, 2023, 485, 181-195.	3.7	4
9469	$\mbox{\ensuremath{\mbox{\sc i}}}\mbox{\sc Helicobacter pylori}\mbox{\ensuremath{\mbox{\sc i}}}\sc is associated with worse overall survival in patients with melanoma treated with immune checkpoint inhibitors. Oncolmmunology, 2022, 11, .$	4.6	11
9470	Bacterial Microbiome in the Phyllo-Endosphere of Highly Specialized Rock Spleenwort. Frontiers in Plant Science, 0, 13, .	3.6	2
9471	Populational and metabolic shifts induced by acetate, butyrate and lactate in dark fermentation. International Journal of Hydrogen Energy, 2022, 47, 28385-28398.	7.1	4
9472	Gut Microbiota and Lymphocyte Subsets in Canine Leishmaniasis. Frontiers in Veterinary Science, 0, 9, .	2.2	0
9474	B cell-mediated regulatory mechanisms control tumor-promoting intestinal inflammation. Cell Reports, 2022, 40, 111051.	6.4	7
9475	Multi-Omics Integration Reveals the Crucial Role of <i>Fusobacterium</i> in the Inflammatory Immune Microenvironment in Head and Neck Squamous Cell Carcinoma. Microbiology Spectrum, 2022, 10, .	3.0	9
9477	The activity and functions of soil microbial communities in the Finnish sub-Arctic vary across vegetation types. FEMS Microbiology Ecology, 2022, 98, .	2.7	8
9478	Exploring methods to summarize gut microbiota composition for microbiability estimation and phenotypic prediction in swine. Journal of Animal Science, 2022, 100, .	0.5	2
9479	Houseflies harbor less diverse microbiota under laboratory conditions but maintain a consistent set of host-associated bacteria. Scientific Reports, 2022, 12, .	3.3	4
9480	Substrate-restricted methanogenesis and limited volatile organic compound degradation in highly diverse and heterogeneous municipal landfill microbial communities. ISME Communications, 2022, 2, .	4.2	8
9481	Community Structure of Nitrifying and Denitrifying Bacteria from Effluents Discharged into Lake Victoria, Kenya. Current Microbiology, 2022, 79, .	2.2	1
9482	Induction of mastitis by cow-to-mouse fecal and milk microbiota transplantation causes microbiome dysbiosis and genomic functional perturbation in mice. Animal Microbiome, 2022, 4, .	3.8	18
9483	Gut Microbiota Diversity of Preterm Neonates Is Associated With Clostridioides Difficile Colonization. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	2
9484	Thrips Microbiome Study in Commercial Avocado (Persea americana Mill.) from Northwest Colombian Andes (Antioquia, Colombia) Shows the Presence of Wolbachia, Ehrlichia, Enterobacter. Diversity, 2022, 14, 540.	1.7	1
9486	Divergence of Biocrust Active Bacterial Communities in the Negev Desert During a Hydration-Desiccation Cycle. Microbial Ecology, 2023, 86, 474-484.	2.8	5
9487	Genomic Insights Into the Interspecific Diversity and Evolution of Mobiluncus, a Pathogen Associated With Bacterial Vaginosis. Frontiers in Microbiology, $0,13,.$	3.5	O

#	Article	IF	CITATIONS
9488	The Bacterial and Fungal Gut Microbiota of the Greater Wax Moth, Galleria mellonella L. Consuming Polyethylene and Polystyrene. Frontiers in Microbiology, 0, 13 , .	3.5	14
9489	Microbial community development during syngas methanation in a trickle bed reactor with various nutrient sources. Applied Microbiology and Biotechnology, 2022, 106, 5317-5333.	3.6	7
9490	Fluctuating selection on bacterial iron regulation in the mammalian gut. Current Biology, 2022, , .	3.9	5
9491	Agricultural management and pesticide use reduce the functioning of beneficial plant symbionts. Nature Ecology and Evolution, 2022, 6, 1145-1154.	7.8	54
9492	Insights into the Gut Microbial Communities of Broiler Chicken Fed Black Soldier Fly Larvae-Desmodium-Based Meal as a Dietary Protein Source. Microorganisms, 2022, 10, 1351.	3.6	9
9493	Diversity of Free-Living and Particle-Attached Prokaryotes in a River-Influenced Coastal Area of the Northern Adriatic Sea. Frontiers in Marine Science, 0, 9, .	2.5	2
9494	Trachymyrmex septentrionalis Ant Microbiome Assembly Is Unique to Individual Colonies and Castes. MSphere, 2022, 7, .	2.9	4
9495	Starch and Fiber Contents of Purified Control Diets Differentially Affect Hepatic Lipid Homeostasis and Gut Microbiota Composition. Frontiers in Nutrition, 0, 9, .	3.7	4
9496	Characterization of the urogenital microbiome in Miniature Schnauzers with and without calcium oxalate urolithiasis. Journal of Veterinary Internal Medicine, 2022, 36, 1341-1352.	1.6	6
9498	Câ€section increases cecal abundance of the archetypal bile acid and glucocorticoid modifying ⟨i⟩Lachnoclostridium [clostridium] scindens⟨ i⟩ in mice. Physiological Reports, 2022, 10, .	1.7	3
9499	Inhibition of Cronobacter sakazakii in an infant simulator of the human intestinal microbial ecosystem using a potential synbiotic. Frontiers in Microbiology, 0, 13, .	3.5	4
9500	The developing airway and gut microbiota in early life is influenced by age of older siblings. Microbiome, 2022, 10, .	11.1	21
9501	A 16S rRNA Sequencing Study Describing the Environmental Microbiota of Two Powdered Infant Formula Built Facilities. Foodborne Pathogens and Disease, 2022, 19, 473-484.	1.8	1
9502	Sedimentary <scp>DNA</scp> records longâ€ŧerm changes in a lake bacterial community in response to varying nutrient availability. Environmental DNA, 2022, 4, 1340-1355.	5. 8	5
9503	<pre><scp>metaPR²</scp>: A database of eukaryotic <scp>18S rRNA</scp> metabarcodes with an emphasis on protists. Molecular Ecology Resources, 2022, 22, 3188-3201.</pre>	4.8	24
9505	Stable carbon isotope values of syndepositional carbonate spherules and micrite record spatial and temporal changes in photosynthesis intensity. Geobiology, 2022, 20, 667-689.	2.4	2
9506	Precipitation, Not Land Use, Primarily Determines the Composition of Both Plant and Phyllosphere Fungal Communities. Frontiers in Fungal Biology, 0, 3, .	2.0	0
9507	Bacterial Communities of the Uterus and Rumen During Heifer Development With Protein Supplementation. Frontiers in Animal Science, 0, 3, .	1.9	2

#	Article	IF	CITATIONS
9510	One bat's waste is another man's treasure: a DNA metabarcoding approach for the assessment of biodiversity and ecosystem services in Ireland using bat faeces. Biodiversity and Conservation, 2022, 31, 2699-2722.	2.6	3
9511	Effects of Tree Composition and Soil Depth on Structure and Functionality of Belowground Microbial Communities in Temperate European Forests. Frontiers in Microbiology, 0, 13, .	3.5	11
9512	Altered Innate Immunity and Damaged Epithelial Integrity in Vaginal Microbial Dysbiosis. Frontiers in Reproductive Health, 0, 4, .	1.9	2
9514	Labâ€scale data and microbial community structure suggest shortcut nitrogen removal as the predominant nitrogen removal mechanism in postâ€eerobic digestion (PAD). Water Environment Research, 2022, 94, .	2.7	3
9515	Dynamics of bacterial and fungal communities of mango: From the tree to ready-to-Eat products. Food Microbiology, 2022, 108, 104095.	4.2	3
9516	Shaping an Open Microbiome for Butanol Production through Process Control. Fermentation, 2022, 8, 333.	3.0	1
9517	Greater functional diversity and redundancy of coral endolithic microbiomes align with lower coral bleaching susceptibility. ISME Journal, 2022, 16, 2406-2420.	9.8	21
9520	Litchi-Derived Polyphenol Alleviates Liver Steatosis and Gut Dysbiosis in Patients with Non-Alcoholic Fatty Liver Disease: A Randomized Double-Blinded, Placebo-Controlled Study. Nutrients, 2022, 14, 2921.	4.1	10
9522	Rectal microbiota are coupled with altered cytokine production capacity following community-acquired pneumonia hospitalization. IScience, 2022, , 104740.	4.1	1
9523	Genomic diversity of genus Limosilactobacillus. Microbial Genomics, 2022, 8, .	2.0	4
9524	Fungal genetic biodiversity and metabolic activity as an indicator of potential biological weathering and soil formation – Case study of towards a better understanding of Earth system dynamics. Ecological Indicators, 2022, 141, 109136.	6.3	4
9525	Effects of municipal wastewater effluents on the digestive gland microbiome of wild freshwater mussels (Lasmigona costata). Ecotoxicology and Environmental Safety, 2022, 241, 113774.	6.0	2
9526	Impact of "chemical cocktails―exposure in shaping mice gut microbiota and the role of selenium supplementation combining metallomics, metabolomics, and metataxonomics. Journal of Hazardous Materials, 2022, 438, 129444.	12.4	9
9527	Profiling microalgal cultures growing on municipal wastewater and fertilizer media in raceway photobioreactors. Bioresource Technology, 2022, 360, 127619.	9.6	4
9528	Fusobacterium is enriched in oral cancer and promotes induction of programmed death-ligand 1 (PD-L1). Neoplasia, 2022, 31, 100813.	5. 3	14
9529	Microbial diversity and geochemistry of groundwater impacted by steel slag leachates. Science of the Total Environment, 2022, 843, 156987.	8.0	6
9530	Remediation of groundwater contaminated with dye using carbon dots technology: Ecotoxicological and microbial community responses. Journal of Environmental Management, 2022, 319, 115634.	7.8	5
9531	The combined enhancement of RL, nZVI and AQDS on the microbial anaerobic-aerobic degradation of PAHs in soil. Chemosphere, 2022, 307, 135609.	8.2	3

#	ARTICLE	IF	CITATIONS
9532	The effect of oxytetracycline treatment on the gut microbiome community dynamics in rainbow trout (Oncorhynchus mykiss) over time. Aquaculture, 2022, 560, 738559.	3.5	11
9533	Cellular stress affects the fate of microbial resistance to folate inhibitors in treatment wetlands. Science of the Total Environment, 2022, 845, 157318.	8.0	3
9534	Condensed tannins increased intestinal permeability of Chinese seabass (Lateolabrax maculatus) based on microbiome-metabolomics analysis. Aquaculture, 2022, 560, 738615.	3.5	6
9535	Comparison of functional-oil blend and anticoccidial antibiotics effects on performance and microbiota of broiler chickens challenged by coccidiosis. PLoS ONE, 2022, 17, e0270350.	2.5	3
9536	Gut microbiome markers in subgroups of HLA class II genotyped infants signal future celiac disease in the general population: ABIS study. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	6
9537	The Interplay Between Use of Biological Therapies, Psychological State, and the Microbiome in IBD. Frontiers in Medicine, 0, 9, .	2.6	0
9538	Host genetic determinants drive compartmentâ€specific assembly of tea plant microbiomes. Plant Biotechnology Journal, 2022, 20, 2174-2186.	8.3	10
9539	Landscape scale ecology of Tetracladium spp. fungal root endophytes. Environmental Microbiomes, 2022, 17, .	5.0	6
9540	Conserved developmental trajectories of the cecal microbiota of broiler chickens in a field study. FEMS Microbiology Ecology, 2022, 98, .	2.7	2
9541	Are microbes growing on flowers evil? Effects of old flower microbes on fruit set in a wild ginger with one-day flowers, Alpinia japonica (Zingiberaceae). Metabarcoding and Metagenomics, 0, 6, .	0.0	0
9542	Marine Microbial Communities of North and South Shelves of Iceland. Frontiers in Marine Science, 0, 9, .	2.5	0
9543	Chronic-Antibiotics Induced Gut Microbiota Dysbiosis Rescues Memory Impairment and Reduces β-Amyloid Aggregation in a Preclinical Alzheimer's Disease Model. International Journal of Molecular Sciences, 2022, 23, 8209.	4.1	12
9544	Degradation Reduces Microbial Richness and Alters Microbial Functions in an Australian Peatland. Microbial Ecology, 0, , .	2.8	3
9545	The digestive tract sections of the sea cucumber Isostichopus badionotus reveal differences in composition, diversity, and functionality of the gut microbiota. Archives of Microbiology, 2022, 204, .	2.2	0
9546	The Relationship Between Maternal and Neonatal Microbiota in Spontaneous Preterm Birth: A Pilot Study. Frontiers in Pediatrics, 0, 10, .	1.9	7
9547	Multiple anthropogenic pressures eliminate the effects of soil microbial diversity on ecosystem functions in experimental microcosms. Nature Communications, 2022, 13, .	12.8	41
9548	The impact of the rice production system (irrigated <i>vs</i> lowland) on root-associated microbiome from farmer's fields in western Burkina Faso. FEMS Microbiology Ecology, 2022, 98, .	2.7	7
9549	Frontloading of stress response genes enhances robustness to environmental change in chimeric corals. BMC Biology, 2022, 20, .	3.8	4

#	Article	IF	CITATIONS
9550	The Fate and Distribution of Microalgal Nitrogen When Applied as an Agricultural Soil Fertiliser and Its Effect on Soil Microbial Communities. Phycology, 2022, 2, 297-318.	3.6	4
9551	Key features of the genetic architecture and evolution of host-microbe interactions revealed by high-resolution genetic mapping of the mucosa-associated gut microbiome in hybrid mice. ELife, 0, 11, .	6.0	9
9552	Increased Soil Fertility in Tea Gardens Leads to Declines in Fungal Diversity and Complexity in Subsoils. Agronomy, 2022, 12, 1751.	3.0	6
9553	Microbial communities associated with mounds of the Orange-footed scrubfowl <i>Megapodius reinwardt</i> . PeerJ, 0, 10, e13600.	2.0	0
9554	Influence of Microplastics on Microbial Structure, Function, and Mechanical Properties of Stream Periphyton. Frontiers in Environmental Science, 0, 10, .	3.3	2
9555	Antibiotic and antifungal use in pediatric leukemia and lymphoma patients are associated with increasing opportunistic pathogens and decreasing bacteria responsible for activities that enhance colonic defense. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	6
9556	Microbial community dispersal from wheat grains to sourdoughs: A contribution of participatory research. Molecular Ecology, 2023, 32, 2413-2427.	3.9	7
9557	Alterations in infant gut microbiome composition and metabolism after exposure to glyphosate and Roundup and/or a spore-based formulation using the SHIME technology. Gut Microbiome, 2022, 3, .	3.2	4
9558	Multiple generations of antibiotic exposure and isolation influence host fitness and the microbiome in a model zooplankton species. FEMS Microbiology Ecology, 2022, 98, .	2.7	0
9559	Truth or Lie: Does the DNA Extraction Procedure Really Affect the Insight in Composition and Diversity of Microbial Communities in Saffron Cultivated Soils?. Applied Microbiology, 2022, 2, 492-501.	1.6	1
9560	Predictable Changes in Eelgrass Microbiomes with Increasing Wasting Disease Prevalence across $23\hat{A}^\circ$ Latitude in the Northeastern Pacific. MSystems, 2022, 7, .	3.8	5
9562	Phosphorus control and dredging decrease methane emissions from shallow lakes. Science of the Total Environment, 2022, 847, 157584.	8.0	5
9563	Analysis of the gut microbiome of susceptible and resistant honeybees (<i>Apis cerana</i>) against sacbrood virus disease. Journal of Applied Entomology, 2022, 146, 1078-1086.	1.8	4
9565	The microbial environment modulates non-genetic maternal effects on egg immunity. Animal Microbiome, 2022, 4, .	3.8	0
9566	Community structure of coral microbiomes is dependent on host morphology. Microbiome, 2022, 10, .	11.1	11
9567	Adaptation to Environmental Extremes Structures Functional Traits in Biological Soil Crust and Hypolithic Microbial Communities. MSystems, 0, , .	3.8	3
9568	Using DNA metabarcoding and a novel canid-specific blocking oligonucleotide to investigate the composition of animal diets of raccoon dogs (Nyctereutes procyonoides) inhabiting the waterside area in Korea. PLoS ONE, 2022, 17, e0271118.	2.5	3
9569	Characterization of the Soil Bacterial Community from Selected Boxwood Gardens across the United States. Microorganisms, 2022, 10, 1514.	3.6	3

#	Article	IF	CITATIONS
9570	Histamine production by the gut microbiota induces visceral hyperalgesia through histamine 4 receptor signaling in mice. Science Translational Medicine, 2022, 14, .	12.4	41
9571	Exploring the microbial composition of Holstein Friesian and Belgian Blue colostrum in relation to the transfer of passive immunity. Journal of Dairy Science, 2022, 105, 7623-7641.	3.4	3
9572	Integrated Fertilization with Bagasse Vermicompost Changes the Microbiome of MencÃa Must and Wine. Fermentation, 2022, 8, 357.	3.0	1
9573	Evaluation of the biodegradation of polymeric materials in the freshwater environment—An attempt to prolong and accelerate the biodegradation experiment. Polymer Degradation and Stability, 2022, 203, 110085.	5.8	3
9574	Composition and functionality of bacterioplankton communities in marine coastal zones adjacent to finfish aquaculture. Marine Pollution Bulletin, 2022, 182, 113957.	5.0	0
9575	Bacterial assemblage in Mediterranean salt marshes: Disentangling the relative importance of seasonality, zonation and halophytes. Science of the Total Environment, 2022, 846, 157514.	8.0	2
9576	Multifactor Progression of Parkinson's Disease: Role of Diet and Exposure to Microbiome-Borne Curli. SSRN Electronic Journal, 0, , .	0.4	0
9577	Emerging tools for understanding the human microbiome. Progress in Molecular Biology and Translational Science, 2022, , .	1.7	0
9579	Proinflammatory mucosal-associated invariant CD8+ T cells react to gut flora yeasts and infiltrate multiple sclerosis brain. Frontiers in Immunology, 0, 13, .	4.8	13
9580	Asthma and Wheeze Severity and the Oropharyngeal Microbiota in Children and Adolescents. Annals of the American Thoracic Society, 0, , .	3.2	7
9581	Crohnâ \in TM s disease recurrence updates: first surgery vs. surgical relapse patients display different profiles of ileal microbiota and systemic microbial-associated inflammatory factors. Frontiers in Immunology, 0, 13, .	4.8	9
9583	Sulfur cycling at natural hydrocarbon and sulfur seeps in Santa Paula Creek, <scp>CA</scp> . Geobiology, 2022, 20, 707-725.	2.4	2
9584	Illuminating protist diversity in pitcher plants and bromeliad tanks. PLoS ONE, 2022, 17, e0270913.	2.5	1
9586	Acute gut microbiome changes after traumatic brain injury are associated with chronic deficits in decision-making and impulsivity in male rats Behavioral Neuroscience, 2023, 137, 15-28.	1.2	3
9587	Combining multi-marker metabarcoding and digital holography to describe eukaryotic plankton across the Newfoundland Shelf. Scientific Reports, 2022, 12, .	3.3	3
9588	The gut microbiome variability of a butterflyfish increases on severely degraded Caribbean reefs. Communications Biology, 2022, 5, .	4.4	12
9589	Invariant natural killer T cells minimally influence gut microbiota composition in mice. Gut Microbes, 2022, 14, .	9.8	3
9590	Interaction between endometrial microbiota and host gene regulation in recurrent implantation failure. Journal of Assisted Reproduction and Genetics, 0, , .	2.5	2

#	Article	IF	CITATIONS
9591	Core Community Persistence Despite Dynamic Spatiotemporal Responses in the Associated Bacterial Communities of Farmed Pacific Oysters. Microbial Ecology, 0, , .	2.8	1
9592	Wild herbivorous mammals (genus Neotoma) host a diverse but transient assemblage of fungi. Symbiosis, 2022, 87, 45-58.	2.3	2
9593	TidyMass an object-oriented reproducible analysis framework for LC–MS data. Nature Communications, 2022, 13, .	12.8	19
9594	Gut microbiota profile of patients on peritoneal dialysis: comparison with household contacts. European Journal of Clinical Nutrition, 2023, 77, 90-97.	2.9	5
9595	Metagenomic analysis reveals associations between salivary microbiota and body composition in early childhood. Scientific Reports, 2022, 12, .	3.3	7
9596	Using metabarcoding and droplet digital PCR to investigate drivers of historical shifts in cyanobacteria from six contrasting lakes. Scientific Reports, 2022, 12, .	3.3	10
9597	Endothelial Caspase-8 prevents fatal necroptotic hemorrhage caused by commensal bacteria. Cell Death and Differentiation, 2023, 30, 27-36.	11.2	5
9598	Whale-Associated Microbial Communities Remain Remarkably Stable despite Massive Water Community Disruption in a Managed Artificial Marine Environment. Oceans, 2022, 3, 289-302.	1.3	0
9599	Gut Microbiome as a Potential Biomarker in Fish: Dietary Exposure to Petroleum Hydrocarbons and Metals, Metabolic Functions and Cytokine Expression in Juvenile Lates calcarifer. Frontiers in Microbiology, $0,13,1$	3.5	10
9600	In Utero Exposure to Caffeine and Acetaminophen, the Gut Microbiome, and Neurodevelopmental Outcomes: A Prospective Birth Cohort Study. International Journal of Environmental Research and Public Health, 2022, 19, 9357.	2.6	3
9601	Low abundance members of the gut microbiome exhibit high immunogenicity. Gut Microbes, 2022, 14, .	9.8	8
9602	The Effect of <i>Septoria glycines </i> and Fungicide Application on the Soybean Phyllosphere Mycobiome. Phytobiomes Journal, 2023, 7, 220-232.	2.7	4
9603	Gut microbiota and host genetics contribute to the phenotypic variation of digestive and feed efficiency traits in growing pigs fed a conventional and a high fiber diet. Genetics Selection Evolution, 2022, 54, .	3.0	4
9604	A Decade of Time Series Sampling Reveals Thermal Variation and Shifts in Pseudo-nitzschia Species Composition That Contribute to Harmful Algal Blooms in an Eastern US Estuary. Frontiers in Marine Science, 0, 9, .	2.5	4
9605	Effect of Various Preterm Infant Milk Formulas on NEC-Like Gut Injury in Mice. Frontiers in Pediatrics, 0, 10, .	1.9	2
9606	Changes in intestinal microbiota in postmenopausal oestrogen receptor-positive breast cancer patients treated with (neo)adjuvant chemotherapy. Npj Breast Cancer, 2022, 8, .	5.2	10
9607	Prophylactic Treatment of Undernourished Mice with Cotrimoxazole Induces a Different Profile of Dysbiosis with Functional Metabolic Alterations. Cells, 2022, 11, 2278.	4.1	2
9609	Tardigrade Community Microbiomes in North American Orchards Include Putative Endosymbionts and Plant Pathogens. Frontiers in Microbiology, 0, 13 , .	3.5	5

#	Article	IF	CITATIONS
9610	Horizontal Gene Transfer of an IncP1 Plasmid to Soil Bacterial Community Introduced by <i>Escherichia coli</i> through Manure Amendment in Soil Microcosms. Environmental Science & Echnology, 2022, 56, 11398-11408.	10.0	15
9611	Mycobiota and the Contribution of Yeasts in Floor Dust of 50 Elementary Schools Characterized with Sequencing Internal Transcribed Spacer Region of Ribosomal DNA. Environmental Science & Eamp; Technology, 2022, 56, 11493-11503.	10.0	O
9613	Feeding black soldier fly larvae (Hermetia illucens) reared on organic rest streams alters gut characteristics of Atlantic salmon (Salmo salar). Journal of Insects As Food and Feed, 2022, 8, 1355-1372.	3.9	6
9614	Microbiota responses to different prebiotics are conserved within individuals and associated with habitual fiber intake. Microbiome, 2022, 10, .	11.1	33
9615	Soil inoculum identity and rate jointly steer microbiomes and plant communities in the field. ISME Communications, 2022, 2, .	4.2	2
9616	One or many? Multi-species livestock grazing influences soil microbiome community structure and antibiotic resistance potential. Frontiers in Sustainable Food Systems, 0, 6, .	3.9	2
9617	Microbiome of the freshwater sponge <i>Ephydatia muelleri</i> shares compositional and functional similarities with those of marine sponges. ISME Journal, 2022, 16, 2503-2512.	9.8	5
9618	Comparing western (Megascops kennicottii) and whiskered (M. trichopsis) screech-owl microbiomes in southern Arizona using a novel 16S rRNA sequencing method. Animal Microbiome, 2022, 4, .	3.8	2
9619	Apyrase-mediated amplification of secretory IgA promotes intestinal homeostasis. Cell Reports, 2022, 40, 111112.	6.4	4
9620	Disturbance by soil mixing decreases microbial richness and supports homogenizing community assembly processes. FEMS Microbiology Ecology, 2022, 98, .	2.7	8
9621	Addressing nontarget amplification in DNA metabarcoding studies of arthropod-feeding rodents. Mammal Research, 0, , .	1.3	2
9623	Surface microbiota of Mediterranean loggerhead sea turtles unraveled by $16\mathrm{S}$ and $18\mathrm{S}$ amplicon sequencing. Frontiers in Ecology and Evolution, $0,10,10$	2.2	4
9624	Patient-Reported Outcomes Correlate With Microbial Community Composition Independent of Mucosal Inflammation in Pediatric Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2023, 29, 286-296.	1.9	4
9625	Teaching genomics to life science undergraduates using cloud computing platforms with open datasets. Biochemistry and Molecular Biology Education, 0, , .	1.2	2
9626	A Winter-to-Summer Transition of Bacterial and Archaeal Communities in Arctic Sea Ice. Microorganisms, 2022, 10, 1618.	3.6	8
9627	Evolved high aerobic capacity has context-specific effects on gut microbiota. Frontiers in Ecology and Evolution, $0,10,1$	2.2	1
9628	Source of human milk (mother or donor) is more important than fortifier type (human or bovine) in shaping the preterm infant microbiome. Cell Reports Medicine, 2022, 3, 100712.	6. 5	17
9629	Geological processes mediate a microbial dispersal loop in the deep biosphere. Science Advances, 2022, 8, .	10.3	17

#	ARTICLE	IF	Citations
9630	Microbial paracetamol degradation involves a high diversity of novel amidase enzyme candidates. Water Research X, 2022, 16, 100152.	6.1	22
9631	Metagenomic Sequencing of the Gallbladder Microbiome: Bacterial Diversity Does Not Vary by Surgical Pathology. Journal of Gastrointestinal Surgery, 2022, 26, 2282-2291.	1.7	1
9632	Comparative Metagenomics Highlight a Widespread Pathway Involved in Catabolism of Phosphonates in Marine and Terrestrial Serpentinizing Ecosystems. MSystems, 2022, 7, .	3.8	4
9633	Isolated Grauer's gorilla populations differ in diet and gut microbiome. Molecular Ecology, 2023, 32, 6523-6542.	3.9	6
9635	Gut microbiota individuality is contingent on temporal scale and age in wild meerkats. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	2.6	11
9636	Detection of Intestinal Dysbiosis in Post-COVID-19 Patients One to Eight Months after Acute Disease Resolution. International Journal of Environmental Research and Public Health, 2022, 19, 10189.	2.6	16
9637	Multiomics assessment of dietary protein titration reveals altered hepatic glucose utilization. Cell Reports, 2022, 40, 111187.	6.4	6
9639	Citizen science monitoring reveals links between honeybee health, pesticide exposure and seasonal availability of floral resources. Scientific Reports, 2022, 12, .	3.3	1
9641	Evaluation of primer pairs for eDNAâ€based assessment of Ephemeroptera, Plecoptera, and Trichoptera across a biogeographically diverse region. Environmental DNA, 2022, 4, 1356-1368.	5.8	6
9642	Soil and Soilless Tomato Cultivation Promote Different Microbial Communities That Provide New Models for Future Crop Interventions. International Journal of Molecular Sciences, 2022, 23, 8820.	4.1	10
9645	Comparison of destructive and nondestructive <scp>DNA</scp> extraction methods for the metabarcoding of arthropod bulk samples. Molecular Ecology Resources, 2023, 23, 92-105.	4.8	13
9646	Environmentally induced reconstruction of microbial communities alters particulate carbon flux of deep chlorophyll maxima in the South China sea. Functional Ecology, 2022, 36, 2493-2507.	3.6	0
9647	Microbial Community, Metabolic Potential and Seasonality of Endosphere Microbiota Associated with Leaves of the Bioenergy Tree Paulownia elongata × fortunei. International Journal of Molecular Sciences, 2022, 23, 8978.	4.1	0
9648	Endospores associated with deep seabed geofluid features in the eastern Gulf of Mexico. Geobiology, 2022, 20, 823-836.	2.4	8
9651	Effect of a Stannous Fluoride Dentifrice on Biofilm Composition, Gene Expression and Biomechanical Properties. Microorganisms, 2022, 10, 1691.	3.6	6
9652	Infection by a eukaryotic gut parasite in wild <i>Daphnia</i> sp. associates with a distinct bacterial community. FEMS Microbiology Ecology, 2022, 98, .	2.7	2
9653	Hepatic metabolism gene expression and gut microbes in offspring, subjected to in-utero PFOS exposure and postnatal diet challenges. Chemosphere, 2022, 308, 136196.	8.2	3
9654	Soil Metabolomics Predict Microbial Taxa as Biomarkers of Moisture Status in Soils from a Tidal Wetland. Microorganisms, 2022, 10, 1653.	3.6	3

#	Article	IF	CITATIONS
9655	Gut microbiota and host genetics modulate the effect of diverse diet patterns on metabolic health. Frontiers in Nutrition, $0, 9, .$	3.7	15
9656	Spatial and temporal variation in New Hampshire bat diets. Scientific Reports, 2022, 12, .	3.3	3
9657	Potential energetic return on investment positively correlated with overall soil microbial activity. Soil Biology and Biochemistry, 2022, 173, 108800.	8.8	5
9658	Current Concentrations of Zn, Cu, and As in Piggery Wastewater Compromise Nutrient Removals in Microalgae–Bacteria Photobioreactors Due to Altered Microbial Communities. Biology, 2022, 11, 1176.	2.8	8
9659	The influence of soil development on the depth distribution and structure of soil microbial communities. Soil Biology and Biochemistry, 2022, 174, 108808.	8.8	14
9660	Fall Armyworm Gut Bacterial Diversity Associated with Different Developmental Stages, Environmental Habitats, and Diets. Insects, 2022, 13, 762.	2.2	12
9661	Shared and contrasting associations in the dynamic nano―and picoplankton communities of two close but contrasting sites from the Bay of Biscay. Environmental Microbiology, 2022, 24, 6052-6070.	3.8	1
9663	Characterization of the bacterial community structure in traditional Gifu ayu-narezushi (fermented) Tj ETQq1	1 0.784314 ı	rgBT /Overlo
9664	Fungal succession on the decomposition of three plant species from a Brazilian mangrove. Scientific Reports, 2022, 12, .	3.3	6
9665	Human gut microbiota after bariatric surgery alters intestinal morphology and glucose absorption in mice independently of obesity. Gut, 2023, 72, 460-471.	12.1	15
9666	Metataxonomic insights into the microbial ecology of farm-scale hay, grass or legume, and corn silage produced with and without inoculants. Frontiers in Systems Biology, 0, 2, .	0.7	5
9667	Host genotype controls ecological change in the leaf fungal microbiome. PLoS Biology, 2022, 20, e3001681.	5.6	14
9668	Host taxonomy determines the composition, structure, and diversity of the earthworm cast microbiome under homogenous feeding conditions. FEMS Microbiology Ecology, 2022, 98, .	2.7	7
9669	On the hidden diversity and niche specialization of the microbial realm of subterranean estuaries. Environmental Microbiology, 2022, 24, 5859-5881.	3.8	11
9670	Faecalibaculum rodentium remodels retinoic acid signaling to govern eosinophil-dependent intestinal epithelial homeostasis. Cell Host and Microbe, 2022, 30, 1295-1310.e8.	11.0	32
9671	Bacterial communities of hookah tobacco products are diverse and differ across brands and flavors. Applied Microbiology and Biotechnology, 2022, 106, 5785-5795.	3.6	2
9672	Oral Administration of Probiotics (Bacillus subtilis and Lactobacillus plantarum) in Nile Tilapia (Oreochromis niloticus) Vaccinated and Challenged with Streptococcus agalactiae. Fishes, 2022, 7, 211.	1.7	2
9673	Northern pike (⟨i⟩Esox lucius⟨/i⟩) youngâ€ofâ€year gut microbiota and associations with wetland nursery water microbial communities in the St. Lawrence River. Aquaculture, Fish and Fisheries, 2022, 2, 384-401.	1.0	1

#	Article	lF	Citations
9674	The quality of organic amendments affects soil microbiome and nitrogen-cycling bacteria in an organic farming system. Frontiers in Soil Science, $0, 2, \ldots$	2.2	4
9675	Effects of Probiotics on Gut Microbiomes of Extremely Preterm Infants in the Neonatal Intensive Care Unit: A Prospective Cohort Study. Nutrients, 2022, 14, 3239.	4.1	9
9676	Optimisation of working parameters for lactic acid bacteria and yeast recovery from table olive biofilms, preserving fruit integrity and reducing chloroplast recovery. LWT - Food Science and Technology, 2022, 166, 113787.	5.2	2
9677	Microbial iron reduction and greenhouse gas production in response to organic matter amendment and temperature increase of periglacial sediments, Bolterdalen, Svalbard. Arctic, Antarctic, and Alpine Research, 2022, 54, 314-334.	1.1	1
9678	Colony self-shading facilitates Symbiodiniaceae cohabitation in a South Pacific coral community. Coral Reefs, 0, , .	2.2	2
9679	Metabolic Strategies Shared by Basement Residents of the Lost City Hydrothermal Field. Applied and Environmental Microbiology, 2022, 88, .	3.1	14
9680	History of fecal transplantation; camel feces contains limited amounts of Bacillus subtilis spores and likely has no traditional role in the treatment of dysentery. PLoS ONE, 2022, 17, e0272607.	2.5	3
9681	Bacterial Community and Chemical Composition of Mixed Fresh Cactus Forage and Buffel Grass Hay during Aerobic Exposure. Agronomy, 2022, 12, 1927.	3.0	1
9682	Temporal variation in skin microbiota of cohabitating amphibians. Canadian Journal of Microbiology, 2022, 68, 583-593.	1.7	2
9684	Characterization of Maladaptive Processes in Acute, Chronic and Remission Phases of Experimental Colitis in C57BL/6 Mice. Biomedicines, 2022, 10, 1903.	3.2	1
9685	Gut microbiota in systemic lupus erythematosus patients and lupus mouse model: a cross species comparative analysis for biomarker discovery. Frontiers in Immunology, 0, 13, .	4.8	15
9686	Investigating the microbial community of <i>Cacopsylla</i> spp. as potential factor in vector competence of phytoplasma. Environmental Microbiology, 2022, 24, 4771-4786.	3.8	10
9687	Experimental methods modestly impact interpretation of the effect of environmental exposures on the larval zebrafish gut microbiome. Scientific Reports, 2022, 12, .	3.3	2
9688	Fluorescence lectin binding analysis of carbohydrate components in dental biofilms grown in situ in the presence or absence of sucrose. Molecular Oral Microbiology, 2022, 37, 196-205.	2.7	3
9690	Systematic profiling of the chicken gut microbiome reveals dietary supplementation with antibiotics alters expression of multiple microbial pathways with minimal impact on community structure. Microbiome, 2022, 10, .	11.1	12
9691	Structure and Dynamics of Periphyton in a Neotropical Freshwater Lake, with Emphasis on Ciliates and Their Relationships with Bacterial Taxa. Microbial Ecology, 2023, 86, 187-199.	2.8	2
9692	Lightella neohaematopini: A new lineage of highly reduced endosymbionts coevolving with chipmunk lice of the genus Neohaematopinus. Frontiers in Microbiology, $0,13,13$	3.5	4
9694	Metabarcoding data reveal vertical multitaxa variation in topsoil communities during the colonization of deglaciated forelands. Molecular Ecology, 2023, 32, 6304-6319.	3.9	6

#	ARTICLE	IF	Citations
9695	Effects of pesticide application and plant sexual identity on leaf physiological traits and phyllosphere bacterial communities. Journal of Plant Ecology, 2023, 16, .	2.3	1
9696	Sulfate- and pH-driven metabolic flexibility in sugarcane vinasse dark fermentation stimulates biohydrogen evolution, sulfidogenesis or homoacetogenesis. International Journal of Hydrogen Energy, 2022, 47, 31202-31222.	7.1	14
9697	Network and machine learning analyses of estuarine microbial communities along a freshwater-marine mixed gradient. Estuarine, Coastal and Shelf Science, 2022, 277, 108026.	2.1	1
9698	First Evaluation of Associated Gut Microbiota in Wild Thick-Lipped Grey Mullets (Chelon labrosus,) Tj ETQq1 1 0.	784314 rg 1.7	BT ₅ /Overlock
9699	Identification of clinical and ecological determinants of strain engraftment after fecal microbiota transplantation using metagenomics. Cell Reports Medicine, 2022, 3, 100711.	6.5	17
9700	Colony but not social phenotype or status structures the gut bacteria of a eusocial mammal. Behavioral Ecology and Sociobiology, 2022, 76, .	1.4	4
9701	Sponge holobionts shift their prokaryotic communities and antimicrobial activity from shallow to lower mesophotic depths. Antonie Van Leeuwenhoek, 2022, 115, 1265-1283.	1.7	3
9702	Crohn's disease in endoscopic remission, obesity, and cases of high genetic risk demonstrate overlapping shifts in the colonic mucosal-luminal interface microbiome. Genome Medicine, 2022, 14, .	8.2	8
9703	Exploring the Bacteriome and Resistome of Humans and Food-Producing Animals in Brazil. Microbiology Spectrum, 2022, 10, .	3.0	4
9704	Fishing for the Microbiome of Tropical Tuna. Microbial Ecology, 2023, 86, 742-755.	2.8	2
9705	Spatial Variation of False Map Turtle (Graptemys pseudogeographica) Bacterial Microbiota in the Lower Missouri River, United States. Journal of Herpetology, 2022, 56, .	0.5	1
9706	Microbiome alterations associated with phthalate exposures in a US-based sample of Latino workers. Environmental Research, 2022, 214, 114126.	7.5	3
9707	Atypical behavioral and thermoregulatory circadian rhythms in mice lacking a microbiome. Scientific Reports, 2022, 12, .	3.3	5
9709	Namco: a microbiome explorer. Microbial Genomics, 2022, 8, .	2.0	4
9710	Longitudinal transmission of bacterial and fungal communities from seed to seed in rice. Communications Biology, 2022, 5, .	4.4	20
9712	Multi-omic Analysis of the Gut Microbiome in Rats with Lithium-Pilocarpine-Induced Temporal Lobe Epilepsy. Molecular Neurobiology, 2022, 59, 6429-6446.	4.0	6
9713	StrainPanDA: Linked reconstruction of strain composition and gene content profiles via pangenomeâ€based decomposition of metagenomic data., 2022, 1,.		8
9714	Metabolic responses of thermophilic endospores to sudden heat-induced perturbation in marine sediment samples. Frontiers in Microbiology, 0, 13 , .	3.5	3

#	Article	IF	CITATIONS
9715	Characterization of presence and activity of microRNAs in the rumen of cattle hints at possible host-microbiota cross-talk mechanism. Scientific Reports, 2022, 12, .	3.3	1
9716	Impact of Stump Removal on Communities of Ectomycorrhizal and Other Soil Fungi in Norway Spruce Stands of Latvia. Diversity, 2022, 14, 673.	1.7	2
9719	Cranberry polyphenols and agave agavins impact gut immune response and microbiota composition while improving gut barrier function, inflammation, and glucose metabolism in mice fed an obesogenic diet. Frontiers in Immunology, 0, 13, .	4.8	24
9720	Free-living and particle-attached bacterial community composition, assembly processes and determinants across spatiotemporal scales in a macrotidal temperate estuary. Scientific Reports, 2022, 12, .	3.3	6
9721	Cascading effects of habitat loss on ectoparasite-associated bacterial microbiomes. ISME Communications, 2022, 2, .	4.2	5
9722	Bacterial community dynamics explain carbon mineralization and assimilation in soils of different landâ€use history. Environmental Microbiology, 2022, 24, 5230-5247.	3.8	4
9723	Crosstalk between mucosal microbiota, host gene expression, and sociomedical factors in the progression of colorectal cancer. Scientific Reports, 2022, 12, .	3.3	3
9724	Impact of microcin J25 on the porcine microbiome in a continuous culture model. Frontiers in Microbiology, 0, 13 , .	3.5	5
9725	Microbiome composition and autochthonous probiotics from contrasting probiosis/dysbiosis states in cobia (Rachycentron canadum) fish epitheliocystis. Access Microbiology, 2022, 4, .	0.5	1
9726	Correlating biodegradation kinetics of 2,3,7,8-tetrachlorodibenzo-p-dioxin to the dynamics of microbial communities originating from soil in Vietnam contaminated with herbicides and dioxins. Frontiers in Microbiology, 0, 13, .	3.5	1
9727	Distinct changes in the colonic microbiome associated with acute diverticulitis. Colorectal Disease, 0, , .	1.4	7
9729	Limited effect of thermal pruning on wild blueberry crop and its root-associated microbiota. Frontiers in Plant Science, 0, 13, .	3.6	3
9731	Potential Therapeutic Skin Microbiomes Suppressing Staphylococcus aureus-Derived Immune Responses and Upregulating Skin Barrier Function-Related Genes via the AhR Signaling Pathway. International Journal of Molecular Sciences, 2022, 23, 9551.	4.1	5
9732	Meta-analysis of larvae of the black soldier fly (<i>Hermetia illucens</i>) microbiota based on 16S rRNA gene amplicon sequencing. FEMS Microbiology Ecology, 2022, 98, .	2.7	8
9733	Adalimumab therapy is associated with increased faecal short chain fatty acids in hidradenitis suppurativa. Experimental Dermatology, 2022, 31, 1872-1880.	2.9	4
9734	Distinguishing the milk microbiota of healthy goats and goats diagnosed with subclinical mastitis, clinical mastitis, and gangrenous mastitis. Frontiers in Microbiology, 0, 13 , .	3.5	6
9735	The microbiome of the pelagic tunicate <i>Dolioletta gegenbauri</i> : AÂpotential link between the grazing and microbial food web. Molecular Ecology, 2023, 32, 6564-6579.	3.9	2
9737	KI Essence extract (a spleen-tonifying formula) promotes neurite outgrowth, alleviates oxidative stress and hypomyelination, and modulates microbiome in maternal immune activation offspring. Frontiers in Pharmacology, 0, 13, .	3.5	2

#	Article	IF	CITATIONS
9738	Global metabolic profiles in a non-human primate model of maternal immune activation: implications for neurodevelopmental disorders. Molecular Psychiatry, 2022, 27, 4959-4973.	7.9	4
9740	Wildfire-dependent changes in soil microbiome diversity and function. Nature Microbiology, 2022, 7, 1419-1430.	13.3	51
9742	Ecosystem size-induced environmental fluctuations affect the temporal dynamics of community assembly mechanisms. ISME Journal, 2022, 16, 2635-2643.	9.8	8
9743	Oral administration of Blautia wexlerae ameliorates obesity and type 2 diabetes via metabolic remodeling of the gut microbiota. Nature Communications, 2022, 13, .	12.8	84
9744	Association between parasite microbiomes and caste development and colony structure in a social trematode. Molecular Ecology, 2022, 31, 5608-5617.	3.9	4
9746	Characterization of interactions of dietary cholesterol with the murine and human gut microbiome. Nature Microbiology, 2022, 7, 1390-1403.	13.3	41
9748	Effects of different duck rearing systems on egg flavor and quality and microbial diversity. Poultry Science, 2022, 101, 102110.	3.4	0
9749	Supplementation of mixed doses of glutamate and glutamine can improve the growth and gut health of piglets during the first 2Âweeks post-weaning. Scientific Reports, 2022, 12, .	3.3	4
9750	Divergent roles for the gut intraepithelial lymphocyte GLP-1R in control of metabolism, microbiota, and TAcell-induced inflammation. Cell Metabolism, 2022, 34, 1514-1531.e7.	16.2	19
9752	Does Host Plant Drive Variation in Microbial Gut Communities in a Recently Shifted Pest?. Microbial Ecology, 2023, 86, 636-646.	2.8	3
9753	Age as a primary driver of the gut microbial composition and function in wild harbor seals. Scientific Reports, 2022, 12, .	3.3	7
9754	Biogeographical survey of soil microbiomes across sub-Saharan Africa: structure, drivers, and predicted climate-driven changes. Microbiome, 2022, 10, .	11.1	14
9755	The Effect of Co-Culture of Two Coral Species on Their Bacterial Composition Under Captive Environments. Marine Biotechnology, 2022, 24, 871-881.	2.4	1
9756	Biodegradable microplastics impact the uptake of Cd in rice: The roles of niche breadth and assembly process. Science of the Total Environment, 2022, 851, 158222.	8.0	10
9757	Hydrolysis capacity of different sized granules in a full-scale aerobic granular sludge (AGS) reactor. Water Research X, 2022, 16, 100151.	6.1	12
9758	The gut microbiota affects the social network of honeybees. Nature Ecology and Evolution, 2022, 6, 1471-1479.	7.8	24
9759	Soil metatranscriptome demonstrates a shift in C, N, and S metabolisms of a grassland ecosystem in response to elevated atmospheric CO2. Frontiers in Microbiology, 0, 13 , .	3.5	6
9760	A systems biology approach to study non-alcoholic fatty liver (NAFL) in women with obesity. IScience, 2022, 25, 104828.	4.1	4

#	Article	IF	CITATIONS
9762	Downregulation of growth plate genes involved with the onset of femoral head separation in young broilers. Frontiers in Physiology, $0,13,13$	2.8	2
9763	Nutrient-limited subarctic caves harbour more diverse and complex bacterial communities than their surface soil. Environmental Microbiomes, 2022, 17, .	5.0	9
9764	Modeling-Guided Amendments Lead to Enhanced Biodegradation in Soil. MSystems, 0, , .	3.8	3
9765	Machine Learning Data Analysis Highlights the Role of Parasutterella and Alloprevotella in Autism Spectrum Disorders. Biomedicines, 2022, 10, 2028.	3.2	10
9766	Human milk nutrient fortifiers alter the developing gastrointestinal microbiota of very-low-birth-weight infants. Cell Host and Microbe, 2022, 30, 1328-1339.e5.	11.0	12
9767	Heritable vaginal bacteria influence immune tolerance and relate to early-life markers of allergic sensitization in infancy. Cell Reports Medicine, 2022, 3, 100713.	6.5	11
9768	MiCloud: A unified web platform for comprehensive microbiome data analysis. PLoS ONE, 2022, 17, e0272354.	2.5	6
9769	Using dietary metabarcoding analyses to characterise waterbirdsâ€agriculture interactions. Journal of Applied Ecology, 0, , .	4.0	1
9770	Nectar resources affect birdâ€dispersed microbial metacommunities in suburban and rural gardens. Environmental Microbiology, 0, , .	3.8	3
9771	Genetic diversity of honeybee colonies predicts gut bacterial diversity of individual colony members. Environmental Microbiology, 2022, 24, 5643-5653.	3.8	1
9772	Quantitative and Qualitative Changes in the Genetic Diversity of Bacterial Communities in Anaerobic Bioreactors with the Diatomaceous Earth/Peat Cell Carrier. Cells, 2022, 11, 2571.	4.1	3
9773	Does swab type matter? Comparing methods for Mannheimia haemolytica recovery and upper respiratory microbiome characterization in feedlot cattle. Animal Microbiome, 2022, 4, .	3.8	5
9776	Maternal soybean diet on prevention of obesity-related breast cancer through early-life gut microbiome and epigenetic regulation. Journal of Nutritional Biochemistry, 2022, 110, 109119.	4.2	8
9777	Metagenomic features of bioburden serve as outcome indicators in combat extremity wounds. Scientific Reports, 2022, 12, .	3.3	4
9778	Cobamide Sharing Is Predicted in the Human Skin Microbiome. MSystems, 2022, 7, .	3.8	15
9779	Deciphering the Tissue Tropism of the RNA Viromes Harbored by Field-Collected Anopheles sinensis and Culex quinquefasciatus. Microbiology Spectrum, 2022, 10, .	3.0	1
9780	Anti-Inflammatory Diet Prevents Subclinical Colonic Inflammation and Alters Metabolomic Profile of Ulcerative Colitis Patients in Clinical Remission. Nutrients, 2022, 14, 3294.	4.1	26
9783	Supplemental Oxygen Alters the Airway Microbiome in Cystic Fibrosis. MSystems, 2022, 7, .	3.8	1

#	Article	IF	CITATIONS
9784	Dietary diversity of multiple shorebird species in an Asian subtropical wetland unveiled by <scp>DNA</scp> metabarcoding. Environmental DNA, 2022, 4, 1381-1396.	5.8	4
9785	Microbial communities on plastic particles in surface waters differ from subsurface waters of the North Pacific Subtropical Gyre. Marine Pollution Bulletin, 2022, 182, 113949.	5.0	9
9786	Investigating the nutritional profile and bacteriome diversity in Bangladeshi sour yogurt. Biocatalysis and Agricultural Biotechnology, 2022, 44, 102451.	3.1	3
9787	Rare biosphere in cultivated Panax rhizosphere shows deterministic assembly and cross-plant similarity. Ecological Indicators, 2022, 142, 109215.	6.3	3
9788	Confluences characteristics determine the influence scope of microbial community from confluence hydrodynamic zone on river network. Journal of Hydrology, 2022, 612, 128288.	5.4	5
9789	DNA metabarcoding reveals the threat of rapidly expanding barred owl populations to native wildlife in western North America. Biological Conservation, 2022, 273, 109678.	4.1	2
9790	Modification of post-traumatic epilepsy by fecal microbiota transfer. Epilepsy and Behavior, 2022, 134, 108860.	1.7	3
9791	Dataset of ileum bacterial diversity in mice after heart failure due to pressure overload. Data in Brief, 2022, 44, 108498.	1.0	0
9792	Modeling of hydrogen and organic acid production using different concentrations of sugarcane vinasse under thermophilic conditions and a link with microbial community 16S rRNA gene sequencing data. Journal of Cleaner Production, 2022, 370, 133437.	9.3	7
9793	Succession of the soil bacterial community as resource utilization shifts from plant residues to rhizodeposits. Soil Biology and Biochemistry, 2022, 173, 108785.	8.8	13
9794	Trade-off for survival: Microbiome response to chemical exposure combines activation of intrinsic resistances and adapted metabolic activity. Environment International, 2022, 168, 107474.	10.0	1
9795	Characterizing and comparing microbial community and biofilm structure in three nitrifying moving bed biofilm reactors. Journal of Environmental Management, 2022, 320, 115883.	7.8	3
9796	Microbial utilization of simple and complex carbon compounds in a temperate forest soil. Soil Biology and Biochemistry, 2022, 173, 108786.	8.8	14
9797	Morpho-anatomical traits explain the effects of bacterial-feeding nematodes on soil bacterial community composition and plant growth and nutrition. Geoderma, 2022, 425, 116068.	5.1	6
9798	Biochar amendment reduces cadmium uptake by stimulating cadmium-resistant PGPR in tomato rhizosphere. Chemosphere, 2022, 307, 136138.	8.2	38
9799	Reduced graphene oxide accelerates the dissipation of 14C-Triclosan in paddy soil via adsorption interactions. Chemosphere, 2022, 307, 136125.	8.2	2
9800	Microbial marker for seawater intrusion in a coastal Mediterranean shallow Lake, Lake Vrana, Croatia. Science of the Total Environment, 2022, 849, 157859.	8.0	2
9801	Microbiome alterations from volatile organic compounds (VOC) exposures among workers in salons primarily serving women of color. Environmental Research, 2022, 214, 114125.	7.5	3

#	Article	IF	Citations
9802	Bees under interactive stressors: the novel insecticides flupyradifurone and sulfoxaflor along with the fungicide azoxystrobin disrupt the gut microbiota of honey bees and increase opportunistic bacterial pathogens. Science of the Total Environment, 2022, 849, 157941.	8.0	29
9803	Prediction of long-term localized corrosion rates in a carbon steel cooling water system is enhanced by metagenome analysis. Engineering Failure Analysis, 2022, 141, 106733.	4.0	7
9804	Insight on bacteria communities in outdoor bronze and marble artefacts in a changing environment. Science of the Total Environment, 2022, 850, 157804.	8.0	3
9805	Modulation of the food microbiome by apple fruit processing. Food Microbiology, 2022, 108, 104103.	4.2	10
9806	Influence of lactate to acetate ratio on biological production of medium chain carboxylates via open culture fermentation. Science of the Total Environment, 2022, 851, 158171.	8.0	7
9807	Prebiotics modify host metabolism in rainbow trout (Oncorhynchus mykiss) fed with a total plant-based diet: Potential implications for microbiome-mediated diet optimization. Aquaculture, 2022, 561, 738699.	3.5	11
9808	Mitochondrial cytochrome c oxidase subunit I (COI) metabarcoding of Foraminifera communities using taxon-specific primers. PeerJ, 0, 10, e13952.	2.0	6
9809	Metaomics unveils the contribution of Alteromonas bacteria to carbon cycling in marine oxygen minimum zones. Frontiers in Marine Science, 0, 9, .	2.5	3
9810	First insight into oral microbiome diversity in Papua New Guineans reveals a specific regional signature. Molecular Ecology, 2023, 32, 2551-2564.	3.9	4
9811	Impact of preservation method and storage period on ribosomal metabarcoding of marine microbes: Implications for remote automated samplings. Frontiers in Microbiology, 0, 13, .	3.5	1
9812	DNA-metabarcoding analyses of the grapevine wood fungal community in the Krasnodar Region and Crimea. Ecological Genetics, 2022, 20, 89-100.	0.5	0
9814	Effects of long-term application of organic manure and chemical fertilizer on soil properties and microbial communities in the agro-pastoral ecotone of North China. Frontiers in Environmental Science, 0, 10, .	3.3	5
9815	Increased DMSP availability during thermal stress influences DMSP-degrading bacteria in coral mucus. Frontiers in Marine Science, 0, 9, .	2.5	6
9816	Microbiome composition is shaped by geography and population structure in the parasitic wasp <i>Asobara japonica </i> , but not in the presence of the endosymbiont <i>Wolbachia </i> . Molecular Ecology, 2023, 32, 6644-6658.	3.9	3
9817	Diversity and structure of soil fungal communities unveil the building history of a burial mound of ancient Japan (Tobiotsuka Kofun, Okayama Prefecture). Journal of Archaeological Science, 2022, 146, 105656.	2.4	5
9818	Effects of a Carnobacterium maltaromaticum strain at natural contamination levels on the microbiota of vacuum-packaged beef steaks during chilled storage. LWT - Food Science and Technology, 2022, 168, 113944.	5.2	2
9819	Wastewater microorganisms impact microbial diversity and important ecological functions of stream periphyton. Water Research, 2022, 225, 119119.	11.3	13
9820	Machine learning on the road to unlocking microbiota's potential for boosting immune checkpoint therapy. International Journal of Medical Microbiology, 2022, 312, 151560.	3.6	1

#	Article	IF	CITATIONS
9821	Aerobiology over the Southern Ocean – Implications for bacterial colonization of Antarctica. Environment International, 2022, 169, 107492.	10.0	6
9822	Fractional factorial experimental design for optimizing volatile fatty acids from anaerobic fermentation of municipal sludge: Microbial community and activity investigation. Renewable Energy, 2022, 199, 733-744.	8.9	3
9823	Ecological niche differences regulate the assembly of bacterial community in endophytic and rhizosphere of Eucalyptus. Forest Ecology and Management, 2022, 524, 120521.	3.2	9
9824	Bacterial and fungal co-occurrence patterns in agricultural soils amended with compost and bokashi. Soil Biology and Biochemistry, 2022, 174, 108831.	8.8	6
9825	Bacterial, fungal, and mycorrhizal communities in the soil differ between clearcuts and insect outbreaks in the boreal forest 50Âyears after disturbance. Forest Ecology and Management, 2022, 523, 120493.	3.2	3
9826	Microbial community composition and hydrochemistry of underexplored geothermal waters in Croatia. Systematic and Applied Microbiology, 2022, 45, 126359.	2.8	5
9827	Centrate as a sustainable growth medium: Impact on microalgal inocula and bacterial communities in tubular photobioreactor cultivation systems. Bioresource Technology, 2022, 363, 127979.	9.6	5
9828	The effect of production parameters on the spatial distribution of bacterial cells in the sausage meat matrix. Meat Science, 2022, 194, 108983.	5.5	0
9829	Effect of fumigants and non-fumigants on nematode and weed control, crop yield, and soil microbial diversity and predicted functionality in a strawberry production system. Science of the Total Environment, 2022, 852, 158285.	8.0	8
9830	Harmful cyanobacterial aerosolization dynamics in the airshed of a eutrophic estuary. Science of the Total Environment, 2022, 852, 158383.	8.0	9
9831	Plutonium mobilization from contaminated estuarine sediments, Esk Estuary (UK). Chemosphere, 2022, 308, 136240.	8.2	2
9832	Field-aged biochar enhances soil organic carbon by increasing recalcitrant organic carbon fractions and making microbial communities more conducive to carbon sequestration. Agriculture, Ecosystems and Environment, 2022, 340, 108177.	5.3	17
9833	Meta-analysis of community composition patterns of halophyte and xerophyte rhizosphere associated bacteria. Rhizosphere, 2022, 24, 100588.	3.0	1
9834	Microbial diversity across compartments in an aquaponic system and its connection to the nitrogen cycle. Science of the Total Environment, 2022, 852, 158426.	8.0	14
9835	Intensity and duration of exposure determine prokaryotic community response to salinization in freshwater wetland soils. Geoderma, 2022, 428, 116138.	5.1	4
9836	Tillage intensity and plant rhizosphere selection shape bacterial-archaeal assemblage diversity and nitrogen cycling genes. Soil and Tillage Research, 2023, 225, 105525.	5.6	4
9837	Microbial communities mediating net methylmercury formation along a trophic gradient in a peatland chronosequence. Journal of Hazardous Materials, 2023, 442, 130057.	12.4	4
9838	Thermal and latitudinal patterns in pace-of-life traits are partly mediated by the gut microbiome. Science of the Total Environment, 2023, 855, 158829.	8.0	4

#	ARTICLE	IF	CITATIONS
9839	Effects of microplastics on common bean rhizosphere bacterial communities. Applied Soil Ecology, 2023, 181, 104649.	4.3	15
9840	Influence of the biofloc bacterial community on the digestive activity of Nile tilapia (Oreochromis) Tj ETQq1	1 0.784314 r	gBT _y Overlock
9841	Intestinal Microbiome Richness of Coral Reef Damselfishes (<i>Actinopterygii: Pomacentridae</i>). Integrative Organismal Biology, 2022, 4, .	1.8	3
9842	Bacterioplankton response to physical stratification following deep convection. Elementa, 2022, 10, .	3.2	1
9843	Hepatic Metabolism Gene Expression and Gut Microbes in Offspring, Subjected to In-Utero PFOS Exposure and Postnatal Diet Challenges. SSRN Electronic Journal, 0, , .	0.4	0
9844	Ankle brachial indices and anaerobes: is peripheral arterial disease associated with anaerobic bacteria in diabetic foot ulcers?. Therapeutic Advances in Endocrinology and Metabolism, 2022, 13, 204201882211187.	3.2	2
9845	Carbon Substrate Selects for Different Lineages of N2O Reducing Communities in Soils Under Anoxic Conditions. SSRN Electronic Journal, 0, , .	0.4	0
9846	Effect of milk protein hydrolysate supplementation on protein energy malnutrition-induced gut dysbiosis. Food and Function, 2022, 13, 10305-10319.	4.6	O
9847	Impavido Attenuates Inflammation, Reduces Atherosclerosis, and Alters Gut Microbiota in Hyperlipidemic Mice. SSRN Electronic Journal, 0, , .	0.4	0
9848	Effect of Doxycycline Addition on Microflora and Microbial Community of Activated Sludge. SSRN Electronic Journal, 0, , .	0.4	O
9849	Dynamics of Microbial Community in Response to Co-Feedstock Composition in an Anaerobic Digester. SSRN Electronic Journal, 0, , .	0.4	0
9850	Diversity and biogeography of planktonic diatoms in Svalbard fjords: The role of dispersal and Arctic endemism in phytoplankton community structuring. Elementa, 2022, 10, .	3.2	8
9851	The microbiome in adult acute appendicitis. Gut Microbiome, 2022, 3, .	3.2	1
9852	Tools to Study Gut Microbiome. , 2022, , 253-270.		O
9853	Response of Microbial Community in Lake Sediments with Various Pac Contamination Levels and Different Exposure Durations. SSRN Electronic Journal, 0, , .	0.4	0
9854	An IBD-Associated Pathobiont Synergises With NSAID to Promote Colitis Which is Blocked by NLRP3 Inflammasome and Caspase-8 Inhibitors. SSRN Electronic Journal, 0, , .	0.4	0
9855	Shifts in uterine bacterial communities associated with endogenous progesterone and $17\hat{l}^2$ -estradiol concentrations in beef cattle. Domestic Animal Endocrinology, 2023, 82, 106766.	1.6	5
9856	Mytilus farming drives higher local bacterial diversity and facilitates the accumulation of aerobic anoxygenic photoheterotrophic related genera. Science of the Total Environment, 2023, 856, 158861.	8.0	0

#	Article	IF	CITATIONS
9857	Pubertal consumption of R. badensis subspecies acadiensis modulates LPS-induced immune responses and gut microbiome dysbiosis in a sex-specific manner. Brain, Behavior, and Immunity, 2023, 107, 62-75.	4.1	9
9858	Characterization of microbial community assembly on new wooden vats for use in cheese production. Food Microbiology, 2023, 109, 104154.	4.2	3
9859	Impact of Norway spruce pre-degradation stages induced by GloeophyllumÂtrabeum on fungal and bacterial communities. Fungal Ecology, 2023, 61, 101188.	1.6	2
9860	Depletion of cyanogenic glycosides in whole flaxseed via Lactobacillaceae fermentation. Food Chemistry, 2023, 403, 134441.	8.2	4
9861	The Effects of Secondary Growth of Spartina alterniflora after Treatment on Sediment Microorganisms in the Yellow River Delta. Microorganisms, 2022, 10, 1722.	3.6	4
9862	Effect of bovine milk fat-based infant formulae on microbiota, metabolites and stool parameters in healthy term infants in a randomized, crossover, placebo-controlled trial. BMC Nutrition, 2022, 8, .	1.6	2
9863	Deposit-feeding worms control subsurface ecosystem functioning in intertidal sediment with strong physical forcing. , 2022, 1 , .		3
9864	Soil pH indirectly determines Ralstonia solanacearum colonization through its impacts on microbial networks and specific microbial groups. Plant and Soil, 2023, 482, 73-88.	3.7	5
9865	Exploration and comparison of bacterial communities present in bovine faeces, milk and blood using 16S rRNA metagenomic sequencing. PLoS ONE, 2022, 17, e0273799.	2.5	11
9866	Factors associated with soils suppressive to black scurf of potato caused by Rhizoctonia solani. New Zealand Plant Protection, 0, 75, 31-49.	0.3	2
9867	Mosquito sex and mycobiota contribute to fructose metabolism in the Asian tiger mosquito Aedes albopictus. Microbiome, 2022, 10, .	11.1	7
9868	Reusing a prepaid health plan's fecal immunochemical tests for microbiome associations with colorectal adenoma. Scientific Reports, 2022, 12, .	3.3	0
9869	Glycerol amendment enhances biosulfidogenesis in acid mine drainage-affected areas: An incubation column experiment. Frontiers in Bioengineering and Biotechnology, $0,10,10$	4.1	1
9872	Land-Use Change and Management Intensification Is Associated with Shifts in Composition of Soil Microbial Communities and Their Functional Diversity in Coffee Agroecosystems. Microorganisms, 2022, 10, 1763.	3.6	3
9874	Linking bacteria, volatiles and insects on carrion: the role of temporal and spatial factors regulating inter-kingdom communication via volatiles. Royal Society Open Science, 2022, 9, .	2.4	8
9875	Gut Microbiome and Mycobiome Alterations in an In Vivo Model of Alzheimer's Disease. Genes, 2022, 13, 1564.	2.4	14
9876	Association of Gut Microbiota with Atherogenic Dyslipidemia, and Its Impact on Serum Lipid Levels after Bariatric Surgery. Nutrients, 2022, 14, 3545.	4.1	17
9877	Exploring the diversity and structural response of sediment-associated microbiota communities to environmental pollution at the siangshan wetland in Taiwan using environmental DNA metagenomic approach. Frontiers in Marine Science, 0, 9, .	2.5	1

#	Article	IF	Citations
9878	Effect of Site and Phenological Status on the Potato Bacterial Rhizomicrobiota. Microorganisms, 2022, 10, 1743.	3.6	1
9879	The phenotype of the gut region is more stably retained than developmental stage in piglet intestinal organoids. Frontiers in Cell and Developmental Biology, 0, 10 , .	3.7	3
9880	Long-Term Fertilization Strategy Impacts Rhizoctonia solani–Microbe Interactions in Soil and Rhizosphere and Defense Responses in Lettuce. Microorganisms, 2022, 10, 1717.	3.6	5
9883	Impact of disturbance and dietary shift on gastrointestinal bacterial community and its invertebrate host system. Molecular Ecology, 2023, 32, 6631-6643.	3.9	3
9885	High Dietary Intake of Rye Affects Porcine Gut Microbiota in a Salmonella Typhimurium Infection Study. Plants, 2022, 11, 2232.	3.5	5
9887	Distinct stages of the intestinal bacterial community of Ampullaceana balthica after salinization. Frontiers in Microbiology, 0, 13, .	3.5	5
9890	Obesity induced gut dysbiosis contributes to disease severity in an animal model of multiple sclerosis. Frontiers in Immunology, 0, 13 , .	4.8	16
9891	Prokaryotes of renowned Karlovy Vary (Carlsbad) thermal springs: phylogenetic and cultivation analysis. Environmental Microbiomes, 2022, 17, .	5.0	7
9892	Analysis of trapped mosquito excreta as a nonâ€invasive method to reveal biodiversity and arbovirus circulation. Molecular Ecology Resources, 0, , .	4.8	3
9893	Nutritional Evaluation of Black Soldier Fly Frass as an Ingredient in Florida Pompano (Trachinotus) Tj ETQq1 1 C	.784314 rgl 2.3	BT / Overlock
9894	The Effect of Feeding with Central European Local Mulberry Genotypes on the Development and Health Status of Silkworms and Quality Parameters of Raw Silk. Insects, 2022, 13, 836.	2.2	3
9895	Skin microbiota analysis in patients with anorexia nervosa and healthy-weight controls reveals microbial indicators of healthy weight and associations with the antimicrobial peptide psoriasin. Scientific Reports, 2022, 12, .	3.3	2
9896	Fellfields of the Kerguelen Islands harbour specific soil microbiomes and rhizomicrobiomes of an endemic plant facing necrosis. Frontiers in Soil Science, 0, 2, .	2.2	0
9897	Correlation between postmortem microbial signatures and substance abuse disorders. PLoS ONE, 2022, 17, e0274401.	2.5	2
9899	A large-scale, multi-year microbial community survey of a freshwater trout aquaculture facility. FEMS Microbiology Ecology, 2022, 98, .	2.7	3
9900	Adipose Tissue, Bile Acids, and Gut Microbiome Species Associated With Gallstones After Bariatric Surgery. Journal of Lipid Research, 2022, 63, 100280.	4.2	3
9901	Intersection of Diet and Exercise with the Gut Microbiome and Circulating Metabolites in Male Bodybuilders: A Pilot Study. Metabolites, 2022, 12, 911.	2.9	2
9902	Maternal effects on early-life gut microbiota maturation in a wild nonhuman primate. Current Biology, 2022, 32, 4508-4520.e6.	3.9	5

#	Article	IF	CITATIONS
9903	MetaPhage: an Automated Pipeline for Analyzing, Annotating, and Classifying Bacteriophages in Metagenomics Sequencing Data. MSystems, 2022, 7, .	3.8	15
9904	Longitudinal analysis of the rectal microbiome in dogs with diabetes mellitus after initiation of insulin therapy. PLoS ONE, 2022, 17, e0273792.	2.5	3
9905	Tropical and Temperate Lineages of <i>Rhipicephalus sanguineus s.l.</i> Ticks (Acari: Ixodidae) Host Different Strains of <i>Coxiella</i> -like Endosymbionts. Journal of Medical Entomology, 0, , .	1.8	0
9906	Assessing the coral microbiome at the scale of tissue-specific habitats within the coral meta-organism. Frontiers in Marine Science, 0, 9, .	2.5	5
9907	Examining ecological succession of diatoms in California Current System cyclonic mesoscale eddies. Limnology and Oceanography, 2022, 67, 2586-2602.	3.1	2
9908	Effect of experimentally increased nutrient availability on the structure, metabolic activities, and potential microbial functions of a maritime Antarctic microbial mat. Frontiers in Microbiology, 0, 13, .	3.5	3
9909	Breathing can be dangerous: Opportunistic fungal pathogens and the diverse community of the small mammal lung mycobiome. Frontiers in Fungal Biology, $0,3,.$	2.0	8
9910	Bacteria communities and water quality parameters in riverine water and sediments near wastewater discharges. Scientific Data, 2022, 9, .	5.3	2
9911	Microbial diversity in various diseases of the stomach Science and Innovations, 2022, 1, 23-26.	0.1	0
9912	Fungicide-Mediated Shifts in the Foliar Fungal Community of an Invasive Grass. Phytobiomes Journal, 2023, 7, 198-207.	2.7	1
9914	Improving environmental monitoring of Vibrionaceae in coastal ecosystems through 16S rRNA gene amplicon sequencing. Environmental Science and Pollution Research, 2022, 29, 67466-67482.	5.3	5
9915	Evolution of the Gut Microbiome in HIV-Exposed Uninfected and Unexposed Infants during the First Year of Life. MBio, 2022, 13, .	4.1	9
9916	Diet-driven microbial ecology underpins associations between cancer immunotherapy outcomes and the gut microbiome. Nature Medicine, 2022, 28, 2344-2352.	30.7	79
9917	Inter- and Intraindividual Differences in the Capacity of the Human Intestinal Microbiome in Fecal Slurries to Metabolize Fructoselysine and Carboxymethyllysine. Journal of Agricultural and Food Chemistry, 2022, 70, 11759-11768.	5.2	2
9918	Influence of plant genotype and soil on the cotton rhizosphere microbiome. Frontiers in Microbiology, 0, 13 , .	3.5	6
9919	DNA metabarcoding the diet of <i>Podarcis</i> lizards endemic to the Balearic Islands. Environmental Epigenetics, O, , .	1.8	4
9921	Intercontinental Gut Microbiome Variances in IBD. International Journal of Molecular Sciences, 2022, 23, 10868.	4.1	3
9922	Are the Bacteria and Their Metabolites Contributing for Gut Inflammation on GSD-la Patients?. Metabolites, 2022, 12, 873.	2.9	3

#	Article	IF	CITATIONS
9923	Expansion of Opportunistic Enteric Fungal Pathogens and Occurrence of Gut Inflammation in Human Liver Echinococcosis. Microbiology Spectrum, 2022, 10, .	3.0	1
9924	Compost Microcosms as Microbially Diverse, Natural-like Environments for Microbiome Research in Caenorhabditis elegans . Journal of Visualized Experiments, 2022, , .	0.3	3
9925	Nicotinamide adenine dinucleotide supplementation drives gut microbiota variation in Alzheimer's mouse model. Frontiers in Aging Neuroscience, 0, 14, .	3.4	8
9926	Natural diversity of the honey bee (Apis mellifera) gut bacteriome in various climatic and seasonal states. PLoS ONE, 2022, 17, e0273844.	2.5	15
9927	High-quality metagenome-assembled genomes from proximal colonic microbiomes of synbiotic-treated korean native black pigs reveal changes in functional capacity. Scientific Reports, 2022, 12, .	3.3	2
9928	Spatial and temporal variation in $\langle i \rangle \hat{l}' \langle i \rangle \langle sup \rangle 13 \langle sup \rangle C$ values of methane emitted from a hemiboreal mire: methanogenesis, methanotrophy, and hysteresis. Biogeosciences, 2022, 19, 4331-4349.	3.3	1
9929	Assessing a megadiverse but poorly known community of fishes in a tropical mangrove estuary through environmental DNA (eDNA) metabarcoding. Scientific Reports, 2022, 12, .	3.3	2
9931	Shallow shotgun sequencing of the microbiome recapitulates <scp>16S</scp> amplicon results and provides functional insights. Molecular Ecology Resources, 2023, 23, 549-564.	4.8	3
9932	Twelve Months of Time-Restricted Feeding Improves Cognition and Alters Microbiome Composition Independent of Macronutrient Composition. Nutrients, 2022, 14, 3977.	4.1	14
9933	Study of gut microbiota alterations in Alzheimer's dementia patients from Kazakhstan. Scientific Reports, 2022, 12, .	3.3	32
9934	Microbial and human transcriptome in vaginal fluid at midgestation: Association with spontaneous preterm delivery. Clinical and Translational Medicine, 2022, 12, .	4.0	1
9936	Metformin modulates the gut microbiome in broiler breeder hens. Frontiers in Physiology, 0, 13 , .	2.8	1
9937	Estuarine microbial networks and relationships vary between environmentally distinct communities. PeerJ, 0, 10, e14005.	2.0	1
9939	Insight into the Fecal Microbiota Signature Associated with Growth Specificity in Korean Jindo Dogs Using 16S rRNA Sequencing. Animals, 2022, 12, 2499.	2.3	1
9940	Study of Wetland Soils of the Salar de Atacama with Different Azonal Vegetative Formations Reveals Changes in the Microbiota Associated with Hygrophile Plant Type on the Soil Surface. Microbiology Spectrum, 2022, 10, .	3.0	5
9942	Review of the Current State of Freely Accessible Web Tools for the Analysis of 16S rRNA Sequencing of the Gut Microbiome. International Journal of Molecular Sciences, 2022, 23, 10865.	4.1	2
9943	Nutrient management and bioaugmentation interactively shape plant–microbe interactions in <i>Miscanthus</i> Â×Â <i>giganteus</i> . GCB Bioenergy, 2022, 14, 1235-1249.	5.6	6
9945	Short- and Long-Term Effects of a Prebiotic Intervention with Polyphenols Extracted from European Black Elderberry—Sustained Expansion of Akkermansia spp Journal of Personalized Medicine, 2022, 12, 1479.	2.5	7

#	Article	IF	CITATIONS
9946	Characterization of Two Zymomonas mobilis Wild Strains and Analysis of Populations Dynamics during Their Leavening of Bread-like Doughs. Foods, 2022, 11, 2768.	4.3	2
9947	Bone app $\tilde{\mathbb{A}}$ ©tit: DNA metabarcoding as a non-lethal alternative to morphological dietary assessment in Atlantic bonefish (Albula vulpes). Environmental Biology of Fishes, 2023, 106, 337-348.	1.0	2
9948	Using Biological Responses to Monitor Freshwater Post-Spill Conditions over 3Âyears in Blacktail Creek, North Dakota, USA. Archives of Environmental Contamination and Toxicology, 2022, 83, 253-271.	4.1	3
9949	Oral microbiota analyses of Saudi sickle cell anemics with dental caries. International Dental Journal, 2022, , .	2.6	0
9951	The microbiome of the dinoflagellate Prorocentrum cordatum in laboratory culture and its changes at higher temperatures. Frontiers in Microbiology, 0 , 13 , .	3.5	3
9953	Particles act as †specialty centers†with expanded enzymatic function throughout the water column in the western North Atlantic. Frontiers in Microbiology, 0, 13, .	3.5	2
9955	Randomized Double-Blind Crossover Study for Evaluating a Probiotic Mixture on Gastrointestinal and Behavioral Symptoms of Autistic Children. Journal of Clinical Medicine, 2022, 11, 5263.	2.4	8
9956	Metabolite Production in <i>Alkanna tinctoria</i> Links Plant Development with the Recruitment of Individual Members of Microbiome Thriving at the Root-Soil Interface. MSystems, 2022, 7, .	3.8	7
9957	Bidirectional Interactions between Arboviruses and the Bacterial and Viral Microbiota in Aedes aegypti and Culex quinquefasciatus. MBio, 2022, 13, .	4.1	13
9958	Exploring the Healthy Eye Microbiota Niche in a Multicenter Study. International Journal of Molecular Sciences, 2022, 23, 10229.	4.1	21
9959	Impact of Antibiotics on the Lung Microbiome and Lung Function in Children With Cystic Fibrosis 1 Year After Hospitalization for an Initial Pulmonary Exacerbation. Open Forum Infectious Diseases, 2022, 9, .	0.9	2
9960	Decreased efficiency of pollen collection due to Sulfoxaflor exposure leads to a reduction in the size of bumble bee workers in late European summer. Frontiers in Ecology and Evolution, 0, 10, .	2.2	2
9961	The Entero-Mammary Pathway and Perinatal Transmission of Gut Microbiota and SARS-CoV-2. International Journal of Molecular Sciences, 2022, 23, 10306.	4.1	6
9962	Interference and co-existence of staphylococci and Cutibacterium acnes within the healthy human skin microbiome. Communications Biology, 2022, 5, .	4.4	14
9963	Environmental and maternal factors shaping tonsillar microbiota development in piglets. BMC Microbiology, 2022, 22, .	3.3	8
9964	Microbial drivers of plant richness and productivity in a grassland restoration experiment along a gradient of landâ€use intensity. New Phytologist, 2022, 236, 1936-1950.	7. 3	6
9965	Intestinal Dysbiosis and Risk of Posttransplant Clostridioides difficile Infection in a Longitudinal Cohort of Liver Transplant Recipients. MSphere, 2022, 7, .	2.9	3
9966	Minimal overall divergence of the gut microbiome in an adaptive radiation of Cyprinodon pupfishes despite potential adaptive enrichment for scale-eating. PLoS ONE, 2022, 17, e0273177.	2.5	1

#	Article	IF	CITATIONS
9967	Dynamics of microbial community and enzyme activities during preparation of <i>Agaricus bisporus</i> compost substrate. ISME Communications, 2022, 2, .	4.2	5
9968	Carbohydrate utilization by the gut microbiome determines host health responsiveness to whole grain type and processing methods. Gut Microbes, 2022, 14 , .	9.8	6
9969	Gut microbiome associations with host genotype vary across ethnicities and potentially influence cardiometabolic traits. Cell Host and Microbe, 2022, 30, 1464-1480.e6.	11.0	13
9970	Adaptive sampling during sequencing reveals the origins of the bovine reproductive tract microbiome across reproductive stages and sexes. Scientific Reports, 2022, 12, .	3.3	4
9971	Riverine drift communities during larval fish dispersal over multiple recruitment years. Hydrobiologia, 2022, 849, 4357-4375.	2.0	1
9972	Pollen <scp>DNA</scp> metabarcoding reveals cryptic diversity and high spatial turnover in alpine plant–pollinator networks. Molecular Ecology, 2023, 32, 6377-6393.	3.9	11
9973	Microbial Interdomain Interactions Delineate the Disruptive Intestinal Homeostasis in Clostridioides difficile Infection. Microbiology Spectrum, 0, , .	3.0	0
9974	Bacterial community of sediments under the Eastern Boundary Current System shows high microdiversity and a latitudinal spatial pattern. Frontiers in Microbiology, 0, 13, .	3.5	4
9975	Bacterial composition in Swedish raw drinking water reveals three major interacting ubiquitous metacommunities. MicrobiologyOpen, 2022, 11 , .	3.0	0
9976	Genetic analysis of seed traits in Sorghum bicolor that affect the human gut microbiome. Nature Communications, 2022, 13, .	12.8	7
9977	Polypharmacy With High Drug Burden Index (DBI) Alters the Gut Microbiome Overriding Aging Effects and Is Reversible With Deprescribing. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2023, 78, 213-222.	3.6	9
9979	Microbial succession in a marine sediment: Inferring interspecific microbial interactions with marine cable bacteria. Environmental Microbiology, 2022, 24, 6348-6364.	3.8	11
9980	Microbes Contribute to Chemopreventive Efficacy, Intestinal Tumorigenesis, and the Metabolome. Cancer Prevention Research, 2022, 15, 803-814.	1.5	3
9981	Inter-annual Persistence of Canopy Fungi Driven by Abundance Despite High Spatial Turnover. Microbial Ecology, 0, , .	2.8	0
9982	Seasonal bacterial niche structures and chemolithoautotrophic ecotypes in a North Atlantic fjord. Scientific Reports, 2022, 12, .	3.3	1
9983	Shifts in water column microbial composition associated to lakes with different trophic conditions: "Lagunas de Montebello―National Park, Chiapas, México. PeerJ, 0, 10, e13999.	2.0	4
9984	Human milk microbiome is shaped by breastfeeding practices. Frontiers in Microbiology, $0,13,.$	3.5	2
9985	Microbiota profile of new-onset celiac disease in children in Saudi Arabia. Gut Pathogens, 2022, 14, .	3.4	5

#	ARTICLE	IF	CITATIONS
9986	Enteric Methane Emission, Rumen Fermentation and Microbial Profiles of Meat-Master Lambs Supplemented with Barley Fodder Sprouts. Fermentation, 2022, 8, 434.	3.0	6
9987	Potential Health-Promoting Effects of Two Candidate Probiotics Isolated from Infant Feces Using an Immune-Based Screening Strategy. Nutrients, 2022, 14, 3651.	4.1	1
9988	Pan-cancer analyses reveal cancer-type-specific fungal ecologies and bacteriome interactions. Cell, 2022, 185, 3789-3806.e17.	28.9	163
9989	Factors structuring microbial communities in highly impacted coastal marine sediments (Mar Menor) Tj ETQq1 1	0.784314	rgBT /Overl
9990	Pinworms are Associated with Taxonomic But Not Functional Differences in the Gut Microbiome of White-Throated Woodrats (Neotoma albigula). Journal of Parasitology, 2022, 108, .	0.7	1
9992	Metabolic Potential of the Gut Microbiome Is Significantly Impacted by Conditioning Regimen in Allogeneic Hematopoietic Stem Cell Transplantation Recipients. International Journal of Molecular Sciences, 2022, 23, 11115.	4.1	4
9994	Long term weight cycling affects fecal microbiota of mice. Molecular Nutrition and Food Research, 0, , 2200439.	3.3	1
9997	Bacterioplankton seasonality in deep high-mountain lakes. Frontiers in Microbiology, 0, 13, .	3.5	O
9998	Impact of irrigation water deficit on two tomato genotypes grown under open field conditions: From the root-associated microbiota to the stress responses. Italian Journal of Agronomy, 2022, 17, .	1.0	4
10000	Rates and physicochemical drivers of microbial anabolic activity in deepâ€sea sediments and implications for deep time. Environmental Microbiology, 2022, 24, 5188-5201.	3.8	1
10001	A pan-cancer mycobiome analysis reveals fungal involvement in gastrointestinal and lung tumors. Cell, 2022, 185, 3807-3822.e12.	28.9	114
10002	Plant communities foraged by the western honeybee (<i>Apis mellifera</i> L.) and their occurrence along urban road networks in Tokyo and Chiba, Japan. Acta Horticulturae, 2022, , 299-308.	0.2	0
10008	Tebufenozide has limited direct effects on simulated aquatic communities. Ecotoxicology, 2022, 31, 1231-1240.	2.4	0
10008	Influence of management practice on the microbiota of a critically endangered species: a longitudinal study of kÄkÄpÅ-chick faeces and associated nest litter. Animal Microbiome, 2022, 4, .	3.8	4
10006	Tracking spoilage bacteria in the tuna microbiome. FEMS Microbiology Ecology, 2022, 98, .	2.7	2
10007	Bitter friends are not always toxic: The loss of acetic acid bacteria and the absence of Komagataeibacter in the gut microbiota of the polyphagous fly Anastrepha ludens could inhibit its development in Psidium guajava in contrast to A. striata and A. fraterculus that flourish in this host. Frontiers in Microbiology, 0, 13.	3.5	5
10008	Comparative metagenomic analysis of human intervertebral disc nucleus nulnosus and cartilaginous	2.4	6
10009	<i>Drosophila melanogaster</i> microbiome is shaped by strict filtering and neutrality along a latitudinal cline. Molecular Ecology, 2022, 31, 5861-5871.	3.9	3

# ARTICLE	IF	Citations
DNA metabarcoding identifies urban foraging patterns of oligolectic and polylectic cavity-nesting bees. Oecologia, 2022, 200, 323-337.	2.0	1
Impact of high pressure treatment on shelf life and microbial profile of wild harvested Ascophyllum 10011 nodosum and aquacultured Alaria esculenta during storage. LWT - Food Science and Technology, 2022, 170, 114022.	5.2	4
10012 Bacterial communities of the oviduct of turkeys. Scientific Reports, 2022, 12, .	3.3	1
Hidden interactions in the intertidal rocky shore: variation in pedal mucus microbiota among marine grazers that feed on epilithic biofilm communities. PeerJ, 0, 10, e13642.	2.0	4
A comprehensive map of microbial biomarkers along the gastrointestinal tract for celiac disease patients. Frontiers in Microbiology, 0, 13 , .	3.5	7
Metaâ€analysis of caries microbiome studies can improve upon disease prediction outcomes. Apmis, 2022, 130, 763-777.	2.0	9
The active core microbiota of two high-yielding laying hen breeds fed with different levels of calcium and phosphorus. Frontiers in Physiology, 0, 13 , .	2.8	5
Sustained Drought, but Not Short-Term Warming, Alters the Gut Microbiomes of Wild <i>Anolis</i> Lizards. Applied and Environmental Microbiology, 2022, 88, .	3.1	10
Antibiotic resistomes and microbial communities in biosolid fertilizers collected from two Canadian wastewater treatment plants in a 10-years interval-potential risks to food chains?. Frontiers in Food Science and Technology, 0, 2, .	1.6	1
Dietary niche breadth influences the effects of urbanization on the gut microbiota of sympatric rodents. Ecology and Evolution, 2022, 12, .	1.9	4
Fish gut-associated bacterial communities in a tropical lagoon (Aghien lagoon, Ivory Coast). Frontiers in Microbiology, 0, 13, .	3.5	4
Characterization of Foliar Fungal Endophyte Communities from White Pine Blister Rust Resistant and 10021 Susceptible <i>Pinus flexilis</i> in Natural Stands in the Southern Rocky Mountains. Phytobiomes Journal, 2023, 7, 259-269.	2.7	2
Evaluation of digestively resistant or soluble fibers, short- and medium-chain fatty acids, trace 10023 minerals, and antibiotics in non-challenged nursery pigs on performance, digestibility, and intestinal integrity. Journal of Animal Science, 0, , .	0.5	2
Searching for a Consensus Among Inflammatory Bowel Disease Studies: A Systematic Meta-Analysis. Inflammatory Bowel Diseases, 2023, 29, 125-139.	1.9	14
Soil Layers Impact Lithocarpus Soil Microbial Composition in the Ailao Mountains Subtropical Forest, Yunnan, China. Journal of Fungi (Basel, Switzerland), 2022, 8, 948.	3.5	1
Characterizing rhizosphere microbial communities associated with tolerance to aboveground herbivory in wild and domesticated tomatoes. Frontiers in Microbiology, 0, 13 , .	3.5	3
Microscopic marine invertebrates are reservoirs for cryptic and diverse protists and fungi. Microbiome, 2022, 10, .	11.1	8
Oral Vaccination Using a Probiotic Vaccine Platform Combined with Prebiotics Impacts Immune Response and the Microbiome. Vaccines, 2022, 10, 1465.	4.4	6

# ARTICLE	IF	Citations
Source and acquisition of rhizosphere microbes in Antarctic vascular plants. Frontiers in Microbiology, $0,13,.$	3.5	6
$_{ m 10030}$ Axial spondyloarthritis patients have altered mucosal IgA response to oral and fecal microbiota. Frontiers in Immunology, 0, 13, .	4.8	3
Additive and non-additive epigenetic signatures of natural hybridization between fish species with different mating systems. Epigenetics, 2022, 17, 2356-2365.	2.7	2
Host and gut bacteria share metabolic pathways for anti-cancer drug metabolism. Nature Microbiology, 2022, 7, 1605-1620.	13.3	28
Highland adaptation of birds on the Qinghai-Tibet Plateau via gut microbiota. Applied Microbiology and Biotechnology, 2022, 106, 6701-6711.	3.6	5
10034 Complete metamorphosis and microbiota turnover in insects. Molecular Ecology, 2023, 32, 6543-6551.	3.9	10
eDNA metabarcoding shows latitudinal eukaryote micro- and mesoplankton diversity stabilizes across 10035 oligotrophic region of a >3000Âkm longitudinal transect in the Indian Ocean. Deep-Sea Research Part II: Topical Studies in Oceanography, 2022, 205, 105178.	1.4	4
Evidence of a selective and biâ€directional relationship between arbuscular mycorrhizal fungal and bacterial communities coâ€inhabiting plant roots. Environmental Microbiology, 2022, 24, 5378-5391.	3.8	3
Exploration of bacterial diversity in leaves and rhizosphere soil of flood affected and unaffected apricot trees. , 0, , .		0
10038 Salt stress in olive tree shapes resident endophytic microbiota. Frontiers in Plant Science, 0, 13, .	3.6	4
What Can We Learn about the Bias of Microbiome Studies from Analyzing Data from Mock Communities?. Genes, 2022, 13, 1758.	2.4	0
10040 Individuals with Inflammatory Bowel Disease Have an Altered Gut Microbiome Composition of Fungi and Protozoa. Microorganisms, 2022, 10, 1910.	3.6	3
Vaginal microbial shifts are unaffected by oral pre-exposure prophylaxis in South African women. Scientific Reports, 2022, 12, .	3.3	2
Analysis of pit latrine microbiota reveals depth-related variation in composition, and key parameters and taxa associated with latrine fill-up rate. Frontiers in Microbiology, 0, 13, .	3.5	3
Minimal impacts on the wheat microbiome when Trichoderma gamsii T6085 is applied as a biocontrol agent to manage fusarium head blight disease. Frontiers in Microbiology, 0, 13, .	3.5	5
Gastric acid and escape to systemic circulation represent major bottlenecks to host infection by <a>i>Citrobacter rodentium : ISME Journal, 2023, 17, 36-46.	9.8	6
Recurrent urinary tract infection and estrogen shape the taxonomic ecology and function of the postmenopausal urogenital microbiome. Cell Reports Medicine, 2022, 3, 100753.	6.5	15
Feeding strategy and dietary preference shape the microbiome of epipelagic copepods in a warm nutrientâ€impoverished ecosystem. Environmental DNA, 2023, 5, 38-55.	5.8	4

# ARTICLE	IF	Citations
10050 Investigating differential abundance methods in microbiome data: A benchmark study. PLoS Computational Biology, 2022, 18, e1010467.	3.2	18
10051 Microbial characteristics of dental caries in HIV positive individuals. Frontiers in Oral Health, 0, 3, .	3.0	1
The Structure of Stable Cellulolytic Consortia Isolated from Natural Lignocellulosic Substrates. International Journal of Molecular Sciences, 2022, 23, 10779.	4.1	9
Characterization of the "gut microbiota-immunity axis―and microbial lipid metabolites in atrophic and potential celiac disease. Frontiers in Microbiology, 0, 13, .	3.5	2
Generalist nematodes dominate the nemabiome of roe deer in sympatry with sheep at a regional level. International Journal for Parasitology, 2022, 52, 751-761.	3.1	8
Engineering an incubation environment that mimics <i>iin situ</i> conditions for <i>iin vitro</i> coastal microbiome studies. BioTechniques, 0, , .	1.8	1
The impact of short-chain fatty acid–producing bacteria of the gut microbiota in hyperuricemia and gout diagnosis. Clinical Rheumatology, 2023, 42, 203-214.	2.2	2
Stromatolite formation by Anaerolineae-dominated microbial communities in hot spring travertine in North Sumatra, Indonesia. Sedimentary Geology, 2022, 440, 106263.	2.1	2
Comparative visual and DNA-based diet assessment extends the prey spectrum of polar cod Boreogadus saida. Marine Ecology - Progress Series, 2022, 698, 139-154.	1.9	5
A case report of improvement on ADHD symptoms after fecal microbiota transplantation with gut 10061 microbiome profiling pre- and post-procedure. Current Medical Research and Opinion, 2022, 38, 1977-1982.	1.9	2
Myeloid-derived suppressor cells prevent disruption of the gut barrier, preserve microbiota 10062 composition, and potentiate immunoregulatory pathways in a rat model of experimental autoimmune encephalomyelitis. Gut Microbes, 2022, 14, .	9.8	6
10063 The Urethral Microbiota of Men with and without Idiopathic Urethritis. MBio, 2022, 13, .	4.1	6
Glyphosate and its formulations Roundup Bioflow and RangerPro alter bacterial and fungal community composition in the rat caecum microbiome. Frontiers in Microbiology, 0, 13, .	3.5	15
Luminal and mucosa-associated caecal microbiota of chickens after experimental Campylobacter jejuni 10065 infection in the absence of Campylobacter-specific phages of group II and III. Microbial Genomics, 2022, 8, .	2.0	0
The State of Play of Reproducibility in Statistics: An Empirical Analysis. American Statistician, 2023, 77, 115-126.	1.6	3
Microbial Diversity in Four Rhizocompartments (Bulk Soil, Rhizosphere, Rhizoplane, and Endosphere) 10067 of Four Winter Wheat Varieties at the Fully Emerged Flag Leaf Growth Stage. Microbiology Resource Announcements, 2022, 11, .	0.6	1
Shotgun metagenomics of fecal samples from children in Peru reveals frequent complex co-infections with multiple Campylobacter species. PLoS Neglected Tropical Diseases, 2022, 16, e0010815.	3.0	5
$_{ m 10070}$ Light and storage time influence the microbial quality of minimally processed rocket. Annals of Applied Biology, 0, , .	2.5	O

# ARTICLE	IF	CITATIONS
Rural environment reduces allergic inflammation by modulating the gut microbiota. Gut Microbes, 2022, 14, .	9.8	10
Emerging harmful algal blooms caused by distinct seasonal assemblages of a toxic diatom. Limnology and Oceanography, 2022, 67, 2341-2359.	3.1	5
Gut microbiota and plasma metabolites associated with bone mineral density in women with or at risk of HIV infection. Aids, 0, Publish Ahead of Print, .	2.2	0
Metatranscriptomic and metataxonomic insights into the ultra-small microbiome of the Korean fermented vegetable, kimchi. Frontiers in Microbiology, $0,13,.$	3.5	3
Microbial features of mature and abandoned soils in refractory clay deposits. BMC Microbiology, 2022, 22, .	3.3	1
Variations in Bacterial Communities and Antibiotic Resistance Genes Across Diverse Recycled and 10078 Surface Water Irrigation Sources in the Mid-Atlantic and Southwest United States: A CONSERVE Two-Year Field Study. Environmental Science & Technology, 2022, 56, 15019-15033.	10.0	6
Adapting to climate with limited genetic diversity: Nucleotide, <scp>DNA </scp> methylation and 10080 microbiome variation among populations of the social spider <i>Stegodyphus dumicola </i> Ecology, 2022, 31, 5765-5783.	3.9	10
Stunted children display ectopic small intestinal colonization by oral bacteria, which cause lipid 10083 malabsorption in experimental models. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
Relation Between Dietary Protein Intake and Gut Microbiome Composition in Community-Dwelling 10084 Older Men: Findings from the Osteoporotic Fractures in Men Study (MrOS). Journal of Nutrition, 2022, 152, 2877-2887.	2.9	6
Gut microbiota shift in layer pullets fed on black soldier fly larvae-based feeds towards enhancing healthy gut microbial community. Scientific Reports, 2022, 12, .	3.3	5
Pharmaceutical Biotransformation is Influenced by Photosynthesis and Microbial Nitrogen Cycling in a Benthic Wetland Biomat. Environmental Science & Technology, 2022, 56, 14462-14477.	10.0	8
Comparing invasive and noninvasive faecal sampling in wildlife microbiome studies: A case study on wild common cranes. Molecular Ecology Resources, 2023, 23, 359-367.	4.8	4
An exploratory study of the gut microbiota in major depression with anxious distress. Journal of Affective Disorders, 2023, 320, 595-604.	4.1	8
Lake Erie field trials to advance autonomous monitoring of cyanobacterial harmful algal blooms. Frontiers in Marine Science, 0, 9, .	2.5	8
Dietary benzoic acid and supplemental enzymes alter fiber-fermenting taxa and metabolites in the cecum of weaned pigs. Journal of Animal Science, 2022, 100 , .	0.5	1
In silico analysis of soil, sediment and groundwater microbial communities to predict biodegradation potential. Journal of Microbiological Methods, 2022, 202, 106595.	1.6	1
Effect of an Escherichia coli F4/F18 bivalent oral live vaccine on gut health and performance of healthy weaned pigs. Animal, 2022, 16, 100654.	3.3	5
Metabology: Analysis of metabolomics data using community ecology tools. Analytica Chimica Acta, 2022, 1232, 340469.	5.4	1

# ARTICLE	IF	CITATIONS
Dynamics of microbial community in response to co-feedstock composition in anaerobic digestion. Bioresource Technology, 2022, 364, 128039.	9.6	12
Environmental DNA-based profiling of benthic bacterial and eukaryote communities along a crude oil spill gradient in a coral reef in the Persian Gulf. Marine Pollution Bulletin, 2022, 184, 114143.	5.0	4
Spatial characterization of microbial sulfur cycling in horizontal-flow constructed wetland models. Chemosphere, 2022, 309, 136605.	8.2	1
Field application of glycerol to enhance reductive dechlorination of chlorinated ethenes and its impact on microbial community. Chemosphere, 2022, 309, 136640.	8.2	1
Postmortem submersion interval estimation of cadavers recovered from freshwater based on gut microbial community succession. Frontiers in Microbiology, 0, 13, .	3 . 5	6
Effects of dietary bamboo (<scp><i>Phyllostachys pubescens</i></scp> Mazel) culm powder on blood properties and intestinal environment of rabbits. Animal Science Journal, 2022, 93, .	1.4	3
Epigenome-Wide Study Identifies Epigenetic Outliers in Normal Mucosa of Patients with Colorectal Cancer. Cancer Prevention Research, 2022, 15, 755-766.	1.5	1
The Role of Carbon to Nitrogen Ratio on the Performance of Denitrifying Biocathodes for Decentralized Wastewater Treatment. Water (Switzerland), 2022, 14, 3076.	2.7	1
Effects of a farm-specific fecal microbial transplant (FMT) product on clinical outcomes and fecal microbiome composition in preweaned dairy calves. PLoS ONE, 2022, 17, e0276638.	2.5	1
Variations in fungal and bacterial microbiome and chemical composition among fermenting <i>Kishu-Narezushi</i> batches. Bioscience, Biotechnology and Biochemistry, 2022, 86, 1705-1717.	1.3	3
Dry-Season Soil and Co-Cultivated Host Plants Enhanced Propagation of Arbuscular Mycorrhizal Fungal Spores from Sand Dune Vegetation in Trap Culture. Journal of Fungi (Basel, Switzerland), 2022, 8, 1061.	3.5	2
Effect of Salmonella Typhimurium Colonization on Microbiota Maturation and Blood Leukocyte Populations in Broiler Chickens. Animals, 2022, 12, 2867.	2.3	4
Effects of repeated lysergic acid diethylamide (LSD) on the mouse brain endocannabinoidome and gut microbiome. British Journal of Pharmacology, 2023, 180, 721-739.	5.4	7
Subgingival host–microbiome metatranscriptomic changes following scaling and root planing in grade <scp> < scp> < scp</scp>	4.9	3
The Arabidopsis thaliana–Streptomyces Interaction Is Controlled by the Metabolic Status of the Holobiont. International Journal of Molecular Sciences, 2022, 23, 12952.	4.1	4
Exploratory analysis of one versus two-day intermittent fasting protocols on the gut microbiome and plasma metabolome in adults with overweight/obesity. Frontiers in Nutrition, 0, 9, .	3.7	8
Random forest analysis reveals taxa predictive of Prunus replant disease in peach root microbiomes. PLoS ONE, 2022, 17, e0275587.	2.5	2
Microbiomes associated with avian malaria survival differ between susceptible Hawaiian 10115 honeycreepers and sympatric malariaâ€resistant introduced birds. Molecular Ecology, 2023, 32, 6659-6670.	3.9	5

# ARTICLE	IF	CITATIONS
Bacterial community in soil and tree roots of <i>Picea abies</i> shows little response to clearcutting. FEMS Microbiology Ecology, 2022, 98, .	2.7	0
10117 The Diversity of Fungal Endophytes from Wild Grape Vitis amurensis Rupr. Plants, 2022, 11, 2897.	3.5	7
ldentification of Human Gut Microbiome Associated with Enterolignan Production. Microorganisms, 2022, 10, 2169.	3.6	0
Beyond Basic Diversity Estimates—Analytical Tools for Mechanistic Interpretations of Amplicon Sequencing Data. Microorganisms, 2022, 10, 1961.	3.6	7
10122 Crop management shapes the diversity and activity of DNA and RNA viruses in the rhizosphere. Microbiome, 2022, 10, .	11.1	12
Lactate addition boosts valerate yields in granular mixed culture carbohydrate fermentation. Journal of Environmental Chemical Engineering, 2022, 10, 108869.	6.7	4
10124 Canine Saliva as a Possible Source of Antimicrobial Resistance Genes. Antibiotics, 2022, 11, 1490.	3.7	4
Microbiota of vaccinated and non-vaccinated clinically inconspicuous and conspicuous piglets under natural Lawsonia intracellularis infection. Frontiers in Veterinary Science, 0, 9, .	2.2	1
Soil Microbiome Influences on Seedling Establishment and Growth of Prosopis chilensis and Prosopis tamarugo from Northern Chile. Plants, 2022, 11, 2717.	3.5	0
An Insight into an Olive Scab on the "lstrska Belica―Variety: Hostâ€Pathogen Interactions and Phyllosphere Mycobiome. Microbial Ecology, 2023, 86, 1343-1363.	2.8	6
Presence of algal symbionts affects denitrifying bacterial communities in the sea anemone Aiptasia coral model. ISME Communications, 2022, 2, .	4.2	5
Microbial Communities of Artisanal Fermented Milk Products from Russia. Microorganisms, 2022, 10, 2140.	3.6	7
Microbial and metabolic characterization of organic artisanal sauerkraut fermentation and study of gut health-promoting properties of sauerkraut brine. Frontiers in Microbiology, 0, 13, .	3.5	5
Sex-based metabolic and microbiota differences in roots and rhizosphere soils of dioecious papaya (Carica papaya L.). Frontiers in Plant Science, $0, 13, .$	3.6	3
The Gut Microbiota in Patients with Polycythemia Vera is Distinct from that of Healthy Controls and Varies by Treatment. Blood Advances, 0, , .	5.2	2
Metagenomic analysis among water masses and sediments from the Southern Gulf of Mexico. Frontiers in Marine Science, 0, 9, .	2.5	0
Characterization and diversity of seed endophytic bacteria of the endemic holoparasitic plant iolis <i>Cistanche armena</i> (Orobanchaceae) from a semi-desert area in Armenia. Seed Science Research, 2022, 32, 264-273.	1.7	7
Understanding the Dynamic of POMS Infection and the Role of Microbiota Composition in the Survival of Pacific Oysters, Crassostrea gigas. Microbiology Spectrum, 2022, 10, .	3.0	4

# ARTICLE	IF	CITATIONS
Maternal supplementation with a casein hydrolysate and yeast beta-glucan from late gestation through lactation improves gastrointestinal health of piglets at weaning. Scientific Reports, 2022, 12, .	3.3	4
10139 80 years later: Marine sediments still influenced by an old war ship. Frontiers in Marine Science, 0, 9, .	2.5	4
Plasticity of the adult human small intestinal stoma microbiota. Cell Host and Microbe, 2022, 30, 1773-1787.e6.	11.0	16
Responses of Ileal and Fecal Microbiota to Withdrawal of Pancreatic Enzyme Replacement Therapy in a Porcine Model of Exocrine Pancreatic Insufficiency. International Journal of Molecular Sciences, 2022, 23, 11700.	4.1	1
Microbiome of Nodules and Roots of Soybean and Common Bean: Searching for Differences Associated with Contrasting Performances in Symbiotic Nitrogen Fixation. International Journal of Molecular Sciences, 2022, 23, 12035.	4.1	10
"Unraveling the Gut Microbiome of the Genus Herichthys (Pisces: Cichlidae): What Can We Learn from Museum Specimens?― Current Microbiology, 2022, 79, .	2.2	1
Plant and Soil Core Mycobiomes in a Two-Year Sorghum–Legume Intercropping System of Underutilized Crops in South Africa. Microorganisms, 2022, 10, 2079.	3.6	2
Shark Provisioning Influences the Gut Microbiota of the Black-Tip Reef Shark in French Polynesia. Fishes, 2022, 7, 312.	1.7	2
4) An R Package for Improving Color Accessibility and Organization of Microbiome Data. Microbiology Resource Announcements, 2022, 11, .	0.6	15
Identification of microbial taxa present in Ctenocephalides felis (cat flea) reveals widespread co-infection and associations with vector phylogeny. Parasites and Vectors, 2022, 15, .	2.5	7
The oral microbiome in treatment $na\tilde{A}$ ve paediatric IBD patients exhibits dysbiosis related to disease severity that resolves following therapy. Journal of Crohn's and Colitis, 0, , .	1.3	5
Contrasting Fecal Methanogenic and Bacterial Profiles of Organic Dairy Cows Located in Northwest Washington Receiving Either a Mixed Diet of Pasture and TMR or Solely TMR. Animals, 2022, 12, 2771.	2.3	1
Host genetic factors related to innate immunity, environmental sensing and cellular functions are associated with human skin microbiota. Nature Communications, 2022, 13, .	12.8	10
Modular, multiâ€barcode amplicon sequencing for improved speciesâ€level detection of fungal 10154 phytopathogens: A case study of pipeline establishment targeting the <i>Ophiostomatales<∫i>Environmental DNA, 2024, 6, .</i>	5.8	5
Osmotic Gradient Is a Factor That Influences the Gill Microbiota Communities in Oryzias melastigma. Biology, 2022, 11, 1528.	2.8	3
Uso de la secuenciación de segunda generación (NGS) para descubrir la diversidad de hongos degradadores de la madera en los bosques Andino Patagónicos. Lilloa, 0, , 155-172.	0.1	O
Screening and characterization of vaginal fluid donations for vaginal microbiota transplantation. Scientific Reports, 2022, 12, .	3.3	6
Changes in Microbial Community Structure in Response to Gummosis in Peach Tree Bark. Plants, 2022, 11, 2834.	3.5	1

# ARTICLE	IF	CITATIONS
LotuS2: an ultrafast and highly accurate tool for amplicon sequencing analysis. Microbiome, 2022, 10,	11.1	22
Inter-annual variability patterns of reef cryptobiota in the central Red Sea across a shelf gradient. Scientific Reports, 2022, 12, .	3.3	1
Net overboard: Comparing marine <scp>eDNA</scp> sampling methodologies at sea to unravel marine biodiversity. Molecular Ecology Resources, 2023, 23, 440-452.	4.8	5
Globallyâ€distributed microbial eukaryotes exhibit endemism at deepâ€sea hydrothermal vents. Molecular Ecology, 2023, 32, 6580-6598.	3.9	7
Mortality by ribosomal sequencing (MoRS) provides a window into taxon-specific cell lysis. ISME Journal, 2023, 17, 105-116.	9.8	6
The duodenal mucosa associated microbiome, visceral sensory function, immune activation and 10166 psychological comorbidities in functional gastrointestinal disorders with and without self-reported non-celiac wheat sensitivity. Gut Microbes, 2022, 14, .	9.8	7
Gut Microbiome Remains Static in Functional Abdominal Pain Disorders Patients Compared to Controls: Potential for Diagnostic Tools. BioTech, 2022, 11, 50.	2.6	0
Role of mucus-bacteria interactions in Enterotoxigenic Escherichia coli (ETEC) H10407 virulence and interplay with human microbiome. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	6
Uteroplacental Insufficiency Causes Microbiota Disruption and Lung Development Impairment in Growth-Restricted Newborn Rats. Nutrients, 2022, 14, 4388.	4.1	6
Contrasting sea ice conditions shape microbial food webs in Hudson Bay (Canadian Arctic). ISME Communications, 2022, 2, .	4.2	4
Impact of Stagnation on the Diversity of Cyanobacteria in Drinking Water Treatment Plant Sludge. Toxins, 2022, 14, 749.	3.4	1
Oral Microcosm Biofilms Grown under Conditions Progressing from Peri-Implant Health, Peri-Implant 10173 Mucositis, and Peri-Implantitis. International Journal of Environmental Research and Public Health, 2022, 19, 14088.	2.6	5
Low-abundance populations distinguish microbiome performance in plant cell wall deconstruction. Microbiome, 2022, 10, .	11.1	10
Environmental DNA reveals diversity and abundance of Alternaria species in neighbouring heterogeneous landscapes in Worcester, UK. Aerobiologia, 2022, 38, 457-481.	1.7	1
Kinetoplastid Species Maintained by a Small Mammal Community in the Pantanal Biome. Pathogens, 2022, 11, 1205.	2.8	3
Helichrysum italicum (Roth) G. Don and Helichrysum arenarium (L.) Moench Infusion Consumption Affects the Inflammatory Status and the Composition of Human Gut Microbiota in Patients with Traits of Metabolic Syndrome: A Randomized Comparative Study. Foods, 2022, 11, 3277.	4.3	3
Mycobiome profiling of nasopharyngeal region of SARS-CoV-2 infected individuals. Microbes and Infection, 2023, 25, 105059.	1.9	1
16S rRNA gene-based assessment of common broiler chicken sampling methods: Evaluating intra-flock sample size, cecal pair similarity, and cloacal swab similarity to other alimentary tract locations. Frontiers in Physiology, 0, 13, .	2.8	5

# ARTICLE	IF	CITATIONS
Leaf Mycobiome and Mycotoxin Profile of Warm-Season Grasses Structured by Plant Species, 10180 Geography, and Apparent Black-Stroma Fungal Structure. Applied and Environmental Microbiology, 2022, 88, .	3.1	1
Environmental DNA (eDNA) detects temporal and habitat effects on community composition and 10181 endangered species in ephemeral ecosystems: A case study in vernal pools. Environmental DNA, 2023, 5, 85-101.	5.8	3
Fecal microbiota composition is related to brown adipose tissue 18F-fluorodeoxyglucose uptake in young adults. Journal of Endocrinological Investigation, 2023, 46, 567-576.	3.3	6
Temporal and spatial dynamics of bacterial and fungal microbiomes in nursery soils post-steaming. PhytoFrontiers, 0, , .	1.6	3
Antibiotic Treatment during Gestation Enhances Susceptibility to Mycobacterium tuberculosis in Offspring. Microbiology Spectrum, 2022, 10, .	3.0	2
Habitat partitioning of soil microbial communities along an elevation gradient: from plant root to landscape scale. Oikos, 2023, 2023, .	2.7	7
Microbial assembly and co-occurrence network in an aquifer under press perturbation. Annals of Microbiology, 2022, 72, .	2.6	2
Metabarcoding assessment of fungal diversity in brown algae and sponges of Mauritius. Frontiers in Microbiology, 0, 13, .	3.5	3
More than an anthropogenic phenomenon: Antimicrobial resistance in ungulates from natural and agricultural environments. Science of the Total Environment, 2023, 858, 159789.	8.0	1
Eggshell microbiome as a potential microbial reservoir in a cavity nesting bird. Journal of Ornithology, 0, , .	1.1	0
10192 Single Seed Microbiota: Assembly and Transmission from Parent Plant to Seedling. MBio, 2022, 13, .	4.1	13
DNA metabarcoding-based study on bacteria and fungi associated with house dust mites (DermatophagoidesÂspp.) in settled house dust. Experimental and Applied Acarology, 0, , .	1.6	0
Tumour microbiomes and Fusobacterium genomics in Vietnamese colorectal cancer patients. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	9
Interactions between Medications and the Gut Microbiome in Inflammatory Bowel Disease. Microorganisms, 2022, 10, 1963.	3.6	4
Gut microbiota analysis in pediatricâ€onset multiple sclerosis compared to pediatric monophasic demyelinating syndromes and pediatric controls. European Journal of Neurology, 0, , .	3.3	0
Effects of different amoxicillin treatment durations on microbiome diversity and composition in the gut. PLoS ONE, 2022, 17, e0275737.	2.5	6
Assessing the relationship between physical activity and the gut microbiome in a large, population-based sample of Wisconsin adults. PLoS ONE, 2022, 17, e0276684.	2.5	3
Red, Gold and Green: Microbial Contribution of Rhodophyta and Other Algae to Green Turtle (Chelonia mydas) Gut Microbiome. Microorganisms, 2022, 10, 1988.	3.6	0

# ARTICLE	IF	CITATIONS
Pathobiology and dysbiosis of the respiratory and intestinal microbiota in 14 months old Golden Syrian hamsters infected with SARS-CoV-2. PLoS Pathogens, 2022, 18, e1010734.	4.7	3
Experimental temperatures shape host microbiome diversity and composition. Global Change Biology, 2023, 29, 41-56.	9.5	29
Deterministic processes drive nationalâ€scale patterns in lake surface sediment bacteria and eukaryotic assemblage composition. Limnology and Oceanography, 2023, 68, 40-55.	3.1	3
10206 Exploratory studies of oral and fecal microbiome in healthy human aging. Frontiers in Aging, 0, 3, .	2.6	5
Acute Endotoxemia-Induced Respiratory and Intestinal Dysbiosis. International Journal of Molecular Sciences, 2022, 23, 11602.	4.1	4
Dynamic trophic shifts in bacterial and eukaryotic communities during the first 30 years of microbial succession following retreat of an Antarctic glacier. FEMS Microbiology Ecology, 2022, 98, .	2.7	3
Comparison of microbial signatures between paired faecal and rectal biopsy samples from healthy volunteers using next-generation sequencing and culturomics. Microbiome, 2022, 10, .	11.1	10
Cytomegalovirus infection disrupts the influence of short-chain fatty acid producers on Treg/Th17 balance. Microbiome, 2022, 10 , .	11.1	6
The Influence of the Degree of Forest Management on Methylmercury and the Composition of Microbial Communities in the Sediments of Boreal Drainage Ditches. Microorganisms, 2022, 10, 1981.	3.6	1
Mycobacteriaceae Mineralizes Micropolyethylene in Riverine Ecosystems. Environmental Science & Samp; Technology, 2022, 56, 15705-15717.	10.0	10
Quantitative real-time PCR analysis of bacterial biomarkers enable fast and accurate monitoring in inflammatory bowel disease. PeerJ, 0, 10, e14217.	2.0	3
The Cynomolgus Macaque Intestinal Mycobiome Is Dominated by the Kazachstania Genus and K. pintolopesii Species. Journal of Fungi (Basel, Switzerland), 2022, 8, 1054.	3.5	6
Oral polio revaccination is associated with changes in gut and upper respiratory microbiomes of infants. Frontiers in Microbiology, 0, 13, .	3.5	2
High carbon resource diversity enhances the certainty of successful plant pathogen and disease control. New Phytologist, 2023, 237, 1333-1346.	7.3	8
Gut-innervating nociceptors regulate the intestinal microbiota to promote tissue protection. Cell, 2022, 185, 4170-4189.e20.	28.9	42
Natural and after colon washing fecal samples: the two sides of the coin for investigating the human gut microbiome. Scientific Reports, 2022, 12, .	3.3	6
Fecal microbiota dynamics and its relationship to diarrhea and health in dairy calves. Journal of Animal Science and Biotechnology, 2022, 13, .	5.3	12
Impact of Physicochemical Parameters on the Diversity and Distribution of Microbial Communities Associated with Three South African Peatlands. Microorganisms, 2022, 10, 2103.	3.6	2

# ARTICLE	IF	Citations
Association of Midgut Bacteria and Their Metabolic Pathways with Zika Infection and Insecticide Resistance in Colombian Aedes aegypti Populations. Viruses, 2022, 14, 2197.	3.3	4
Probiotic human alcohol dehydrogenase-4 expressing bacteria protects from diet-induced obesity and metabolic impairment: a new concept of disease prevention. , 0, , 118-136.		0
Quantitative Stable-Isotope Probing (qSIP) with Metagenomics Links Microbial Physiology and Activity to Soil Moisture in Mediterranean-Climate Grassland Ecosystems. MSystems, 2022, 7, .	3.8	9
A novel biological sources consistency evaluation method reveals high level of biodiversity within 10225 wild natural medicine: A case study of Amynthas earthworms as "Guang Dilong― Acta Pharmaceutica Sinica B, 2023, 13, 1755-1770.	12.0	4
10226 Changes in the foliar fungal community between oak leaf flushes along a latitudinal gradient in Europe. Journal of Biogeography, 2022, 49, 2269-2280.	3.0	2
Degradation Rates and Bacterial Community Compositions Vary among Commonly Used Bioplastic 10228 Materials in a Brackish Marine Environment. Environmental Science & Enp.; Technology, 2022, 56, 15760-15769.	10.0	14
Microplastic polymer properties as deterministic factors driving terrestrial plastisphere microbiome assembly and succession in the field. Environmental Microbiology, 2023, 25, 2681-2697.	3.8	12
Real world population pharmacokinetic study in children and young adults with inflammatory bowel 10230 disease discovers novel blood and stool microbial predictors of vedolizumab clearance. Alimentary Pharmacology and Therapeutics, 2023, 57, 524-539.	3.7	6
Microbial Properties of Raw Milk throughout the Year and Their Relationships to Quality Parameters. Foods, 2022, 11, 3077.	4.3	10
Year-around survey and manipulation experiments reveal differential sensitivities of soil prokaryotic 10232 and fungal communities to saltwater intrusion in Florida Everglades wetlands. Science of the Total Environment, 2023, 858, 159865.	8.0	1
Soil bacterial community response to cover crops, cover crop termination, and predicted climate conditions in a dryland cropping system. Frontiers in Sustainable Food Systems, 0, 6, .	3.9	1
Long-term life history predicts current gut microbiome in a population-based cohort study. Nature Aging, 2022, 2, 885-895.	11.6	11
Innate and Peripheral Immune Alterations after Traumatic Brain Injury Are Regulated in a Gut Microbiota-Dependent Manner in Mice. Journal of Neurotrauma, 2023, 40, 772-787.	3.4	6
Commensal oral microbiota impacts ulcerative oral mucositis clinical course in allogeneic stem cell transplant recipients. Scientific Reports, 2022, 12, .	3.3	9
10238 Gut microbiome diversity of porcine peritonitis model of sepsis. Scientific Reports, 2022, 12, .	3.3	1
Early stage biofilm formation on bio-based microplastics in a freshwater reservoir. Science of the Total Environment, 2023, 858, 159569.	8.0	7
Microbiota Modulation in Blueberry Rhizosphere by Biocontrol Bacteria. Microbiology Research, 2022, 13, 809-824.	1.9	6
Fecal microbiome alterations in treatment-naive de novo Parkinson's disease. Npj Parkinson's Disease, 2022, 8, .	5. 3	10

# ARTICLE	IF	Citations
Gut microbiome composition better reflects host phylogeny than diet diversity in breeding woodâ€warblers. Molecular Ecology, 2023, 32, 518-536.	3.9	2
First experimental evidence for active farming in ambrosia beetles and strong heredity of garden microbiomes. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	2.6	11
Optimization of conditions for in vitro modeling of subgingival normobiosis and dysbiosis. Frontiers in Microbiology, 0, 13, .	3.5	0
Life Underground: Investigating Microbial Communities and Their Biomarkers in Marsâ€Analog Lava 10245 Tubes at Craters of the Moon National Monument and Preserve. Journal of Geophysical Research E: Planets, 2022, 127, .	3.6	5
10246 Inulin fibre promotes microbiota-derived bile acids and type 2 inflammation. Nature, 2022, 611, 578-584.	27.8	50
Arsenolipids reduce butyrate levels and influence human gut microbiota in a donor-dependent way. Ecotoxicology and Environmental Safety, 2022, 246, 114175.	6.0	3
The microbial profile of rivers and lagoons three years after the impact of the world's largest mining disaster (Fundão dam, Brazil). Environmental Research, 2023, 216, 114710.	7.5	4
The ability of <i>Phaeobacter inhibens</i> to produce tropodithietic acid influences the community dynamics of a microalgal microbiome. ISME Communications, 2022, 2, .	4.2	2
Phylogenetic diversity only weakly mitigates climateâ€changeâ€driven biodiversity loss in insect communities. Molecular Ecology, 2023, 32, 6147-6160.	3.9	2
Incipiently social carpenter bees (<i>Xylocopa</i>) host distinctive gut bacterial communities and 10251 display geographical structure as revealed by fullâ€length PacBio 16S rRNA sequencing. Molecular Ecology, 2023, 32, 1530-1543.	3.9	16
Calcium enhances polyhydroxyalkanoate production and promotes selective growth of the polyhydroxyalkanoate-storing biomass in municipal activated sludge. Water Research, 2022, 226, 119259.	11.3	6
Impacts of Dietary Protein and Niacin Deficiency on Reproduction Performance, Body Growth, and Gut 10253 Microbiota of Female Hamsters (Tscherskia triton) and Their Offspring. Microbiology Spectrum, 2022, 10, .	3.0	7
Multiomics Characterization of the Canada Goose Fecal Microbiome Reveals Selective Efficacy of Simulated Metagenomes. Microbiology Spectrum, 2022, 10, .	3.0	5
Bacterioplankton dispersal and biogeochemical function across Alaskan Arctic catchments. Environmental Microbiology, 2022, 24, 5690-5706.	3.8	1
Microbial community dynamics from a fast-receding glacier of Western Himalayas highlight the importance of microbes in primary succession, nutrient recycling, and xenobiotics degradation. Ecological Indicators, 2022, 144, 109565.	6.3	6
Methanogen Levels Are Significantly Associated with Fecal Microbiota Composition and Alpha Diversity in Healthy Adults and Irritable Bowel Syndrome Patients. Microbiology Spectrum, 2022, 10, .	3.0	5
10258 Effect of Resistant Dextrin on Intestinal Gas Homeostasis and Microbiota. Nutrients, 2022, 14, 4611.	4.1	6
Urban forest soils harbour distinct and more diverse communities of bacteria and fungi compared to less disturbed forest soils. Molecular Ecology, 2023, 32, 504-517.	3.9	14

# ARTICLE	IF	CITATIONS
Metagenomic characterization of bacterial community and antibiotic resistance genes found in the mass transit system in Seoul, South Korea. Ecotoxicology and Environmental Safety, 2022, 246, 114176.	6.0	3
The gut microbiome of wild American marten in the Upper Peninsula of Michigan. PLoS ONE, 2022, 17, e0275850.	2.5	1
Albic Podzols of Boreal Pine Forests of Russia: Soil Organic Matter, Physicochemical and Microbiological Properties across Pyrogenic History. Forests, 2022, 13, 1831.	2.1	5
Uneven response of microbial communities to intense dust deposition across the coastal transition zone off Mauritania. Frontiers in Marine Science, $0, 9, .$	2.5	1
The Appendix Orchestrates T-Cell Mediated Immunosurveillance in Colitis-Associated Cancer. Cellular and Molecular Gastroenterology and Hepatology, 2023, 15, 665-687.	4.5	7
Sampling from four geographically divergent young female populations demonstrates forensic geolocation potential in microbiomes. Scientific Reports, 2022, 12, .	3.3	3
Fire and land use impact soil properties in a Mediterranean dry sclerophyll woodland. Journal of Environmental Management, 2022, 324, 116245.	7.8	5
Rationale and study protocol for a randomized controlled feeding study to determine the structural- 10269 and functional-level effects of diet-specific interventions on the gut microbiota of non-Hispanic black and white adults. Contemporary Clinical Trials, 2022, 123, 106968.	1.8	0
Gut microbiota and holobiont metabolome composition of the medaka fish (Oryzias latipes) are affected by a short exposure to the cyanobacterium Microcystis aeruginosa. Aquatic Toxicology, 2022, 253, 106329.	4.0	8
Effects of low salinities on growth, fatty acid composition, and transcriptome in Florida pompano (Trachinotus carolinus) at early developmental stages. Aquaculture, 2023, 563, 738964.	3.5	2
Optimization of bacterial DNA and endotoxin extraction from settled airborne dust. Science of the Total Environment, 2023, 857, 159455.	8.0	3
Maternal anxiety, depression and stress affects offspring gut microbiome diversity and bifidobacterial abundances. Brain, Behavior, and Immunity, 2023, 107, 253-264.	4.1	30
Sediment metagenomics reveals the impacts of poultry industry wastewater on antibiotic resistance and nitrogen cycling genes in tidal creek ecosystems. Science of the Total Environment, 2023, 857, 159496.	8.0	8
Microbial communities associated with kelp detritus in temperate and subantarctic intertidal sediments. Science of the Total Environment, 2023, 857, 159392.	8.0	5
Active microbial communities during biodegradation of biodegradable plastics by mesophilic and thermophilic anaerobic digestion. Journal of Hazardous Materials, 2023, 443, 130208.	12.4	24
Determination and quantification of microbial communities and antimicrobial resistance on food through host DNA-depleted metagenomics. Food Microbiology, 2023, 110, 104162.	4.2	9
Full-scale aerobic granular sludge for municipal wastewater treatment – granule formation, microbial succession, and process performance. Environmental Science: Water Research and Technology, 2022, 8, 3138-3154.	2.4	11
Understanding the impact of different source water types on the biofilm characteristics and 10279 microbial communities of manganese removing biofilters. Environmental Science: Water Research and Technology, 0, , .	2.4	0

# ARTICLE	IF	Citations
Removing chemical and biological pollutants from swine wastewater through constructed wetlands aiming reclaimed water reuse. Journal of Environmental Management, 2023, 326, 116642.	7.8	5
DNA metabarcoding reveals compositional and functional differences in fungal communities among Amazonian canga formations. Fungal Ecology, 2023, 61, 101209.	1.6	0
Bacteroidota structure in the face of varying agricultural practices as an important indicator of soil quality – a culture independent approach. Agriculture, Ecosystems and Environment, 2023, 342, 108252.	5.3	13
Multiomic analysis reveals microbiome-related relationships between cocaine use and metabolites. Aids, 2022, 36, 2089-2099.	2.2	1
Tissue-dependent transcriptional and bacterial associations in primary sclerosing cholangitis-associated inflammatory bowel disease. Wellcome Open Research, 0, 6, 199.	1.8	0
Sugarcane cultivation practices modulate rhizosphere microbial community composition and structure. Scientific Reports, 2022, 12, .	3.3	0
Function-Based Rhizosphere Assembly along a Gradient of Desiccation in the Former Aral Sea. MSystems, 2022, 7, .	3.8	6
Homogenisation of water and sediment bacterial communities in a shallow lake (lake Balihe, China). Freshwater Biology, 2023, 68, 155-171.	2.4	3
Mycoplasmataceae dominate microbial community differences between gut regions in mammals with a simple gut architecture. Journal of Mammalogy, 0, , .	1.3	0
Defining Composition and Function of the Rhizosphere Microbiota of Barley Genotypes Exposed to Growth-Limiting Nitrogen Supplies. MSystems, 2022, 7, .	3.8	12
Syntrophic acetate oxidation having a key role in thermophilic phenol conversion in anaerobic membrane bioreactor under saline conditions. Chemical Engineering Journal, 2023, 455, 140305.	12.7	2
C3NA: correlation and consensus-based cross-taxonomy network analysis for compositional microbial data. BMC Bioinformatics, 2022, 23, .	2.6	1
Fiber-like Action of d-Fagomine on the Gut Microbiota and Body Weight of Healthy Rats. Nutrients, 2022, 14, 4656.	4.1	0
Effects of crude oil and gas condensate spill on coastal benthic microbial populations. Frontiers in Environmental Science, $0,10,10$	3.3	8
The gut microbiome reflects ancestry despite dietary shifts across a hybrid zone. Ecology Letters, 2023, 26, 63-75.	6.4	4
The Blueberry Fruit Mycobiome Varies by Tissue Type and Fungicide Treatment. Phytobiomes Journal, 2023, 7, 208-219.	2.7	3
Hidden Tenants: Microbiota of the Rhizosphere and Phyllosphere of Cordia dodecandra Trees in Mayan Forests and Homegardens. Plants, 2022, 11, 3098.	3.5	1
Optimization of Low-Biomass Sample Collection and Quantitative PCR-Based Titration Impact 16S rRNA Microbiome Resolution. Microbiology Spectrum, 2022, 10, .	3.0	4

# ARTICLE	IF	CITATIONS
Application of Coagulation and Foam Concentration Method to Quantify Waterborne Pathogens in River Water Samples. Water (Switzerland), 2022, 14, 3642.	2.7	0
Steelhead trout (Oncorhynchus mykiss) fed probiotic during the earliest developmental stages have 10303 enhanced growth rates and intestinal microbiome bacterial diversity. Frontiers in Marine Science, 0, 9, .	2.5	5
Human access and deterministic processes play a major role in structuring planktonic and sedimentary bacterial and eukaryotic communities in lakes. PeerJ, 0, 10, e14378.	2.0	4
Disrupted gut microbiota aggravates working memory dysfunction induced by high-altitude exposure in mice. Frontiers in Microbiology, 0, 13 , .	3.5	2
Comprehensive Phenotyping in Inflammatory Bowel Disease: Search for Biomarker Algorithms in the Transkingdom Interactions Context. Microorganisms, 2022, 10, 2190.	3.6	1
Composition and Structural Characteristics of Rhizosphere Microorganisms of Polygonum sibiricum (Laxm.) Tzvelev in the Yellow River Delta. Diversity, 2022, 14, 965.	1.7	1
Long-term effects of early-life rumen microbiota modulation on dairy cow production performance and methane emissions. Frontiers in Microbiology, 0, 13, .	3.5	3
$_{10310}^{}$ Human milk microbial species are associated with infant head-circumference during early and late lactation in Guatemalan mother-infant dyads. Frontiers in Microbiology, 0, 13, .	3.5	2
Soil microbiome disruption reveals specific and general plant-bacterial relationships in three agroecosystem soils. PLoS ONE, 2022, 17, e0277529.	2.5	8
10312 Reshuffling of the Coral Microbiome during Dormancy. Applied and Environmental Microbiology, 0, , .	3.1	0
Benthic invertebrates in Svalbard fjords—when metabarcoding does not outperform traditional biodiversity assessment. PeerJ, 0, 10, e14321.	2.0	0
Linking migration and microbiota at a major stopover site in a long-distance avian migrant. Movement Ecology, 2022, 10, .	2.8	5
Microbial Community in the Permafrost Thaw Gradient in the South of the Vitim Plateau (Buryatia,) Tj ETQq0 (ว 0 rgBT /Ove	erlock 10 Tf 5
Years After a Fire, Biocrust Microbial Communities are Similar to Unburned Communities in a Coastal Grassland. Microbial Ecology, 0, , .	2.8	1
How do microbial communities deal with chronic hydrocarbon presence in oil seep soils? Data from historical handâ€dug oil wells. Land Degradation and Development, 2023, 34, 1283-1296.	3.9	2
Oral microbiota and periodontitis severity among Hispanic adults. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	8
Metagenomic insights into the impacts of phytochemicals on bacterial and archaeal community structure and biogas production patterns during anaerobic digestion of avocado oil processing waste feedstocks. Biomass Conversion and Biorefinery, 0, , .	4.6	4
Deciphering the microbial composition of biodynamic preparations and their effects on the apple rhizosphere microbiome. Frontiers in Soil Science, 0, 2, .	2.2	3

# ARTICLE	IF	Citations
10324 Pro-Inflammatory Oral Microbiota in Juvenile Spondyloarthritis: A Pilot Study. Children, 2022, 9, 1764.	1.5	1
Assessment of the Gut Microbiota during Juice Fasting with and without Inulin Supplementation: A Feasibility Study in Healthy Volunteers. Foods, 2022, 11, 3673.	4.3	O
10326 Influential factors of saliva microbiota composition. Scientific Reports, 2022, 12, .	3.3	3
Effects of Reductive Soil Disinfestation Combined with Liquid-Readily Decomposable Compounds and Solid Plant Residues on the Bacterial Community and Functional Composition. Microbial Ecology, 2023, 86, 1132-1144.	2.8	5
Gut Microbiota Associated with Gestational Health Conditions in a Sample of Mexican Women. Nutrients, 2022, 14, 4818.	4.1	2
SSU rRNA sequencing data for bacterial communities associated with Vibrio-infected rainbow trout (Oncorhynchus mykiss). Data in Brief, 2022, , 108752.	1.0	0
Microbial ecology of a shallow alkaline hydrothermal vent: $Str\tilde{A}\frac{1}{2}tan$ Hydrothermal Field, Eyjaf \tilde{A} ¶rdur, northern Iceland. Frontiers in Microbiology, 0, 13, .	3. 5	6
Narrowband ultraviolet B response in cutaneous T-cell lymphoma is characterized by increased 10331 bacterial diversity and reduced Staphylococcus aureus and Staphylococcus lugdunensis. Frontiers in Immunology, 0, 13, .	4.8	9
Prolonged mask wearing does not alter the oral microbiome, salivary flow rate or gingival health status – A pilot study. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	2
Dynamics of Gut Microbiota and Clinical Variables after Ketogenic and Mediterranean Diets in Drug-NaÃ-ve Patients with Type 2 Diabetes Mellitus and Obesity. Metabolites, 2022, 12, 1092.	2.9	16
Dysbiosis and reduced small intestinal function are required to induce intestinal insufficiency in mice. American Journal of Physiology - Renal Physiology, 2023, 324, G10-G23.	3.4	4
Dissemination of antibiotic resistance in antibiotic-free recirculating aquaculture systems. Journal of Hazardous Materials Advances, 2022, 8, 100201.	3.0	0
Predator dispersal influences predator distribution but not prey diversity in pitcher plant microbial metacommunities. Ecology, 2023, 104, .	3.2	0
10340 Indian sewage microbiome has unique community characteristics and potential for population-level disease predictions. Science of the Total Environment, 2023, 858, 160178.	8.0	5
Bladder cancer is associated with decreased urinary microbiota diversity and alterations in microbial community composition. Urologic Oncology: Seminars and Original Investigations, 2023, 41, 107.e15-107.e22.	1.6	5
Microbiota of healthy and bleached corals of the species Siderastrea stellata in response to river influx and seasonality in Brazilian northeast. Environmental Science and Pollution Research, 0, , .	5.3	0
Establishment of the Bacterial Microbiota in a Lab-Reared Model Teleost Fish, the Medaka Oryzias latipes. Microorganisms, 2022, 10, 2280.	3.6	5
Microplastic contamination and microbial colonization in coastal area of Busan City, Korea. Frontiers in Marine Science, 0, 9, .	2.5	5

# ARTICLE	IF	CITATIONS
Bioremediation of Petroleum-Contaminated Soils with Biosurfactant-Producing Degraders Isolated from the Native Desert Soils. Microorganisms, 2022, 10, 2267.	3.6	1
In vitro study of the modulatory effects of heat-killed bacterial biomass on aquaculture bacterioplankton communities. Scientific Reports, 2022, 12, .	3.3	2
Fungal Metabarcoding Data for Two Grapevine Varieties (Regent and <i>Vitis vinifera</i>) Tj ETQq0 0 0 rgBT /O ¹ 10348 Conditions. Phytobiomes Journal, 2022, 6, 358-367.	verlock 10 2.7	Tf 50 667 Td 2
The rhizosphere microbiome and host plant glucosinolates exhibit feedback cycles in <i>Brassica rapa</i> . Molecular Ecology, 2023, 32, 741-751.	3.9	6
Soil characteristics and redox properties of infiltrating water are determinants of microbial communities at managed aquifer recharge sites. FEMS Microbiology Ecology, 2022, 98, .	2.7	1
Mode of delivery modulates the intestinal microbiota and impacts the response to vaccination. Nature Communications, 2022, 13, .	12.8	9
10352 Skin microbiome sampling in the preterm neonate. Pediatric Dermatology, 2023, 40, 129-131.	0.9	1
Identifying the Role of Elevation, Geography, and Species Identity in Structuring Turtle Ant (Cephalotes Latreille, 1802) Bacterial Communities. Microbial Ecology, 2023, 86, 1240-1253.	2.8	3
Water Stress, Cadmium, and Plant Genotype Modulate the Rhizosphere Microbiome of Pisum sativum L Plants, 2022, 11, 3013.	3.5	3
A combined microbial and biogeochemical dataset from high-latitude ecosystems with respect to methane cycle. Scientific Data, 2022, 9, .	5.3	6
Proton Pump Inhibitor Pantoprazole Modulates Intestinal Microbiota and Induces TLR4 Signaling and Fibrosis in Mouse Liver. International Journal of Molecular Sciences, 2022, 23, 13766.	4.1	1
The microbial community associated with Parascaris spp. infecting juvenile horses. Parasites and Vectors, 2022, 15 , .	2.5	2
Short-Term Tomato Consumption Alters the Pig Gut Microbiome toward a More Favorable Profile. Microbiology Spectrum, 2022, 10, .	3.0	1
Sapwood mycobiome varies across host, plant compartment and environments in <i>Nothofagus</i> forests from Northern Patagonia. Molecular Ecology, 2023, 32, 6599-6618.	3.9	4
Geographic Location, Management Strategy, and Huanglongbing Disease Affect Arbuscular Mycorrhizal Fungal Communities Across U.S. Citrus Orchards. Phytobiomes Journal, 2022, 6, 342-353.	2.7	2
Genetic variants in taste genes play a role in oral microbial composition and severe early childhood caries. IScience, 2022, 25, 105489.	4.1	6
Autoimmune-associated genetics impact probiotic colonization of the infant gut. Journal of Autoimmunity, 2022, 133, 102943.	6.5	2
Colonic innate immune defenses and microbiota alterations in acute swine dysentery. Microbial Pathogenesis, 2022, 173, 105873.	2.9	1

# ARTICLE	IF	Citations
Provenance of rhizobial symbionts is similar for invasive and non-invasive acacias introduced to California. FEMS Microbiology Ecology, 0 , , .	2.7	2
Modulation of the porcine intestinal microbiota in the course of Ascaris suum infection. Parasites and Vectors, 2022, 15, .	2.5	3
10370 The effects of urban land use gradients on wild bee microbiomes. Frontiers in Microbiology, 0, 13, .	3.5	5
Rubble fields shape planktonic protist communities in Indonesia at a local scale. Journal of Eukaryotic Microbiology, 2023, 70, .	1.7	3
Diversity and dynamics of bacterial communities in the drinking water distribution network of a mid-sized city in Brazil. Journal of Water and Health, 2022, 20, 1733-1747.	2.6	0
Disentangling the role of soil bacterial diversity in phosphorus transformation in the maize rhizosphere. Applied Soil Ecology, 2023, 182, 104739.	4.3	2
Aquaculture rearing systems induce no legacy effects in Atlantic cod larvae or their rearing water bacterial communities. Scientific Reports, 2022, 12, .	3.3	3
Bacterial gut microbiomes of aculeate brood parasites overlap with their aculeate hosts', but have higher diversity and specialization. FEMS Microbiology Ecology, 2022, 98, .	2.7	3
The Kitty Microbiome Project: Defining the Healthy Fecal "Core Microbiome―in Pet Domestic Cats. Veterinary Sciences, 2022, 9, 635.	1.7	6
Enteroendocrine peptides, growth, and the microbiome during the porcine weaning transition. Animal Microbiome, 2022, 4, .	3.8	3
$_{10380}$ Gut microbiota composition as a candidate risk factor for dimethyl fumarate-induced lymphopenia in multiple sclerosis. Gut Microbes, 2022, 14, .	9.8	10
Both abundant and rare fungi colonizing Fagus sylvatica ectomycorrhizal root-tips shape associated bacterial communities. Communications Biology, 2022, 5, .	4.4	1
Influence of short and long term processes on SAR11 communities in open ocean and coastal systems. ISME Communications, 2022, 2, .	4.2	2
Modulation of gut microbiota, blood metabolites, and disease resistance by dietary \hat{l}^2 -glucan in rainbow trout (Oncorhynchus mykiss). Animal Microbiome, 2022, 4, .	3.8	6
Arsenic-triggered bacterial minorities correlate with arsenic accumulation in cabbage. Geoderma, 2023, 429, 116278.	5.1	0
A randomized, double-blinded study evaluating effect of matcha green tea on human fecal microbiota. Journal of Clinical Biochemistry and Nutrition, 2023, 72, 165-170.	1.4	0
lmpacts of sea ice melting procedures on measurements of microbial community structure. Elementa, 2022, 10 , .	3.2	2
End-of-life MoS ₂ -enabled device and material transformation in landfill leachate and its effect on the landfill microbiome. Environmental Science: Nano, 2023, 10, 203-214.	4.3	1

# ARTICLE	IF	CITATIONS
10390 Universal drivers of cheese microbiomes. IScience, 2023, 26, 105744.	4.1	3
Metagenomics analysis of the morphological aspects and bacterial composition of broiler feces. Poultry Science, 2023, 102, 102401.	3.4	2
Nitrogen-fixing sulfate reducing bacteria in shallow coastal sediments under simulated resuspension. Estuarine, Coastal and Shelf Science, 2023, 280, 108165.	2.1	5
Prenatal arsenic exposure stymies gut butyrate production and enhances gut permeability in post 10393 natal life even in absence of arsenic deftly through miR122-Occludin pathway. Toxicology Letters, 2023, 374, 19-30.	0.8	0
Putative metabolism of Ca. Accumulibacter via the utilization of glucose. Water Research, 2023, 229, 119446.	11.3	12
The gut microbiome and child mental health: A population-based study. Brain, Behavior, and Immunity, 2023, 108, 188-196.	4.1	6
Active populations and growth of soil microorganisms are framed by mean annual precipitation in three California annual grasslands. Soil Biology and Biochemistry, 2023, 177, 108886.	8.8	4
Variations in oral responsiveness associate with specific signatures in the gut microbiota and modulate dietary habits. Food Quality and Preference, 2023, 106, 104790.	4.6	3
New insights into microbial community coalescence in the land-sea continuum. Microbiological Research, 2023, 267, 127259.	5.3	2
Taxonomic and functional dynamics of the soil microbiome from a tropical dry forest in kraft lignin-amended microcosms. Applied Soil Ecology, 2023, 183, 104766.	4.3	0
Responses of soil rare and abundant microorganisms to recurring biotic disturbances. Soil Biology and Biochemistry, 2023, 177, 108913.	8.8	5
Response of sediment microbial communities to different levels of PAC contamination and exposure time. Science of the Total Environment, 2023, 861, 160683.	8.0	6
Microscale dynamics of dark zone alterations in anthropized karstic cave shows abrupt microbial community switch. Science of the Total Environment, 2023, 862, 160824.	8.0	2
Alteration of oral microbiome composition in children living with pesticide-exposed farm workers. International Journal of Hygiene and Environmental Health, 2023, 248, 114090.	4.3	0
Two problems in one shot: Vinasse and glycerol co-digestion in a thermophilic high-rate reactor to 10404 improve process stability even at high sulfate concentrations. Science of the Total Environment, 2023, 862, 160823.	8.0	7
Response of a temperate coral to temperature stress: A comparison of populations across sites. Journal of Experimental Marine Biology and Ecology, 2023, 560, 151863.	1.5	0
Pseudomonas-specific 16S rRNA insect gut-microbiome profiling using next-generation sequencing. STAR Protocols, 2023, 4, 101941.	1.2	0
Which soil microbiome? Bacteria, fungi, and protozoa communities show different relationships with urban green space type and use-intensity. Science of the Total Environment, 2023, 863, 160468.	8.0	2

# ARTICLE	IF	Citations
In grapevine decline, microbiomes are affected differently in symptomatic and asymptomatic soils. Applied Soil Ecology, 2023, 183, 104767.	4.3	5
Comparative study of the rhizosphere microbiome of Coffea arabica grown in different countries reveals a small set of prevalent and keystone taxa. Rhizosphere, 2023, 25, 100652.	3.0	2
Assessment of poultry process hygiene and bacterial dynamics along two broiler slaughter lines in Norway. Food Control, 2023, 146, 109526.	5 . 5	5
Evolution of the spontaneous sourdoughs microbiota prepared with organic or conventional whole wheat flours from South Brazil. Anais Da Academia Brasileira De Ciencias, 2022, 94, .	0.8	1
Methane-related community of a carbonate-enriched pockmark, Brazilian Southeastern continental slope. Ocean and Coastal Research, 2022, 70, .	0.6	3
Long-Term Soil Fungal Community Recovery After Fire is Impacted by Climate Change. Western North American Naturalist, 2022, 82, .	0.4	0
10414 Assessment of Hippocampus guttulatus diet using DNA metabarcoding of faeces., 2022,,.		1
10415 A Miniaturized and Automated eDNA Sampler: Application to a Marine Environment. , 2022, , .		2
Piglet cardiopulmonary bypass induces intestinal dysbiosis and barrier dysfunction associated with systemic inflammation. DMM Disease Models and Mechanisms, 2023, 16, .	2.4	6
High diversity and low specificity of fungi associated with seedless epiphytic plants. Biotropica, 2023, 55, 268-276.	1.6	0
Prevalence and ecological features of deep chlorophyll layers in Lake of the Woods, a complex 10418 hydrological system with strong trophic, physical, and chemical gradients. Journal of Great Lakes Research, 2023, 49, 122-133.	1.9	6
A gut microbial metabolite of dietary polyphenols reverses obesity-driven hepatic steatosis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
Detritusâ€hosted methanogenesis sustains the methane paradox in an alpine lake. Limnology and Oceanography, 2023, 68, 248-264.	3.1	5
Differences in gut microbial fructoselysine degradation activity between breast-fed and formula-fed infants. FEMS Microbiology Ecology, 2022, 99, .	2.7	2
Do we need to change our perspective about gut biomarkers? A public data mining approach to identify differentially abundant bacteria in intestinal inflammatory diseases. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	1
Comparison of two acidophilic sulfidogenic consortia for the treatment of acidic mine water. Frontiers in Bioengineering and Biotechnology, 0, 10, .	4.1	0
Catchment characteristics and seasonality control the composition of microbial assemblages exported from three outlet glaciers of the Greenland Ice Sheet. Frontiers in Microbiology, 0, 13, .	3 . 5	1
Integrative web cloud computing and analytics using MiPair for design-based comparative analysis with paired microbiome data. Scientific Reports, 2022, 12, .	3. 3	2

# ARTICLE	IF	CITATIONS
Novel application of metagenomics for the strain-level detection of bacterial contaminants within non-sterile industrial products – a retrospective, real-time analysis. Microbial Genomics, 2022, 8, .	2.0	0
Plasma Levels of Omega-3 and Omega-6 Derived Oxylipins Are Associated with Fecal Microbiota Composition in Young Adults. Nutrients, 2022, 14, 4991.	4.1	5
Effective degradation of organophosphate ester flame retardants and plasticizers in coastal sediments under high urban pressure. Scientific Reports, 2022, 12, .	3.3	5
Changes in the Cervical Microbiota of Women with Different High-Risk Human Papillomavirus Loads. Viruses, 2022, 14, 2674.	3.3	2
Functional Diversification of Oyster Big Defensins Generates Antimicrobial Specificity and Synergy against Members of the Microbiota. Marine Drugs, 2022, 20, 745.	4.6	5
Significance of <i>Limosilactobacillus fermentum</i> and <i>Saccharomyces cerevisia</i> on the 10435 Growth Performance, Haematological Traits, Serum Biochemistry, Faecal and Caeca Microbiota of Broiler Chickens., 0, , 1-20.		1
Age matters: Microbiome depletion prior to repeat mild traumatic brain injury differentially alters microbial composition and function in adolescent and adult rats. PLoS ONE, 2022, 17, e0278259.	2.5	6
Mycobiome Diversity of the Cave Church of Sts. Peter and Paul in Serbia—Risk Assessment Implication 10438 for the Conservation of Rare Cavern Habitat Housing a Peculiar Fresco Painting. Journal of Fungi (Basel, Switzerland), 2022, 8, 1263.	3.5	6
Genetics and Nutrition Drive the Gut Microbiota Succession and Host-Transcriptome Interactions through the Gilthead Sea Bream (Sparus aurata) Production Cycle. Biology, 2022, 11, 1744.	2.8	8
Human milk microbial species are associated with mild growth deficits during early infancy among Guatemalan mother–infant dyads. , 0, 1, .		1
Risk Factors Associated with Severe Clostridioides difficile Infection in Patients with Cancer. Infectious Diseases and Therapy, 2023, 12, 209-225.	4.0	2
10444 Bacterial and Fungal Co-Occurrence in the Nudibranch, Pteraeolidia semperi. Life, 2022, 12, 1988.	2.4	1
The Analysis of the Mycobiota in Plastic Polluted Soil Reveals a Reduction in Metabolic Ability. Journal of Fungi (Basel, Switzerland), 2022, 8, 1247.	3.5	2
Deciphering the community structure and the functional potential of a hypersaline marsh microbial mat community. FEMS Microbiology Ecology, 2022, 98, .	2.7	1
Screen the unforeseen: Microbiomeâ€profiling for detection of zoonotic pathogens in wild rats. Transboundary and Emerging Diseases, 2022, 69, 3881-3895.	3.0	3
Back to the roots: defining the core microbiome of <i>Sorghum bicolor</i> in agricultural field soils from the centre of origin. FEMS Microbiology Ecology, 2022, 98, .	2.7	7
Impact of Daily Consumption of Whole-Grain Quinoa-Enriched Bread on Gut Microbiome in Males. Nutrients, 2022, 14, 4888.	4.1	2
The Gill Microbiota of Argopecten purpuratus Scallop Is Dominated by Symbiotic Campylobacterota and Upwelling Intensification Differentially Affects Their Abundance. Microorganisms, 2022, 10, 2330.	3.6	2

# ARTICLE	IF	CITATIONS
Effect of Wastewater on the Composition of Bacterial Microbiota of Phragmites australis Used in Constructed Wetlands for Phytodepuration. Plants, 2022, 11, 3210.	3.5	0
Human Gut Microbiota in Coronary Artery Disease: A Systematic Review and Meta-Analysis. Metabolites, 2022, 12, 1165.	2.9	20
Environmental and Anthropogenic Factors Shape the Skin Bacterial Communities of a Semi-Arid Amphibian Species. Microbial Ecology, 2023, 86, 1393-1404.	2.8	2
Wild microbiomes of striped plateau lizards vary with reproductive season, sex, and body size. Scientific Reports, 2022, 12 , .	3.3	3
Ancient oral microbiomes support gradual Neolithic dietary shifts towards agriculture. Nature Communications, 2022, 13, .	12.8	13
Short- and Long-Term Effects of Different Antibiotics on the Gut Microbiota and Cytokines Level in Mice. Infection and Drug Resistance, 0, Volume 15, 6785-6797.	2.7	5
Composition and metabolic potential of microbiomes associated with mesopelagic animals from Monterey Canyon. ISME Communications, 2022, 2, .	4,2	3
Biodiversity of freshwater ciliates (Protista, Ciliophora) in the Lake Weishan Wetland, China: the state of the art. Marine Life Science and Technology, 2022, 4, 429-451.	4.6	31
Consumption of the cell-free or heat-treated fractions of a pitched kefir confers some but not all positive impacts of the corresponding whole kefir. Frontiers in Microbiology, 0, 13, .	3.5	4
10466 Early season soil microbiome best predicts wheat grain quality. FEMS Microbiology Ecology, 2022, 99, .	2.7	2
Molecular diet analysis enables detection of diatom and cyanobacteria DNA in the gut of Macoma balthica. PLoS ONE, 2022, 17, e0278070.	2.5	1
Effects of long-term fertilization with contemporary Danish human urine, composted household 10468 waste and sewage sludge on soil nematode abundance and community structure. Science of the Total Environment, 2023, 860, 160485.	8.0	7
Molecular characterization of gut microbiome in weaning pigs supplemented with multi-strain probiotics using metagenomic, culturomic, and metabolomic approaches. Animal Microbiome, 2022, 4, .	3.8	0
Host identity is the dominant factor in the assembly of nematode and tardigrade gut microbiomes in Antarctic Dry Valley streams. Scientific Reports, 2022, 12, .	3.3	3
Lack of host phylogenetic structure in the gut bacterial communities of New Zealand cicadas and their interspecific hybrids. Scientific Reports, 2022, 12, .	3.3	4
10474 Mycobial community assemblages in sink drains across a university campus. Environmental DNA, 0, , .	5.8	O
Mycobiota and diet-derived fungal xenosiderophores promote Salmonella gastrointestinal colonization. Nature Microbiology, 2022, 7, 2025-2038.	13.3	13
10476 Influence of Geochemistry in the Tropical Hot Springs on Microbial Community Structure and Function. Current Microbiology, 2023, 80, .	2.2	1

# ARTICLE	IF	CITATIONS
Diversity and composition of the microbiome associated with eggs of the Southern green stinkbug, <i>Nezara viridula</i> (Hemiptera: Pentatomidae). MicrobiologyOpen, 2022, 11, .	3.0	4
Chronic consumption of probiotics, oats, and apples has differential effects on postprandial bile acid profile and cardiometabolic disease risk markers compared with an isocaloric control (cornflakes): a randomized trial. American Journal of Clinical Nutrition, 2023, 117, 252-265.	4.7	3
Honeybees affect floral microbiome composition in a central food source for wild pollinators in boreal ecosystems. Oecologia, 2023, 201, 59-72.	2.0	5
Forests influence yeast populations vectored by insects into vineyards. Frontiers in Microbiology, 0, 13, .	3.5	5
Metabolism of Scenedesmus obliquus cultivated with raw plant substrates. Frontiers in Plant Science, 0, 13, .	3.6	3
Differential modulation of the bacterial endophytic microbiota of Festuca arundinaceae (tall fescue) 10482 cultivars by the plant-growth promoting strain Streptomyces albidoflavus UYFA156. Plant and Soil, 2023, 485, 317-332.	3.7	3
More than <i>Mycobacterium tuberculosis: </i> site-of-disease microbial communities, and their functional and clinical profiles in tuberculous lymphadenitis. Thorax, 2023, 78, 297-308.	5.6	1
Exploration of the rhizosphere microbiome of native plant Ceanothus velutinus – an excellent resource of plant growth-promoting bacteria. Frontiers in Plant Science, 0, 13, .	3.6	5
Dysbiotic but nonpathogenic shift in the fecal mycobiota of patients with rheumatoid arthritis. Gut Microbes, 2022, 14, .	9.8	9
Skin dysbiosis and Cutibacterium acnes biofilm in inflammatory acne lesions of adolescents. Scientific Reports, 2022, 12, .	3.3	16
Dark-purple rice extract modulates gut microbiota composition in acetic acid– and indomethacin-induced inflammatory bowel disease in rats. International Microbiology, 2023, 26, 423-434.	2.4	3
The microbiome shifts throughout the gastrointestinal tract of Bradford cattle in the Pampa biome. PLoS ONE, 2022, 17, e0279386.	2.5	1
Treatment of peanut allergy and colitis in mice via the intestinal release of butyrate from polymeric micelles. Nature Biomedical Engineering, 2023, 7, 38-55.	22.5	36
Chronic exposure to synthetic food colorant Allura Red AC promotes susceptibility to experimental colitis via intestinal serotonin in mice. Nature Communications, 2022, 13, .	12.8	18
A Reproducible and Tunable Synthetic Soil Microbial Community Provides New Insights into Microbial Ecology. MSystems, 2022, 7, .	3.8	12
Does plastic type matter? Insights into non-indigenous marine larvae recruitment under controlled conditions. PeerJ, 0, 10, e14549.	2.0	0
Divergent responses of soil microorganisms to throughfall exclusion across tropical forest soils driven by soil fertility and climate history. Soil Biology and Biochemistry, 2023, 177, 108924.	8.8	2
Influence of Dietary Inulin on Fecal Microbiota, Cardiometabolic Risk Factors, Eicosanoids, and Oxidative Stress in Rats Fed a High-Fat Diet. Foods, 2022, 11, 4072.	4.3	2

#	Article	IF	CITATIONS
10496	Plant microbiomes harbor potential to promote nutrient turnover in impoverished substrates of a Brazilian biodiversity hotspot. ISME Journal, 2023, 17, 354-370.	9.8	14
10497	Ozone modified hypothalamic signaling enhancing thermogenesis in the TDP-43A315T transgenic model of Amyotrophic Lateral Sclerosis. Scientific Reports, 2022, 12, .	3.3	2
10498	Vertical and temporal distribution of chytrids infecting diatoms in the Gulf of Naples (Italy,) Tj ETQq0 0 0 rgBT /Ov	verlock 10 1.1	Tf 50 662 To
10499	Diversity dynamics of aerobic anoxygenic phototrophic bacteria in a freshwater lake. Environmental Microbiology Reports, 2023, 15, 60-71.	2.4	8
10500	Hatchery tanks induce intense reduction in microbiota diversity associated with gills and guts of two endemic species of the SÃ \pm o Francisco River. Frontiers in Microbiology, 0, 13, .	3. 5	0
10501	Characterization of the gut microbiome and resistome of Galapagos marine iguanas (Amblyrhynchus) Tj ETQq $1\ 1$	0,7,84314	rgBT /Overlo
10502	High Level of Interaction between Phages and Bacteria in an Artisanal Raw Milk Cheese Microbial Community. MSystems, 2023, 8, .	3.8	5
10503	A rare loss-of-function genetic mutation suggest a role of dermcidin deficiency in hidradenitis suppurativa pathogenesis. Frontiers in Immunology, $0,13,.$	4.8	6
10504	Evaluating Ruminal and Small Intestinal Morphology and Microbiota Composition of Calves Fed a Macleaya cordata Extract Preparation. Animals, 2023, 13, 54.	2.3	0
10505	MGnify: the microbiome sequence data analysis resource in 2023. Nucleic Acids Research, 2023, 51, D753-D759.	14.5	70
10506	The devil is in the details: Variable impacts of season, BMI, sampling site temperature, and presence of insects on the post-mortem microbiome. Frontiers in Microbiology, 0, 13, .	3. 5	4
10508	Suppression of Streptococcosis and Modulation of the Gut Bacteriome in Nile Tilapia (<i>Oreochromis niloticus</i>) by the Marine Sediment Bacteria Bacillus haynesii and Advenella mimigardefordensis. Microbiology Spectrum, 2022, 10, .	3.0	1
10509	Impact of Dietary Arachidonic Acid on Gut Microbiota Composition and Gut–Brain Axis in Male BALB/C Mice. Nutrients, 2022, 14, 5338.	4.1	1
10510	Micro-fractionation shows microbial community changes in soil particles below 20 \hat{l} 4m. Frontiers in Ecology and Evolution, 0, 10, .	2.2	6
10511	Gut microbiome of helminth-infected indigenous Malaysians is context dependent. Microbiome, 2022, 10, .	11.1	6
10512	Legacy effects of fumigation on soil bacterial and fungal communities and their response to metam sodium application. Environmental Microbiomes, 2022, 17, .	5.0	6
10514	Acute high-fat diet impairs macrophage-supported intestinal damage resolution. JCI Insight, 2023, 8, .	5.0	3
10515	Targeted single-cell genomics reveals novel host adaptation strategies of the symbiotic bacteria Endozoicomonas in Acropora tenuis coral. Microbiome, 2022, 10, .	11.1	6

# ARTICLE	IF	CITATIONS
Marked Effects of Larval Salt Exposure on the Life History and Gut Microbiota of the Malaria Vector Anopheles merus (Diptera: Culicidae). Insects, 2022, 13, 1165.	2.2	0
Biodegradable Polyesters and Low Molecular Weight Polyethylene in Soil: Interrelations of Material Properties, Soil Organic Matter Substances, and Microbial Community. International Journal of Molecular Sciences, 2022, 23, 15976.	4.1	2
Efficient computation of contributional diversity metrics from microbiome data with <i>FuncDiv</i> Bioinformatics, 2023, 39, .	4.1	1
Changes in Phylogenetic and Functional Diversity of Ciliates along the Course of a Mediterranean Karstic River. Microorganisms, 2022, 10, 2493.	3.6	1
Phytogenics and encapsulated sodium butyrate can replace antibiotics as growth promoters for lightly weaned piglets. PLoS ONE, 2022, 17, e0279197.	2.5	1
Elevated estuary water temperature drives fish gut dysbiosis and increased loads of pathogenic vibrionaceae. Environmental Research, 2023, 219, 115144.	7.5	8
Meta-analysis of sputum microbiome studies identifies airway disease-specific taxonomic and functional signatures. Journal of Medical Microbiology, 2022, 72, .	1.8	0
Gut microbiota analyses of Saudi populations for type 2 diabetes-related phenotypes reveals significant association. BMC Microbiology, 2022, 22, .	3.3	5
Mycorrhizal fungi alter root exudation to cultivate a beneficial microbiome for plant growth. Functional Ecology, 2023, 37, 664-675.	3.6	11
Healthy adult gut microbiota sustains its own vitamin B12 requirement in an in vitro batch fermentation model. Frontiers in Nutrition, 0, 9, .	3.7	3
10531 Exploring the Viability of a Liquid-Permeable Membrane Biofilm Reactor. ACS ES&T Water, 2023, 3, 70-78.	4.6	0
Longitudinal analysis of the faecal microbiome in pigs fed Cyberlindnera jadinii yeast as a protein 10532 source during the weanling period followed by a rapeseed- and faba bean-based grower-finisher diet. Animal Microbiome, 2022, 4, .	3.8	2
Tare Soil Alters the Composition of the Developing Potato Rhizosphere Microbiome. Phytobiomes Journal, 2023, 7, 91-99.	2.7	2
Enterocyte-specific deletion of metal transporter Zip14 (Slc39a14) alters intestinal homeostasis 10535 through epigenetic mechanisms. American Journal of Physiology - Renal Physiology, 2023, 324, G159-G176.	3.4	4
Dietary supplementation with Mexican foods, Opuntia ficus indica, Theobroma cacao, and Acheta domesticus: Improving obesogenic and microbiota features in obese mice. Frontiers in Nutrition, 0, 9, .	3.7	2
Age and micronutrient effects on the microbiome in a mouse model of zinc depletion and supplementation. PLoS ONE, 2022, 17, e0275352.	2.5	3
Gut microbiota of endangered Australian sea lion pups is unchanged by topical ivermectin treatment for endemic hookworm infection. Frontiers in Microbiology, 0, 13, .	3.5	0
Enhanced Arbovirus Surveillance with High-Throughput Metatranscriptomic Processing of Field-Collected Mosquitoes. Viruses, 2022, 14, 2759.	3.3	5

#	Article	IF	Citations
10540	Maternal Mycobiome, but Not Antibiotics, Alters Fungal Community Structure in Neonatal Piglets. Applied and Environmental Microbiology, 2022, 88, .	3.1	3
10541	Decay of oil residues in the soil is enhanced by the presence of Spartina alterniflora, with no additional effect from microbiome manipulation. Frontiers in Soil Science, 0, 2, .	2.2	O
10542	AMF Inoculum Enhances Crop Yields of Zea mays L.  Chenghai No. 618' and Glycine max L.  Zhonghuang No. 17' without Disturbing Native Fugal Communities in Coal Mine Dump. International Journal of Environmental Research and Public Health, 2022, 19, 17058.	2.6	2
10543	Taxonomic, Genomic, and Functional Variation in the Gut Microbiomes of Wild Spotted Hyenas Across 2 Decades of Study. MSystems, 0, , .	3.8	1
10544	Characterization of membrane vesicles in <i>Alteromonas macleodii</i> indicates potential roles in their copiotrophic lifestyle. MicroLife, 2023, 4, .	2.1	3
10545	Microbiome Profiling from Fecal Immunochemical Test Reveals Microbial Signatures with Potential for Colorectal Cancer Screening. Cancers, 2023, 15, 120.	3.7	3
10546	Ecology, Not Host Phylogeny, Shapes the Oral Microbiome in Closely Related Species. Molecular Biology and Evolution, 2022, 39, .	8.9	8
10547	Effects of sea ice retreat and ocean warming on the Laptev Sea continental slope ecosystem (1993 vs) Tj ETQq $1\ 1$	0.784314 2:5	1 _. rgBT /Ove
10549	Evaluation of primers for the detection of deadwood-inhabiting archaea <i>via</i> amplicon sequencing. PeerJ, 0, 10, e14567.	2.0	0
10550	Crop rotations in organic greenhouse production – effects of increased crop diversity on the soil microbiome. Acta Horticulturae, 2022, , 47-54.	0.2	O
10551	Effects of maternal supplementation of fish oil during late gestation and lactation on growth performance, fecal microbiota structure and post-weaning diarrhoea of offspring piglets. British Journal of Nutrition, 2023, 130, 966-977.	2.3	2
10553	Assembly of Endophytic Communities of <i>Setaria viridis</i> Plants when Grown in Different Soils and Derived from Different Seeds. Phytobiomes Journal, 2024, 8, 34-45.	2.7	O
10554	Evaluation of co-circulating pathogens and microbiome from COVID-19 infections. PLoS ONE, 2022, 17, e0278543.	2.5	2
10555	Elevated Dietary Carbohydrate and Glycemic Intake Associate with an Altered Oral Microbial Ecosystem in Two Large U.S. Cohorts. Cancer Research Communications, 2022, 2, 1558-1568.	1.7	O
10556	Habitats within the plant root differ in bacterial network topology and taxonomic assortativity. Molecular Plant-Microbe Interactions, 0, , .	2.6	0
10557	Human Microbiome Mixture Analysis Using Weighted Quantile Sum Regression. International Journal of Environmental Research and Public Health, 2023, 20, 94.	2.6	8
10558	Wheat genome architecture influences interactions with phytobeneficial microbial functional groups in the rhizosphere. Plant, Cell and Environment, 2023, 46, 1018-1032.	5.7	2
10559	Impact of HIV infection and integrase strand transfer inhibitors-based treatment on the gut virome. Scientific Reports, 2022, 12, .	3.3	6

# ARTICLE	IF	CITATIONS
Cloacal microbiomes of sympatric and allopatric Sceloporus lizards vary with environment and host relatedness. PLoS ONE, 2022, 17, e0279288.	2.5	1
Increase of intestinal bacterial sialidase activity exacerbates acute colitis in mice. Frontiers in Molecular Biosciences, $0, 9, .$	3.5	1
Prokaryotic and eukaryotic microbial diversity from three soda lakes in the East African Rift Valley determined by amplicon sequencing. Frontiers in Microbiology, $0,13,.$	3.5	5
Kombuchas from Green and Black Tea Modulate the Gut Microbiota and Improve the Intestinal Health of Wistar Rats Fed a High-Fat High-Fructose Diet. Nutrients, 2022, 14, 5234.	4.1	2
Characterization of the bacterial microbiome of Amblyomma scalpturatum and Amblyomma ovale collected from Tapirus terrestris and Amblyomma sabanerae collected from Chelonoidis denticulata, Madre de Dios- Peru. BMC Microbiology, 2022, 22, .	3.3	1
Conditionality of soil microbial mediation of Solidago plant phenotype: indicator taxa within complex microbiomes influence some, but not all Solidago traits. Plant and Soil, 0, , .	3.7	2
Urine and fecal microbiota in a canine model of bladder cancer and comparison of canine and human urine microbiota. International Journal of Transgender Health, 2022, 15, 1245-1263.	2.3	3
10568 Symbioses are restructured by repeated mass coral bleaching. Science Advances, 2022, 8, .	10.3	14
Revisiting fecal metatranscriptomics analyses of macaques with idiopathic chronic diarrhoea with a focus on trichomonad parasites. Parasitology, 2023, 150, 248-261.	1.5	0
Deterministic Assembly Processes Strengthen the Effects of \hat{l}^2 -Diversity on Community Biomass of Marine Bacterioplankton. MSystems, 0, , .	3.8	2
Alterations in the cutaneous microbiome of patients with psoriasis and psoriatic arthritis reveal similarities between non-lesional and lesional skin. Annals of the Rheumatic Diseases, 2023, 82, 507-514.	0.9	6
lmpacts of disinfected wastewater irrigation on soil characteristics, microbial community composition, and crop yield. Blue-Green Systems, 2022, 4, 247-271.	2.0	3
Airway microbiota and immune mediator relationships differ in obesity and asthma. Journal of Allergy and Clinical Immunology, 2023, 151, 931-942.	2.9	3
Impact of Hurricane Maria on mold levels in the homes of Piñones, Puerto Rico. Air Quality, Atmosphere and Health, 2023, 16, 661-668.	3.3	2
Stochastic variational variable selection for high-dimensional microbiome data. Microbiome, 2022, 10,	11.1	2
Microbial communities and main features of labneh Ambaris, a traditional Lebanese fermented goat milk product. Journal of Dairy Science, 2023, 106, 868-883.	3.4	1
Ensiled Mixed Vegetables Enriched Carbohydrate Metabolism in Heterofermentative Lactic Acid Bacteria. Fermentation, 2022, 8, 699.	3.0	1
Bioprospecting for Novel Bacterial Sources of Hydrolytic Enzymes and Antimicrobials in the Romanian Littoral Zone of the Black Sea. Microorganisms, 2022, 10, 2468.	3.6	3

# ARTICLE	IF	CITATIONS
Microbial communities and biogeochemical functioning across peatlands in the Athabasca Oil Sands region of Canada: Implications for reclamation and management. Land Degradation and Development, 2023, 34, 1504-1521.	3.9	1
Characterizing a subtropical hypereutrophic lake: From physicochemical variables to shotgun metagenomic data. Frontiers in Microbiology, 0, 13 , .	3.5	0
Effects of Moss-Dominated Biocrusts on Soil Microbial Community Structure in an Ionic Rare Earth Tailings Area of Southern China. Toxics, 2022, 10, 782.	3.7	0
Analysis of bronchoalveolar lavage fluid metatranscriptomes among patients with COVID-19 disease. Scientific Reports, 2022, 12, .	3.3	0
Characterizing Variation in the Bacterial and Fungal Tare Soil Microbiome of Seed Potato. Phytobiomes Journal, 2023, 7, 78-90.	2.7	2
Inputs don't equal outputs: Bacterial microbiomes of the ingesta, gut, and feces of the keystone deposit feeder <i>Ilyanassa obsoleta</i> . FEMS Microbiology Ecology, 0, , .	2.7	0
Trophic State Drives the Diversity of Protists in a Tropical River (New River, Belize). Microorganisms, 2022, 10, 2425.	3.6	3
Shifts in soil phosphorus fractions during seasonal transitions in a riparian floodplain wetland. Frontiers in Environmental Science, 0, 10, .	3.3	1
Gut microbiota modulates bleomycin-induced acute lung injury response in mice. Respiratory Research, 2022, 23, .	3.6	9
Metatranscriptomes reveal the diverse responses of <scp> <i>Thaumarchaeota</i> </scp> ecotypes to environmental variations in the northern slope of the South China Sea. Environmental Microbiology, 0, , .	3.8	2
benchdamic: benchmarking of differential abundance methods for microbiome data. Bioinformatics, 2023, 39, .	4.1	1
Sources of Fungal Symbionts in the Microbiome of a Mobile Insect Host, Spodoptera frugiperda. Microbial Ecology, 2023, 86, 900-913.	2.8	3
Idiosyncratic effects of coinfection on the association between systemic pathogens and the gut microbiota of a wild rodent, the bank vole <i>Myodes glareolus</i> . Journal of Animal Ecology, 2023, 92, 826-837.	2.8	5
Combined organic-inorganic fertilization builds higher stability of soil and root microbial networks than exclusive mineral or organic fertilization. Soil Ecology Letters, 2023, 5, .	4.5	7
Dysbiosis in Head and Neck Cancer: Determining Optimal Sampling Site for Oral Microbiome Collection. Pathogens, 2022, 11, 1550.	2.8	3
Relating biomass composition and the distribution of metabolic functions in the co-fermentation of sugarcane vinasse and glycerol. International Journal of Hydrogen Energy, 2023, 48, 8837-8853.	7.1	5
Genomic and Environmental Factors Shape the Active Gill Bacterial Community of an Amazonian Teleost Holobiont. Microbiology Spectrum, 2022, 10, .	3.0	2
Healthy dietary patterns are associated with the gut microbiome in the Hispanic Community Health Study/Study of Latinos. American Journal of Clinical Nutrition, 2023, 117, 540-552.	4.7	7

# ARTICLE	IF	Citations
Selective Enrichment of Nitrososphaera viennensis-Like Ammonia-Oxidizing Archaea over Ammonia-Oxidizing Bacteria from Drinking Water Biofilms. Microbiology Spectrum, 2022, 10 , .	3.0	1
Effect of Parthenium hysterophorus L. Invasion on Soil Microbial Communities in the Yellow River Delta, China. Microorganisms, 2023, 11, 18.	3.6	2
10602 Interplay between Cruciferous Vegetables and the Gut Microbiome: A Multi-Omic Approach. Nutrients, 2023, 15, 42.	4.1	7
Microbiota of the Rearing Water of <i>Penaeus stylirostris < li>Larvae Influenced by Lagoon Seawater and Specific Key Microbial Lineages of Larval Stage and Survival. Microbiology Spectrum, 2022, 10, .</i>	3.0	5
Host's genetic background determines the outcome of reciprocal faecal transplantation on life-history traits and microbiome composition. Animal Microbiome, 2022, 4, .	3.8	2
10605 The gut microbiota and depressive symptoms across ethnic groups. Nature Communications, 2022, 13, .	12.8	25
Dietary supplementation of Bacillus subtilis or antibiotics modified intestinal microbiome of weaned pigs under enterotoxigenic Escherichia coli infection. Frontiers in Microbiology, 0, 13, .	3.5	3
Data on the temporal changes in soil properties and microbiome composition after a jet-fuel contamination during the pot and field experiments. Data in Brief, 2022, , 108860.	1.0	1
10608 Multi-Task Learning for Compositional Data via Sparse Network Lasso. Entropy, 2022, 24, 1839.	2.2	1
Aphid species specializing on milkweed harbor taxonomically similar bacterial communities that differ in richness and relative abundance of core symbionts. Scientific Reports, 2022, 12, .	3.3	1
An insight into the commercial piglet's microbial gut colonization: from birth towards weaning. Animal Microbiome, 2022, 4, .	3.8	8
Depth-related patterns in microbial community responses to complex organic matter in the western North Atlantic Ocean. Biogeosciences, 2022, 19, 5617-5631.	3.3	3
Methanogenic consortia from thermophilic molasses-fed structured-bed reactors: microbial characterization and responses to varying food-to-microorganism ratios. Brazilian Journal of Chemical Engineering, 0, , .	1.3	0
Experimental inheritance of antibiotic acquired dysbiosis affects host phenotypes across generations. Frontiers in Microbiology, 0, 13 , .	3.5	2
Coâ€substrate composition is critical for enrichment of functional key species and for process efficiency during biogas production from cattle manure. Microbial Biotechnology, 2023, 16, 350-371.	4.2	3
Impact of Cultivation and Origin on the Fruit Microbiome of Apples and Blueberries and Implications for the Exposome. Microbial Ecology, 2023, 86, 973-984.	2.8	6
Comparative analysis of scalp and gut microbiome in androgenetic alopecia: A Korean cross-sectional study. Frontiers in Microbiology, 0, 13, .	3.5	3
Oral Microbiome in Nonsmoker Patients with Oral Cavity Squamous Cell Carcinoma, Defined by Metagenomic Shotgun Sequencing. Cancers, 2022, 14, 6096.	3.7	4

# ARTICLE	IF	Citations
Studying Plant–Insect Interactions through the Analyses of the Diversity, Composition, and Functional Inference of Their Bacteriomes. Microorganisms, 2023, 11, 40.	3.6	4
ITS Metabarcoding Reveals the Effects of Oregano Essential Oil on Fusarium oxysporum and Other Fungal Species in Soil Samples. Plants, 2023, 12, 62.	3.5	1
Guts within guts: the microbiome of the intestinal helminth parasite Ascaris suum is derived but distinct from its host. Microbiome, 2022, 10 , .	11.1	6
Gut microbiota of homing pigeons shows summer–winter variation under constant diet indicating a substantial effect of temperature. Animal Microbiome, 2022, 4, .	3.8	3
Dominating taxonomic composition of the early life gut microbiota and influencing factors in infants up to seven months of age in Latvia. Proceedings of the Latvian Academy of Sciences, 2022, 76, 657-664.	0.1	0
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. Gut Microbes, 2023, 15 , .	9.8	3
Influence of a sodium-saccharin sweetener on the rumen content and rumen epithelium microbiota in dairy cattle during heat stress. Journal of Animal Science, 0, , .	0.5	1
Transjugular intrahepatic Porto-systemic shunt positively influences the composition and metabolic functions of the gut microbiota in cirrhotic patients. Digestive and Liver Disease, 2022, , .	0.9	0
Intelectin-1 binds and alters the localization ofÂthe mucus barrier–modifying bacteriumÂ <i>Akkermansia muciniphila</i> Journal of Experimental Medicine, 2023, 220, .	8.5	8
Human soft tissue sarcomas harbor an intratumoral viral microbiome which is linked with natural killer cell infiltrate and prognosis. , 2023, 11, e004285.		8
Large-diameter trees and deadwood correspond with belowground ectomycorrhizal fungal richness. Ecological Processes, 2023, 12, .	3.9	5
Stability of the Fecal and Oral Microbiome over 2 Years at â^80°C for Multiple Collection Methods. Cancer Epidemiology Biomarkers and Prevention, 2023, 32, 444-451.	2.5	1
Soil Chemistry and Soil History Significantly Structure Oomycete Communities in <i>Brassicaceae</i> Crop Rotations. Applied and Environmental Microbiology, 2023, 89, .	3.1	3
Selective and differential feeding on marine prokaryotes by mucous mesh feeders. Environmental Microbiology, 2023, 25, 880-893.	3.8	6
Molecular Detection of Rickettsia and Other Bacteria in Ticks and Birds in an Urban Fragment of Tropical Dry Forest in Magdalena, Colombia. Life, 2023, 13, 145.	2.4	2
10637 Beehives possess their own distinct microbiomes. Environmental Microbiomes, 2023, 18, .	5.0	6
Personalized Dietary Advice to Increase Protein Intake in Older Adults Does Not Affect the Gut 10638 Microbiota, Appetite or Central Processing of Food Stimuli in Community-Dwelling Older Adults: A Six-Month Randomized Controlled Trial. Nutrients, 2023, 15, 332.	4.1	4
3-Nitrooxypropanol supplementation of a forage diet decreased enteric methane emissions from beef cattle without affecting feed intake and apparent total-tract digestibility. Journal of Animal Science, 2023, 101, .	0.5	3

# ARTICLE	IF	CITATIONS
Succession of the microbiota in the gut of reproductives of Macrotermes subhyalinus (Termitidae) at colony foundation gives insights into symbionts transmission. Frontiers in Ecology and Evolution, 0, 10, .	2.2	3
Discovery of Nylon 11 ingestion by mealworm (<i>Tenebrio molitor</i>) larvae and detection of monomer-degrading bacteria in gut microbiota. AIMS Microbiology, 2022, 8, 612-623.	2.2	1
The gut-microbiota-brain axis in a Spanish population in the aftermath of the COVID-19 pandemic: microbiota composition linked to anxiety, trauma, and depression profiles. Gut Microbes, 2023, 15, .	9.8	10
Soil Microbial Community Responses to Different Management Strategies in Almond Crop. Journal of Fungi (Basel, Switzerland), 2023, 9, 95.	3.5	3
10645 Modelling the Gastrointestinal Carriage of Klebsiella pneumoniae Infections. MBio, 2023, 14, .	4.1	4
ApoE isoform– and microbiota-dependent progression of neurodegeneration in a mouse model of tauopathy. Science, 2023, 379, .	12.6	75
Responses of roots and rhizosphere of female papaya to the exogenous application of GA3. BMC Plant Biology, 2023, 23, .	3 . 6	3
Study of a Pilot Scale Microbial Electrosynthesis Reactor for Organic Waste Biorefinery. Energies, 2023, 16, 591.	3.1	3
Studying the Association between Antibiotic Resistance Genes and Insertion Sequences in Metagenomes: Challenges and Pitfalls. Antibiotics, 2023, 12, 175.	3.7	2
Multi-omics profiles of the intestinal microbiome in irritable bowel syndrome and its bowel habit subtypes. Microbiome, 2023, 11 , .	11.1	25
A deep continental aquifer downhole sampler for microbiological studies. Frontiers in Microbiology, 0, 13, .	3 . 5	3
Hidden Decomposers: the Role of Bacteria and Fungi in Recently Intermittent Alpine Streams Heterotrophic Pathways. Microbial Ecology, 2023, 86, 1499-1512.	2.8	3
10653 Fecal Microbiome Does Not Represent Whole Gut Microbiome. Cellular Microbiology, 2023, 2023, 1-14.	2.1	9
Microbial diversity and proxy species for human impact in Italian karst caves. Scientific Reports, 2023, 13 , .	3.3	10
Precision Monitoring of Honey Bee (Hymenoptera: Apidae) Activity and Pollen Diversity during Pollination to Evaluate Colony Health. Insects, 2023, 14, 95.	2.2	0
Breast cancer patients from the Midwest region of the United States have reduced levels of short-chain fatty acid-producing gut bacteria. Scientific Reports, 2023, 13 , .	3.3	10
Structure and metabolic potential of the prokaryotic communities from the hydrothermal system of Paleochori Bay, Milos, Greece. Frontiers in Microbiology, 0, 13, .	3.5	1
Longitudinal, Multi-Platform Metagenomics Yields a High-Quality Genomic Catalog and Guides an <i>In Vitro</i>	3.8	4

# ARTICLE	IF	Citations
Bacterial, Archaeal, and Eukaryote Diversity in Planktonic and Sessile Communities Inside an Abandoned and Flooded Iron Mine (Quebec, Canada). Applied Microbiology, 2023, 3, 45-63.	1.6	1
10661 Arbuscular mycorrhizal fungi in oat-pea intercropping. Scientific Reports, 2023, 13, .	3. 3	1
Investigating host-gut microbial relationship in Penaeus monodon upon exposure to Vibrio harveyi. Aquaculture, 2023, 567, 739252.	3 . 5	5
10663 Microbiome analysis of raw honey reveals important factors influencing the bacterial and fungal communities. Frontiers in Microbiology, 0, 13, .	3.5	5
Phyllosphere Exudates Select for Distinct Microbiome Members in Sorghum Epicuticular Wax and Aerial Root Mucilage. Phytobiomes Journal, 2023, 7, 184-197.	2.7	5
SpPdp11 Administration in Diet Modified the Transcriptomic Response and Its Microbiota Associated in Mechanically Induced Wound Sparus aurata Skin. Animals, 2023, 13, 193.	2.3	0
Local and non″ocal soil microbiota impede germination of the endangered <i>Acacia whibleyana</i> Austral Ecology, 0, , .	1.5	0
Breastfeeding enrichment of B.Âlongum subsp. infantis mitigates the effect of antibiotics on the microbiota and childhood asthma risk. Med, 2023, 4, 92-112.e5.	4.4	15
lnvestigating geological records of tsunamis in Western Thailand with environmental DNA. Marine Geology, 2023, , 106989.	2.1	1
Ecological insights into soil health according to the genomic traits and environment-wide associations of bacteria in agricultural soils. ISME Communications, 2023, 3, .	4.2	12
Celiac Disease Predisposition and Genital Tract Microbiota in Women Affected by Recurrent Pregnancy Loss. Nutrients, 2023, 15, 221.	4.1	8
Using metabolic potential within the airway microbiome as predictors of clinical state in persons with cystic fibrosis. Frontiers in Medicine, 0, 9, .	2.6	2
The thermal degradation and soil recovery of thermal treatment of field-weathered decabrominated diphenyl ether-contaminated soil. Chemosphere, 2023, 318, 137736.	8.2	1
Viral Community Structure and Potential Functions in the Dried-Out Aral Sea Basin Change along a Desiccation Gradient. MSystems, 2023, 8, .	3.8	1
Environmental and geographical factors structure cauliflower coral's algal symbioses across the Indoâ€Pacific. Journal of Biogeography, 2023, 50, 669-684.	3.0	1
10676 Insular holobionts: persistence and seasonal plasticity of the Balearic wall lizard (<i>Podarcis) Tj ETQq1 1 0.784</i>	314 rgBT /	Overlock 10 1
Above- and below-ground microbiome in the annual developmental cycle of two olive tree varieties. FEMS Microbes, 2023, 4, .	2.1	2
10678 The microbiome of kidney stones and urine of patients with nephrolithiasis. Urolithiasis, 2023, 51, .	2.0	2

# Article	IF	CITATIONS
The gestational membrane microbiome in the presence or absence of intraamniotic infection. American Journal of Obstetrics & Samp; Gynecology MFM, 2023, 5, 100837.	2.6	1
The person-to-person transmission landscape of the gut and oral microbiomes. Nature, 2023, 614, 125-135.	27.8	111
8-HQA adjusts the number and diversity of bacteria in the gut microbiome of Spodoptera littoralis. Frontiers in Microbiology, 0, 14, .	3.5	3
The gut microbiota of people with asthma influences lung inflammation in gnotobiotic mice. IScience, 2023, 26, 105991.	4.1	4
Interactions between perceived stress and microbial-host immune components: two demographically and geographically distinct pregnancy cohorts. Translational Psychiatry, 2023, 13, .	4.8	5
lnsights into the effects of sublethal doses of pesticides glufosinate-ammonium and sulfoxaflor on honey bee health. Science of the Total Environment, 2023, 868, 161331.	8.0	3
Changes in the Ixodes ricinus microbiome associated with artificial tick feeding. Frontiers in Microbiology, 0, 13, .	3. 5	3
Different patterns and drivers of fungal communities between phyllosphere and rhizosphere in alpine grasslands. Functional Ecology, 2023, 37, 523-535.	3.6	1
Seasonal Shifts in Bacterial and Fungal Microbiomes of Leaves and Associated Leaf-Mining Larvae Reveal Persistence of Core Taxa Regardless of Diet. Microbiology Spectrum, 2023, 11, .	3.0	7
Effect on microbial communities in apple orchard soil when exposed short-term to climate change abiotic factors and different orchard management practices. Journal of Applied Microbiology, 2023, 134, .	3.1	1
Distribution and diversity of anaerobic thermophiles and putative anaerobic nickel-dependent carbon monoxide-oxidizing thermophiles in mesothermal soils and sediments. Frontiers in Microbiology, 0, 13, .	3.5	3
Comparative Analysis of Metagenomic (Amplicon and Shotgun) DNA Sequencing to Characterize 10692 Microbial Communities in Household On-Site Wastewater Treatment Systems. Water (Switzerland), 2023, 15, 271.	2.7	1
The role of the gut microbiota in patients with Kleefstra syndrome. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 0, , .	1.7	0
Effect of Long-Term Inorganic Fertilization on Diversity and Abundance of Bacterial and Archaeal Communities at Tillage in Irrigated Rice Field. Advances in Bioscience and Biotechnology (Print), 2023, 14, 18-33.	0.7	O
$_{10696}$ A global perspective on bacterial diversity in the terrestrial deep subsurface. Microbiology (United) Tj ETQq0 () 0 rgBT ₈ /Ove	erlogk 10 Tf 50
Fungal community composition and genetic potential regulate fine root decay in northern temperate forests. Molecular Ecology, 2023, 32, 2005-2021.	3.9	3
Exposure to global change and microplastics elicits an immune response in an endangered coral. Frontiers in Marine Science, 0, 9, .	2.5	4
Glycosidic linkage of rare and new-to-nature disaccharides reshapes gut microbiota in vitro. Food Chemistry, 2023, , 135440.	8.2	1

# ARTICLE	IF	CITATIONS
Microbial communities on eelgrass (Zostera marina) thriving in Tokyo Bay and the possible source of leaf-attached microbes. Frontiers in Microbiology, 0, 13, .	3.5	2
The Saccharina latissima microbiome: Effects of region, season, and physiology. Frontiers in Microbiology, $0,13,.$	3.5	6
Untangling the complex interactions between turtle ants and their microbial partners. Animal Microbiome, 2023, 5, .	3.8	3
Airway bacterial community composition in persons with advanced cystic fibrosis lung disease. Journal of Cystic Fibrosis, 2023, 22, 623-629.	0.7	1
Rectal swabs as a viable alternative to faecal sampling for the analysis of gut microbiota functionality and composition. Scientific Reports, 2023, 13, .	3.3	5
Dynamics of the gut microbiome, IgA response, and plasma metabolome in the development of pediatric celiac disease. Microbiome, 2023, 11 , .	11.1	8
Distinct Microbiotas Are Associated with Different Production Lines in the Cutting Room of a Swine Slaughterhouse. Microorganisms, 2023, 11, 133.	3.6	3
DNA Metabarcoding-Based Evaluation of the Diet of Big Brown Bats (Eptesicus fuscus) in the Mid-Atlantic Region. Northeastern Naturalist, 2023, 29, .	0.3	0
Altered gastrointestinal tract structure and microbiome following cerebral malaria infection. Parasitology Research, 0, , .	1.6	0
Co-invasive ectomycorrhizal fungi alter native soil fungal communities. Plant and Soil, 2023, 484, 547-567.	3.7	3
Involucrin Modulates Vitamin D Receptor Activity in the Epidermis. Journal of Investigative Dermatology, 2023, 143, 1052-1061.e3.	0.7	0
Study of altered gut microbial dynamics and their association with gestational diabetes mellitus. Systems Microbiology and Biomanufacturing, 2024, 4, 263-273.	2.9	0
lnvestigation of systemic granulomatosis in cultured meagre, Argyrosomus regius, using clinical metagenomics. Aquaculture, 2023, 567, 739249.	3.5	4
10716 New Negombata species discovered: latrunculin mystery solved. Coral Reefs, 0, , .	2.2	0
10717 Characterizing the gut microbiome changes with aging in a novel Alzheimer's disease rat model. Aging, 2022, 15, 459-471.	3.1	8
Natural rubber reduces herbivory and alters the microbiome below ground. New Phytologist, 2023, 239, 1475-1489.	7.3	4
The salivary and nasopharyngeal microbiomes are associated with SARS oVâ€2 infection and disease severity. Journal of Medical Virology, 2023, 95, .	5.0	6
Soil depth as a driver of microbial and carbon dynamics in a planted forest (<i>Pinus radiata</i>) pumice soil. Soil, 2023, 9, 55-70.	4.9	2

# ARTICLE	IF	CITATIONS
Fructooligosaccharides (FOS) differentially modifies the in vitro gut microbiota in an age-dependent manner. Frontiers in Nutrition, $0, 9, .$	3.7	4
The aerobiome in a hospital environment: Characterization, seasonal tendencies and the effect of window opening ventilation. Building and Environment, 2023, 230, 110024.	6.9	3
Microbial Motility at the Bottom of North America: Digital Holographic Microscopy and Genomic Motility Signatures in Badwater Spring, Death Valley National Park. Astrobiology, 0, , .	3.0	1
Grape-associated fungal community patterns persist from berry to wine on a fine geographical scale. FEMS Yeast Research, 2023, 23, .	2.3	4
Hydrological connections in a glaciated Andean catchment under permafrost conditions (33°S). Journal of Hydrology: Regional Studies, 2023, , 101311.	2,4	0
Spatial co-occurrence patterns of benthic microbial assemblage in response to trace metals in the Atacama Desert Coastline. Frontiers in Microbiology, 0, 13, .	3.5	0
Unique Features of the Gut Microbiome Characterized in Animal Models of Angelman Syndrome. MSystems, 2023, 8, .	3.8	1
Variation in the Early Life and Adult Intestinal Microbiome of Intra-Uterine Growth Restricted Rat Offspring Exposed to a High Fat and Fructose Diet. Nutrients, 2023, 15, 217.	4.1	1
Topography of the respiratory, oral, and guttural pouch bacterial and fungal microbiotas in horses. Journal of Veterinary Internal Medicine, 2023, 37, 349-360.	1.6	2
Geography and elevation as drivers of cloacal microbiome assemblages of a passerine bird distributed across Sulawesi, Indonesia. Animal Microbiome, 2023, 5, .	3.8	3
Antenatal gut microbiome profiles and effect on pregnancy outcome in HIV infected and HIV uninfected women in a resource limited setting. BMC Microbiology, 2023, 23, .	3.3	3
Effects of short-term experimental manipulation of captive social environment on uropygial gland microbiome and preen oil volatile composition. Frontiers in Ecology and Evolution, 0, 10, .	2.2	1
Malaria disrupts the rhesus macaque gut microbiome. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	4
Metabarcoding of eDNA for tracking the floral and geographical origins of bee honey. Food Research International, 2023, 164, 112413.	6.2	2
Limited influence of seasonality on coral microbiomes and endosymbionts in an equatorial reef. Ecological Indicators, 2023, 146, 109878.	6.3	5
Encapsulated in sediments: eDNA deciphers the ecosystem history of one of the most polluted European marine sites. Environment International, 2023, 172, 107738.	10.0	11
Fate of dissolved organics and generated sulfate ions during biofiltration of oil sands process water pretreated with sulfate radical advanced oxidation process. Chemical Engineering Journal, 2023, 458, 141390.	12.7	6
The gut microbiota and metabolome are associated with diminished COVID-19 vaccine-induced antibody responses in immunosuppressed inflammatory bowel disease patients. EBioMedicine, 2023, 88, 104430	y). 6.1	19

# ARTICLE	IF	CITATIONS
Gut microbiota might influence the risk of rejection after liver transplantation. Journal of Liver Transplantation, 2023, 9, 100140.	0.4	3
Diversity of the holopelagic Sargassum microbiome from the Great Atlantic Sargassum Belt to coastal stranding locations. Harmful Algae, 2023, 122, 102369.	4.8	9
Long-term organic fertilization promotes the resilience of soil multifunctionality driven by bacterial communities. Soil Biology and Biochemistry, 2023, 177, 108922.	8.8	19
A protocol for the extraction of viable bacteria for identification of bacterial communities in bentonite. Applied Clay Science, 2023, 232, 106809.	5.2	2
Time is a stronger predictor of microbiome community composition than tissue in external mucosal surfaces of Atlantic salmon (Salmo salar) reared in a semi-natural freshwater environment. Aquaculture, 2023, 566, 739211.	3.5	3
Inflammatory profiles, gut microbiome, and kidney function are impacted after high-fidelity firefighter training. International Journal of Hygiene and Environmental Health, 2023, 248, 114107.	4.3	1
Contrasting responses of microbial diversity and community structure in decaying root bark and xylem to N addition in an alpine shrubland. Soil Biology and Biochemistry, 2023, 178, 108937.	8.8	0
Title: Obesogenic microbial signatures and the development of obesity in childhood acute lymphoblastic leukemia. Leukemia Research, 2023, 126, 107017.	0.8	0
Comparative study of bacterial community dynamics in different soils following application of the herbicide atrazine. Environmental Research, 2023, 220, 115189.	7.5	3
10750 Protocol for microbiota analysis of a murine stroke model. STAR Protocols, 2023, 4, 101969.	1.2	1
Distinctive role of soil type and land use in driving bacterial communities and carbon cycling functions down soil profiles. Catena, 2023, 223, 106903.	5.0	6
Profiling of phenol content and microbial community dynamics during pâté olive cake fermentation. Food Bioscience, 2023, 52, 102358.	4.4	4
Adverse impacts of Roundup on soil bacteria, soil chemistry and mycorrhizal fungi during restoration of a Colorado grassland. Applied Soil Ecology, 2023, 185, 104778.	4.3	4
Belowground crop responses to root herbivory are associated with the community structure of native arbuscular mycorrhizal fungi. Applied Soil Ecology, 2023, 185, 104797.	4.3	6
Comparing earthworm biodiversity estimated by DNA metabarcoding and morphology-based approaches. Applied Soil Ecology, 2023, 185, 104798.	4.3	3
Disease-induced assemblage of the rhizosphere fungal community in successive plantings of wheat. Phytobiomes Journal, 0, , .	2.7	2
Growth Performance, Gut Health, Welfare and Qualitative Behavior Characteristics of Broilers Fed Diets Supplemented with Dried Common (Olea europaea) Olive Pulp. Sustainability, 2023, 15, 501.	3.2	2
10759 Bacterial Profiles of Brain in Downer Cattle with Unknown Etiology. Microorganisms, 2023, 11, 98.	3.6	0

# ARTICLE	IF	CITATIONS
Phage-Host Prediction Using a Computational Tool Coupled with 16S rRNA Gene Amplicon Sequencing. Viruses, 2023, 15, 76.	3.3	O
The Impact of Different Inoculation Schemes on the Microbiota, Physicochemical and Sensory 10762 Characteristics of Greek Kopanisti Cheese throughout Production and Ripening. Microorganisms, 2023, 11, 66.	3.6	2
Snow Surface Microbial Diversity at the Detection Limit within the Vicinity of the Concordia Station, Antarctica. Life, 2023, 13, 113.	2.4	2
Effects of Phycosphere Bacteria on Their Algal Host Are Host Species-Specific and Not Phylogenetically Conserved. Microorganisms, 2023, 11, 62.	3.6	2
Vaccination with an HIV T-cell immunogen induces alterations in the mouse gut microbiota. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	5
Critical Assessment of Whole Genome and Viral Enrichment Shotgun Metagenome on the Characterization of Stool Total Virome in Hepatocellular Carcinoma Patients. Viruses, 2023, 15, 53.	3.3	1
Coumarin biosynthesis genes are required after foliar pathogen infection for the creation of a microbial soil-borne legacy that primes plants for SA-dependent defenses. Scientific Reports, 2022, 12, .	3.3	10
Assessing the causes and consequences of gut mycobiome variation in a wild population of the Seychelles warbler. Microbiome, 2022, 10 , .	11.1	3
Rapid bacterial and fungal successional dynamics in first year after chaparral wildfire. Molecular Ecology, 2023, 32, 1685-1707.	3.9	18
96. Variance component estimation of longitudinal alpha diversity metrics of the ocular microbiome in preweaned beef cattle. , 2022, , .		0
Contrasting Nitrogen Fertilization and <i>Brassica napus</i> (Canola) Variety Development Impact Recruitment of the Root-Associated Microbiome. Phytobiomes Journal, 2023, 7, 125-137.	2.7	2
Microbially produced vitamin B12 contributes to the lipid-lowering effect of silymarin. Nature Communications, 2023, 14, .	12.8	12
Effect of ospemifene on vaginal microbiome in postmenopausal women with vulvovaginal atrophy. Menopause, 2023, 30, 361-369.	2.0	3
Environmental Filtering Drives Fungal Phyllosphere Community in Regional Agricultural Landscapes. Plants, 2023, 12, 507.	3.5	1
Gut microbiome composition associated with <i>Plasmodium</i> infection in the Eurasian tree sparrow. Journal of Avian Biology, 2023, 2023, .	1.2	4
Leveraging microbiome rediversification for the ecological rescue of soil function. Environmental Microbiomes, 2023, 18, .	5.0	1
Lettuce Soil Microbiome Modulated by an L-α-Amino Acid-Based Biostimulant. Agriculture (Switzerland), 2023, 13, 344.	3.1	4
Spatial comparison and temporal evolution of two marine iron-rich microbial mats from the Lucky Strike Hydrothermal Field, related to environmental variations. Frontiers in Marine Science, 0, 10, .	2.5	4

# ARTICLE	IF	CITATIONS
An IBD-associated pathobiont synergises with NSAID to promote colitis which is blocked by NLRP3 inflammasome and Caspase-8 inhibitors. Gut Microbes, 2023, 15, .	9.8	4
Acute appendicitis manifests as two microbiome state types with oral pathogens influencing severity. Gut Microbes, 2023, 15, .	9.8	5
Surfeit folic acid, protein, and exercise modify oncogenic inflammatory biomarkers and fecal microbiota. Frontiers in Nutrition, 0, 9, .	3.7	1
Viral infection switches the balance between bacterial and eukaryotic recyclers of organic matter during coccolithophore blooms. Nature Communications, 2023, 14, .	12.8	11
A Case of Successful Treatment of Recurrent Urinary Tract Infection by Extended-Spectrum β-Lactamase 10787 Producing <i>Klebsiella pneumoniae</i> Using Oral Lyophilized Fecal Microbiota Transplant. Microbial Drug Resistance, 2023, 29, 34-38.	2.0	3
Transcriptome analysis reveals increased abundance and diversity of opportunistic fungal pathogens in nasopharyngeal tract of COVID-19 patients. PLoS ONE, 2023, 18, e0278134.	2.5	2
Strain-specific alterations in gut microbiome and host immune responses elicited by tolerogenic Bifidobacterium pseudolongum. Scientific Reports, 2023, 13, .	3.3	8
Combining vertebrate mitochondrial 12S rRNA gene sequencing and shotgun metagenomic sequencing to investigate the diet of the leopard cat (Prionailurus bengalensis) in Korea. PLoS ONE, 2023, 18, e0281245.	2.5	1
10793 Bacterial topography of the upper and lower respiratory tract in pigs. Animal Microbiome, 2023, 5, .	3.8	7
Association between Legionella species and humic substances during early summer in the northern Baltic Sea. Frontiers in Marine Science, 0, 9, .	2.5	1
Response of the Soil Fungal Community and Its Function during the Conversion of Forestland to Tea Plantations: A Case Study in Southeast China. Forests, 2023, 14, 209.	2.1	2
Orofacial clefts alter early life oral microbiome maturation towards higher levels of potentially pathogenic species: A prospective observational study. Journal of Oral Microbiology, 2023, 15, .	2.7	1
A Cross-Sectional Study of Potential Antimicrobial Resistance and Ecology in Gastrointestinal and 10800 Oral Microbial Communities of Young Normoweight Pakistani Individuals. Microorganisms, 2023, 11, 279.	3.6	2
Therapeutic beta-lactam dosages and broad-spectrum antibiotics are associated with reductions in microbial richness and diversity in persons with cystic fibrosis. Scientific Reports, 2023, 13, .	3.3	1
Microbiome Alterations in Alcohol Use Disorder and Alcoholic Liver Disease. International Journal of Molecular Sciences, 2023, 24, 2461.	4.1	8
Transmission Mode and Assembly of Seed Fungal Endophyte Communities in Wheat and Wheat Wild Relatives. Phytobiomes Journal, 2023, 7, 113-124.	2.7	3
Testing the passive sampling hypothesis: The role of dispersal in shaping microbial species-area relationship. Frontiers in Microbiology, 0, 14, .	3.5	4
Modulatory Effects of Heat-Inactivated Streptococcus Thermophilus Strain 7 on the Inflammatory 10805 Response: A Study on an Animal Model with TLR3-Induced Intestinal Injury. Microorganisms, 2023, 11, 278.	3.6	0

# ARTICLE	IF	CITATIONS
Frizzled 7 modulates goblet and Paneth cell fate, and maintains homeostasis in mouse intestine. Development (Cambridge), 2023, 150, .	2.5	2
Insufficient Evidence of a Breastmilk Microbiota at Six-Weeks Postpartum: A Pilot Study. Nutrients, 2023, 15, 696.	4.1	0
Dietary Impacts on Changes in Diversity and Abundance of the Murine Microbiome during Progression and Treatment of Cancer. Nutrients, 2023, 15, 724.	4.1	2
10810 Human liver microbiota modeling strategy at the early onset of fibrosis. BMC Microbiology, 2023, 23, .	3.3	1
Copper intrauterine device increases vaginal concentrations of inflammatory anaerobes and depletes lactobacilli compared to hormonal options in a randomized trial. Nature Communications, 2023, 14, .	12.8	7
Correspondence analysis for dimension reduction, batch integration, and visualization of single-cell RNA-seq data. Scientific Reports, 2023, 13, .	3.3	2
Modeling geographic distribution of arbuscular mycorrhizal fungi from molecular evidence in soils of Argentinean Puna using a maximum entropy approach. Peerl, 0, 11, e14651.	2.0	3
Cryptic Diversity of Black Band Disease Cyanobacteria in Siderastrea siderea Corals Revealed by Chemical Ecology and Comparative Genome-Resolved Metagenomics. Marine Drugs, 2023, 21, 76.	4.6	4
Bark-inhabiting fungal communities of European chestnut undergo substantial alteration by canker formation following chestnut blight infection. Frontiers in Microbiology, 0, 14, .	3.5	0
How does heat stress affect sponge microbiomes? Structure and resilience of microbial communities of marine sponges from different habitats. Frontiers in Marine Science, 0, 9, .	2.5	5
Dietary Supplementation with Botanical Blends Modified Intestinal Microbiota and Metabolomics of Weaned Pigs Experimentally Infected with Enterotoxigenic Escherichia coli. Microorganisms, 2023, 11, 320.	3.6	1
Genetic and Structural Diversity of Prokaryotic Ice-Binding Proteins from the Central Arctic Ocean. Genes, 2023, 14, 363.	2.4	5
Genes mcr improve the intestinal fitness of pathogenic E. coli and balance their lifestyle to commensalism. Microbiome, 2023, 11 , .	11.1	9
Impacts of winter wheat and cover crops on soil microbial diversity in a corn–soybean noâ€till cropping system in Quebec (Canada). , 2023, 6, .		0
Artisanal and farmer bread making practices differently shape fungal species community composition in French sourdoughs. , 0, 3, .		4
A High Dose of Dietary Berberine Improves Gut Wall Morphology, Despite an Expansion of 10823 <1>Enterobacteriaceae 1 and a Reduction in Beneficial Microbiota in Broiler Chickens. MSystems, 2023, 8, .	3.8	8
Experimental bacterial dysbiosis with consequent immune alterations increase intrarectal SIV acquisition susceptibility. Cell Reports, 2023, 42, 112020.	6.4	1
Individuality and stability of the koala (<i>Phascolarctos cinereus</i>) faecal microbiota through time. PeerJ, 0, 11, e14598.	2.0	3

# ARTICLE	IF	CITATIONS
lnteraction between genetics and inulin affects host metabolism in rainbow trout fed a sustainable all plant-based diet. British Journal of Nutrition, 2023, 130, 1105-1120.	2.3	3
Bacterial community structure of electrogenic biofilm developed on modified graphite anode in microbial fuel cell. Scientific Reports, 2023, 13, .	3.3	15
Gut Dysbiosis in Experimental Kidney Disease: A Meta-Analysis of Rodent Repository Data. Journal of the American Society of Nephrology: JASN, 2023, 34, 533-553.	6.1	3
Functional significance of microbial diversity in arid soils: biological soil crusts and nitrogen fixation as a model system. FEMS Microbiology Ecology, 0 , , .	2.7	0
ldentifying the core microbiome of the sea star <i>Pisaster ochraceus</i> in the context of sea star wasting disease. FEMS Microbiology Ecology, 0, , .	2.7	3
Characterization of the bacterial microbiome of Swedish ticks through 16S rRNA amplicon sequencing of whole ticks and of individual tick organs. Parasites and Vectors, 2023, 16 , .	2.5	6
10833 S100B Affects Gut Microbiota Biodiversity. International Journal of Molecular Sciences, 2023, 24, 2248.	4.1	4
Accumulation of Black Carbon Particles in Placenta, Cord Blood, and Childhood Urine in Association 10834 with the Intestinal Microbiome Diversity and Composition in Four- to Six-Year-Old Children in the ENVIR <i>ON</i> AGE Birth Cohort. Environmental Health Perspectives, 2023, 131, .	6.0	5
Metabarcoding reveals seasonal and spatial patterns of arthropod community assemblages in two contrasting habitats: Desert and oasis of the Baja California Peninsula, Mexico. Diversity and Distributions, 2023, 29, 438-461.	4.1	0
A microbial tale of farming, invasion and conservation: on the gut bacteria of European and American mink in Western Europe. Biological Invasions, 2023, 25, 1693-1709.	2.4	1
The quorum quenching enzyme Aii20J modifies in vitro periodontal biofilm formation. Frontiers in Cellular and Infection Microbiology, 0, 13 , .	3.9	12
Time-dependent fermentation of different structural units of commercial pectins with intestinal bacteria. Carbohydrate Polymers, 2023, 308, 120642.	10.2	4
Land use effects on soil protists and their top-down regulation on bacteria and fungi in soil profiles. Applied Soil Ecology, 2023, 185, 104799.	4.3	7
Potential interactions between diatoms and bacteria are shaped by trace element gradients in the Southern Ocean. Frontiers in Marine Science, 0, 9, .	2.5	3
Limited cross-species virus transmission in a spatially restricted coral reef fish community. Virus Evolution, 2023, 9, .	4.9	4
Aerial transport of bacteria by dust plumes in the Eastern Mediterranean revealed by complementary rRNA/rRNA-gene sequencing. Communications Earth & Environment, 2023, 4, .	6.8	4
Characteristics of The Bleached Microbiome of The Generalist Coral <i>Pocillopora damicornis</i> from Two Distinct Reef Habitats. Integrative Organismal Biology, 2023, 5, .	1.8	2
Biofilm thickness controls the relative importance of stochastic and deterministic processes in microbial community assembly in moving bed biofilm reactors. Interface Focus, 2023, 13, .	3.0	2

# ARTICLE	IF	Citations
Three-way relationships between gut microbiota, helminth assemblages and bacterial infections in wild rodent populations. , 0, 3, .		2
Diet Quality and Liver Health in People Living with HIV in the MASH Cohort: A Multi-Omic Analysis of the Fecal Microbiome and Metabolome. Metabolites, 2023, 13, 271.	2.9	2
AQP1 in the Gastrointestinal Tract of Mice: Expression Pattern and Impact of AQP1 Knockout on Colonic Function. International Journal of Molecular Sciences, 2023, 24, 3616.	4.1	2
Effect of two milk supplements and two ways of administration on growth performance, welfare and fecal microbial ecology of suckling piglets. Frontiers in Veterinary Science, 0, 10 , .	2.2	0
Red mark syndrome: Is the aquaculture water microbiome a keystone for understanding the disease aetiology?. Frontiers in Microbiology, 0, 14, .	3 . 5	1
Analysis of the core bacterial community associated with consumer-ready Eastern oysters (Crassostrea virginica). PLoS ONE, 2023, 18, e0281747.	2.5	4
Gut Microbiota Remodeling and Intestinal Adaptation to Lipid Malabsorption After Enteroendocrine Cell Loss in Adult Mice. Cellular and Molecular Gastroenterology and Hepatology, 2023, 15, 1443-1461.	4. 5	5
Opportunistic vs selective feeding strategies of zooplankton under changing environmental conditions. Journal of Plankton Research, 2023, 45, 389-403.	1.8	3
Altered Faecal Microbiota Composition and Structure of Ghanaian Children with Acute Gastroenteritis. International Journal of Molecular Sciences, 2023, 24, 3607.	4.1	4
Highâ€resolution phylogenetic analysis reveals longâ€term microbial dynamics and microdiversity in phytoplankton microbiome. Journal of Eukaryotic Microbiology, 2023, 70, .	1.7	2
Bacteroidetes to Firmicutes: captivity changes the gut microbiota composition and diversity in a social subterranean rodent. Animal Microbiome, 2023, 5, .	3.8	8
Insects in water towers: Hibernating flies could compromise microbial drinking water quality. Frontiers in Water, 0, 5, .	2.3	1
Distinguishable Influence of the Delivery Mode, Feeding Pattern, and Infant Sex on Dynamic Alterations in the Intestinal Microbiota in the First Year of Life. Microbial Ecology, 0, , .	2.8	1
High Abundance of Candidatus Arthromitus in Intestinal Microbiota of Seriolella violacea (Palm Ruff) under Reared Conditions. Fishes, 2023, 8, 109.	1.7	2
Understanding the impact of radical changes in diet and the gut microbiota on brain function and structure: rationale and design of the EMBRACE study. Surgery for Obesity and Related Diseases, 2023, 19, 1000-1012.	1.2	0
Dietary tryptophan deficiency promotes gut RORγt+ Treg cells at the expense of Gata3+ Treg cells and alters commensal microbiota metabolism. Cell Reports, 2023, 42, 112135.	6.4	9
Environment and shipping drive environmental <scp>DNA</scp> betaâ€diversity among commercial ports. Molecular Ecology, 2023, 32, 6696-6709.	3.9	5
Omega-3-Supplemented Fat Diet Drives Immune Metabolic Response in Visceral Adipose Tissue by Modulating Gut Microbiota in a Mouse Model of Obesity. Nutrients, 2023, 15, 1404.	4.1	7

# ARTICLE	IF	Citations
ls there a placental microbiota? A critical review and re-analysis of published placental microbiota datasets. BMC Microbiology, 2023, 23, .	3.3	16
Strip intercropping with local crops increased Aconitum carmichaeli yield and soil quality. Frontiers in Plant Science, 0, 14, .	3.6	1
Bacterial communities of Aedes aegypti mosquitoes differ between crop and midgut tissues. PLoS Neglected Tropical Diseases, 2023, 17, e0011218.	3.0	5
10874 Fungal Biostarter Effect on the Quality of Dry-Aged Beef. Foods, 2023, 12, 1330.	4.3	1
Nlrp12 deficiency alters gut microbiota and ameliorates Faslpr-mediated systemic autoimmunity in male mice. Frontiers in Immunology, 0, 14, .	4.8	1
Plant species shape the bacterial communities on the phyllosphere in a hyper-arid desert. Microbiological Research, 2023, 269, 127314.	5.3	4
Agaricus subrufescens fermented rye affects the development of intestinal microbiota, local intestinal and innate immunity in suckling-to-nursery pigs. Animal Microbiome, 2023, 5, .	3.8	0
Out of site, out of mind: Changes in feather moss phyllosphere microbiota in mine offsite boreal landscapes. Frontiers in Microbiology, 0, 14, .	3.5	1
E-Cigarette Vapour Alters High-Fat Diet-Induced Systemic Inflammatory Responses but Has No Effect on High-Fat Diet-Induced Changes in Gut Microbiota. Nutrients, 2023, 15, 1783.	4.1	0
Commercial production of Florida pompano (Trachinotus carolinus) larvae at low salinity induces 10880 variable changes in whole-larvae microbial diversity, gene expression, and gill histopathology. Frontiers in Marine Science, 0, 10, .	2.5	0
Diversity and structure of feather mite communities on seabirds from the north–east Atlantic and Mediterranean Sea. Scientific Reports, 2023, 13, .	3.3	0
The gut microbiome and regional fat distribution: Findings from the Baltimore Longitudinal Study of Aging. Obesity, 2023, 31, 1425-1435.	3.0	1
Metabarcoding inventory of an arctic tundra soil ecosystem reveals highly heterogeneous communities at a small scale. Polar Biology, 2023, 46, 461-471.	1.2	2
Plastisphere assemblages differ from the surrounding bacterial communities in transitional coastal environments. Science of the Total Environment, 2023, 869, 161703.	8.0	8
Plant sexual variation modulates rhizospheric nutrient processes through the soil microbiome 10886 response to drought and rewetting in Populus cathayana. Biology and Fertility of Soils, 2023, 59, 571-587.	4.3	1
Maternal polychlorinated biphenyl 126 (PCB 126) exposure modulates offspring gut microbiota irrespective of diet and exercise. Reproductive Toxicology, 2023, 118, 108384.	2.9	1
The selection of software and database for metagenomics sequence analysis impacts the outcome of microbial profiling and pathogen detection. PLoS ONE, 2023, 18, e0284031.	2.5	0
Soil fungal diversity and assembly along a xeric stress gradient in the central Namib Desert. Fungal Biology, 2023, 127, 997-1003.	2.5	2

# ARTICLE	IF	Citations
Relationship Functioning and Gut Microbiota Composition among Older Adult Couples. International Journal of Environmental Research and Public Health, 2023, 20, 5435.	2.6	0
Gut Microbiota–Derived Trimethylamine N-Oxide Contributes to Abdominal Aortic Aneurysm Through Inflammatory and Apoptotic Mechanisms. Circulation, 2023, 147, 1079-1096.	1.6	16
Maternal Rumen Bacteriota Shapes the Offspring Rumen Bacteriota, Affecting the Development of Young Ruminants. Microbiology Spectrum, 2023, 11 , .	3.0	1
Microbial life in 25-m-deep boreholes in ancient permafrost illuminated by metagenomics. Environmental Microbiomes, 2023, 18, .	5.0	1
Fe(III) Biomineralization in the Surface Microlayer of Acid Mine Waters Catalyzed by Neustonic Fe(II)-Oxidizing Microorganisms. Minerals (Basel, Switzerland), 2023, 13, 508.	2.0	1
Meta-Analysis Reveals Compositional and Functional Microbial Changes Associated with Osteoporosis. Microbiology Spectrum, 2023, 11, .	3.0	5
The preterm gut microbiota and administration routes of different probiotics: a randomized controlled trial. Pediatric Research, 2023, 94, 1480-1487.	2.3	3
Effect of yeast species and processing on intestinal microbiota of Atlantic salmon (Salmo salar) fed soybean meal-based diets in seawater. Animal Microbiome, 2023, 5, .	3.8	4
Arthropod co-occurrence networks indicate environmental differences between islands and signal introduced species in Azorean native forest remnants. Frontiers in Ecology and Evolution, 0, 11 , .	2.2	1
An inexpensive, reproducible method to quantify activated sludge foaming potential: Validation 10901 through labâ€scale studies and yearâ€long fullâ€scale sampling campaign. Water Environment Research, 2023, 95, .	2.7	0
Effects of phenyl acids on different degradation phases during thermophilic anaerobic digestion. Frontiers in Microbiology, 0, 14, .	3.5	1
Contribution of soil bacteria to the atmosphere across biomes. Science of the Total Environment, 2023, 871, 162137.	8.0	3
Enhanced removal of warfare agent tri-nitro-toluene by a Methylophaga-dominated microbiome. Marine Pollution Bulletin, 2023, 190, 114866.	5.0	4
Microplastic biofilm, associated pathogen and antimicrobial resistance dynamics through a 10905 wastewater treatment process incorporating a constructed wetland. Water Research, 2023, 235, 119936.	11.3	14
Enrichment of antibiotic resistant genes and pathogens in face masks from coastal environments. Journal of Hazardous Materials, 2023, 449, 131038.	12.4	4
Long-term implementation of a silvopastoral system enhances soil P availability and bacterial diversity. Geoderma, 2023, 433, 116458.	5.1	2
Effects of Granular Activated Carbon Amendment, Temperature, and Organic Loading Rate on 10908 Microbial Communities in Up-Flow Anaerobic Sludge Blanket Reactors. Journal of Environmental Engineering, ASCE, 2023, 149, .	1.4	2
Effects of global change on the ability of stream biofilm to dissipate the herbicide glyphosate. Environmental Pollution, 2023, 324, 121406.	7. 5	2

# ARTICLE	IF	Citations
How does particulate matter affect plant transcriptome and microbiome?. Environmental and Experimental Botany, 2023, 209, 105313.	4.2	2
Physicochemical and bacterial changes during composting of vegetable and animal-derived agro-industrial wastes. Bioresource Technology, 2023, 376, 128842.	9.6	13
Molecular insights informing factors affecting low temperature anaerobic applications: Diversity, collated core microbiomes and complexity stability relationships in LCFA-fed systems. Science of the Total Environment, 2023, 874, 162420.	8.0	4
Effects of pair-housing pubertal and adult male and female mice on LPS-induced age-dependent immune responses: A potential role for the gut microbiota. Brain, Behavior, and Immunity, 2023, 110, 297-309.	4.1	3
The effects of glyphosate, pure or in herbicide formulation, on bumble bees and their gut microbial communities. Science of the Total Environment, 2023, 872, 162102.	8.0	11
Characterization of the eukaryotic microbial communities in the chicken ileum in cage-free and conventional commercial housing systems. Poultry Science, 2023, 102, 102621.	3.4	0
No bacterial-mediated alleviation of thermal stress in a brown seaweed suggests the absence of ecological bacterial rescue effects. Science of the Total Environment, 2023, 876, 162532.	8.0	1
The effects of mixed-species root zones on the resistance of soil bacteria and fungi to long-term 10917 experimental and natural reductions in soil moisture. Science of the Total Environment, 2023, 873, 162266.	8.0	6
Enhanced plant growth in the presence of earthworms correlates with changes in soil microbiota but not nutrient availability. Geoderma, 2023, 433, 116426.	5.1	5
How arsenic contamination influences downslope wetland plant and microbial community structure and function. Science of the Total Environment, 2023, 876, 162839.	8.0	2
Prairie strips remove swine manure associated antimicrobial resistance genes and bacteria from runoff. Agriculture, Ecosystems and Environment, 2023, 349, 108469.	5. 3	1
Effects of heat and pesticide stress on life history, physiology and the gut microbiome of two 10921 congeneric damselflies that differ in stressor tolerance. Science of the Total Environment, 2023, 875, 162617.	8.0	0
History of childhood physical abuse is associated with gut microbiota diversity among adult psychiatric inpatients. Journal of Affective Disorders, 2023, 331, 50-56.	4.1	1
Deciphering the contribution of microbial biomass to the properties of dissolved and particulate organic matter in anaerobic digestates. Science of the Total Environment, 2023, 877, 162882.	8.0	4
Ammonia recovery from organic nitrogen in synthetic dairy manure with a microbial fuel cell. Chemosphere, 2023, 325, 138388.	8.2	9
The prokaryotic community of Chondrosia reniformis Nardo, 1847: from diversity to mercury detection. Zoology, 2023, 158, 126091.	1.2	0
Enrichment and chemical fractionation of plant nutrients, potentially toxic and economically valuable elements in digestate from mesophilic and thermophilic fermentation. Biomass and Bioenergy, 2023, 173, 106779.	5.7	1
Journey to the morpho-textural traits, microbiota, and volatilome of Ciauscolo PGI salami. Food Bioscience, 2023, 53, 102582.	4.4	4

# Article	IF	CITATIONS
A meta-analysis of the effect of Eimeria spp. and/or Clostridium perfringens infection on the microbiota of broiler chickens. Poultry Science, 2023, 102, 102652.	3.4	3
Reduced growth of Pinus radiata in the presence of the Australian native Allocasuarina nana via 10929 direct allelopathy and inhibition of the pine-supporting mycorrhizal community. Applied Soil Ecology, 2023, 187, 104852.	4.3	0
Response of soil fungal community to chromium contamination in agricultural soils with different physicochemical properties. Science of the Total Environment, 2023, 879, 163244.	8.0	4
Greener residential environment is associated with increased bacterial diversity in outdoor ambient air. Science of the Total Environment, 2023, 880, 163266.	8.0	1
Soil amendment with insect exuviae causes species-specific changes in the rhizosphere bacterial community of cabbage plants. Applied Soil Ecology, 2023, 188, 104854.	4.3	7
Delving into the study of lactic acid bacteria and yeasts distribution in table olive biofilms using a non-destructive procedure. Food Microbiology, 2023, 113, 104250.	4.2	1
Altered gut bacterial–fungal interkingdom networks in children and adolescents with depression. Journal of Affective Disorders, 2023, 332, 64-71.	4.1	5
Short-term prescribed fire-induced changes in soil microbial communities and nutrients in native rangelands of Florida. Applied Soil Ecology, 2023, 189, 104914.	4.3	3
10936 Environmental sponge sampling: We are only scraping the surface., 2023, 1, 13-21.		0
Microbiome diversity from sponges biogeographically distributed between South America and Antarctica. Science of the Total Environment, 2023, 879, 163256.	8.0	1
Altered human gut virome in patients undergoing antibiotics therapy for Helicobacter pylori. Nature Communications, 2023, 14, .	12.8	3
Grapefruit Root and Rhizosphere Responses to Varying Planting Densities, Fertilizer Concentrations and Application Methods. Plants, 2023, 12, 1659.	3.5	0
The Effect of a Planetary Health Diet on the Human Gut Microbiome: A Descriptive Analysis. Nutrients, 2023, 15, 1924.	4.1	4
Potential reservoirs of antimicrobial resistance in livestock waste and treated wastewater that can be disseminated to agricultural land. Science of the Total Environment, 2023, 872, 162194.	8.0	15
Sedum as host plants for caterpillars? Introducing gut content metabarcoding to green roof research. Urban Ecosystems, 0, , .	2.4	1
Spatio-temporal variation of the microbiome and resistome repertoire along an anthropogenically dynamic segment of the Ganges River, India. Science of the Total Environment, 2023, 872, 162125.	8.0	9
Plastic litter changes the rhizosphere bacterial community of coastal dune plants. Science of the Total Environment, 2023, 880, 163293.	8.0	1
eDNA metabarcoding reveals shifts in sediment eukaryote communities in a metal contaminated estuary. Marine Pollution Bulletin, 2023, 191, 114896.	5.0	1

# ARTICLE	IF	Citations
Metaviromic analyses of DNA virus community from sediments of the N-Choe stream, North India. Virus Research, 2023, 330, 199110.	2.2	0
Longitudinal analysis of changes in the gut microbiota of zebrafish following acute spring viremia of carp virus infection. Aquaculture, 2023, 572, 739499.	3 . 5	1
Impacts of microplastics and the associated plastisphere on physiological, biochemical, genetic expression and gut microbiota of the filter-feeder amphioxus. Environment International, 2023, 172, 107750.	10.0	9
Reactive iron, not fungal community, drives organic carbon oxidation potential in floodplain soils. Soil Biology and Biochemistry, 2023, 178, 108962.	8.8	5
Yellow mealworms (Tenebrio molitor) as an alternative animal feed source: A comprehensive characterization of nutritional values and the larval gut microbiome. Journal of Cleaner Production, 2023, 389, 136104.	9.3	11
Revisiting Mt Fuji's groundwater origins with helium, vanadium and environmental DNA tracers. , 2023, 1, 60-73.		10
Host identity affects the response of mycorrhizal fungal communities to high severity fires in Alaskan boreal forests. Fungal Ecology, 2023, 62, 101222.	1.6	1
Assessing the impacts of light synthetic crude oil on microbial communities within Laurentian Great Lakes' sediment habitats. Journal of Great Lakes Research, 2023, 49, 440-452.	1.9	1
Continuous bioreactors enable high-level bioremediation of diesel-contaminated seawater at low and mesophilic temperatures using Antarctic bacterial consortia: Pollutant analysis and microbial community composition. Environmental Pollution, 2023, 321, 121139.	7.5	2
Species interactions, stability, and resilience of the gut microbiota - Helminth assemblage in horses. IScience, 2023, 26, 106044.	4.1	13
The fate of sulfonamide resistance genes and anthropogenic pollution marker intl1 after discharge of wastewater into a pristine river stream. Frontiers in Microbiology, 0, 14, .	3 . 5	13
Short-term feeding of defatted bovine colostrum mitigates inflammation in the gut via changes in metabolites and microbiota in a chicken animal model. Animal Microbiome, 2023, 5, .	3.8	1
Local conditions matter: Minimal and variable effects of soil disturbance on microbial communities and functions in European vineyards. PLoS ONE, 2023, 18, e0280516.	2.5	4
Diversity and Dynamics of Marine Arenicolous Fungi in Three Seasides of the Korean Peninsula. Journal of Microbiology, 0, , .	2.8	1
Recycling eutrophic lake sediments into grass production: A four-year field experiment on agronomical and environmental implications. Science of the Total Environment, 2023, 870, 161881.	8.0	7
High abundance of hydrocarbon-degrading <i>Alcanivorax</i> in plumes of hydrothermally active volcanoes in the South Pacific Ocean. ISME Journal, 2023, 17, 600-610.	9.8	5
Dredged sediments contain potentially beneficial microorganisms for agriculture and little harmful cyanobacteria., 2023, 2, 45-57.		2
10972 Dynamic of the Soil Microbiota in Short-Term Crop Rotation. Life, 2023, 13, 400.	2.4	1

# ARTICLE	IF	CITATIONS
10973 Immune priming prior to pathogen exposure sheds light on the relationship between host, microbiome and pathogen in disease. Royal Society Open Science, 2023, 10, .	2.4	2
Soil water extract and bacteriome determine N2O emission potential in soils. Biology and Fertility of Soils, 2023, 59, 217-232.	4.3	3
Microbiota composition in the lower respiratory tract is associated with severity in patients with acute respiratory distress by influenza. Virology Journal, 2023, 20, .	3.4	5
Community Profiling of Seed Endophytes from the Pb-Zn Hyperaccumulator Noccaea caerulescens and Their Plant Growth Promotion Potential. Plants, 2023, 12, 643.	3.5	3
Salp blooms drive strong increases in passive carbon export in the Southern Ocean. Nature Communications, 2023, 14, .	12.8	13
A 17-year time-series of fungal environmental DNA from a coastal marine ecosystem reveals long-term 10979 seasonal-scale and inter-annual diversity patterns. Proceedings of the Royal Society B: Biological Sciences, 2023, 290, .	2.6	3
A dark matter in sake brewing: Origin of microbes producing a Kimoto-style fermentation starter. Frontiers in Microbiology, 0, 14 , .	3.5	12
Maturational patterns of the infant gut mycobiome are associated with early-life body mass index. Cell Reports Medicine, 2023, 4, 100928.	6.5	4
10983 Characterizing the Effect of Amylase Inhibitors on Maltodextrin Metabolism by Gut Bacteria Using Fluorescent Glycan Labeling. ACS Chemical Biology, 2023, 18, 356-366.	3.4	1
Natural variation of <i>Macrocystis pyrifera</i> gametophyte germplasm culture microbiomes and applications for improving yield in offshore farms. Journal of Phycology, 2023, 59, 402-417.	2.3	1
The mycobiota of faeces from the critically endangered kÄkÄpÅ•and associated nest litter. New Zealand Journal of Zoology, 0, , 1-22.	1.1	0
Ecological diversity methods improve quantitative examination of student language in short constructed responses in STEM. Frontiers in Education, 0, 8, .	2.1	1
Implications of a short carbon pulse on biofilm formation on mica schist in microcosms with deep crystalline bedrock groundwater. Frontiers in Microbiology, 0, 14, .	3.5	1
Combining <i>Geobacter</i> spp. Dominated Biofilms and Anaerobic Digestion Effluents─The Effect of 10988 Effluent Composition and Electrode Potential on Biofilm Activity and Stability. Environmental Science & Environmental & En	10.0	1
MicrobiotaProcess: A comprehensive R package for deep mining microbiome. Innovation(China), 2023, 4, 100388.	9.1	22
Metagenomic Analysis of the Abundance and Composition of Antibiotic Resistance Genes in Hospital Wastewater in Benin, Burkina Faso, and Finland. MSphere, 2023, 8, .	2.9	11
Pathogen-Specific Alterations in the Gut Microbiota Predict Outcomes in Flare of Inflammatory Bowel Disease Complicated by Gastrointestinal Infection. Clinical and Translational Gastroenterology, 2023, 14, e00550.	2.5	1
Symbiont diversity in the eukaryotic microbiomes of marine crustacean zooplankton. Journal of Plankton Research, 2023, 45, 338-359.	1.8	2

# ARTICLE	IF	CITATIONS
Effects of adding different carbon sources on the microbial behavior of sulfate-reducing bacteria in sulfate-containing wastewater. Journal of Cleaner Production, 2023, 392, 136332.	9.3	12
Triazoles and Strobilurin Mixture Affects Soil Microbial Community and Incidences of Wheat Diseases. Plants, 2023, 12, 660.	3.5	4
The impact of cefuroxime prophylaxis on human intestinal microbiota in surgical oncological patients. , 0, 1, .		0
The Epibiotic Microbiota of Wild Caribbean Sea Urchin Spines Is Species Specific. Microorganisms, 2023, 11, 391.	3.6	1
Over supplementation with vitamin B12 alters microbe-host interactions in the gut leading to accelerated Citrobacter rodentium colonization and pathogenesis in mice. Microbiome, 2023, 11, .	11.1	4
10999 Seasonal variation in the Canastra cheese mycobiota. Frontiers in Microbiology, 0, 13, .	3.5	3
Large-scale impact of the 2016 Marine Heatwave on the plankton-associated microbial communities of the Great Barrier Reef (Australia). Marine Pollution Bulletin, 2023, 188, 114685.	5.0	11
The mystery of the ice cold rose—Microbiome of an Arctic winter frost flower. MicrobiologyOpen, 2023, 12, .	3.0	0
Microbiological Changes during Long-Storage of Beef Meat under Different Temperature and Vacuum-Packaging Conditions. Foods, 2023, 12, 694.	4.3	5
Cultivar Susceptibility to Olive Knot Disease and Association with Endophytic Microbiota Community. Agronomy, 2023, 13, 468.	3.0	0
Effect of Abscisic Acid on Growth, Fatty Acid Profile, and Pigment Composition of the Chlorophyte ChlorellaÂ(Chromochloris) zofingiensis and Its Co-Culture Microbiome. Life, 2023, 13, 452.	2.4	4
Comparative Analysis of Core Microbiome Assignments: Implications for Ecological Synthesis. MSystems, 2023, 8, .	3.8	14
Supergroup F Wolbachia with extremely reduced genome: transition to obligate insect symbionts. Microbiome, 2023, 11, .	11.1	5
The utility of dust for forensic intelligence: Exploring collection methods and detection limits for environmental DNA, elemental and mineralogical analyses of dust samples. Forensic Science International, 2023, 344, 111599.	2.2	8
lsotopic and microbial evidence for biodegradation of diluted bitumen in the unsaturated zone. Environmental Pollution, 2023, 322, 121170.	7.5	2
Diversity, distribution and organic substrates preferences of microbial communities of a low anthropic activity cave in North-Western Romania. Frontiers in Microbiology, 0, 14, .	3.5	5
Intratumoral microbiome is driven by metastatic site and associated with immune histopathological parameters: An ancillary study of the SHIVA clinical trial. European Journal of Cancer, 2023, 183, 152-161.	2.8	6
Warmer winters result in reshaping of the European beech forest soil microbiome (bacteria, archaea) Tj ETQq1 11014 2023, 25, 1118-1135.	1 0.784314 3.8	1 rgBT /Overlo

# ARTICLE	IF	CITATIONS
Microbial Dynamics in Mixed-Culture Biofilms of Salmonella Typhimurium and Escherichia coli O157:H7 and Bacteria Surviving Sanitation of Conveyor Belts of Meat Processing Plants. Microorganisms, 2023, 11, 421.	3.6	5
Limosilactobacillus reuteri administration alters the gut-brain-behavior axis in a sex-dependent manner in socially monogamous prairie voles. Frontiers in Microbiology, 0, 14, .	3.5	2
Subtle Responses of Soil Bacterial Communities to Corn-Soybean-Wheat Rotation. Phytobiomes Journal, 2023, 7, 392-400.	2.7	1
11020 Fecal identification markers impact the feline fecal microbiota. Frontiers in Veterinary Science, 0, 10 , .	2.2	1
Spatio-temporal connectivity of the aquatic microbiome associated with cyanobacterial blooms along a Great Lake riverine-lacustrine continuum. Frontiers in Microbiology, 0, 14, .	3.5	5
Prokaryotic community interchange between distinct microhabitats causes community pressure on anammox biofilm development. Water Research, 2023, 233, 119726.	11.3	11
The dynamics of the microbiome in Ixodidae are shaped by tick ontogeny and pathogens in Sarawak, Malaysian Borneo. Microbial Genomics, 2023, 9, .	2.0	0
Leveraging Scheme for Cross-Study Microbiome Machine Learning Prediction and Feature Evaluations. Bioengineering, 2023, 10, 231.	3.5	1
498. Preliminary investigation into the association of members of the rumen biome with production traits in Afrikaner cattle. , 2022, , .		0
501. Comparing methods to summarize gut microbiota composition in estimating microbiability of host phenotypes in swine. , 2022, , .		0
A comparison of free-living and sponge-associated bacterial communities from a remote oceanic island with a focus on calcareous sponges. FEMS Microbiology Ecology, 2023, 99, .	2.7	1
Bacterial microbiome variation across symbiotic states and clonal lines in a cnidarian model. Frontiers in Marine Science, 0, 10 , .	2.5	2
Temporal variability of microbial response to crude oil exposure in the northern Gulf of Mexico. Frontiers in Ecology and Evolution, $0,11,100$	2.2	0
Soil Bacterial Assemblage Across a Production Landscape: Agriculture Increases Diversity While Revegetation Recovers Community Composition. Microbial Ecology, 2023, 85, 1098-1112.	2.8	3
Microbial community structure analysis of hypersaline niches and elucidation of their role in the biogeochemical cycling of nitrogen, sulphur and methane. Ecological Informatics, 2023, 75, 102023.	5.2	2
11034 The gut microbiome–Does stool represent right?. Heliyon, 2023, 9, e13602.	3.2	5
Taxonomic Diversity of the Microbial Biofilms Collected along the Thermal Streams on Kunashir Island. Ecologies, 2023, 4, 106-123.	1.6	2
Recycled Household Ash in Rice Paddies of Bangladesh for Sustainable Production of Rice Without Altering Grain Arsenic and Cadmium. Exposure and Health, 2024, 16, 87-99.	4.9	2

# ARTICLE	IF	Citations
Cloacal microbiota are biogeographically structured in larks from desert, tropical and temperate areas. BMC Microbiology, 2023, 23, .	3.3	0
Microbial Community Succession Along a Chronosequence in Constructed Salt Marsh Soils. Microbial Ecology, 2023, 85, 931-950.	2.8	O
Characterization of the Nero Siciliano Pig Fecal Microbiota after a Liquid Whey-Supplemented Diet. Animals, 2023, 13, 642.	2.3	8
Insights on the particle-attached riverine archaeal community shifts linked to seasons and to 11041 multipollution during a Mediterranean extreme storm event. Environmental Science and Pollution Research, 2023, 30, 49685-49702.	5.3	1
Intestinal homeostasis disruption in mice chronically exposed to arsenite-contaminated drinking water. Chemico-Biological Interactions, 2023, 373, 110404.	4.0	7
Genomic microbiome analyses of surface sand samples from the Kyzyl-Kum Desert (Uzbekistan): characterization and comparative study. Archives of Microbiology, 2023, 205, .	2.2	O
Maternal Î ³ Î TÂcells shape offspring pulmonary type 2 immunity in a microbiota-dependent manner. Cell Reports, 2023, 42, 112074.	6.4	6
N ₂ â€fixation can sustain wastewater treatment performance of photogranules under nitrogenâ€limiting conditions. Biotechnology and Bioengineering, 2023, 120, 1303-1315.	3.3	O
Diversity and putative interactions of parasitic alveolates belonging to Syndiniales at a coastal Pacific site. Environmental Microbiology Reports, 2023, 15, 157-169.	2.4	2
Environmental Selection and Biogeography Shape the Microbiome of Subsurface Petroleum Reservoirs. MSystems, 2023, 8, .	3.8	1
Virulence Factors of the Gut Microbiome Are Associated with BMI and Metabolic Blood Parameters in Children with Obesity. Microbiology Spectrum, 2023, 11, .	3.0	3
The activity of the aryl hydrocarbon receptor in T cells tunes the gut microenvironment to sustain autoimmunity and neuroinflammation. PLoS Biology, 2023, 21, e3002000.	5.6	9
Timing and delivery route effects of cecal microbiome transplants on Salmonella Typhimurium infections in chickens: potential for in-hatchery delivery of microbial interventions. Animal Microbiome, 2023, 5, .	3.8	3
Functional and Compositional Changes in the Fecal Microbiome of a Shorebird during Migratory Stopover. MSystems, 2023, 8, .	3.8	3
Competitive Reactions during Ethanol Chain Elongation Were Temporarily Suppressed by Increasing Hydrogen Partial Pressure through Methanogenesis Inhibition. Environmental Science & Echnology, 2023, 57, 3369-3379.	10.0	8
Carbon Emission and Biodiversity of Arctic Soil Microbial Communities of the Novaya Zemlya and Franz Josef Land Archipelagos. Microorganisms, 2023, 11, 482.	3.6	3
Interspecific plant-plant interactions increase the soil microbial network stability, shift keystone microbial taxa, and enhance their functions in mixed stands. Forest Ecology and Management, 2023, 533, 120851.	3.2	11
Gradual Recovery of Building Plumbing-Associated Microbial Communities after Extended Periods of Altered Water Demand during the COVID-19 Pandemic. Environmental Science & Emp; Technology, 2023, 57, 3248-3259.	10.0	8

# ARTICLE	IF	CITATIONS
Reliability of species detection in 16S microbiome analysis: Comparison of five widely used pipelines and recommendations for a more standardized approach. PLoS ONE, 2023, 18, e0280870.	2.5	6
Network-based multi-omics integration reveals metabolic at-risk profile within treated HIV-infection. ELife, 0, 12 , .	6.0	5
Changes in the Rhizosphere Prokaryotic Community Structure of Halodule wrightii Monospecific Stands Associated to Submarine Groundwater Discharges in a Karstic Costal Area. Microorganisms, 2023, 11, 494.	3.6	0
First insights into the gut microbiome of Diatraea saccharalis: From a sugarcane pest to a reservoir of new bacteria with biotechnological potential. Frontiers in Ecology and Evolution, 0, 11 , .	2.2	O
Root and rhizosphere fungi associated with the yield of diverse Brassica napus genotypes. Rhizosphere, 2023, 25, 100677.	3.0	3
Subgingival microbiome in periodontal health, gingivitis and different stages of periodontitis. Journal of Clinical Periodontology, 2023, 50, 905-920.	4.9	8
Metagenomic mapping of cyanobacteria and potential cyanotoxin producing taxa in large rivers of th United States. Scientific Reports, 2023, 13, .	ne 3.3	2
11066 Exercise-induced microbial changes in preventing type 2 diabetes. Science China Life Sciences, 0, , .	4.9	7
Inulin prebiotic reinforces host cancer immunosurveillance via $\text{\'E}\hat{E}^T$ cell activation. Frontiers in Immunology, 0, 14, .	4.8	8
Maximum summer temperatures predict the temperature adaptation of Arctic soil bacterial communities. Biogeosciences, 2023, 20, 767-780.	3.3	4
11069 Co-diversification of an intestinal <i>Mycoplasma</i> and its salmonid host. ISME Journal, 2023, 17, 682-692.	9.8	14
Transcriptionally active nasopharyngeal commensals and opportunistic microbial dynamics define mild symptoms in the COVID 19 vaccination breakthroughs. PLoS Pathogens, 2023, 19, e1011160.	4.7	5
Extreme Niche Partitioning and Microbial Dark Matter in a Mauna Loa Lava Tube. Journal of Geophysical Research E: Planets, 2023, 128, .	3.6	3
Moss and Liverwort Covers Structure Soil Bacterial and Fungal Communities Differently in the Icelandic Highlands. Microbial Ecology, 2023, 86, 1893-1908.	2.8	2
Diverse Marine T4-like Cyanophage Communities Are Primarily Comprised of Low-Abundance Species Including Species with Distinct Seasonal, Persistent, Occasional, or Sporadic Dynamics. Viruses, 2023 15, 581.	3.3	3
Microbiome response in an urban river system is dominated by seasonality over wastewater treatmen upgrades. Environmental Microbiomes, 2023, 18, .	nt 5.0	0
Stochasticity causes high î²â€diversity and functional divergence of bacterial assemblages in closed systems. Ecology, 2023, 104, .	3.2	5
Steering the product spectrum in high-pressure anaerobic processes: CO2 partial pressure as a novel tool in biorefinery concepts. , 2023, 16, .		1

# ARTICLE	IF	Citations
Strong restructuration of skin microbiota during captivity challenges ex-situ conservation of amphibians. Frontiers in Microbiology, 0, 14, .	3.5	1
Assessing the Effects of Rotifer Feed Enrichments on Turbot (Scophthalmus maximus) Larvae and Post-Larvae Gut-Associated Bacterial Communities. Microorganisms, 2023, 11, 520.	3.6	1
Analysis of 16S rRNA Gene Sequence of Nasopharyngeal Exudate Reveals Changes in Key Microbial Communities Associated with Aging. International Journal of Molecular Sciences, 2023, 24, 4127.	4.1	3
An Exploratory Case-Control Study on the Associations of Bacterially-Derived Vitamin K Forms with the Intestinal Microbiome and Obesity-Related Osteoarthritis. Current Developments in Nutrition, 2023, 7, 100049.	0.3	2
11082 Comparison of genomic and transcriptional microbiome analysis in gastric cancer patients and healthy individuals. World Journal of Gastroenterology, 0, 29, 1202-1218.	3.3	7
Gut microbiome composition is associated with long-term disability worsening in multiple sclerosis. Gut Microbes, 2023, 15, .	9.8	4
Water column dynamics control nitrite-dependent anaerobic methane oxidation by ⟨i⟩Candidatus⟨/i⟩ "Methylomirabilis―in stratified lake basins. ISME Journal, 2023, 17, 693-702.	9.8	7
Earthworms shape prokaryotic communities and affect extracellular enzyme activities in agricultural soil. European Journal of Soil Biology, 2023, 115, 103474.	3.2	4
Design of the Building Research in CRC prevention (BRIDGE-CRC) trial: a 6-month, parallel group Mediterranean diet and weight loss randomized controlled lifestyle intervention targeting the bile acid-gut microbiome axis to reduce colorectal cancer risk among African American/Black adults with obesity. Trials, 2023, 24, .	1.6	1
The Pathogen Aeromonas salmonicida achromogenes Induces Fast Immune and Microbiota Modifications in Rainbow Trout. Microorganisms, 2023, 11, 539.	3.6	3
Metagenomics and metabarcoding experimental choices and their impact on microbial community characterization in freshwater recirculating aquaculture systems. Environmental Microbiomes, 2023, 18, .	5.0	3
Microbial community dynamics of a sequentially fed anaerobic digester treating solid organic waste. FEMS Microbiology Ecology, 2023, 99, .	2.7	3
Elevated atmospheric CO2 concentrations caused a shift of the metabolically active microbiome in vineyard soil. BMC Microbiology, 2023, 23, .	3.3	1
The Gut Commensal Escherichia coli Aggravates High-Fat-Diet-Induced Obesity and Insulin Resistance in Mice. Applied and Environmental Microbiology, 2023, 89, .	3.1	6
Short-chain fatty acids improve inflamm-aging and acute lung injury in old mice. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2023, 324, L480-L492.	2.9	4
The use of different <scp>16S rRNA</scp> gene variable regions in biogeographical studies. Environmental Microbiology Reports, 2023, 15, 216-228.	2.4	6
Taxonomic composition, community structure and molecular novelty of microeukaryotes in a temperate oligomesotrophic lake as revealed by metabarcoding. Scientific Reports, 2023, 13, .	3.3	1
Microbiome diversity, composition and assembly in a California citrus orchard. Frontiers in Microbiology, 0, 14, .	3.5	4

# ARTICLE	IF	CITATIONS
The waxy mutation in sorghum and other cereal grains reshapes the gut microbiome by reducing levels of multiple beneficial species. Gut Microbes, 2023 , 15 , .	9.8	5
Effect of fabric mulch ground covers on lemon trees rhizosphere microbiome in Florida flatwood soils. Frontiers in Soil Science, 0, 3, .	2.2	1
Do antimicrobial peptide levels alter performance of insect-based aquaculture feeds – a study using genetic models of insect immune activation. Journal of Insects As Food and Feed, 2023, 9, 919-934.	3.9	0
Microbiota-derived 3-IAA influences chemotherapy efficacy in pancreatic cancer. Nature, 2023, 615, 168-174.	27.8	89
The geographical and seasonal effects on the composition of marine microplastic and its microbial communities: The case study of Israel and Portugal. Frontiers in Microbiology, 0, 14, .	3. 5	7
Upper respiratory tract microbiota dynamics following COVID-19 in adults. Microbial Genomics, 2023, 9, .	2.0	1
Persistent flocks of diverse motile bacteria in long-term incubations of electron-conducting cable bacteria, Candidatus Electronema aureum. Frontiers in Microbiology, 0, 14, .	3.5	5
Environment or genetic isolation? An atypical intestinal microbiota in the Maltese honey bee Apis mellifera spp. ruttneri. Frontiers in Microbiology, 0, 14, .	3.5	4
Facial Skin Microbiome: Aging-Related Changes and Exploratory Functional Associations with Host Genetic Factors, a Pilot Study. Biomedicines, 2023, 11, 684.	3.2	4
11108 Multiomic spatial analysis reveals a distinct mucosa-associated virome. Gut Microbes, 2023, 15, .	9.8	5
Sour Orange Microbiome Is Affected by Infections of Plenodomus tracheiphilus Causal Agent of Citrus Mal Secco Disease. Agronomy, 2023, 13, 654.	3.0	2
The Taxonomic Structure of the Prokaryotic Biome of the Rhizosphere Triticum Aestivum L. Depending on the Variety and Application of Associative Bacteria. Lecture Notes in Networks and Systems, 2023, , 1878-1887.	0.7	O
The effects of antibiotics and illness on gut microbial composition in the fawn-footed mosaic-tailed rat (Melomys cervinipes). PLoS ONE, 2023, 18, e0281533.	2.5	0
High diversity of microsporidian parasites and new planktonic hosts in freshwater and marine ecosystems. Limnology and Oceanography, 2023, 68, 928-941.	3.1	0
Comparing the gut microbiome of obese, African American, older adults with and without mild cognitive impairment. PLoS ONE, 2023, 18, e0280211.	2.5	6
Saccharomyces cerevisiae fermentation product improves robustness of equine gut microbiome upon stress. Frontiers in Veterinary Science, 0, 10, .	2.2	1
Environmental changes associated with drying climate are expected to affect functional groups of pro- and microeukaryotes differently in temporary saline waters. Scientific Reports, 2023, 13, .	3.3	2
Estuarine Sediment Microbiomes from a Chronosequence of Restored Urban Salt Marshes. Microbial Ecology, 0, , .	2.8	O

#	ARTICLE	IF	Citations
11117	Anthropogenic Nitrate Contamination Impacts Nitrous Oxide Emissions and Microbial Communities in the Marchica Lagoon (Morocco). Sustainability, 2023, 15, 4077.	3.2	2
11118	Prebiotic Consumption Alters Microbiota but Not Biological Markers of Stress and Inflammation or Mental Health Symptoms in Healthy Adults: A Randomized, Controlled, Crossover Trial. Journal of Nutrition, 2023, 153, 1283-1296.	2.9	5
11119	Post-weaning diarrhea in pigs from a single Danish production herd was not associated with the pre-weaning fecal microbiota composition and diversity. Frontiers in Microbiology, 0, 14, .	3.5	1
11120	Interpersonal variability of the human gut virome confounds disease signal detection in IBD. Communications Biology, 2023, 6, .	4.4	5
11121	Biostimulation of <i>Salicornia europaea</i> L. crops with plant growth-promoting bacteria in laboratory and field conditions: effects on growth and metabolite profile. Journal of Applied Microbiology, 2023, 134, .	3.1	2
11123	A longitudinal survey in the wild reveals major shifts in fish host microbiota after parasite infection. Molecular Ecology, 2023, 32, 3014-3024.	3.9	2
11125	Homogeneous Environmental Selection Structures the Bacterial Communities of Benthic Biofilms in Proglacial Floodplain Streams. Applied and Environmental Microbiology, 2023, 89, .	3.1	3
11127	Short-Term Impact of Oxytetracycline Administration on the Fecal Microbiome, Resistome and Virulome of Grazing Cattle. Antibiotics, 2023, 12, 470.	3.7	0
11128	Cholestasis impairs gut microbiota development and bile salt hydrolase activity in preterm neonates. Gut Microbes, 2023, 15, .	9.8	1
11129	Effects on rumen microbiome and milk quality of dairy cows fed a grass silage-based diet supplemented with the macroalga Asparagopsis taxiformis. Frontiers in Animal Science, 0, 4, .	1.9	7
11130	Longitudinal study of the short- and long-term effects of hospitalisation and oral trimethoprim-sulfadiazine administration on the equine faecal microbiome and resistome. Microbiome, 2023, 11 , .	11.1	3
11131	Red Meat Intake, Indole-3-Acetate, and Dorea longicatena Together Affect Insulin Resistance after Gastric Bypass. Nutrients, 2023, 15, 1185.	4.1	3
11132	Successful invasions to freshwater systems double with climate warming. Limnology and Oceanography, 2023, 68, 953-962.	3.1	1
11133	Comparing environmental DNA collection methods for sampling community composition on marine infrastructure. Estuarine, Coastal and Shelf Science, 2023, 283, 108283.	2.1	1
11134	The Gut Microbiome of an Indigenous Agropastoralist Population in a Remote Area of Colombia with High Rates of Gastrointestinal Infections and Dysbiosis. Microorganisms, 2023, 11, 625.	3.6	1
11135	Zearalenone and Its Emerging Metabolites Promptly Affect the Rumen Microbiota in Holstein Cows Fed a Forage-Rich Diet. Toxins, 2023, 15, 185.	3.4	1
11137	Spatiotemporal dynamics of benthic bacterial communities in the Perdido Fold Belt, Northwestern Gulf of Mexico. Frontiers in Marine Science, 0, 10, .	2.5	2
11138	Leaf Microbiome Data for European Cultivated Grapevine (<i>Vitis vinifera</i>) During Downy Mildew (<i>Plasmopara viticola</i>) Epidemics in Three Wine-Producing Regions in France. PhytoFrontiers, 0, , .	1.6	O

#	ARTICLE	IF	CITATIONS
11139	The endometrial microbiota of women with or without a live birth within $12 \hat{A}$ months after a first failed IVF/ICSI cycle. Scientific Reports, 2023, 13, .	3.3	4
11141	A New Technique for Use in Culturing Prokaryotes Comprising the Mouse Intestinal Microbiome. Advances in Microbiology, 2023, 13, 119-147.	0.6	O
11142	Habitat severity characteristics structure soil communities at regional and local spatial scales along the Antarctica Peninsula. Antarctic Science, 2023, 35, 103-119.	0.9	2
11143	Potential Exposure to Respiratory and Enteric Bacterial Pathogens among Wastewater Treatment Plant Workers, South Africa. International Journal of Environmental Research and Public Health, 2023, 20, 4338.	2.6	2
11144	Interactive effects of depth and differential irrigation on soil microbiome composition and functioning. , 0, 2, .		4
11145	Disentangling the mixed effects of soil management on microbial diversity and soil functions: A case study in vineyards. Scientific Reports, 2023, 13 , .	3.3	2
11146	Self-organized metabotyping of obese individuals identifies clusters responding differently to bariatric surgery. PLoS ONE, 2023, 18, e0279335.	2.5	0
11147	Evaluation of the rbcL marker for metabarcoding of marine diatoms and inference of population structure of selected genera. Frontiers in Microbiology, 0, 14, .	3.5	3
11148	Different assembly mechanisms of leaf epiphytic and endophytic bacterial communities underlie their higher diversity in more diverse forests. Journal of Ecology, 2023, 111, 970-981.	4.0	3
11149	Probiotic BioPlus® PS modulate shrimp-tilapia polyculture pond soil microbiome and exhibit bioremediation potential. Journal of Applied Aquaculture, 2024, 36, 252-269.	1.4	1
11150	Insights from Bacterial 16S rRNA Gene into Bacterial Genera and Predicted Metabolic Pathways Associated with Stool Consistency in Rectal Cancer Patients: A Proof of Concept. Biological Research for Nursing, 0, , 109980042311596.	1.9	0
11151	Metabarcoding Reveals Impact of Different Land Uses on Fungal Diversity in the South-Eastern Region of Antioquia, Colombia. Plants, 2023, 12, 1126.	3.5	0
11152	Soil and tree phyllosphere microbial communities differ between coniferous and broadleaf deciduous boreal forests. Plant and Soil, 2023, 488, 233-253.	3.7	3
11153	Fine-scale spatial variation shape fecal microbiome diversity and composition in black-tailed prairie dogs (Cynomys ludovicianus). BMC Microbiology, 2023, 23, .	3.3	1
11154	Selection processes of Arctic seasonal glacier snowpack bacterial communities. Microbiome, 2023, 11, .	11.1	1
11156	Microbiome analysis revealed distinct microbial communities occupying different sized nodules in field-grown peanut. Frontiers in Microbiology, 0, 14 , .	3.5	1
11157	Microbiomes of a disease-resistant genotype of Acropora cervicornis are resistant to acute, but not chronic, nutrient enrichment. Scientific Reports, 2023, 13, .	3.3	1
11158	A mouthwash formulated with o-cymen-5-ol and zinc chloride specifically targets potential pathogens without impairing the native oral microbiome in healthy individuals. Journal of Oral Microbiology, 2023, 15, .	2.7	2

#	Article	IF	CITATIONS
11159	Fluorescence activated cell sorting and fermentation analysis to study rumen microbiome responses to administered live microbials and yeast cell wall derived prebiotics. Frontiers in Microbiology, 0, 13, \cdot	3.5	1
11160	Evaluation of the effects of Lake HévÃz sulfur thermal water on skin microbiome in plaque psoriasis: An open label, pilot study. International Journal of Biometeorology, 2023, 67, 661-673.	3.0	0
11161	Omics and imaging combinatorial approach reveals butyrate-induced inflammatory effects in the zebrafish gut. Animal Microbiome, 2023, 5, .	3.8	3
11162	First morphological and molecular investigation of the mycobiota associated with <i> Astragalus nebrodensis < i > in its natural environment (Madonie mountains, Sicily). Plant Biosystems, 2023, 157, 688-698.</i>	1.6	1
11163	Disparate population and holobiont structure of pocilloporid corals across the Red Sea gradient demonstrate speciesâ€specific evolutionary trajectories. Molecular Ecology, 2023, 32, 2151-2173.	3.9	10
11164	Local environment drives rapid shifts in composition and phylogenetic clustering of seagrass microbiomes. Scientific Reports, 2023, 13, .	3.3	1
11165	Soil Inoculation and Blocker-Mediated Sequencing Show Effects of the Antibacterial T6SS on Agrobacterial Tumorigenesis and Gallobiome. MBio, 2023, 14, .	4.1	3
11166	Encouraging news for in situ conservation: Translocation of salamander larvae has limited impacts on their skin microbiota. Molecular Ecology, 0, , .	3.9	1
11168	Habitat and tree species identity shape aboveground and belowground fungal communities in central European forests. Frontiers in Microbiology, 0, 14, .	3.5	2
11170	Trophic level and proteobacteria abundance drive antibiotic resistance levels inÂfish from coastal New England. Animal Microbiome, 2023, 5, .	3.8	3
11172	Nested PCR Approach for <i>petB</i> Gene Metabarcoding of Marine <i>Synechococcus</i> Populations. Microbiology Spectrum, 2023, 11, .	3.0	0
11173	Identifying characteristics of the natural and built environment associated with child development: A pilot study integrating google street view, computer vision models, and bioinformatic approaches. Remote Sensing Applications: Society and Environment, 2023, 30, 100950.	1.5	O
11174	Comparative analysis of two nonlethal methods for the study of the gut bacterial communities in wild lizards. Integrative Zoology, 2023, 18, 1056-1071.	2.6	2
11176	Moss and underlying soil bacterial community structures are linked to moss functional traits. Ecosphere, 2023, 14, .	2.2	4
11177	Fine characterization and microbiota assessment as keys to understanding the positive effect of standardized natural citrus extract on broiler chickens. Journal of Animal Science, 2023, 101, .	0.5	0
11178	Productive and physiological implications of top-dress addition of branched-chain amino acids and arginine on lactating sows and offspring. Journal of Animal Science and Biotechnology, 2023, 14, .	5.3	4
11180	Monitoring the birds and the bees: Environmental <scp>DNA</scp> metabarcoding of flowers detects plant–animal interactions. Environmental DNA, 2023, 5, 488-502.	5.8	14
11181	Nasal Bacteriomes of Patients with Asthma and Allergic Rhinitis Show Unique Composition, Structure, Function and Interactions. Microorganisms, 2023, 11, 683.	3.6	6

#	Article	IF	CITATIONS
11182	The association between anemia and hypovitaminosis D. The Egyptian Journal of Haematology, 2022, 47, 308.	0.1	0
11183	Association of the gut microbiome with kidney function and damage in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Gut Microbes, 2023, 15, .	9.8	3
11185	Mother-to-infant microbiota transmission and infant microbiota development across multiple body sites. Cell Host and Microbe, 2023, 31, 447-460.e6.	11.0	31
11187	Captive and urban environments are associated with distinct gut microbiota in deer mice () Tj ETQq1 1 0.784314	rgBT /Ovei	lock 10 Tf
11188	Leaf microbiome data for European beech (Fagus sylvatica) at the leaf and canopy scales collected in a gallery forest in South-West France. Annals of Forest Science, 2023, 80, .	2.0	0
11189	Functional variability in specific root respiration translates to autotrophic differences in soil respiration in a temperate deciduous forest. Geoderma, 2023, 432, 116414.	5.1	1
11190	Surface Bacterioplankton Community Structure Crossing the Antarctic Circumpolar Current Fronts. Microorganisms, 2023, 11, 702.	3.6	2
11191	Association of soil fungal community composition with incidence of Fusarium wilt of banana in Malaysia. Mycologia, 2023, 115, 178-186.	1.9	1
11192	Multiomics profiling of the impact of an angiotensin ($1\hat{a}\in$ "7)-expressing probiotic combined with exercise training in aged male rats. Journal of Applied Physiology, 2023, 134, 1135-1153.	2.5	2
11193	A meta-analysis of the stony coral tissue loss disease microbiome finds key bacteria in unaffected and lesion tissue in diseased colonies. ISME Communications, 2023, 3, .	4.2	11
11195	Characterization of the Lower Airways and Oral Microbiota in Healthy Young Persons in the Community. Biomedicines, 2023, 11, 841.	3.2	3
11196	Bacterial aerobic methane cycling by the marine sponge-associated microbiome. Microbiome, 2023, 11, .	11.1	3
11197	The Effects of Lakitelek Thermal Water and Tap Water on Skin Microbiome, a Randomized Control Pilot Study. Life, 2023, 13, 746.	2.4	1
11203	Bacterial, but not fungal, communities show spatial heterogeneity in European beech (<i>Fagus) Tj ETQq1 1 0.784</i>	1314 rgBT 2.7	/Pverlock
11204	Individual variation in the avian gut microbiota: The influence of host state and environmental heterogeneity. Molecular Ecology, 2023, 32, 3322-3339.	3.9	2
11205	The impact of diet and ethnicity on gut microbiota variation in irritable bowel syndrome: A multiâ€center study. Journal of Gastroenterology and Hepatology (Australia), 2023, 38, 1259-1268.	2.8	2
11206	16S Amplicon Metabarcoding of the Nest Materials of Native Australian Stingless Bees. Microbiology Resource Announcements, 2023, 12, .	0.6	O
11207	Disentangling the Functional Role of Fungi in Cold Seep Sediment. Microbiology Spectrum, 2023, 11, .	3.0	2

#	ARTICLE	IF	CITATIONS
11208	Microbial Enrichment Techniques on Syngas and CO2 Targeting Production of Higher Acids and Alcohols. Molecules, 2023, 28, 2562.	3.8	1
11209	Integrated multiomic wastewater-based epidemiology can elucidate population-level dietary behaviour and inform public health nutrition assessments. Nature Food, 2023, 4, 257-266.	14.0	4
11210	Title Pending 16086. Meat and Muscle Biology, 0, , .	1.9	0
11211	Microbial Composition on Abandoned and Reclaimed Mining Sites in the Komi Republic (North Russia). Microorganisms, 2023, 11, 720.	3.6	2
11212	Thrive or survive: prokaryotic life in hypersaline soils. Environmental Microbiomes, 2023, 18, .	5.0	4
11214	The Oral Microbiome as Mediator between Oral Hygiene and Its Impact on Nasopharyngeal Carcinoma. Microorganisms, 2023, 11, 719.	3.6	1
11215	Beyond purified dietary fibre supplements: Compositional variation between cell wall fibre from different plants influences human faecal microbiota activity and growth in vitro. Environmental Microbiology, 2023, 25, 1484-1504.	3.8	O
11216	Trophic diversification and parasitic invasion as ecological niche modulators for gut microbiota of whitefish. Frontiers in Microbiology, $0,14,.$	3.5	5
11217	Acetoclastic archaea adaptation under increasing temperature in lake sediments and wetland soils from Alaska. Polar Biology, 2023, 46, 259-275.	1.2	1
11218	A Longitudinal Characterization of the Seminal Microbiota and Antibiotic Resistance in Yearling Beef Bulls Subjected to Different Rates of Gain. Microbiology Spectrum, 2023, 11 , .	3.0	7
11219	Host–microbiome interactions in apical periodontitis: The endodontic microbiome in relation to circulatory immunologic markers. International Endodontic Journal, 2023, 56, 748-764.	5.0	5
11221	Characterization of the Endometrial Microbiome in Patients with Recurrent Implantation Failure. Microorganisms, 2023, 11, 741.	3.6	8
11222	The dietary sweetener sucralose is a negative modulator of T cell-mediated responses. Nature, 2023, 615, 705-711.	27.8	24
11223	Effects of supplementation of Bacillus amyloliquefaciens on performance, systemic immunity, and intestinal microbiota of weaned pigs experimentally infected with a pathogenic enterotoxigenic E. coli F18. Frontiers in Microbiology, 0, 14 , .	3.5	2
11224	Gut microbiota in a mouse model of obesity and peripheral neuropathy associated with plasma and nerve lipidomics and nerve transcriptomics. Microbiome, 2023, 11 , .	11.1	6
11225	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. Frontiers in Animal Science, 0, 4, .	1.9	2
11226	Soluble TNF mediates amyloid-independent, diet-induced alterations to immune and neuronal functions in an Alzheimerâ \in [™] s disease mouse model. Frontiers in Cellular Neuroscience, 0, 17, .	3.7	3
11228	Temporal dynamics of geothermal microbial communities in Aotearoa-New Zealand. Frontiers in Microbiology, 0, 14, .	3.5	1

#	Article	IF	CITATIONS
11231	\hat{l}^2 -mannanase supplementation in diets reduced in 85 kcal metabolizable energy/kg containing xylanase-phytase improves gain to feed ratio, nutrient usage, and backfat thickness in finisher pigs. Frontiers in Veterinary Science, 0, 10, .	2.2	4
11232	Characterization of the cervicovaginal microbiota of female beef cattle harboring <i>Campylobacter fetus</i> subsp. <i>venerealis</i> using 16S rDNA gene sequencing. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
11233	Bioinformatic and Statistical Analysis of Microbiome Data. Methods in Molecular Biology, 2023, , 183-229.	0.9	2
11234	Combined Effects of Temperature and Dietary Lipid Level on Body Composition, Growth, and Freshness Profile in European Seabass, Dicentrarchus labrax. Animals, 2023, 13, 1068.	2.3	2
11236	Integrated analysis reveals important differences in the gut and oropharyngeal microbiota between children with mild and severe hand, foot, and mouth disease. Emerging Microbes and Infections, 2023, 12, .	6.5	1
11237	High-Resolution Taxonomic Characterization Reveals Novel Human Microbial Strains with Potential as Risk Factors and Probiotics for Prediabetes and Type 2 Diabetes. Microorganisms, 2023, 11, 758.	3.6	4
11238	pH and microbial community determine the denitrifying activity in the presence of nitrate-containing radioactive waste. Frontiers in Microbiology, 0, 13 , .	3.5	5
11239	The Microbial Terroir of the Nemea Zone Agiorgitiko cv.: A First Metataxonomic Approach. Australian Journal of Grape and Wine Research, 2023, 2023, 1-18.	2.1	1
11240	Spatial variation of the gut microbiome in response to long-term metformin treatment in high-fat diet-induced type 2 diabetes mouse model of both sexes. Gut Microbes, 2023, 15, .	9.8	4
11241	Evaluating coevolution in a horizontally transmitted mutualism. Evolution; International Journal of Organic Evolution, 2023, 77, 166-185.	2.3	2
11242	Chlorine Dioxide Reprograms Rhizosphere Microbial Communities to Enrich Interactions with Tobacco (<i>Nicotiana tabacum</i>). Polish Journal of Microbiology, 2023, 72, 47-60.	1.7	0
11244	Hippocampus guttulatus diet based on DNA metabarcoding. Frontiers in Marine Science, 0, 10, .	2.5	2
11245	Garden soil bacteria transiently colonize gardeners' skin after direct soil contact. Urban Agriculture & Regional Food Systems, 2023, 8, .	0.9	1
11246	Geography shapes the microbial community in <i>Heliconius</i> butterflies. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
11248	Eucommia Polysaccharides Ameliorate Aging-Associated Gut Dysbiosis: A Potential Mechanism for Life Extension in Drosophila. International Journal of Molecular Sciences, 2023, 24, 5881.	4.1	1
11249	Bacterial gut microbiome differences in adults with ADHD and in children with ADHD on psychostimulant medication. Brain, Behavior, and Immunity, 2023, 110, 310-321.	4.1	2
11250	Snow Microorganisms Colonise Arctic Soils Following Snow Melt. Microbial Ecology, 2023, 86, 1661-1675.	2.8	0
11251	A multi-angle analysis of injury induced by supplementation of soybean meal in Litopenaeus vannamei diets. , $0, 2, .$		O

#	ARTICLE	IF	Citations
11252	Microeukaryotic Communities of the Long-Term Ice-Covered Freshwater Lakes in the Subarctic Region of Yakutia, Russia. Diversity, 2023, 15, 454.	1.7	0
11253	Sexual behavior shapes male genitourinary microbiome composition. Cell Reports Medicine, 2023, 4, 100981.	6.5	4
11254	Evaluating the efficacy of non-thermal microbial load reduction treatments of heat labile food components for in vitro fermentation experiments. PLoS ONE, 2023, 18, e0283287.	2.5	0
11255	Microbial Drivers of Plant Performance during Drought Depend upon Community Composition and the Greater Soil Environment. Microbiology Spectrum, 2023, 11, .	3.0	4
11257	Effects of Hanwoo (Korean cattle) manure as organic fertilizer on plant growth, feed quality, and soil bacterial community. Frontiers in Plant Science, 0, 14, .	3.6	5
11258	Structure vs. chemistry: Alternate mechanisms for controlling leaf microbiomes. PLoS ONE, 2023, 18, e0275734.	2.5	O
11261	Impavido attenuates inflammation, reduces atherosclerosis, and alters gut microbiota in hyperlipidemic mice. IScience, 2023, 26, 106453.	4.1	2
11262	Rumen biogeographical regions and their impact on microbial and metabolome variation. Frontiers in Animal Science, 0, 4, .	1.9	O
11263	Colonization order of bacterial isolates on treefrog embryos impacts microbiome structure in tadpoles. Proceedings of the Royal Society B: Biological Sciences, 2023, 290, .	2.6	0
11265	Parasitism causes changes in caterpillar odours and associated bacterial communities with consequences for host-location by a hyperparasitoid. PLoS Pathogens, 2023, 19, e1011262.	4.7	1
11266	The Vaginal Microbiome of Transgender and Gender Nonbinary Individuals. Transgender Health, 0, , .	2.5	0
11267	Combining air sampling and DNA metabarcoding to monitor plant pathogens. PhytoFrontiers, 0, , .	1.6	0
11268	Fungal Symbionts Generate Water-Saver and Water-Spender Plant Drought Strategies via Diverse Effects on Host Gene Expression. Phytobiomes Journal, 2023, 7, 172-183.	2.7	3
11269	Diversity and function of methyl-coenzyme M reductase-encoding archaea in Yellowstone hot springs revealed by metagenomics and mesocosm experiments. ISME Communications, 2023, 3, .	4.2	10
11270	Revisiting Microbial Diversity in Hypersaline Microbial Mats from Guerrero Negro for a Better Understanding of Methanogenic Archaeal Communities. Microorganisms, 2023, 11, 812.	3.6	2
11271	Exploring the Potential of Lactobacillus helveticus R0052 and Bifidobacterium longum R0175 as Promising Psychobiotics Using SHIME. Nutrients, 2023, 15, 1521.	4.1	4
11272	SARS oVâ€⊋ infection alters the gut microbiome in diabetes patients: A crossâ€sectional study from Bangladesh. Journal of Medical Virology, 2023, 95, .	5.0	6
11273	Fineâ€scale mapping of physicochemical and microbial landscapes of the coral skeleton. Environmental Microbiology, 2023, 25, 1505-1521.	3.8	4

#	ARTICLE	IF	Citations
11274	Microbe-mineral interactions in the Plastisphere: Coastal biogeochemistry and consequences for degradation of plastics. Frontiers in Marine Science, $0,10,10$	2.5	6
11275	Functional Potential of Soil Microbial Communities and Their Subcommunities Varies with Tree Mycorrhizal Type and Tree Diversity. Microbiology Spectrum, 2023, 11, .	3.0	7
11276	Microbial and Biogeochemical Shifts in a Highly Anthropogenically Impacted Estuary ("El Sauceâ€) Tj ETQq0 0	0 rgBT /O 2.7	verlock 10 1
11278	Impact of oestrus synchronization devices on ewes vaginal microbiota and artificial insemination outcome. Frontiers in Microbiology, 0, 14 , .	3.5	3
11280	Longitudinal changes in subgingival biofilm composition following periodontal treatment. Journal of Periodontology, 2023, 94, 1065-1077.	3.4	0
11281	Studies on the Composition and Diversity of Seagrass Ruppia sinensis Rhizosphere Mmicroorganisms in the Yellow River Delta. Plants, 2023, 12, 1435.	3.5	1
11282	Nasal microbiota profiles in shelter dogs with dermatological conditions carrying methicillin-resistant and methicillin-sensitive Staphylococcus species. Scientific Reports, 2023, 13, .	3.3	1
11284	Skin and Blood Microbial Signatures of Sedentary and Migratory Trout (Salmo trutta) of the Kerguelen Islands. Fishes, 2023, 8, 174.	1.7	3
11285	Evidence for wastewaters as environments where mobile antibiotic resistance genes emerge. Communications Biology, 2023, 6, .	4.4	14
11287	Infant gut microbiome composition correlated with type 1 diabetes acquisition in the general population: the ABIS study. Diabetologia, 2023, 66, 1116-1128.	6.3	12
11288	No evidence for associations between brood size, gut microbiome diversity and survival in great tit (Parus major) nestlings. Animal Microbiome, 2023, 5, .	3.8	1
11290	Microbial composition of tumorous and adjacent gastric tissue is associated with prognosis of gastric cancer. Scientific Reports, 2023, 13, .	3.3	8
11291	Bacillus subtilis KMO Impacts gut Microbiota Profile and Transcription of Genes Related to Transcellular Transport in Zebrafish (Danio rerio). Current Microbiology, 2023, 80, .	2.2	0
11293	Microbial Diversity of Deep-sea Sediments from Three Newly Discovered Hydrothermal Vent Fields in the Central Indian Ridge. Ocean Science Journal, 2023, 58, .	1.3	1
11294	Prospective, longitudinal analysis of the gut microbiome in patients with locally advanced rectal cancer predicts response to neoadjuvant concurrent chemoradiotherapy. Journal of Translational Medicine, 2023, 21, .	4.4	4
11295	Potato root-associated microbiomes adapt to combined water and nutrient limitation and have a plant genotype-specific role for plant stress mitigation. Environmental Microbiomes, 2023, 18, .	5.0	15
11296	Mock community as an in situ positive control for amplicon sequencing of microbiotas from the same ecosystem. Scientific Reports, 2023, 13, .	3.3	2
11297	The microbiome of the marine flatworm Macrostomum lignano provides fitness advantages and exhibits circadian rhythmicity. Communications Biology, 2023, 6, .	4.4	0

# ARTICLE	IF	Citations
Connecting Gut Microbial Diversity with Plasma Metabolome and Fecal Bile Acid Changes the Antibiotics Tobramycin and Colistin Sulfate. Chemical Research in Toxicology, 2023, 36	Induced by 3.3 6, 598-616.	1
Simultaneous profiling of host expression and microbial abundance by spatial metatranscr sequencing. Genome Research, 2023, 33, 401-411.	iptome 5.5	2
Water deficits shape the microbiome of Bermudagrass roots to be Actinobacteria rich. FEM Microbiology Ecology, 2023, 99, .	MS 2.7	2
Emerging investigator series: differential effects of carbon nanotubes and graphene on the rhizosphere microbiome. Environmental Science: Nano, 2023, 10, 1570-1584.	e tomato 4.3	1
<i>Xanthomonas ii> infection and ozone stress distinctly influence the microbial communications at ructure and interactions in the pepper phyllosphere. ISME Communications, 2023, 3, .</i>	nity 4.2	4
Current levels of microplastic pollution impact wild seabird gut microbiomes. Nature Ecolo Evolution, 2023, 7, 698-706.	ogy and 7.8	22
Similar Skin Barrier Function in Persons with Type 1 Diabetes Compared with Healthy Cont Innovations, 2023, 3, 100200.	trols. JID 2.4	1
Impact of testosterone use on the vaginal microbiota of transgender men, including susce bacterial vaginosis: study protocol for a prospective, observational study. BMJ Open, 2023	ptibility to , 13, e073068.	0
The Succession of the Cellulolytic Microbial Community from the Soil during Oat Straw Decomposition. International Journal of Molecular Sciences, 2023, 24, 6342.	4.1	1
Pharmacologic improvement of CFTR function rapidly decreases sputum pathogen density infections generally persist. Journal of Clinical Investigation, 2023, 133, .	, but lung 8.2	38
Intestinal microbiota of <scp>Nearcticâ€Neotropical</scp> migratory birds vary more over years than between host species. Molecular Ecology, 2023, 32, 3290-3307.	r seasons and 3.9	2
High throughput screening of fungal phytopathogens caught in Australian forestry insect surveillance traps. Frontiers in Forests and Global Change, 0, 6, .	2.3	1
The microbial composition and functional roles of different kombucha products in Singapo Journal of Food, 2023, 21, 269-274.	ore. CYTA - 1.9	2
Variations and gradients between methane seep and off-seep microbial communities in a s canyon system in the Northeast Pacific. PeerJ, 0, 11, e15119.	submarine 2.0	1
Microbiome and Physicochemical Features Associated with Differential Listeria monocytog Growth in Soft, Surface-Ripened Cheeses. Applied and Environmental Microbiology, 2023,	genes 89, . 3.1	4
From the Surface Ocean to the Seafloor: Linking Modern and Paleoâ€Genetics at the Sabri Antarctica (IN2017_V01). Journal of Geophysical Research G: Biogeosciences, 2023, 128,	ina Coast, East 3.0	1
Fish waste to sustainable additives: Fish protein hydrolysates alleviate intestinal dysbiosis atrophy induced by poultry by-product meal in Lates calcarifer juvenile. Frontiers in Nutrition	and muscle on, 0, 10, . 3.7	3
Legacy Effects of Phytoremediation on Plant-Associated Prokaryotic Communities in Reme 11317 Subarctic Soil Historically Contaminated with Petroleum Hydrocarbons. Microbiology Spec 2023, 11, .	ediated strum, 3.0	O

# ARTICLE	IF	Citations
Microbial Diversity Using a Metataxonomic Approach, Associated with Coffee Fermentation Processin the Department of QuindÃo, Colombia. Fermentation, 2023, 9, 343.	sses 3.0	5
Impact of the bacterial nasopharyngeal microbiota on the severity of genus enterovirus lower 11319 respiratory tract infection in children: A case–control study. Pediatric Pulmonology, 2023, 58, 1728-1737.	2.0	1
11320 Effects of Inbreeding on Microbial Community Diversity of Zea mays. Microorganisms, 2023, 11, 8	3.6	1
Exploiting a targeted resistome sequencing approach in assessing antimicrobial resistance in retail foods. Environmental Microbiomes, 2023, 18, .	5.0	5
Arresting microbiome development limits immune system maturation and resistance to infection i mice. Cell Host and Microbe, 2023, 31, 554-570.e7.	in 11.0	22
Gut Microbiota of Freshwater Gastropod (Bellamya aeruginosa) Assist the Adaptation of Host to Toxic Cyanobacterial Stress. Toxins, 2023, 15, 252.	3.4	3
Anaerobic Microbial Degradation of Polypropylene and Polyvinyl Chloride Samples. Microbiology, 2023, 92, 83-93.	1.2	1
Infection strategies of different chytrids in a diatom spring bloom. Freshwater Biology, 2023, 68, 972-986.	2.4	2
Dominant bacterial taxa drive microbiome differences of juvenile Pacific oysters of the same age a variable sizes. , 0, 2, .	nd	1
Reducing bias in microbiome research: Comparing methods from sample collection to sequencing Frontiers in Microbiology, 0, 14, .	. 3.5	1
Compact and automated eDNA sampler for in situ monitoring of marine environments. Scientific Reports, 2023, 13, .	3.3	7
Dynamics of oral microbiome acquisition in healthy infants: A pilot study. Frontiers in Oral Health, 4, .	0, 3.0	2
The Bacterial Microbiome of the Coral Skeleton Algal Symbiont Ostreobium Shows Preferential Associations and Signatures of Phylosymbiosis. Microbial Ecology, 0, , .	2.8	3
Development of a biomarker signature using grating-coupled fluorescence plasmonic microarray for diagnosis of MIS-C. Frontiers in Bioengineering and Biotechnology, 0, 11, .	or 4.1	1
High resolution functional analysis and community structure of photogranules. ISME Journal, 2023 17, 870-879.	3, 9.8	4
Interrogating the Diversity of Vaginal, Endometrial, and Fecal Microbiomes in Healthy and Metritis Dairy Cattle. Animals, 2023, 13, 1221.	2.3	2
Metabolic and microbiota response to arginine supplementation and cyclic heat stress in broiler chickens. Frontiers in Physiology, 0, 14, .	2.8	3
Uniform selective pressures within redox zones drive gradual changes in microbial community composition in hadal sediments. Environmental Microbiology, 2023, 25, 1594-1604.	3.8	2

#	ARTICLE	IF	CITATIONS
11339	Effects of anthropogenic stress on hosts and their microbiomes: Treated wastewater alters performance and gut microbiome of a key detritivore (<i>Asellus aquaticus</i>). Evolutionary Applications, 2023, 16, 824-848.	3.1	0
11340	A First Insight into the Microbial and Viral Communities of Comau Fjord—A Unique Human-Impacted Ecosystem in Patagonia (42â~ S). Microorganisms, 2023, 11, 904.	3.6	1
11341	Contamination detection and microbiome exploration with GRIMER. GigaScience, 2022, 12, .	6.4	2
11342	A Randomized Controlled Trial of Probiotics Targeting Gut Dysbiosis in Huntington's Disease. Journal of Huntington's Disease, 2023, 12, 43-55.	1.9	5
11343	Metagenomic assessment of nitrate-contaminated mine wastewaters and optimization of complete denitrification by indigenous enriched bacteria. Frontiers in Environmental Science, 0, 11, .	3.3	2
11344	Taking e <scp>DNA</scp> underground: Factors affecting e <scp>DNA</scp> detection of subterranean fauna in groundwater. Molecular Ecology Resources, 2023, 23, 1257-1274.	4.8	4
11347	Antibacterial plant combinations prevent postweaning diarrhea in organically raised piglets challenged with enterotoxigenic Escherichia coli F18. Frontiers in Veterinary Science, 0, 10, .	2.2	3
11348	Composition and function of the Galapagos penguin gut microbiome vary with age, location, and a putative bacterial pathogen. Scientific Reports, 2023, 13 , .	3.3	5
11349	$\mbox{\sc i}\mbox{\sc Rothia}\mbox{\sc lin}\mbox{\sc i}\mbox{\sc Moraxella catarrhalis}\mbox{\sc lin}\mbox{\sc Colonization with a Secreted Peptidoglycan Endopeptidase. MBio, 2023, 14, .}$	4.1	10
11350	Inter―and intraspecific phytochemical variation correlate with epiphytic flower and leaf bacterial communities. Environmental Microbiology, 2023, 25, 1624-1643.	3.8	3
11351	Successional dynamics of the cultivated kelp microbiome. Journal of Phycology, 2023, 59, 538-551.	2.3	4
11352	Comparative analysis of macroalgae supplementation on the rumen microbial community: Asparagopsis taxiformis inhibits major ruminal methanogenic, fibrolytic, and volatile fatty acid-producing microbes in vitro. Frontiers in Microbiology, 0, 14, .	3.5	3
11353	Soil Suppressiveness Against Pythium ultimum and Rhizoctonia solani in Two Land Management Systems and Eleven Soil Health Treatments. Microbial Ecology, 0, , .	2.8	1
11354	Plant domestication shapes rhizosphere microbiome assembly and metabolic functions. Microbiome, 2023, 11, .	11.1	33
11355	Red clover root-associated microbiota is shaped by geographic location and choice of farming system. Journal of Applied Microbiology, 2023, 134, .	3.1	2
11357	The Impact of MOSE (Experimental Electromechanical Module) Flood Barriers on Microphytobenthic Community of the Venice Lagoon. Microorganisms, 2023, 11, 936.	3.6	1
11358	Microbial mat compositions and localization patterns explain the virulence of black band disease in corals. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	1
11359	Date Palm Waste Compost Application Increases Soil Microbial Community Diversity in a Cropping Barley (Hordeum vulgare L.) Field. Biology, 2023, 12, 546.	2.8	O

#	ARTICLE	IF	CITATIONS
11360	Gluconic acid improves performance of newly weaned piglets associated with alterations in gut microbiome and fermentation. Porcine Health Management, $2023, 9, \ldots$	2.6	8
11361	Isha yoga practices, vegan diet, and participation in Samyama meditation retreat: impact on the gut microbiome & amp; metabolome – a non-randomized trial. BMC Complementary Medicine and Therapies, 2023, 23, .	2.7	3
11362	Unveiling the role of emerging metagenomics for the examination of hypersaline environments. Biotechnology and Genetic Engineering Reviews, 0, , 1-39.	6.2	2
11363	A cryopreservation method to recover laboratory- and field-derived bacterial communities from mosquito larval habitats. PLoS Neglected Tropical Diseases, 2023, 17, e0011234.	3.0	4
11365	Reconnaissance of Oxygenic Denitrifiers in Agriculturally Impacted Soils. MSphere, 0, , .	2.9	0
11366	Feeding effects of the keystone deposit feeder <i>llyanassa obsoleta</i> (Neogastropoda, Gastropoda) on sedimentary diatoms. Journal of Phycology, 0, , .	2.3	0
11367	Impacts of Nutrients on Alkene Biodegradation Rates and Microbial Community Composition in Enriched Consortia from Natural Inocula. Microbiology Spectrum, 0, , .	3.0	0
11368	Quantification of diversity sampling bias resulting from rice root bacterial isolation on popular and nitrogen-free culture media using 16S amplicon barcoding. PLoS ONE, 2023, 18, e0279049.	2.5	2
11369	Exploring the microbiome of oral epithelial dysplasia as a predictor of malignant progression. BMC Oral Health, 2023, 23, .	2.3	2
11370	Microscale pollen release and dispersal patterns in flowering grass populations. Science of the Total Environment, 2023, 880, 163345.	8.0	3
11372	Selecting 16S rRNA Primers for Microbiome Analysis in a Host–Microbe System: The Case of the Jellyfish Rhopilema nomadica. Microorganisms, 2023, 11, 955.	3.6	2
11373	Land use modification causes slow, but predictable, change in soil microbial community composition and functional potential. Environmental Microbiomes, 2023, 18, .	5.0	2
11374	Intratumoral microbiota is associated with prognosis in patients with adrenocortical carcinoma. , 2023, 2, .		6
11375	Agroecosystem edge effects on vegetation, soil properties, and the soil microbial community in the Canadian prairie. PLoS ONE, 2023, 18, e0283832.	2.5	3
11376	Wildlife gut microbiomes of sympatric generalist species respond differently to anthropogenic landscape disturbances. Animal Microbiome, 2023, 5, .	3.8	2
11377	Different approaches to processing environmental DNA samples in turbid waters have distinct effects for fish, bacterial and archaea communities. , 0, 3, .		O
11378	Freshwater transfer affected intestinal microbiota with correlation to cytokine gene expression in Asian sea bass. Frontiers in Microbiology, $0,14,.$	3.5	3
11379	Problematic Cannabis Use Is Associated with Reduced Rectal Microbial Species Richness and Diversity Among a Pilot Sample of Young Sexual and Gender Minorities. AIDS Research and Human Retroviruses, 2024, 40, 1-6.	1.1	O

# AI	RTICLE	IF	Citations
	ongevity of centenarians is reflected by the gut microbiome with youth-associated signatures. ature Aging, 2023, 3, 436-449.	11.6	11
11381 th	ontinuous single-stage elemental sulfur reduction and copper sulfide precipitation under ermoacidophilic conditions. Water Research, 2023, 236, 119948.	11.3	2
	ungal Diversity Associated with Armadillidium Isopods: A Case Study in Central Park of Gwacheon, outh Korea. Diversity, 2023, 15, 533.	1.7	1
11385 (⊦	Vater temperature and disease alters bacterial diversity and cultivability from American lobster Homarus americanus) shells. IScience, 2023, 26, 106606.	4.1	1
11386 In	fluence of carbon-based cathodes on biofilm composition and electrochemical performance in soil icrobial fuel cells. Environmental Science and Ecotechnology, 2023, 16, 100276.	13.5	9
11389 A	metabarcoding analysis of the wrackbed microbiome indicates a phylogeographic break along the orth Sea–Baltic Sea transition zone. Environmental Microbiology, 0, , .	3.8	0
	laternal Psychosocial Stress Is Associated with Reduced Diversity in the Early Infant Gut Microbiome. licroorganisms, 2023, 11, 975.	3.6	5
11391 pa	upilumab but not cyclosporine treatment shifts the microbiome toward a healthy skin flora in atients with moderateâ€toâ€severe atopic dermatitis. Allergy: European Journal of Allergy and Clinical nmunology, 2023, 78, 2290-2300.	5.7	5
11393 Ex	xpanding known viral diversity in the healthy infant gut. Nature Microbiology, 2023, 8, 986-998.	13.3	31
	ark-zone alterations expand throughout Paleolithic Lascaux Cave despite spatial heterogeneity of ne cave microbiome. Environmental Microbiomes, 2023, 18, .	5.0	3
11396 Bo	ody Size Poorly Predicts Host-Associated Microbial Diversity in Wild Birds. Microbiology Spectrum, 023, 11, .	3.0	3
11397 Cl	haracterization of rumen microbiome and metabolome from oro-esophageal tubing and rumen annula in Holstein dairy cows. Scientific Reports, 2023, 13, .	3.3	1
	hemical Characterization and Metagenomic Identification of Endophytic Microbiome from South frican Sunflower (Helianthus annus) Seeds. Microorganisms, 2023, 11, 988.	3.6	5
	liSurv: an Integrative Web Cloud Platform for User-Friendly Microbiome Data Analysis with Survival esponses. Microbiology Spectrum, 2023, $11,\ldots$	3.0	2
11400 N	itrogen transformation processes catalyzed by manure microbiomes in earthen pit and concrete corages on commercial dairy farms. Environmental Microbiomes, 2023, 18, .	5.0	1
11401 la	omprehensive Microbiome and Metabolome Analyses Reveal the Medicinal Components of Paeonia ctiflora. Plants, 2023, 12, 1612.	3.5	4
	sights into the circulating microbiome of Atlantic and Greenland halibut populations: the role of pecies-specific and environmental factors. Scientific Reports, 2023, 13, .	3.3	3
11405 C	omparison of two molecular barcodes for the study of equine strongylid communities with mplicon sequencing. PeerJ, 0, 11, e15124.	2.0	6

# ARTICLE	IF	Citations
Staphylococcal diversity in atopic dermatitis from an individual to a global scale. Cell Host and Microbe, 2023, 31, 578-592.e6.	11.0	9
A network perspective on the ecology of gut microbiota and progression of type 2 diabetes: Linkages to keystone taxa in a Mexican cohort. Frontiers in Endocrinology, 0, 14, .	3.5	9
Micro-photoautotroph predation as a driver for trophic niche specialization in 12 syntopic Indo-Pacific parrotfish species. Biological Journal of the Linnean Society, 2023, 139, 91-114.	1.6	5
Microplastic ingestion affects hydrogen production and microbiomes in the gut of the terrestrial isopod <scp><i>Porcellio scaber</i>Scaponolic Environmental Microbiology, 2023, 25, 2776-2791.</scp>	3.8	5
The impact of urine collection method on canine urinary microbiota detection: a cross-sectional study. BMC Microbiology, 2023, 23, .	3.3	1
Subgingival microbial diversity and respiratory decline: A crossâ€sectional study. Journal of Clinical Periodontology, 2023, 50, 921-931.	4.9	2
The microbiomes of two Singaporean corals show site-specific differentiation and variability that correlates with the seasonal monsoons. Coral Reefs, 2023, 42, 677-691.	2.2	1
Constellation of the endophytic mycobiome in spring and winter wheat cultivars grown under various conditions. Scientific Reports, 2023, 13, .	3.3	0
Congeneric temperate orchids recruit similarâ€"yet differentially abundantâ€"endophytic bacterial communities that are uncoupled from soil, but linked to host phenology and population size. American Journal of Botany, 2023, 110, .	1.7	0
Bringing Antarctica to the lab: a polar desert environmental chamber to study the response of Antarctic microbial communities to climate change. Polar Biology, 2023, 46, 445-459.	1.2	1
Randomized controlled pilot study assessing fructose tolerance during fructose reintroduction in <scp>nonâ€constipated</scp> irritable bowel syndrome patients successfully treated with a low <scp>FODMAP</scp> diet. Neurogastroenterology and Motility, 2023, 35, .	3.0	2
Fungal succession in decomposing ash leaves colonized by the ash dieback pathogen Hymenoscyphus fraxineus or its harmless relative Hymenoscyphus albidus. Frontiers in Microbiology, 0, 14, .	3.5	0
The nasal microbiome in patients suffering from non-steroidal anti-inflammatory drugs-exacerbated respiratory disease in absence of corticosteroids. Frontiers in Immunology, 0, 14, .	4.8	2
Identification of microbial community in the urban environment: The concordance between conventional culture and nanopore 16S rRNA sequencing. Frontiers in Microbiology, 0, 14, .	3.5	2
Versatile microbial communities rapidly assimilate ammonium hydroxide-treated plastic waste. Journal of Industrial Microbiology and Biotechnology, 2023, 50, .	3.0	1
Characterization of the lung microbiome and inflammatory cytokine levels in women exposed to environmental risk factors: A pilot study. Immunity, Inflammation and Disease, 2023, 11, .	2.7	1
A westernized diet changed the colonic bacterial composition and metabolite concentration in a dextran sulfate sodium pig model for ulcerative colitis. Frontiers in Microbiology, 0, 14, .	3.5	3
Evaluation of DNA extraction methods and direct PCR in metabarcoding of mock and marine bacterial communities. Frontiers in Microbiology, 0, 14, .	3.5	4

#	ARTICLE	IF	CITATIONS
11428	Biochar significantly reduced nutrient-induced positive priming in a subtropical forest soil. Biology and Fertility of Soils, 2023, 59, 589-607.	4.3	16
11430	Screening the maize rhizobiome for consortia that improve Azospirillum brasilense root colonization and plant growth outcomes. Frontiers in Sustainable Food Systems, 0, 7, .	3.9	4
11431	Sympatric rodents in a desert shrubland differ in arthropod consumption. Journal of Arid Environments, 2023, 214, 104999.	2.4	0
11432	Microbiomic profiles of bile in patients with benign and malignant pancreaticobiliary disease. PLoS ONE, 2023, 18, e0283021.	2.5	5
11433	Integrative Metatranscriptomic Analysis Reveals Disease-specific Microbiome–host Interactions in Oral Squamous Cell Carcinoma. Cancer Research Communications, 2023, 3, 807-820.	1.7	2
11434	Novel Sources of Biodiversity and Biomolecules from Bacteria Isolated from a High Middle Ages Soil Sample in Palermo (Sicily, Italy). Microbiology Spectrum, 2023, 11, .	3.0	1
11435	The microbiome of the endosymbiotic Symbiodiniaceae in corals exposed to thermal stress. Hydrobiologia, 2023, 850, 3685-3704.	2.0	4
11436	Effects of non-protein nitrogen on buffel grass fiber and ruminal bacterial composition in sheep. Livestock Science, 2023, 272, 105237.	1.6	1
11437	Free-Living and Particle-Associated Microbial Communities of Lake Baikal Differ by Season and Nutrient Intake. Diversity, 2023, 15, 572.	1.7	0
11438	Environmental Impacts on Skin Microbiomes of Sympatric High Arctic Salmonids. Fishes, 2023, 8, 214.	1.7	3
11439	Bacterial community responses to planktonic and terrestrial substrates in coastal northern Baltic Sea. Frontiers in Marine Science, 0, 10 , .	2.5	2
11440	Slight Temperature Deviation during a 56-Day Storage Period Does Not Affect the Microbiota of Fresh Vacuum-Packed Pork Loins. Foods, 2023, 12, 1695.	4.3	1
11442	Effect of Antibiotics and Gut Microbiota on the Development of Sepsis in Children with Hematopoietic Stem Cell Transplants. Journal of Pediatric Infectious Diseases, 0, , .	0.2	0
11443	Metagenomic profile of the bacterial communities associated with <i>lxodes granulatus</i> (Acari:) Tj ETQq1 1	0.784314 r	gBT /Overlo
11444	Specific host metabolite and gut microbiome alterations are associated with bone loss during spaceflight. Cell Reports, 2023, 42, 112299.	6.4	4
11445	Impact of <i>in situ</i> solar irradiation on snow bacterial communities and functional potential. FEMS Microbiology Ecology, 0, , .	2.7	1
11447	Vibrio cholerae Invasion Dynamics of the Chironomid Host Are Strongly Influenced by Aquatic Cell Density and Can Vary by Strain. Microbiology Spectrum, 2023, 11, .	3.0	3
11450	DNA extraction protocol impacts ocular surface microbiome profile. Frontiers in Microbiology, 0, 14,	3.5	3

#	ARTICLE	IF	CITATIONS
11451	Oral and fecal microbiota perturbance in cocaine users: Can rTMS-induced cocaine abstinence support eubiosis restoration?. IScience, 2023, 26, 106627.	4.1	1
11452	Analysis of two sampling treatments of beef for microbiome studies based on metataxonomic. Letters in Applied Microbiology, 0, , .	2.2	0
11453	Characteristics of the esophageal microbiome in patients with achalasia and its changes before and after peroral endoscopic myotomy: A pilot study. Journal of Gastroenterology and Hepatology (Australia), 2023, 38, 1307-1315.	2.8	3
11454	Pruning Wound Protection Products Induce Alterations in the Wood Mycobiome Profile of Grapevines. Journal of Fungi (Basel, Switzerland), 2023, 9, 488.	3.5	O
11455	Paired environmental <scp>DNA</scp> and dive surveys provide distinct but complementary snapshots of marine biodiversity in a temperate fjord. Environmental DNA, 2023, 5, 597-612.	5.8	2
11456	Comparing the succession of microbial communities throughout development in field and laboratory nests of the ambrosia beetle Xyleborinus saxesenii. Frontiers in Microbiology, 0, 14, .	3.5	3
11458	Interactions between rootstocks and compost influence the active rhizosphere bacterial communities in citrus. Microbiome, 2023, 11 , .	11.1	5
11459	Human microbiome transfer in the built environment differs based on occupants, objects, and buildings. Scientific Reports, 2023, 13, .	3.3	2
11460	Assessment of Multidimensional Health Care Parameters Among Adults in Japan for Developing a Virtual Human Generative Model: Protocol for a Cross-sectional Study. JMIR Research Protocols, 0, 12, e47024.	1.0	0
11461	Beech Leaf Disease Severity Affects Ectomycorrhizal Colonization and Fungal Taxa Composition. Journal of Fungi (Basel, Switzerland), 2023, 9, 497.	3.5	3
11462	Mucin-microbiome signatures shape the tumor microenvironment in gastric cancer. Microbiome, 2023, 11, .	11.1	3
11464	Field scale biodegradation of total petroleum hydrocarbons and soil restoration by Ecopiles: microbiological analysis of the process. Frontiers in Microbiology, 0, 14, .	3.5	2
11465	Metapangenomics of wild and cultivated banana microbiome reveals a plethora of host-associated protective functions. Environmental Microbiomes, 2023, 18, .	5.0	3
11466	Dynamics of Microbial Communities in Nitrite-Free and Nutritionally Improved Dry Fermented Sausages. Fermentation, 2023, 9, 403.	3.0	2
11468	Recovery of the soil fungal microbiome after steam disinfection to manage the plant pathogen Fusarium solani. Frontiers in Plant Science, 0, 14, .	3.6	0
11469	Effects of recurrent summer droughts on arbuscular mycorrhizal and total fungal communities in experimental grasslands differing in plant diversity and community composition. Frontiers in Soil Science, 0, 3, .	2.2	1
11470	From waste to feed: Microbial fermented abalone waste improves the digestibility, gut health, and immunity in marron, Cherax cainii. Fish and Shellfish Immunology, 2023, 137, 108748.	3.6	2
11471	In situ growth of modern oncoids from Salado river, Salar de la Laguna Verde Complex, Argentina. Sedimentary Geology, 2023, 451, 106396.	2.1	O

#	Article	IF	CITATIONS
11472	Genomic and 16S metabarcoding data of Holothuria tubulosa Gmelin, 1791. Data in Brief, 2023, 48, 109171.	1.0	1
11473	Fungal Diversity and Community Composition across Ecosystems. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314	FrgBT/Ove	erlock 10 Tf 50
11474	Selective enrichment of the raw milk microbiota in cheese production: Concept of a natural adjunct milk culture. Frontiers in Microbiology, 0, 14 , .	3 . 5	4
11475	Benchmarking microbial DNA enrichment protocols from human intestinal biopsies. Frontiers in Genetics, $0,14,.$	2.3	3
11476	Bacterial inoculation of ⟨i⟩Quercus pyrenaica⟨ i⟩ trees alters coâ€occurrence patterns but not the composition of the rhizosphere bacteriome in wild conditions. Environmental Microbiology, 2023, 25, 1747-1761.	3.8	0
11477	Successional changes in fungal communities occur a few weeks following wildfire in a mixed Douglas-fir-ponderosa pine forest. Fungal Ecology, 2023, 63, 101246.	1.6	1
11478	Cecal Microbiota Development and Physiological Responses of Broilers Following Early Life Microbial Inoculation Using Different Delivery Methods and Microbial Sources. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
11479	Modulation of milking performance, methane emissions, and rumen microbiome on dairy cows by dietary supplementation of a blend of essential oils. Animal, 2023, 17, 100825.	3.3	3
11480	Metatranscriptomic analysis of the gut microbiome of black soldier fly larvae reared on lignocellulose-rich fiber diets unveils key lignocellulolytic enzymes. Frontiers in Microbiology, 0, 14, .	3.5	3
11481	Predicting feed efficiency traits in growing lambs from their ruminal microbiota. Animal, 2023, 17, 100824.	3.3	O
11483	The phyto-bacterioplankton couple in a shallow freshwater ecosystem: Who leads the dance?. Harmful Algae, 2023, 126, 102436.	4.8	3
11485	Bact-to-Batch: A Microbiota-Based Tool to Determine Optimal Animal Allocation in Experimental Designs. International Journal of Molecular Sciences, 2023, 24, 7912.	4.1	2
11487	Prokaryotic Responses to Estuarine Coalescence Contribute to Planktonic Community Assembly in a Mediterranean Nutrient-Rich Estuary. Journal of Marine Science and Engineering, 2023, 11, 933.	2.6	1
11488	Host selection has a stronger impact on leaf microbiome assembly compared to landâ€management practices. , 2023, 2, 99-111.		1
11489	Unraveling microbial community by next-generation sequencing in living membrane bioreactors for wastewater treatment. Science of the Total Environment, 2023, 886, 163965.	8.0	3
11491	A Metagenomic and Amplicon Sequencing Combined Approach Reveals the Best Primers to Study Marine Aerobic Anoxygenic Phototrophs. Microbial Ecology, 2023, 86, 2161-2172.	2.8	1
11492	Bacterial Diversity in Egg Capsular Fluid of the Spotted Salamander Ambystoma maculatum Decreases with Embryonic Development. Microbial Ecology, 0, , .	2.8	0
11493	Peat loss collocates with a threshold in plant–mycorrhizal associations in drained peatlands encroached by trees. New Phytologist, 2023, 240, 412-425.	7.3	8

# ARTICLE	IF	Citations
11494 Childhood lower respiratory tract infections linked to residential airborne bacterial and fungal microbiota. Environmental Research, 2023, 231, 116063.	7.5	1
Mitomycin C-induced effects on aerobic methanotrophs in a landfill cover soil; implications of a viral shunt?. FEMS Microbiology Ecology, 2023, 99, .	2.7	1
Spontaneously occurring tumors in different wild-derived strains of hydra. Scientific Reports, 2023, 13, .	3.3	6
Gut microbiota maturity mediates the protective effect of siblings on food allergy. Journal of Allergy and Clinical Immunology, 2023, 152, 667-675.	2.9	3
Spatial scale impacts microbial community composition and distribution within and across stream ecosystems in North and Central America. Environmental Microbiology, 2023, 25, 1860-1874.	3.8	0
<i>Mycena</i> species can be opportunistâ€generalist plant root invaders. Environmental Microbiology, 2023, 25, 1875-1893.	3.8	5
Dietary protein shapes the profile and repertoire of intestinal CD4+ T cells. Journal of Experimental Medicine, 2023, 220, .	8.5	3
Permanent cover crop as a strategy to promote soil health and vineyard performance. Environmental Sustainability, 2023, 6, 243-258.	2.8	1
Microbiota and pathogens in an invasive bee: <i>Megachile sculpturalis</i> from native and invaded regions. Insect Molecular Biology, 0, , .	2.0	2
Disruption of fish gut microbiota composition and holobiont's metabolome during a simulated Microcystis aeruginosa (Cyanobacteria) bloom. Microbiome, 2023, 11, .	11.1	5
Gut microbiome diversity and composition is associated with exploratory behavior in a wild-caught songbird. Animal Microbiome, 2023, 5, .	3.8	3
Characterisation of the koala (Phascolarctos cinereus) pouch microbiota in a captive population reveals a dysbiotic compositional profile associated with neonatal mortality. Microbiome, 2023, 11 , .	11.1	0
CX3CR1 modulates SLE-associated glomerulonephritis and cardiovascular disease in MRL/lpr mice. Inflammation Research, 2023, 72, 1083-1097.	4.0	3
ldentifying Gut Microbiota associated with Gastrointestinal Symptoms upon Roux-en-Y Gastric Bypass. Obesity Surgery, 2023, 33, 1635-1645.	2.1	2
Arsenic (As) oxidation by core endosphere microbiome mediates As speciation in Pteris vittata roots. Journal of Hazardous Materials, 2023, 454, 131458.	12.4	5
Anaerobic oxidation of methane does not attenuate methane emissions from thermokarst lakes. Limnology and Oceanography, 0, , .	3.1	0
Rumen Microbiota Predicts Feed Efficiency of Primiparous Nordic Red Dairy Cows. Microorganisms, 2023, 11, 1116.	3.6	2
Microbiome Network Connectivity and Composition Linked to Disease Resistance in Strawberry Plants. Phytobiomes Journal, 0, , .	2.7	4

#	ARTICLE	IF	CITATIONS
11513	Profiling the Urobiota in a Pediatric Population with Neurogenic Bladder Secondary to Spinal Dysraphism. International Journal of Molecular Sciences, 2023, 24, 8261.	4.1	4
11516	<i>Convivina</i> is a specialised core gut symbiont of the invasive hornet <i>Vespa velutina</i> Insect Molecular Biology, 2023, 32, 510-527.	2.0	2
11517	Metabolic effects of early life stress and preâ€pregnancy obesity are long lasting and sex specific in mice. European Journal of Neuroscience, 2023, 58, 2215-2231.	2.6	0
11518	The role of land use, management, and microbial diversity depletion on glyphosate biodegradation in tropical soils. Environmental Research, 2023, 231, 116178.	7.5	2
11519	Deciphering effect of maternal postpartum antibiotic prophylaxis on infant gut microbiome: a whole metagenomic analysis. Future Microbiology, 0, , .	2.0	0
11520	Net cleaning impacts Atlantic salmon gill health through microbiome dysbiosis. , 0, 2, .		O
11521	Root microbiome diversity and structure of the Sonoran desert buffelgrass (Pennisetum ciliare L.). PLoS ONE, 2023, 18, e0285978.	2.5	1
11522	Resilience of barley (Hordeum vulgare) plants upon exposure to tramadol: Implication for the root-associated bacterial community and the antioxidative plant defence system. Science of the Total Environment, 2023, 892, 164260.	8.0	0
11523	Environmental DNA surveillance of biocontamination in a drinking water treatment plant. Journal of Hazardous Materials, 2023, 456, 131656.	12.4	1
11524	Microbial Diversity and Activity of Biofilms from Geothermal Springs in Croatia. Microbial Ecology, 2023, 86, 2305-2319.	2.8	1
11525	Taxonomic and functional responses of soil and root bacterial communities associated with poplar exposed to a contamination gradient of phenanthrene. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
11526	In the right place, at the right time: the integration of bacteria into the Plankton Ecology Group model. Microbiome, 2023, 11 , .	11.1	4
11527	Composition of mucus- and digesta-associated bacteria in growing pigs with and without diarrhea differed according to the presence of colonic inflammation. BMC Microbiology, 2023, 23, .	3.3	4
11531	Structures of Get3d reveal a distinct architecture associated with the emergence of photosynthesis. Journal of Biological Chemistry, 2023, 299, 104752.	3.4	0
11532	Diversity and functional roles of the symbiotic microbiome associated to marine sponges off Karah Island, Terengganu, Malaysia. Regional Studies in Marine Science, 2023, 62, 102967.	0.7	1
11533	Postmortem Nasopharyngeal Microbiome Analysis of Zambian Infants With and Without Respiratory Syncytial Virus Disease: A Nested Case Control Study. Pediatric Infectious Disease Journal, 2023, 42, 637-643.	2.0	1
11534	Species composition of root-associated mycobiome of ruderal invasive Anthemis cotula L. varies with elevation in Kashmir Himalaya. International Microbiology, 0, , .	2.4	0
11535	Divergence of the Host-Associated Microbiota with the Genetic Distance of Host Individuals Within a Parthenogenetic Daphnia Species. Microbial Ecology, 0, , .	2.8	O

# ARTICLE	IF	Citations
Hive Transplantation Has Minimal Impact on the Core Gut Microbiome of the Australian Stingle Tetragonula carbonaria. Microbial Ecology, 2023, 86, 2086-2096.	ss Bee, 2.8	1
Microbial communities in the deep-sea sediments of the South São Paulo Plateau, Southwest Atlantic Ocean. International Microbiology, 2023, 26, 1041-1051.	ern 2.4	2
The natural product chlorotonil A preserves colonization resistance and prevents relapsing Clostridioides difficile infection. Cell Host and Microbe, 2023, 31, 734-750.e8.	11.0	O
Hydrochemical and Seasonally Conditioned Changes of Microbial Communities in the Tufa-Form Freshwater Network Ecosystem. MSphere, 2023, 8, .	ning 2.9	5
The Inherited Intestinal Microbiota from Myeloid-Specific ZIP8KO Mice Impairs Pulmonary Host against Pneumococcal Pneumonia. Pathogens, 2023, 12, 639.	Defense 2.8	1
Dedomestication of modern soybean is potentially revealed by variation in the root-associated bacterial community along a domestication gradient. Plant and Soil, 0, , .	3.7	1
Association of Vitamin D Level and Maternal Gut Microbiome during Pregnancy: Findings from a Randomized Controlled Trial of Antenatal Vitamin D Supplementation. Nutrients, 2023, 15, 205	a 59. 4.1	0
Indirect maternal effects via nest microbiome composition drive gut colonization in altricial chic Molecular Ecology, 2023, 32, 3657-3671.	cks. 3.9	1
Methane-Oxidizing Activity Enhances Sulfamethoxazole Biotransformation in a Benthic Constru Wetland Biomat. Environmental Science & Scie	ucted 10.0	2
Use of carrion fly iDNA metabarcoding to monitor invasive and native mammals. Conservation Biology, 2023, 37, .	4.7	4
Salinity Impacts the Functional mcrA and dsrA Gene Abundances in Everglades Marshes. Microorganisms, 2023, 11, 1180.	3.6	0
Long-term impact of pulses crop rotation on soil fungal diversity in aerobic and wetland rice cultivation. Fungal Biology, 2023, 127, 1053-1066.	2.5	1
11549 Sex differences in the skin microbiome of burn scars. Wound Repair and Regeneration, 2023, 3	1, 547-558. 3.0	2
11550 The best practice for microbiome analysis using R. Protein and Cell, 2023, 14, 713-725.	11.0	13
Resilience of swine nasal microbiota to influenza A virus challenge in a longitudinal study. Veter Research, 2023, 54, .	rinary 3.0	0
Only a minority of bacteria grow after wetting in both natural and post-mining biocrusts in a hyperarid phosphate mine. Soil, 2023, 9, 231-242.	4.9	O
Land use in the Prairie Pothole Region influences the soil bacterial community composition and relative abundance of nitrogen cycling genes. Canadian Journal of Soil Science, 0, , .	1.2	1
Study on Effects of Probiotics on Gut Microbiome and Clinical Course in Patients with Critical C Illnesses. Microbial Ecology, 2023, 86, 1814-1828.	Care 2.8	2

# ARTICLE		IF	CITATIONS
The soil microbiomes of forest ecos Scientific Reports, 2023, 13, .	systems in Kenya: their diversity and environmental drivers.	3.3	1
11559 Vaginal Microbiome in Pregnant Wo	omen with and without Short Cervix. Nutrients, 2023, 15, 2173.	4.1	3
Water availability alters the commu plant mycorrhizal benefit. Plants Pe	unity structure of arbuscular mycorrhizal fungi and determines cople Planet, 2023, 5, 683-689.	3.3	1
Characterization of the equine plac Theriogenology, 2023, 206, 60-70.	ental microbial population in healthy pregnancies.	2.1	6
Sexual Dimorphism in Lipid Metabo 15, 2175.	olism and Gut Microbiota in Mice Fed a High-Fat Diet. Nutrients, 2023,	4.1	2
Novel <scp>eDNA</scp> approache and arthropod communities. Enviro	es to monitor Western honey bee (<i>Apis mellifera</i> L.) microbial onmental DNA, 2024, 6, .	5.8	2
Gut microbiome profiles may be rela 11564 children with psychiatric disorder: a Microbiology, 0, 13, .	ated to atypical antipsychotic associated overweight in Asian a preliminary study. Frontiers in Cellular and Infection	3.9	1
Crohn's disease proteolytic mic mice. Gut Microbes, 2023, 15, .	crobiota enhances inflammation through PAR2 pathway in gnotobiotic	9.8	O
Drivers of stability and transience ir litter-decomposing microbial comm	n composition-functioning links during serial propagation of nunities. MSystems, 2023, 8, .	3.8	0
	bial community development during organic pinot noir wine ermentation conditions. Heliyon, 2023, 9, e15658.	3.2	3
Repeated applications of fipronil, procommunity composition: A laborate	ropyzamide and flutriafol affect soil microbial functions and ory-to-field assessment. Chemosphere, 2023, 331, 138850.	8.2	2
A core of functional complementary Animal Microbiome, 2023, 5, .	y bacteria infects oysters in Pacific Oyster Mortality Syndrome.	3.8	4
11570 Influence of amino acids on bacterio Ocean Station Papa in the subarction	oplankton production, biomass and community composition at c Pacific. Elementa, 2023, 11, .	3.2	1
Genome-Resolved Metagenomics o Microbiome on Marginal Lands. Agr	of Nitrogen Transformations in the Switchgrass Rhizosphere ronomy, 2023, 13, 1294.	3.0	1
Effects of different fertilization con 11573 and composition of the rhizosphere growth stages. Frontiers in Microbia	ditions and different geographical locations on the diversity e microbiota of Qingke (Hordeum vulgare L.) plants in different ology, 0, 14, .	3.5	1
Fecal virome transfer improves prol unexpectedly enhances the fertility	iferation of commensal gut <i>Akkermansia muciniphila</i> and rate in laboratory mice. Gut Microbes, 2023, 15, .	9.8	7
	act soil nutrient cycling and the soil microbiome after three years and Fertility of Soils, 2023, 59, 659-678.	4.3	4
Temperature-Related Short-Term Su Genes, 2023, 14, 1051.	uccession Events of Bacterial Phylotypes in Potter Cove, Antarctica.	2.4	3

#	Article	IF	CITATIONS
11578	Highly diverse and unknown viruses may enhance Antarctic endoliths' adaptability. Microbiome, 2023, 11, .	11.1	3
11579	Effects on rumen pH and feed intake of a dietary concentrate challenge in cows fed rations containing pH modulators with different neutralizing capacity. Journal of Dairy Science, 2023, 106, 4580-4598.	3.4	2
11581	Survey of the Endophytic Bacteria Inhabiting Wild <i>Daucus</i> Seed Using 16S rRNA Gene Amplicon Sequencing. Microbiology Resource Announcements, 2023, 12, .	0.6	1
11582	Universal gut microbial relationships in the gut microbiome of wild baboons. ELife, 0, 12, .	6.0	5
11583	Close but different: Metabarcoding analyses reveal different microbial communities in ancient Roman nymphaea. International Biodeterioration and Biodegradation, 2023, 181, 105619.	3.9	0
11584	Microbiome Structure of a Wild <i>Drosophila</i> Community along Tropical Elevational Gradients and Comparison to Laboratory Lines. Applied and Environmental Microbiology, 2023, 89, .	3.1	3
11585	Plasma virome dynamics in chronic hepatitis B virus infected patients. Frontiers in Microbiology, 0, 14,	3.5	5
11586	Factors shaping the gut microbiome of five species of lizards from different habitats. PeerJ, 0, 11, e15146.	2.0	1
11587	Effects of the supplementation with a multispecies probiotic on clinical and laboratory recovery of children with newly diagnosed celiac disease: A randomized, placebo-controlled trial. Digestive and Liver Disease, 2023, , .	0.9	2
11588	Profiling the human intestinal environment under physiological conditions. Nature, 2023, 617, 581-591.	27.8	78
11589	Human gene and microbial analyses in rectal cancer complete responses to radiotherapy. BJS Open, 2023, 7, .	1.7	1
11590	Microbiome analysis of thai traditional fermented soybeans reveals short-chain fatty acid-associated bacterial taxa. Scientific Reports, 2023, 13, .	3.3	5
11591	Distinct Features Based on Partitioning of the Endophytic Fungi of Cereals and Other Grasses. Microbiology Spectrum, 2023, 11, .	3.0	1
11592	Integrative multi-omics deciphers the spatial characteristics of host-gut microbiota interactions in Crohn's disease. Cell Reports Medicine, 2023, 4, 101050.	6.5	4
11593	Out of the stable: Social disruption and concurrent shifts in the feral mare (<i>Equus caballus</i>) fecal microbiota. Ecology and Evolution, 2023, 13, .	1.9	0
11594	Pre-pregnancy body mass index and gut microbiota of mothers and children 5 years postpartum. International Journal of Obesity, 0, , .	3.4	0
11595	Spatial and temporal niche separation of Methanomassiliicoccales phylotypes in temperate fens. FEMS Microbiology Ecology, 2023, 99, .	2.7	4
11596	Anthropogenic and natural disturbances along a river and its estuary alter the diversity of pathogens and antibiotic resistance mechanisms. Science of the Total Environment, 2023, 887, 164108.	8.0	3

# ARTICLE	IF	Citations
Impact of a Blend of Microencapsulated Organic Acids and Botanicals on the Microbiome of Commercial Broiler Breeders under Clinical Necrotic Enteritis. Animals, 2023, 13, 1627.	2.3	O
Wavelet clustering analysis as a tool for characterizing community structure in the human microbiome. Scientific Reports, 2023, 13, .	3.3	1
Colocalization and potential interactions of <i>Endozoicomonas</i> and chlamydiae in microbial aggregates of the coral <i>Pocillopora acuta</i> . Science Advances, 2023, 9, .	10.3	19
Inclusion of database outgroups reduces false positives in fungal metabarcoding taxonomic assignments. Mycologia, 2023, 115, 571-577.	1.9	2
Gut Microbiota and B Cell Receptor (BCR) Inhibitors for the Treatment of Chronic Lymphocytic Leukemia: Is Biodiversity Correlated with Clinical Response or Immune-Related Adverse Event Occurrence? A Cross-Sectional Study. Microorganisms, 2023, 11, 1305.	3.6	1
Rice developmental stages modulate rhizosphere bacteria and archaea co-occurrence and sensitivity 11604 to long-term inorganic fertilization in a West African Sahelian agro-ecosystem. Environmental Microbiomes, 2023, 18, .	5.0	3
Succession of bacterial biofilm communities following removal of chloramine from a full-scale drinking water distribution system. Npj Clean Water, 2023, 6, .	8.0	3
Feeding hempseed cake alters the bovine gut, respiratory and reproductive microbiota. Scientific Reports, 2023, 13, .	3.3	7
Urban food forestry transforms fine-scale soil function for rapid and uniform carbon sequestration. Urban Ecosystems, 0, , .	2.4	0
Nitrogen input on organic amendments alters the pattern of soil–microbe-plant co-dependence. Science of the Total Environment, 2023, 890, 164347.	8.0	1
Host habitat shapes the core gut bacteria of decapod crustaceans: A meta-analysis. Heliyon, 2023, 9 e16511.	9, 3.2	0
A Method of DNA Extraction from Plants for Metagenomic Analysis Based on the Example of Grape Vitis amurensis Rupr Applied Biochemistry and Microbiology, 2023, 59, 361-367.	0.9	3
Single-Chamber Electrofermentation of Rumen Fluid Increases Microbial Biomass and Volatile Fatty Acid Production without Major Changes in Diversity. Fermentation, 2023, 9, 502.	3.0	0
Gut microbiota fermentation profiles of pre-digested mycoprotein (Quorn) using faecal batch cultures <i>in vitro</i> : a preliminary study. International Journal of Food Sciences and Nutrition, 2023, 74, 327-337.	2.8	0
Legume Overseeding and P Fertilization Increases Microbial Activity and Decreases the Relative Abundance of AM Fungi in Pampas Natural Pastures. Microorganisms, 2023, 11, 1383.	3.6	3
Effects of Degradation on Microbial Communities of an Amazonian Mangrove. Microorganisms, 202 11, 1389.	23, 3.6	4
Altered gut microbiota in older adults with mild cognitive impairment: a case-control study. Frontiers in Aging Neuroscience, 0, 15, .	3.4	3
Characterisation of †Candidatus Methylobacter titanis†sp. nov., a putative novel species of Methylobacter clade 2 and their distribution in sediments of freshwater lakes in maritime Antarctica. Antonie Van Leeuwenhoek, 2023, 116, 721-738.	. 1.7	1

# ARTICLE	IF	Citations
11622 Fertilization Enhances Grain Inorganic Arsenic Assimilation in Rice. Exposure and Health, 0, , .	4.9	2
Gut microbiota, circulating inflammatory markers and metabolites, and carotid artery atherosclerosis in HIV infection. Microbiome, 2023, 11, .	11.1	4
Microbial communities of the upper respiratory tract in mild and severe COVID-19 patients: a possible link with the disease course. , 0, 2, .	2	2
Comparative <scp>16S rRNA</scp> gene sequencing study of subgingival microbiota of healthy subjects and patients with periodontitis from four different countries. Journal of Clinical Periodontology, 2023, 50, 1176-1187.	4.9	1
Association between lipid-A-producing oral bacteria of different potency and fractional exhaled nitric oxide in a Norwegian population-based adult cohort. Journal of Translational Medicine, 2023, 21, .	4.4	0
Effects of Early Emollient Use in Children at High Risk of Atopic Dermatitis: A German Pilot Study. Act Dermato-Venereologica, 0, 103, adv5671.	a 1.3	3
Service-lines as major contributor to water quality deterioration at customer ends. Water Research, 2023, 241, 120143.	11.3	1
Long-Term Simulated Nitrogen Deposition Has Moderate Impacts on Soil Microbial Communities across Three Bioclimatic Domains of the Eastern Canadian Forest. Forests, 2023, 14, 1124.	2.1	2
Profiling the microbiome of oral and genital mucosal surfaces in Behçet's disease. Clinical Immunology, 2023, 253, 109654.	3.2	3
The summer bacterial and archaeal community composition of the northern Barents Sea. Progress in Oceanography, 2023, 215, 103054.	3.2	4
Maternal transmission gives way to social transmission during gut microbiota assembly in wild mice. Animal Microbiome, 2023, 5, .	3.8	6
11636 Amplicon Sequencing Pipelines in Metagenomics. Methods in Molecular Biology, 2023, , 69-83.	0.9	O
Host-diet-gut microbiome interactions influence human energy balance: a randomized clinical trial. Nature Communications, 2023, 14, .	12.8	16
Prevalence and Persistence of Antibiotic Resistance Determinants in the Gut of Travelers Returning to the United Kingdom is Associated with Colonization by Pathogenic Escherichiacoli. Microbiology Spectrum, 2023, 11, .	3.0	3
Dairy Manure-Derived Biochar in Soil Enhances Nutrient Metabolism and Soil Fertility, Altering the Soil Prokaryote Community. Agronomy, 2023, 13, 1512.	3.0	0
Physiological changes during torpor favor association with Endozoicomonas endosymbionts in the urochordate Botrylloides leachii. Frontiers in Microbiology, 0, 14, .	3.5	4
Advanced Glycation End Products (AGEs) in Diet and Skin in Relation to Stool Microbiota: The Rotterdam Study. Nutrients, 2023, 15, 2567.	4.1	5
Comprehensive Guideline for Microbiome Analysis Using R. Methods in Molecular Biology, 2023, , 393-436.	0.9	1

# ARTICLE	IF	CITATIONS
Preharvest Maize Fungal Microbiome and Mycotoxin Contamination: Case of Zambia's Difformation Preharvest Maize Fungal Microbiome and Mycotoxin Contamination: Case of Zambia's Difformation Preharvest Maize Fungal Microbiome and Mycotoxin Contamination: Case of Zambia's Difformation Preharvest Maize Fungal Microbiome and Mycotoxin Contamination: Case of Zambia's Difformation Preharvest Maize Fungal Microbiome and Mycotoxin Contamination: Case of Zambia's Difformation Preharvest Maize Fungal Microbiome and Mycotoxin Contamination Preharvest Maize Fungal Microbiome Preharvest Microbiome Preharvest Microbiome Preharves	erent 3.1	0
Anaerobutyricum and Subdoligranulum Are Differentially Enriched in Broilers with Disparate Web Gains. Animals, 2023, 13, 1834.	eight 2.3	2
The microbiome of Riccia liverworts is an important reservoir for microbial diversity in temporar agricultural crusts. Environmental Microbiomes, 2023, 18, .	y 5.0	1
No impacts of glyphosate or Crithidia bombi, or their combination, on the bumblebee microbiol Scientific Reports, 2023, 13, .	me. 3.3	5
Salivary microbial profiles associate with responsiveness to warning oral sensations and dietary intakes. Food Research International, 2023, 171, 113072.	6.2	0
Diversity of fecal parasitomes of wild carnivores inhabiting Korea, including zoonotic parasites a parasites of their prey animals, as revealed by 18S rRNA gene sequencing. International Journal Parasitology: Parasites and Wildlife, 2023, 21, 179-184.		O
Altered Gut Microbiota as Potential Biomarkers for Autism Spectrum Disorder in Early Childhoo Neuroscience, 2023, 523, 118-131.	od. 2.3	3
Mix of almond baru (Dipteryx alata Vog.) and goat whey modulated intestinal microbiota, impro 11653 memory and induced anxiolytic like behavior in aged rats. Journal of Psychiatric Research, 2023 98-117.	oved , 164, 3.1	2
11654 Characterizing the gut microbiome of broilers raised under conventional and no antibiotics eve practices. Poultry Science, 2023, 102, 102832.	r 3.4	O
Host- and <i>Fusarium </i> -Adapted Bacterial Consortia Alter Microbial Community Structures i <i>Arabidopsis </i> Roots and Suppress <i>Fusarium oxysporum </i> -I>. Phytobiomes Journal, 2024		O
Biological mechanisms underlying priming of vascular plant material in the presence of diatoms Aquatic Microbial Ecology, 2023, 89, 99-117.	5. 1.8	2
Breast cancer: the first comparative evaluation of oncobiome composition between males and females. Biology of Sex Differences, 2023, 14, .	4.1	2
A comparison of mesophotic and shallow sponge holobionts resilience to predicted future temperature elevation. Frontiers in Marine Science, 0, 10, .	2.5	0
The impact of vitamin D3 supplementation on the faecal and oral microbiome of dairy calves in or at pasture. Scientific Reports, 2023, 13 , .	doors 3.3	O
Valorisation of hydrothermal liquefaction wastewater in agriculture: effects on tobacco plants a rhizosphere microbiota. Frontiers in Plant Science, 0, 14, .	and 3.6	2
Distinct Signatures of Tumor-Associated Microbiota and Metabolome in Low-Grade vs. High-Gra 11664 Dysplastic Colon Polyps: Inference of Their Role in Tumor Initiation and Progression. Cancers, 2 3065.		1
Deterministic processes have limited impacts on foliar fungal endophyte communities along a savanna-forest successional gradient. Fungal Ecology, 2023, 64, 101249.	1.6	2
Frequent pulse disturbances shape resistance and resilience in tropical marine microbial commu ISME Communications, 2023, 3, .	unities. 4.2	3

# ARTICLE	IF	CITATIONS
Environmental concentrations of surfactants as a trigger for climax of horizonal gene transfer of antibiotic resistance. Heliyon, 2023, 9, e17034.	3.2	1
Adoption of alternative life cycles in a parasitic trematode is linked to microbiome differences. Biology Letters, 2023, 19, .	2.3	0
Geology and land use shape nitrogen and sulfur cycling groundwater microbial communities in Pacific Island aquifers. ISME Communications, 2023, 3, .	4.2	1
Effect of labile and recalcitrant carbon on heterotrophic nitrification in a subtropical forest soil. European Journal of Soil Science, 2023, 74, .	3.9	0
11672 Cover cropping reduces the negative effect of salinity on soil microbiomes., 2023, 2, 140-152.		1
Potential impacts of environmental bacteria on the microbiota of loggerhead (<i>Caretta caretta</i>) and green (<i>Chelonia mydas</i>) sea turtle eggs and their hatching success. MicrobiologyOpen, 2023, 12, .	3.0	0
Landscape characteristics shape surface soil microbiomes in the Chihuahuan Desert. Frontiers in Microbiology, 0, 14, .	3.5	1
The oral bacteriomes of patients with allergic rhinitis and asthma differ from that of healthy controls. Frontiers in Microbiology, 0, 14, .	3.5	2
Treatment of soybean processing residues for energy recovery and environmental compliance: Technical and economic feasibility. Energy, 2023, 279, 128061.	8.8	0
Natural populations of the putative ancient asexual Darwinula stevensoni (Crustacea, Ostracoda) differ in their microbiomes. Hydrobiologia, 0, , .	2.0	0
Biodegradable polymers boost reproduction in the earthworm Eisenia fetida. Science of the Total Environment, 2023, 892, 164670.	8.0	2
Mass-Immigration Shapes the Antibiotic Resistome of Wastewater Treatment Plants. SSRN Electronic Journal, 0, , .	0.4	0
11681 Patterns in soil microbial diversity across Europe. Nature Communications, 2023, 14, .	12.8	24
Thermal Hydrolysis Pretreatment Effects on Endocrine Disrupting Compounds and Microbial Communities in Wastewater Sludge from Anaerobic Digestion. Environmental Engineering Science, 2023, 40, 219-232.	1.6	2
Host genotype affects endotoxin release in excreta of broilers at slaughter age. Frontiers in Genetics, 0, 14, .	2.3	0
Soil microbiomes in lawns reveal land-use legacy impacts on urban landscapes. Oecologia, 2023, 202, 337-351.	2.0	0
Disruption of the skin, gill, and gut mucosae microbiome of gilthead seabream fingerlings after bacterial infection and antibiotic treatment. FEMS Microbes, 2023, 4, .	2.1	2
Temporal dynamics of soil fungi in a pyrodiverse dryâ€sclerophyll forest. Molecular Ecology, 2023, 32, 4181-4198.	3.9	1

#	ARTICLE	IF	CITATIONS
11687	Microbiomes of Blood-Feeding Triatomines in the Context of Their Predatory Relatives and the Environment. Microbiology Spectrum, 0 , , .	3.0	0
11688	A new approach of microbiome monitoring in the built environment: feasibility analysis of condensation capture. Microbiome, 2023, 11 , .	11.1	0
11689	Microbiome species diversity and seasonal stability of two temperate marine sponges Hymeniacidon perlevis and Suberites massa. Environmental Microbiomes, 2023, 18, .	5.0	2
11692	Woodland wildfire enables fungal colonization of encroaching Douglasâ€fir. Functional Ecology, 0, , .	3.6	0
11693	Changes in arbuscular mycorrhizal fungal communities, mycorrhizal soil infectivity, and phosphorus availability under Chromolaena odorata (Asteraceae) invasions in a West-African forest-savanna ecotone. Mycorrhiza, 2023, 33, 257-275.	2.8	2
11694	<i>Haemophilus influenzae</i> and <i>Moraxella catarrhalis</i> in sputum of severe asthma with inflammasome and neutrophil activation. Allergy: European Journal of Allergy and Clinical Immunology, 2023, 78, 2906-2920.	5.7	2
11695	Community structure and abundance of ACC deaminase containing bacteria in soils with 16S-PICRUSt2 inference or direct acdS gene sequencing. Journal of Microbiological Methods, 2023, 211, 106740.	1.6	6
11696	Metagenomic Study of Fungal Microbial Communities in Two PDO Somontano Vineyards (Huesca,) Tj ETQq1 1 C their Associated Microorganisms. Plants, 2023, 12, 2251.	3.5 3.5	gBT /Overloc 1
11697	Tree Root-Associated Microbial Communities Depend on Various Floor Management Systems in an Intensive Apple (Malus × domestica Borkh.) Orchard. International Journal of Molecular Sciences, 2023, 24, 9898.	4.1	2
11698	Porewater constituents inhibit microbially mediated greenhouse gas production (GHG) and regulate the response of soil organic matter decomposition to warming in anoxic peat from a <i>Sphagnum</i> -dominated bog. FEMS Microbiology Ecology, 2023, 99, .	2.7	3
11699	Faecal Microbiota Characterisation of Potamochoerus porcus Living in a Controlled Environment. Microorganisms, 2023, 11, 1542.	3.6	0
11700	Honey bees and bumble bees occupying the same landscape have distinct gut microbiomes and amplicon sequence variant-level responses to infections. PeerJ, 0, 11, e15501.	2.0	3
11701	The impact of environmental conditions and milk type on microbial communities of wooden vats and cheeses produced therein. Food Microbiology, 2023, 115, 104319.	4.2	1
11702	Evaluation of the microbiota-sparing properties of the anti-staphylococcal antibiotic afabicin. Journal of Antimicrobial Chemotherapy, 2023, 78, 1900-1908.	3.0	2
11703	An analysis of the cecum microbiome of three breeds of the guinea pig: Andina, Inti, and Peru. Research in Veterinary Science, 2023, 161, 50-61.	1.9	2
11704	Exposure to cooking fumes is associated with perturbations in nasal microbiota composition: A pilot study. Environmental Research, 2023, 234, 116392.	7.5	1
11706	Biodegradation of trace sulfonamide antibiotics accelerated by substrates across oxic to anoxic conditions during column infiltration experiments. Water Research, 2023, 242, 120193.	11.3	3
11707	Effects of liquefied sake lees on growth performance and faecal and blood characteristics in Japanese Black calves. Animal, 2023, 17, 100873.	3.3	1

#	ARTICLE	IF	CITATIONS
11708	Dynamic <i>Phaeodactylum tricornutum </i> exometabolites shape surrounding bacterial communities. New Phytologist, 2023, 239, 1420-1433.	7.3	4
11709	Coprophagy rapidly matures juvenile gut microbiota in a precocial bird. Evolution Letters, 2023, 7, 240-251.	3.3	1
11710	Decreased diversity and connectivity of endophytic fungal assemblages within cultivated European olive trees compared to their native African counterpart. Fungal Ecology, 2023, 65, 101261.	1.6	1
11711	A metabarcoding protocol targeting two DNA regions to analyze rootâ \in associated fungal communities in ferns and lycophytes. Applications in Plant Sciences, 2023, 11, .	2.1	2
11712	Predicting soil fungal communities from chemical and physical properties., 0,,.		3
11714	Social signal manipulation and environmental challenges have independent effects on physiology, internal microbiome, and reproductive performance in tree swallows (<i>Tachycineta bicolor</i>). Journal of Experimental Zoology Part A: Ecological and Integrative Physiology, 2023, 339, 723-735.	1.9	0
11715	Temporal progression of anaerobic fungal communities in dairy calves from birth to maturity. Environmental Microbiology, 2023, 25, 2088-2101.	3.8	1
11716	The Role of Microbiota in Pancreatic Cancer. Cancers, 2023, 15, 3143.	3.7	3
11717	Effects of respiratory virus vaccination and bovine respiratory disease on the respiratory microbiome of feedlot cattle. Frontiers in Microbiology, 0, 14 , .	3 . 5	1
11719	Biofilm Formation and Genetic Diversity of Microbial Communities in Anaerobic Batch Reactor with Polylactide (PLA) Addition. International Journal of Molecular Sciences, 2023, 24, 10042.	4.1	3
11720	Comparison of microbial colonization between natural and plastic substrata in a polluted watershed. FEMS Microbiology Ecology, 2023, 99, .	2.7	1
11721	Synthase-selected sorting approach identifies a beta-lactone synthase in a nudibranch symbiotic bacterium. Microbiome, 2023, 11 , .	11.1	0
11722	Diversity, composition, and networking of saliva microbiota distinguish the severity of COVID-19 episodes as revealed by an analysis of 16S rRNA variable V1-V3 region sequences. MSystems, 0, , .	3.8	0
11723	Metabarcoding of fecal pellets in wild muskox populations reveals negative relationships between microbiome and diet alpha diversity. Ecology and Evolution, 2023, 13, .	1.9	0
11724	RNA-based amplicon sequencing is ineffective in measuring metabolic activity in environmental microbial communities. Microbiome, 2023, 11 , .	11.1	11
11725	Microbial community structure and settlement induction capacity of marine biofilms developed under varied reef conditions. Marine Pollution Bulletin, 2023, 193, 115138.	5.0	2
11727	Distinct fungal and bacterial responses to fire severity and soil depth across a ten-year wildfire chronosequence in beetle-killed lodgepole pine forests. Forest Ecology and Management, 2023, 544, 121160.	3.2	3
11729	Globally consistent response of plant microbiome diversity across hosts and continents to soil nutrients and herbivores. Nature Communications, 2023, 14, .	12.8	2

#	ARTICLE	IF	CITATIONS
11730	Initial diet influences future development paths of gut microbiota in larval northern pike (Esox) Tj ETQq0 0 0 rgBT	/Qverlock	10 Tf 50 74
11731	Host Phylogeny Structures the Gut Bacterial Community Within Galerucella Leaf Beetles. Microbial Ecology, 2023, 86, 2477-2487.	2.8	1
11732	Gut microbiome composition may be an indicator of preclinical Alzheimer's disease. Science Translational Medicine, 2023, 15, .	12.4	38
11733	Relative and Quantitative Characterization of the Bovine Bacterial Ocular Surface Microbiome in the Context of Suspected Ocular Squamous Cell Carcinoma. Animals, 2023, 13, 1976.	2.3	2
11735	The Impact of Sea Ice Cover on Microbial Communities in Antarctic Shelf Sediments. Microorganisms, 2023, 11, 1572.	3.6	1
11736	A comparison of biomonitoring methodologies for surf zone fish communities. PLoS ONE, 2023, 18, e0260903.	2.5	3
11737	Composition of Bacterial Communities in Oil-Contaminated Bottom Sediments of the Kamenka River. Moscow University Biological Sciences Bulletin, 2023, 78, 14-20.	0.7	1
11738	Determining resident microbial community members and their correlations with geochemistry in a serpentinizing spring. Frontiers in Microbiology, 0, 14, .	3.5	1
11739	Diet-induced changes in fecal microbiota composition and diversity in dogs (Canis lupus familiaris): A comparative study of BARF-type and commercial diets. Comparative Immunology, Microbiology and Infectious Diseases, 2023, 98, 102007.	1.6	1
11740	Host and Water Microbiota Are Differentially Linked to Potential Human Pathogen Accumulation in Oysters. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
11741	Total and arbuscular mycorrhizal fungal communities in the first 3 years after the collapse of the Fundão Dam: are we on the ecosystem recovery pathway?. Restoration Ecology, 0, , .	2.9	0
11742	Gastrointestinal Microbial Ecology of Weaned Piglets Fed Diets with Different Levels of Glyphosate. Microbiology Spectrum, 2023, 11 , .	3.0	1
11743	Influence of agroecology practices on rumen microbiota associated with methane emission in dairy cattle. Animal Feed Science and Technology, 2023, 303, 115716.	2.2	0
11744	Antibiotics reduce <i>Pocillopora</i> coralâ€associated bacteria diversity, decrease holobiont oxygen consumption and activate immune gene expression. Molecular Ecology, 2023, 32, 4677-4694.	3.9	4
11746	Effects of Rhizosphere Microbial Communities on Cucumber Fusarium wilt Disease Suppression. Microorganisms, 2023, 11, 1576.	3.6	5
11747	Vineyard renewal reduces copper and zinc bioavailability and increases microbial diversity in southern Brazil. Ecological Engineering, 2023, 194, 106995.	3.6	1
11748	Metagenomic analysis of gut microbiome from tilapia species across several regions in Japan. Aquaculture, 2023, 576, 739809.	3.5	0
11749	Accelerated dissipation, soil microbial toxicity and dispersal of antimicrobial resistance in soils repeatedly exposed to tiamulin, tilmicosin and sulfamethoxazole. Science of the Total Environment, 2023, 893, 164817.	8.0	1

#	ARTICLE	IF	Citations
11750	Bioinoculants and organic soil amendments affect nematode diversity in apple orchards. Applied Soil Ecology, 2023, 190, 105004.	4.3	0
11751	Changes in rice rhizosphere and bulk soil bacterial communities in the Doñana wetlands at different growth stages. Applied Soil Ecology, 2023, 190, 105013.	4.3	2
11752	Comparative Microbial Community Analysis of Fur Seals and Aquaculture Salmon Gut Microbiomes in Tasmania. Oceans, 2023, 4, 200-219.	1.3	1
11753	Seasonal assembly of skin microbiota driven by neutral and selective processes in the greater horseshoe bat. Molecular Ecology, 0, , .	3.9	2
11755	Cultivation potential of Vanilla crop wild relatives in two contrasting land use systems. European Journal of Agronomy, 2023, 149, 126890.	4.1	1
11756	Gut Microbiota and Aging: Traditional Chinese Medicine and Modern Medicine. Clinical Interventions in Aging, 0, Volume 18, 963-986.	2.9	6
11757	Hydrodynamic and anthropogenic disturbances co-shape microbiota rhythmicity and community assembly within intertidal groundwater-surface water continuum. Water Research, 2023, 242, 120236.	11.3	6
11758	Exploring the mycobiota of bromeliads phytotelmata in Brazilian Campos Rupestres. Brazilian Journal of Microbiology, 0, , .	2.0	0
11761	On the legacy of cover crop-specific microbial footprints. Soil Biology and Biochemistry, 2023, 184, 109080.	8.8	2
11762	Analysis of gut microbiota in patients with Williams–Beuren Syndrome reveals dysbiosis linked to clinical manifestations. Scientific Reports, 2023, 13, .	3.3	1
11763	Rookery through rehabilitation: Microbial community assembly in newborn harbour seals after maternal separation. Environmental Microbiology, 0, , .	3.8	0
11764	Next-generation sequencing analysis of semen microbiome taxonomy in men with nonobstructive azoospermia vs. fertile controls: a pilot study. F&S Science, 2023, 4, 257-264.	0.9	1
11765	Social transmission of bacterial symbionts homogenizes the microbiome within and across generations of group-living spiders. ISME Communications, 2023, 3, .	4.2	1
11767	Amplicon sequencing allows differential quantification of closely related parasite species: an example from rodent Coccidia (Eimeria). Parasites and Vectors, 2023, 16, .	2.5	1
11768	Respiratory Activity and Biodiversity of Microbiomes in Podzolic Soils of Post-Pyrogenic Spruce Forests in the Krasnoyarsk Krai and Komi Republic. Eurasian Soil Science, 2023, 56, 793-806.	1.6	3
11769	Biological treatment and microbial composition of landfill leachate using a compost process in an airlift bioreactor. Journal of Cleaner Production, 2023, 415, 137748.	9.3	5
11771	Synthesis and evaluation of metal-impregnated carbon cloth supplementation to improve anaerobic digestion performance from municipal sludge. Chemical Engineering Journal, 2023, 471, 144164.	12.7	1
11772	Whole metagenome sequencing reveals host plant influences microbial community associated with larvae of <i>Anastrepha obliqua </i> Entomologia Experimentalis Et Applicata, 2023, 171, 668-680.	1.4	1

#	ARTICLE	IF	CITATIONS
11773	A genetic system for Akkermansia muciniphila reveals a role for mucin foraging in gut colonization and host sterol biosynthesis gene expression. Nature Microbiology, 2023, 8, 1450-1467.	13.3	16
11775	Effects of biostimulant application on soil biological and physicochemical properties: A field study. , 2023, 2, 285-300.		2
11776	Gut microbiome dysbiosis is associated with host genetics in the Norwegian Lundehund. Frontiers in Microbiology, $0,14,.$	3.5	0
11777	Premise plumbing bacterial communities in four European cities and their association with Legionella. $0, 2, .$		1
11778	Host genotype and microbiome associations in coâ€occurring clonal and nonâ€clonal kelp, <i>Ecklonia radiata</i> . Molecular Ecology, 2023, 32, 4584-4598.	3.9	1
11779	Microbial Profiling of Amniotic Fluid, Umbilical Blood and Placenta of the Foaling Mare. Animals, 2023, 13, 2029.	2.3	O
11780	In situ field experiment shows the potential of methanogenic archaea for biomethane production from underground gas storage in natural rock environment. Environmental Technology and Innovation, 2023, 32, 103253.	6.1	1
11782	Glacial meltwater and seasonality influence community composition of diazotrophs in Arctic coastal and open waters. FEMS Microbiology Ecology, 2023, 99, .	2.7	2
11783	A Globally Distributed Bacteroides caccae Strain Is the Most Prevalent Mother-Child Shared <i>Bacteroidaceae</i> Strain in a Large Scandinavian Cohort. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
11784	Wildfires disturb the natural skin microbiota of terrestrial salamanders. Environmental Microbiology, 2023, 25, 2203-2215.	3.8	1
11785	Phytoplankton Diversity and Co-Dependency in a Stratified Oligotrophic Ecosystem in the South Adriatic Sea. Water (Switzerland), 2023, 15, 2299.	2.7	0
11786	Profiling Walnut Fungal Pathobiome Associated with Walnut Dieback Using Community-Targeted DNA Metabarcoding. Plants, 2023, 12, 2383.	3.5	2
11787	Filtration of environmentally sourced aquatic media impacts laboratory olonised <i>Aedes albopictus</i> early development and adult bacteriome composition. Medical and Veterinary Entomology, 0, , .	1.5	0
11788	Pinpointing the distinctive impacts of ten cover crop species on the resident and active fractions of the soil microbiome. Applied Soil Ecology, 2023, 190, 105012.	4.3	3
11789	The promotion of stress tolerant Symbiodiniaceae dominance in juveniles of two coral species under simulated future conditions of ocean warming and acidification. Frontiers in Ecology and Evolution, $0,11,.$	2.2	0
11790	Higher convergence of human-great ape enteric eukaryotic viromes in central African forest than in a European zoo: a One Health analysis. Nature Communications, 2023, 14 , .	12.8	2
11791	Metagenomics reveals novel microbial signatures of farm exposures in house dust. Frontiers in Microbiology, 0, 14 , .	3. 5	4
11792	Concordance of microbial and visual health indicators of white-band disease in nursery reared Caribbean coral <i>Acropora cervicornis</i>). PeerJ, 0, 11, e15170.	2.0	1

# ARTICLE	IF	Citations
The correlation between gut and intra-tumor microbiota and PDAC: Etiology, diagnostics and therapeutics. Biochimica Et Biophysica Acta: Reviews on Cancer, 2023, 1878, 188943.	7.4	0
Can dietary magnesium sources and buffer change the ruminal microbiota composition and fermentation of lactating dairy cows?. Journal of Animal Science, 2023, 101, .	0.5	1
Optimizing metaproteomics database construction: lessons from a study of the vaginal microbio MSystems, 0, , .	ome. 3.8	1
Bacterial community diversity and underlying assembly patterns along vertical soil profiles in wetland and meadow habitats on the Zoige Plateau, China. Soil Biology and Biochemistry, 2023 109076.	, 184, 8.8	2
Pleural Empyema Caused by <i>Streptococcus intermedius</i> and <i>Fusobacterium nucleatur Distinct Entity of Pleural Infections. Clinical Infectious Diseases, 2023, 77, 1361-1371.</i>	m: A 5.8	4
Reintroduction of threatened digging mammals influences soil microbial communities differently along a rainfall gradient. Pedobiologia, 2023, 99-100, 150889.	y 1.2	1
Bacterial dysbiosis and epithelial status of the California sea lion (Zalophus californianus) in the Gulf of California. Infection, Genetics and Evolution, 2023, , 105474.	2.3	O
Differential impact of two major polychaete guilds on microbial communities in marine sediment microcosm study. Frontiers in Marine Science, 0, 10, .	ts: a 2.5	O
Microbiome analysis of Litopenaeus vannamei reveals Vibrio as main risk factor of white faeces syndrome. Aquaculture, 2023, 576, 739829.	3.5	3
Rumen microbiome response to sustained release mineral bolus supplement with low- and high-forages. Frontiers in Animal Science, 0, 4, .	quality 1.9	1
Current concepts, advances, and challenges in deciphering the human microbiota with metatranscriptomics. Trends in Genetics, 2023, 39, 686-702.	6.7	9
Intestinal Epithelial Inactivity of Dual Oxidase 2 Results in Microbiome-Mediated Metabolic Synd Cellular and Molecular Gastroenterology and Hepatology, 2023, 16, 557-572.	rome. 4.5	3
Effects of sample collection and storage methods on fecal bacterial diversity in California ground squirrels (<i>Otospermophilus beecheyi</i>). Journal of Mammalogy, 0, , .	d 1.3	0
Impact of compacted bentonite microbial community on the clay mineralogy and copper caniste corrosion: a multidisciplinary approach in view of a safe Deep Geological Repository of nuclear wastes. Journal of Hazardous Materials, 2023, 458, 131940.	er 12.4	5
Soil carbon storage and compositional responses of soil microbial communities under perennial grain IWG vs. annual wheat. Soil Biology and Biochemistry, 2023, 184, 109111.	8.8	3
A DNA-barcode biodiversity standard analysis method (DNA-BSAM) reveals a large variance in th of a range of biological, chemical and physical soil management interventions at different sites, location is one of the most important aspects determining the nature of agricultural soil microbiology. Soil Biology and Biochemistry, 2023, 184, 109104.		1
Dietary restriction mitigates the age-associated decline in mouse B cell receptor repertoire diver Cell Reports, 2023, 42, 112722.	sity. 6.4	2
Absence of gut microbiota reduces neonatal survival and exacerbates liver disease in 11814 <i>Cyp2c70</i> deficient mice with a human-like bile acid composition. Clinical Science, 2023, 1 995-1011.	137, 4.3	4

# ARTICLE		IF	Citations
Glacier retreat alters downstream fjord ecosystem structure an Geoscience, 2023, 16, 671-674.	nd function in Greenland. Nature	12.9	2
Similar connectivity of gut microbiota and brain activity netwo lipid intake in children from a Mexican indigenous population.	orks is mediated by animal protein and PLoS ONE, 2023, 18, e0281385.	2.5	2
Nutrient availability and grazing influence the strength of prior bacterial community coalescence. Environmental Microbiology	rity effects during freshwater v, 0, , .	3.8	0
Soil pH fitness of residents contributes more to the invasion so the invader itself. Applied Soil Ecology, 2023, 190, 105032.	uccess of Ralstonis solanacearum than	4.3	0
The microbiota knows: handling-stress and diet transform the of rainbow trout in RAS. Animal Microbiome, 2023, 5, .	microbial landscape in the gut content	3.8	1
Regular consumption of lacto-fermented vegetables has greated compared with the microbiome. Gut Microbiome, 2023, 4, .	er effects on the gut metabolome	3.2	2
The Nitrogen Cycling Key Functional Genes and Related Microl Determined by Crop Rotation Plans in the Loess Plateau. Agro		3.0	2
Long-term follow-up of colorectal cancer screening attendees Phascolarctobacterium spp. using 16S rRNA and metagenome	identifies differences in sequencing. Frontiers in Oncology, 0, 13, .	2.8	4
The Gut Microbiome Responds Progressively to Fat and/or Sug Modified by Dietary Fat and Sugar. Nutrients, 2023, 15, 2097.	ar-Rich Diets and Is Differentially	4.1	4
11828 Impact of sterilization and chemical fertilizer on the microbiote Microbiology, 0, 14, .	a of oil palm seedlings. Frontiers in	3.5	1
Exploring the Association between Citrus Nutraceutical Eriocit Pre-Diabetes in a Dynamic Microbiome Model. Pharmaceutical		3.8	2
Glycomacropeptide Impacts Amylin-Mediated Satiety, Postpra and the Fecal Microbiome in Obese Postmenopausal Women.		2.9	6
Compositional Changes in Sediment Microbiota Are Associated Column in High-Altitude Hyperarid Andean Lake Systems. Microbiota Are Associated Column in High-Altitude Hyperarid Andean Lake Systems.		3.0	0
11832 Tropical lacustrine sediment microbial community response to Reports, 2023, 13, .	an extreme El Niño event. Scientific	3.3	0
Assembly and comparative genome analysis of a Patagonian < reveals unexpected intraspecific variation. Yeast, 2023, 40, 19		1.7	0
Leveraging the microbiome to understand clinical heterogenei T-RAD study. Translational Psychiatry, 2023, 13, .	ty in depression: findings from the	4.8	5
Bacterial communities shift and influence in an acid mine drain disperse alkaline substrate system. Science of the Total Enviro		8.0	2
Phenanthrene Degradation by Photosynthetic Bacterial Conso 2023, 13, 1108.	rtium Dominated by Fischerella sp Life,	2.4	O

# ARTICLE	IF	CITATIONS
Mucosal Microbiota from Colorectal Cancer, Adenoma and Normal Epithelium Reveals the Imprint of Fusobacterium nucleatum in Cancerogenesis. Microorganisms, 2023, 11, 1147.	3.6	1
11838 Building a genome-based understanding of bacterial pH preferences. Science Advances, 2023, 9, .	10.3	12
Exploring the Bacterial Community in Aged Fecal Sources from Dairy Cows: Impacts on Fecal Source Tracking. Microorganisms, 2023, 11, 1161.	3.6	0
Plant and soil health in organic strawberry farms – Greater importance of fungal trophic modes and networks than α-diversity of the mycobiome. Applied Soil Ecology, 2023, 188, 104925.	4.3	1
Feeding an unsalable carrot total-mixed ration altered bacterial amino acid degradation in the rumen of lambs. Scientific Reports, 2023, 13, .	3.3	1
A tensor decomposition model for longitudinal microbiome studies. Annals of Applied Statistics, 2023, 17, .	1.1	0
MPrESS: An R-Package for Accurately Predicting Power for Comparisons of 16S rRNA Microbiome Taxa Distributions including Simulation by Dirichlet Mixture Modeling. Microorganisms, 2023, 11, 1166.	3.6	0
TRAF3 suppression encourages B cell recruitment and prolongs survival of microbiome-intact mice with ovarian cancer. Journal of Experimental and Clinical Cancer Research, 2023, 42, .	8.6	3
Comparative assessment of the bacterial communities associated with Anopheles darlingi immature stages and their breeding sites in the Brazilian Amazon. Parasites and Vectors, 2023, 16, .	2.5	1
Investigating the oral microbiome in retrospective and prospective cases of prostate, colon, and breast cancer. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	4
Dispersal changes soil bacterial interactions with fungal wood decomposition. ISME Communications, 2023, 3, .	4.2	1
Host filtering, not competitive exclusion, may be the main driver of arbuscular mycorrhizal fungal community assembly under high phosphorus. Functional Ecology, 2023, 37, 1856-1869.	3.6	2
Effects of Coenzyme Q10 on the Biomarkers (Hydrogen, Methane, SCFA and TMA) and Composition of the Gut Microbiome in Rats. Pharmaceuticals, 2023, 16, 686.	3.8	6
11851 MBECS: Microbiome Batch Effects Correction Suite. BMC Bioinformatics, 2023, 24, .	2.6	1
Dynamics of bacterial and archaeal communities during horse bedding and green waste composting. PeerJ, 0, 11, e15239.	2.0	1
Lemur Gut Microeukaryotic Community Variation Is Not Associated with Host Phylogeny, Diet, or Habitat. Microbial Ecology, 0, , .	2.8	0
Impact of phosphorus limitation on medium-chain-length polyhydroxyalkanoate production by activated sludge. Applied Microbiology and Biotechnology, 2023, 107, 3509-3522.	3.6	0
Influence of olive cake dietary supplementation on fecal microbiota of dairy cows. Frontiers in Microbiology, 0, 14 , .	3.5	2

# ARTICL	E	IF	CITATIONS
	nian dark earths enhance the establishment of tree species in forest ecological restoration. rs in Soil Science, $0, 3, .$	2.2	2
11857 Ecolog estuary	ical status of Urdaibai Biosphere reserve based on bacterial communities in a small-drainage 7. Marine and Freshwater Research, 2023, 74, 651-664.	1.3	O
	ersistence of Novel Polyfluoroalkyl Betaines in Aerobic Soils. Environmental Science & ology, 2023, 57, 7442-7453.	10.0	2
	ed microbial diversity of the nasopharyngeal microbiome in household contacts with latent ulosis infection. Scientific Reports, 2023, 13, .	3.3	2
	iome structure of milt and ovarian fluid in farmed Arctic charr (Salvelinus alpinus). ılture, 2023, 574, 739648.	3.5	0
11863 High-re	solution characterization of short-term temporal variability in the taxonomic and resistome sition of wastewater influent. Microbial Genomics, 2023, 9, .	2.0	О
11865 The mi	crobiome of the ice-capped Cayambe Volcanic Complex in Ecuador. Frontiers in Microbiology, 0,	3.5	2
11866 Crop ro canola	otation significantly influences the composition of soil, rhizosphere, and root microbiota in (Brassica napus L.). Environmental Microbiomes, 2023, 18, .	5.0	8
11867 Inhibiti Used ir	on of Listeria monocytogenes by Broth Cultures of Surface Microbiota of Wooden Boards n Cheese Ripening. Applied Sciences (Switzerland), 2023, 13, 5872.	2.5	2
	s of biofilm and bacterial communities in the towel environment with daily use. Scientific s, 2023, 13, .	3.3	2
11869 treated	Eterm changes in the subgingival microbiota in patients with stage <scp>Ill–IV</scp> periodontitis by mechanical therapy and adjunctive systemic antibiotics: A secondary analysis of a nized controlled trial. Journal of Clinical Periodontology, 2023, 50, 1101-1112.	4.9	2
11870 Microb Microb	iome Analysis of Sugarcane Juices and Biofilms from Louisiana Raw Sugar Factories. iology Spectrum, 2023, 11, .	3.0	3
	nkton diversity in an oligotrophic and high salinity environment in the central Adriatic Sea. fic Reports, 2023, 13, .	3.3	1
11872 contan	ng the shaping factors for archaeal and bacterial communities in tidal wetland soils ninated with polycyclic aromatic hydrocarbons. Environmental Technology and Innovation, 31, 103191.	6.1	2
11873 Diet, G Transla	ut Microbiome, and Their End Metabolites Associate With Acute Pancreatitis Risk. Clinical and tional Gastroenterology, 2023, 14, e00597.	2.5	1
11874 Variation	on in Temperature Dependences across Europe Reveals the Climate Sensitivity of Soil Microbial posers. Applied and Environmental Microbiology, 2023, 89, .	3.1	5
	crobial communities are sensitive to differences in fertilization intensity in organic and tional farming systems. FEMS Microbiology Ecology, 2023, 99, .	2.7	2
11876 with ar	oxide nanoparticles (nCeO2) exert minimal adverse effects on microbial communities in soils ad without biosolids amendment. Environmental Science and Pollution Research, 2023, 30, 72353.	5.3	О

#	Article	IF	Citations
11877	Positive fungal interactions are key drivers in Antarctic endolithic microcosms at the boundaries for life sustainability. FEMS Microbiology Ecology, 2023, 99, .	2.7	2
11878	Synecological response of spring benthic prokaryotes and macroinvertebrates to Paleozoic roof pendantâ€derived calcium. Ecosphere, 2023, 14, .	2.2	0
11880	Impact of ionizing radiation on the environmental microbiomes of Chornobyl wetlands. Environmental Pollution, 2023, 330, 121774.	7.5	4
11882	Early-Life Skin Microbial Biomarkers for Eczema Phenotypes in Chinese Toddlers. Pathogens, 2023, 12, 697.	2.8	1
11883	Factors Affecting the Gut Microbiome in Pediatric Intestinal Failure. Journal of Pediatric Gastroenterology and Nutrition, 2023, 77, 426-432.	1.8	2
11884	Insect phylogeny structures the bacterial communities in the microbiome of psyllids (Hemiptera:) Tj ETQq1 1 0.78	4314 rgBT 2.5	Overlock
11885	Home-site advantage for host species–specific gut microbiota. Science Advances, 2023, 9, .	10.3	7
11886	The influence of liver transplantation on the interplay between gut microbiome and bile acid homeostasis in children with biliary atresia. Hepatology Communications, 2023, 7, .	4.3	O
11887	Development of early life gut resistome and mobilome across gestational ages and microbiota-modifying treatments. EBioMedicine, 2023, 92, 104613.	6.1	5
11888	Development of Martian saline seep models and their implications for planetary protection. Biofilm, 2023, 5, 100127.	3.8	1
11889	Microbiome Characterization after Aerobic Digestate Reactivation of Anaerobically Digested Sewage Sludge. Fermentation, 2023, 9, 471.	3.0	0
11890	Introduction to R for Microbiome Data. , 2023, , 11-63.		0
11891	Low-dose glyphosate exposure alters gut microbiota composition and modulates gut homeostasis. Environmental Toxicology and Pharmacology, 2023, 100, 104149.	4.0	5
11892	Microbial biomarker detection in shrimp larvae rearing water as putative bio-surveillance proxies in shrimp aquaculture. PeerJ, 0, 11, e15201.	2.0	5
11893	Multiomics Reveals Symbionts, Pathogens, and Tissue-Specific Microbiome of Blacklegged Ticks (Ixodes) Tj ETQq0 2023, 11, .	0 0 o rgBT / 3.0	/Overlock 10 2
11894	Modulation of the gut microbiome with nisin. Scientific Reports, 2023, 13, .	3.3	4
11895	Bacterioplankton Communities in Dissolved Organic Carbon-Rich Amazonian Black Water. Microbiology Spectrum, 2023, 11, .	3.0	2
11896	Depth drives the distribution of microbial ecological functions in the coastal western Antarctic Peninsula. Frontiers in Microbiology, 0, 14 , .	3.5	1

# Ar	TICLE	IF	CITATIONS
11897 Gu Co	t microbial communities of hybridising pygmy angelfishes reflect species boundaries. mmunications Biology, 2023, 6, .	4.4	0
11898 Do	e Effect of Oral Iron Supplementation on Gut Microbial Composition: a Secondary Analysis of a uble-Blind, Randomized Controlled Trial among Cambodian Women of Reproductive Age. crobiology Spectrum, 2023, 11, .	3.0	1
11900 Ge of	nder-specific changes of the gut microbiome correlate with tumor development in murine models pancreatic cancer. IScience, 2023, 26, 106841.	4.1	1
	sterboard sheet applied in vertical-flow constructed wetlands: Nutrients removal, microbial ersity, and mechanisms. Journal of Water Process Engineering, 2023, 53, 103811.	5.6	O
11902 Ch	emolithotrophic microbiome of buried soil layers following volcanic eruptions: A potential huge bon sink. Soil Biology and Biochemistry, 2023, 183, 109055.	8.8	1
11903 Infl mid	uence of feedstock source on the development of polyhydroxyalkanoates-producing mixed crobial cultures in continuously stirred tank reactors. New Biotechnology, 2023, 76, 90-97.	4.4	2
	versity and composition of gut microbiota in healthy individuals and patients at different stages of patitis B virus-related liver disease. Gut Pathogens, 2023, 15, .	3.4	3
11906 Cat	ffeine Consumption Helps Honey Bees Fight a Bacterial Pathogen. Microbiology Spectrum, 2023, 11, .	3.0	O
11907 Rhi in l	zosphere microbial community composition shifts diurnally and in response to natural variation nost clock phenotype. MSystems, 2023, 8, .	3.8	0
11909 The	e making of the oral microbiome in Agta hunter–gatherers. Evolutionary Human Sciences, 2023, 5, .	1.7	2
11910 Ecc Imp	oinformatic Analysis of the Gut Ecological Diversity of Wild and Captive Long-Tailed Gorals Using proved ITS2 Region Primers to Support Their Conservation. Microorganisms, 2023, 11, 1368.	3.6	0
	ney-based diet containing medium chain triglycerides modulates the gut microbiota and protects the estinal mucosa from chemotherapy while maintaining therapy efficacy. Cell Death and Disease, 2023,	6.3	4
	erations in the Fungal Microbiome in Ulcerative Colitis. Inflammatory Bowel Diseases, 2023, 29, 13-1621.	1.9	5
	nning alters the network patterns and keystone taxa of rhizosphere soil microbial communities in inese fir plantation. Applied Soil Ecology, 2023, 189, 104956.	4.3	3
11914 in (tential long consequences from internal and external ecology: loss of gut microbiota antifragility children from an industrialized population compared with an indigenous rural lifestyle. Journal of velopmental Origins of Health and Disease, 0, , 1-12.	1.4	0
11915 Enr ter	richment of rare methanogenic Archaea shows their important ecological role in natural high-CO2 restrial subsurface environments. Frontiers in Microbiology, $0,14,.$	3.5	1
	rtheast Pacific eelgrass fish communities characterized by environmental <scp>DNA</scp> oresent local diversity and show habitat specificity. Environmental DNA, 0, , .	5.8	0
	stagenomic analysis and antibacterial activity of kefir microorganisms. Journal of Food Science, 23, 88, 2933-2949.	3.1	5

# ARTICLE		IF	Citations
	on of Phenotypes in Microbiome Networks for Designing Synthetic Communities: a Study of mes in the Grafted Tomato System. Applied and Environmental Microbiology, 2023, 89, .	3.1	2
11920 Capturir the critic	g speciesâ€wide diversity of the gut microbiota and its relationship with genomic variation in ally endangered kÄkÄpÅ• Molecular Ecology, 2023, 32, 4224-4241.	3.9	1
	uencing reveals high arbuscular mycorrhizal fungi diversity in the rhizosphere soil of fricana trees in fragmented Afromontane forests. Annals of Microbiology, 2023, 73, .	2.6	0
	en Species to Alien Communities: Host- and Habitat-Associated Microbiomes in an Alien an. Microbial Ecology, 2023, 86, 2373-2385.	2.8	1
11923 Helicoba in the ab	acter spp. are prevalent in wild mice and protect from lethal Citrobacter rodentium infection sence of adaptive immunity. Cell Reports, 2023, 42, 112549.	6.4	0
11924 The dist Scientifi	ibution and diversity of eukaryotic phytoplankton in the Icelandic marine environment. c Reports, 2023, 13, .	3.3	1
	son of two methods for bioaerosol sampling and characterization in a low-biomass chamber nent. Building and Environment, 2023, 240, 110458.	6.9	0
	obiome associated with low anterior resection syndrome after rectal cancer surgery. c Reports, 2023, 13, .	3.3	O
	nic Structure of Planktonic Protist Communities in Saline and Hypersaline Continental Revealed by Metabarcoding. Water (Switzerland), 2023, 15, 2008.	2.7	1
	of diet shift on the gut microbiota of the critically endangered Siberian Crane. Avian n, 2023, 14, 100108.	1.2	1
11930 Sexual t Journal o	ransmission may drive pair similarity of the cloacal microbiome in a polyandrous species. of Animal Ecology, 0, , .	2.8	1
	l and/or post-weaning supplementation with Bacillus altitudinis spores modulates the l composition of colostrum, digesta and faeces in pigs. Scientific Reports, 2023, 13, .	3.3	3
Diversity 11932 Ecosyste	of Arbuscular Mycorrhizal Fungi Associated with Six Rice Cultivars in Italian Agricultural om Managed with Alternate Wetting and Drying. Rice Science, 2023, 30, 348-358.	3.9	0
11933 Genome quantita	-wide mapping of gene-microbe interactions in the murine lung microbiota based on tive microbial profiling. Animal Microbiome, 2023, 5, .	3.8	1
11934 Old-grov other ro	oth <i>Acer macrophyllum</i> trees host a unique suite of arbuscular mycorrhizal fungi and ot-associated fungal taxa in their canopy soil environment. Mycologia, 2023, 115, 470-483.	1.9	1
	m as galactomannan source induces dysbiosis and reduces performance in broiler chickens ary \hat{l}^2 -mannanase restores the gut homeostasis. Poultry Science, 2023, 102, 102810.	3.4	4
	one attenuates colitis associated colorectal tumorigenesis through Ras/Raf/ERK pathway sion and SCFA-producing bacteria promotion. Biomedicine and Pharmacotherapy, 2023, 164,	5.6	3
	and Cotton Spermosphere Soil Microbiome Shows Dominance of Soilborne Copiotrophs. ology Spectrum, 0, , .	3.0	O

# A	RTICLE	IF	Citations
	White kidney bean extract as a nutraceutical: effects on gut microbiota, alpha-amylase inhibition, and ser experiences. Gut Microbiome, 2023, 4, .	3.2	1
	Oral Microbiome Traits of Type 1 Diabetes and Phenylketonuria Patients in Latvia. Microorganisms, 023, 11, 1471.	3.6	O
11940 e	PR43 stimulation on $TCR\hat{1}\pm\hat{1}^2+$ intraepithelial colonic lymphocytes inhibits the recruitment of ncephalitogenic T-cells into the central nervous system and attenuates the development of utoimmunity. Journal of Neuroinflammation, 2023, 20, .	7.2	2
	he core mangrove microbiome reveals shared taxa potentially involved in nutrient cycling and romoting host survival. Environmental Microbiomes, 2023, 18, .	5.0	2
11942 R	tock pools as a source of environmental DNA for the detection of the threatened Pilbara olive python Liasis olivaceus barroni). Frontiers in Environmental Science, 0, 11 , .	3.3	0
11943 E	Deconstructed Plastic Substrate Preferences of Microbial Populations from the Natural nvironment. Microbiology Spectrum, 2023, 11, .	3.0	2
	dicrobiota members from body sites of dairy cows are largely shared within individual hosts hroughout lactation but sharing is limited in the herd. Animal Microbiome, 2023, 5, .	3.8	1
11945 C	he effect of low-abundance OTU filtering methods on the reliability and variability of microbial omposition assessed by 16S rRNA amplicon sequencing. Frontiers in Cellular and Infection dicrobiology, 0, 13, .	3.9	5
11946 N	lant community stability is associated with a decoupling of prokaryote and fungal soil networks. lature Communications, 2023, 14, .	12.8	4
11947 C	Growth Increase in the Herbaceous Plant Centella asiatica by the Plant Growth-Promoting hizobacteria Priestia megaterium HyangYak-01. Plants, 2023, 12, 2398.	3.5	1
11948 C	Composition of the colon microbiota in the individuals with inflammatory bowel disease and colon ancer. Folia Microbiologica, 0, , .	2.3	2
11949 C	Comparing the impact of mixed-culture microbial communities and fecal transplant on the intestinal nicrobiota and metabolome of weaned piglets. FEMS Microbiology Ecology, 2023, 99, .	2.7	1
	xploring associations between the gut microbiota and full-scale intelligence in preschool children. Jeuroscience Letters, 2023, 810, 137357.	2.1	2
11952 N	Microbial Communities in Gynecological Cancers and Their Association with Tumor Somatic Pariation. Cancers, 2023, 15, 3316.	3.7	O
	Characterization of the Human Blood Virome in Iranian Multiple Transfused Patients. Viruses, 2023, 15, 425.	3.3	2
11954 V s	Whole-body microbiota of newborn calves and their response to prenatal vitamin and mineral upplementation. Frontiers in Microbiology, $0,14,.$	3.5	5
11956 T	he microbiota of pregnant women with SARS-CoV-2 and their infants. Microbiome, 2023, $11,\ldots$	11.1	1
11957 L b	inking the shifts in the metabolically active microbiota in a UASB and hybrid anaerobic-aerobic ioreactor for swine wastewater treatment. Journal of Environmental Management, 2023, 344, 118435.	7.8	1

#	Article	IF	CITATIONS
11958	An initial genomic blueprint of the healthy human oesophageal microbiome. Access Microbiology, 2023, 5, .	0.5	О
11959	Unrecognized diversity and distribution of soil algae from Maritime Antarctica (Fildes Peninsula, King) Tj ETQq1 1	0,7,84314	rgBT /Overlo
11960	Positive interactions between mycorrhizal fungi and bacteria are widespread and benefit plant growth. Current Biology, 2023, 33, 2878-2887.e4.	3.9	5
11961	Soil Microbiomes Associated with a Novel Perennial Grain Cultivated under Temperate Agricultural Conditions. Microbiology Resource Announcements, 2023, 12, .	0.6	0
11962	BONCAT-FACS-Seq reveals the active fraction of a biocrust community undergoing a wet-up event. Frontiers in Microbiology, 0, 14, .	3.5	0
11964	Shotgun Metagenomic Sequencing Revealed the Prebiotic Potential of a Fruit Juice Drink with Fermentable Fibres in Healthy Humans. Foods, 2023, 12, 2480.	4.3	0
11966	Indigenously produced biochar retains fertility in sandy soil through unique microbial diversity sustenance: a step toward the circular economy. Frontiers in Microbiology, 0, 14, .	3.5	0
11967	Red Ginseng Dietary Fiber Shows Prebiotic Potential by Modulating Gut Microbiota in Dogs. Microbiology Spectrum, 2023, 11, .	3.0	2
11968	Characterization of fungal communities associated with the lenticel-like damage of avocado cv. Hass in two geographical locations in Colombia. Phytobiomes Journal, 0, , .	2.7	1
11969	Diversity of plant DNA in stool is linked to dietary quality, age, and household income. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	4
11970	Leaf Endophyte Community Composition and Network Structures Differ Between Tolerant and Susceptible English Boxwood. Phytobiomes Journal, 2023, 7, 160-171.	2.7	2
11971	Intensive vegetable production under plastic mulch: A field study on soil plastic and pesticide residues and their effects on the soil microbiome. Science of the Total Environment, 2023, 900, 165179.	8.0	2
11972	Microbiota-produced indole metabolites disrupt mitochondrial function and inhibit Cryptosporidium parvum growth. Cell Reports, 2023, 42, 112680.	6.4	7
11974	Comparison of the gill and gut microbiomes of common carp (Cyprinus carpio) and zebrafish (Danio) Tj ${\sf ETQq1\ 1}$	0.784314	rgBT /Ove <mark>rlo</mark>
11976	Effect of feed concentration and residence time on anaerobic fermentation in CSTR and SBR to produce short-chain organic acids. Journal of Environmental Chemical Engineering, 2023, 11, 110461.	6.7	0
11977	Wood fibers are a crucial microhabitat for cellulose- and xylan- degrading bacteria in the hindgut of the wood-feeding beetle Odontotaenius disjunctus. Frontiers in Microbiology, 0, 14, .	3.5	6
11978	The Community Structure of eDNA in the Los Angeles River Reveals an Altered Nitrogen Cycle at Impervious Sites. Diversity, 2023, 15, 823.	1.7	0
11979	Metabolic response of intestinal microbiota to guar gum consumption. Frontiers in Nutrition, 0, 10, .	3.7	3

#	Article	IF	CITATIONS
11981	Continued Organic Fertigation after Basal Manure Application Does Not Impact Soil Fungal Communities, Tomato Yield or Soil Fertility. Microorganisms, 2023, 11, 1715.	3.6	0
11982	Exploring the feasibility of biological hydrogen production using seed sludge pretreated with agro-industrial wastes. Renewable Energy, 2023, 215, 118934.	8.9	3
11983	Influence of redox condition and inoculum on micropollutant biodegradation by soil and activated sludge communities. Science of the Total Environment, 2023, 897, 165233.	8.0	2
11984	Seasonal Dynamics of Marine Bacterial Communities in Aquaculture Farms: The case of the Northern Ionian Coastal Ecosystem (Mediterranean Sea). Journal of Marine Science and Engineering, 2023, 11, 1332.	2.6	0
11985	Identification of Antibiotic Resistance Gene Hosts in Treatment Wetlands Using a Single-Cell Based High-Throughput Approach. Water (Switzerland), 2023, 15, 2432.	2.7	1
11986	Connecting gut microbiome changes with fish health conditions in juvenile Atlantic cod (Gadus) Tj ETQq $1\ 1\ 0.784$	1314 rgBT 7.5	/gverlock 1
11987	Correlating the succession of microbial communities from Nigerian soils to petroleum biodegradation. World Journal of Microbiology and Biotechnology, 2023, 39, .	3.6	1
11988	Exogenous microorganisms promote moss biocrust restoration and shape microbiomes in a sandy desert. Plant and Soil, 0, , .	3.7	0
11989	Influence of dietary oils rich in omega-6 or omega-3 fatty acids on rumen microbiome of dairy cows. Translational Animal Science, 2023, 7, .	1.1	0
11991	Microbiomic and Metabolomic Analyses Unveil the Protective Effect of Saffron in a Mouse Colitis Model. Current Issues in Molecular Biology, 2023, 45, 5558-5574.	2.4	1
11992	Spontaneous body wall contractions stabilize the fluid microenvironment that shapes host–microbe associations. ELife, 0, 12, .	6.0	1
11993	Bacterial populations in different parts of domestic drinking water systems are distinct and adapted to the given ambient temperatures. Frontiers in Water, 0, 5, .	2.3	4
11994	Inhibition of nitrous oxide reduction in forest soil microcosms by different forms of methanobactin. Environmental Microbiology, 2023, 25, 2338-2350.	3.8	0
11995	Interactive Effects of Ceftriaxone and Chitosan Immobilization on the Production of Arachidonic Acid by and the Microbiome of the Chlorophyte Lobosphaera sp. IPPAS C-2047. International Journal of Molecular Sciences, 2023, 24, 10988.	4.1	O
11996	Ecoevolutionary processes structure milk microbiomes across the mammalian tree of life. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	3
11998	Rhizobial nitrogen fixation efficiency shapes endosphere bacterial communities and Medicago truncatula host growth. Microbiome, 2023, 11 , .	11.1	6
11999	Shifting biogeochemical conditions and capping media impact composition and behavior of PAH-enriched microbial communities. Journal of Soils and Sediments, 2023, 23, 3262-3274.	3.0	1
12000	Gut barrier-microbiota imbalances in early life lead to higher sensitivity to inflammation in a murine model of C-section delivery. Microbiome, 2023, 11 , .	11.1	4

#	ARTICLE	IF	Citations
12001	Microbial community structural and functional differentiation in capped thickened oil sands tailings planted with native boreal species. Frontiers in Microbiology, 0, 14, .	3.5	1
12002	<i>In vitro</i> adhesion, pilus expression, and <i>in vivo</i> amelioration of antibiotic-induced microbiota disturbance by <i>Bifidobacterium</i> spp. strains from fecal donors. Gut Microbes, 2023, 15, .	9.8	3
12003	Validation of a batch cultivation protocol for fecal microbiota of Kenyan infants. BMC Microbiology, 2023, 23, .	3.3	1
12004	Microbiota in Umbilical Dirt and Its Relationship with Odor. Microbes and Environments, 2023, 38, n/a.	1.6	0
12005	Exploring Gut Microbial Dynamics and Symbiotic Interaction in Blattella germanica Using Rifampicin. Biology, 2023, 12, 955.	2.8	2
12007	Evaluating nanopore sequencing for microbial community characterization in catfish pond water. Journal of the World Aquaculture Society, 2024, 55, 289-301.	2.4	0
12008	Blood orange juice intake changes specific bacteria of gut microbiota associated with cardiometabolic biomarkers. Frontiers in Microbiology, 0, 14, .	3. 5	2
12009	Inter-row cropping and rootstock genotype selection in a UK cider orchard to combat apple replant disease. Phytopathology Research, 2023, 5, .	2.4	1
12010	Microbial Communities Associated with Alternative Fuels in Model Seawater-Compensated Fuel Ballast Tanks. Corrosion and Materials Degradation, 2023, 4, 382-397.	2.4	2
12012	Effect of operational parameters on the performance of an anaerobic sequencing batch reactor (AnSBR) treating protein-rich wastewater. Environmental Science and Ecotechnology, 2024, 17, 100296.	13.5	0
12013	Harnessing diversity and antagonism within the pig skin microbiota to identify novel mediators of colonization resistance to methicillin-resistant <i>Staphylococcus aureus</i> . MSphere, 2023, 8, .	2.9	5
12014	Development of the intestinal microbiome in cystic fibrosis in early life. MSphere, 2023, 8, .	2.9	6
12015	Age-related effects on the modulation of gut microbiota by pectins and their derivatives: an in vitro study. Frontiers in Microbiology, 0, 14 , .	3.5	2
12016	Effect of ozone nanobubbles on the microbial ecology of pond water and safety for jade perch (Scortum barcoo). Aquaculture, 2023, 576, 739866.	3.5	0
12017	Gypsum endolithic phototrophs under moderate climate (Southern Sicily): their diversity and pigment composition. Frontiers in Microbiology, 0, 14, .	3 . 5	1
12020	Important role of endogenous microbial symbionts of fish gills in the challenging but highly biodiverse Amazonian blackwaters. Nature Communications, 2023, 14, .	12.8	2
12021	Innovative approaches to accurately assess the effectiveness of biocide-based treatments to fight biodeterioration of Cultural Heritage monuments. Science of the Total Environment, 2023, 897, 165318.	8.0	2
12022	Characterizing the blood microbiota of omnivorous and frugivorous bats (Chiroptera:) Tj ETQq1 1 0.784314 rgBT	/Overlock 2.0	10 Tf 50 62

# ARTICLE	IF	Citations
Examining the gut microbiota from several human-biting tick species in Northwestern Spain. Journal of Medical Entomology, 0 , , .	1.8	0
Intratumoral Microbiota Changes with Tumor Stage and Influences the Immune Signature of Oral Squamous Cell Carcinoma. Microbiology Spectrum, 0, , .	3.0	2
Digging deep: lessons learned from meiofaunal responses to a disturbance experiment in the Clarion-Clipperton Zone. Marine Biodiversity, 2023, 53, .	1.0	0
Combining frass and fatty acid co-products derived from Black soldier fly larvae farming shows potential as a slow release fertiliser. Science of the Total Environment, 2023, 899, 165371.	8.0	1
Fecal microbiota transplantation plus anti-PD-1 immunotherapy in advanced melanoma: a phase I trial. Nature Medicine, 2023, 29, 2121-2132.	30.7	39
New insights into the structure, microbial diversity and ecology of yellow biofilms in a Paleolithic rock art cave (Pindal Cave, Asturias, Spain). Science of the Total Environment, 2023, 897, 165218.	8.0	6
Effects of FODMAPs and Gluten on Gut Microbiota and Their Association with the Metabolome in Irritable Bowel Syndrome: A Double-Blind, Randomized, Cross-Over Intervention Study. Nutrients, 2023, 15, 3045.	4.1	2
12030 Extreme summers impact cropland and grassland soil microbiomes. ISME Journal, 2023, 17, 1589-1600.	9.8	10
12032 Long-Term Persistence of Three Microbial Wildfire Biomarkers in Forest Soils. Forests, 2023, 14, 1383.	2.1	1
Seasonality of the bacterial and archaeal community composition of the Northern Barents Sea. Frontiers in Microbiology, 0, 14 , .	3.5	3
Multiscale Spatial Variability and Stability in the Structure and Diversity of Bacterial Communities Associated with the Kelp Eisenia cokeri in Peru. Microbial Ecology, 2023, 86, 2574-2582.	2.8	1
Clonality, local population structure and gametophyte sex ratios in cryptic species of the <a>i>Sphagnum magellanicum complex. Annals of Botany, 2023, 132, 77-94.	2.9	2
Serotonin Transporter (SERT) Expression Modulates the Composition of the Western-Diet-Induced Microbiota in Aged Female Mice. Nutrients, 2023, 15, 3048.	4.1	0
Type of intrinsic resistant starch type 3 determines in vitro fermentation by pooled adult faecal inoculum. Carbohydrate Polymers, 2023, 319, 121187.	10.2	4
Differential contribution of nitrifying prokaryotes to groundwater nitrification. ISME Journal, 2023, 17, 1601-1611.	9.8	1
Impact of HIV on the Oral Microbiome of Children Living in Sub-Saharan Africa, Determined by Using an	3.0	2
4) Akkermansia muciniphila 4) reduces susceptibility to <i>Listeria monocytogenes 6) infection in mice fed a high-fat diet. Gut Microbes, 2023, 15, .</i>	9.8	3
Gut Colonization by ESBL-Producing Escherichia coli in Dogs Is Associated with a Distinct Microbiome and Resistome Composition. Microbiology Spectrum, 2023, 11, .	3.0	3

# ARTICLE	IF	CITATIONS
Temporal Microbial Dynamics in Feces Discriminate by Nutrition, Fecal Color, Consistency and Sample Type in Suckling and Newly Weaned Piglets. Animals, 2023, 13, 2251.	2.3	0
12046 Expanding Antarctic biogeography: microbial ecology of Antarctic island soils. Ecography, 2023, 2023, .	4.5	1
Winery by-products as a feed source with functional properties: dose–response effect of grape pomace, grape seed meal, and grape seed extract on rumen microbial community and their fermentation activity in RUSITEC. Journal of Animal Science and Biotechnology, 2023, 14, .	5 . 3	2
Quantitative differences in synthetic gut microbial inoculums do not affect the final stabilized <i>in vitro</i> community compositions. MSystems, 0, , .	3.8	O
Bacterial Diversity on Historical Audio-Visual Materials and in the Atmosphere of Czech Depositories. Microbiology Spectrum, 0, , .	3.0	1
Comparison of swab DNA extraction methods for examining sea star dermal microbiomes. Aquatic Microbial Ecology, 0 , , .	1.8	O
A decade of microbial community dynamics on sinking particles during high carbon export events in the eastern Fram Strait. Frontiers in Marine Science, 0, 10, .	2.5	1
Post-fire wood mulch negatively affects the moss biocrust cover and its positive effects on microbial diversity in a semi-arid Mediterranean forest. Applied Soil Ecology, 2023, 191, 105026.	4.3	2
Synergistic adverse effects of microfibers and freshwater acidification on host-microbiota interactions in the water flea Daphnia magna. Journal of Hazardous Materials, 2023, 459, 132026.	12.4	3
DNA metabarcoding reveals rangewide variation in aquatic diet of a riparian avian insectivore, the Prothonotary Warbler. Auk, 0, , .	1.4	1
Antibiotic use during pregnancy is linked to offspring gut microbial dysbiosis, barrier disruption, and altered immunity along the gut–lung axis. European Journal of Immunology, 2023, 53, .	2.9	1
Rhizosphere bacteria show a stronger response to antibiotic-based biopesticide than to conventional pesticides. Journal of Hazardous Materials, 2023, 458, 132035.	12.4	1
Analyzing microbial communities and their biodegradation of multiple pharmaceuticals in membrane bioreactors. Applied Microbiology and Biotechnology, 2023, 107, 5545-5554.	3.6	3
Leaf side determines the relative importance of dispersal versus host filtering in the phyllosphere microbiome. MBio, 0, , .	4.1	2
12059 Integrating seed microbiome knowledge into restoration and ex situ conservation of native Australian plants. Australian Journal of Botany, 2023, 71, 379-394.	0.6	2
168 microbiome analysis of microbial communities in distribution centers handling fresh produce. Frontiers in Microbiology, 0, 14, .	3.5	O
Targeted metagenomics using bait-capture to detect antibiotic resistance genes in retail meat and seafood. Frontiers in Microbiology, 0, 14, .	3.5	0
Oral and anal microbiome from HIV-exposed individuals: role of host-associated factors in taxa composition and metabolic pathways. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	1

# ARTICLE	IF	Citations
Short-Term Dietary Intervention with Whole Oats Protects from Antibiotic-Induced Dysbiosis. Microbiology Spectrum, 0, , .	3.0	1
Abrupt perturbation and delayed recovery of the vaginal ecosystem following childbirth. Nature Communications, 2023, 14 , .	12.8	4
12068 Contribution of farms to the microbiota in the swine value chain. Frontiers in Systems Biology, 0, 3, .	0.7	0
Bioaugmentation has temporary effect on anaerobic pesticide biodegradation in simulated groundwater systems. Biodegradation, 0, , .	3.0	0
12070 Association of mycoheterotrophic Gentianaceae with specific Glomus lineages. Mycorrhiza, 0, , .	2.8	0
Bacterial endophytes of sugar maple leaves vary more idiosyncratically than epiphytes across a large geographic area. FEMS Microbiology Ecology, 0, , .	2.7	1
Examining the microbial composition of natural springs in Bhaderwah, Jammu and Kashmir, India. Environmental Monitoring and Assessment, 2023, 195, .	2.7	2
Antibiotic induced restructuring of the gut microbiota does not affect oral uptake and accumulation of perfluorooctane sulfonic acid (PFOS) in rats. Environmental Pollution, 2023, 334, 122179.	7.5	1
Metagenomic Analysis to Uncover the Subgingival and Atherosclerotic Plaque Microbiota in Patients with Coronary Artery Disease. Indian Journal of Microbiology, 0, , .	2.7	0
Glyphosate affects larval gut microbiota and metamorphosis of honey bees with differences between rearing procedures. Environmental Pollution, 2023, 334, 122200.	7. 5	2
Mining-impacted rice paddies select for Archaeal methylators and reveal a putative (Archaeal) regulator of mercury methylation. ISME Communications, 2023, 3, .	4.2	0
Organic and conventional farming systems shape soil bacterial community composition in tropical arable farming. Applied Soil Ecology, 2023, 191, 105054.	4.3	0
Biological soil crusts on agricultural soils of mesic regions promote microbial cross-kingdom co-occurrences and nutrient retention. Frontiers in Microbiology, 0, 14, .	3.5	0
Seasonality and bacterial community assembly processes dominate prairie ecosystem service disruption during invasion. Soil Biology and Biochemistry, 2023, 184, 109120.	8.8	1
Evaluation of the Effect of Incorporating Olive Mill Wastewater on Nutrients, Quality, and Bacterial Flora in Fermented Total Mixed Ration. Fermentation, 2023, 9, 665.	3.0	1
Metagenomic comparisons reveal a highly diverse and unique viral community in a seasonally fluctuating hypersaline microbial mat. Microbial Genomics, 2023, 9, .	2.0	2
Circulating TÂcell profiles associate with enterotype signatures underlying hematological malignancy relapses. Cell Host and Microbe, 2023, 31, 1386-1403.e6.	11.0	4
Soil bacteria and fungi communities are shaped by elevation influences in Colombian forest and p \tilde{A}_i ramo natural ecosystems. International Microbiology, 0, , .	2.4	0

# ARTICLE	IF	Citations
$2\hat{a}\in^2$ -fucosyllactose alone or combined with resistant starch increases circulating short-chain fatty acids in lean men and men with prediabetes and obesity. Frontiers in Nutrition, 0, 10, .	3.7	O
12091 Presence of an ultra-small microbiome in fermented cabbages. PeerJ, 0, 11, e15680.	2.0	0
Maternal Diet May Modulate Breast Milk Microbiota—A Case Study in a Group of Colombian Women. Microorganisms, 2023, 11, 1812.	3.6	1
Changes in the Microbial Composition of the Rhizosphere of Hop Plants Affected by Verticillium Wilt Caused by Verticillium nonalfalfae. Microorganisms, 2023, 11, 1819.	3.6	2
Heterotrophy, microbiome, and location effects on restoration efficacy of the threatened coral Acropora palmata. Communications Earth & Environment, 2023, 4, .	6.8	0
Spatial and temporal dynamics of coastal benthic microbial communities along a salinity gradient. Aquatic Microbial Ecology, 0 , , .	1.8	0
Comparison of the Faecal Microbiota Composition Following a Dairy By-Product Supplemented Diet in Nero Siciliano and Large White × Landrace Pig Breeds. Animals, 2023, 13, 2323.	2.3	1
Effects of rearing mode on gastro-intestinal microbiota and development, immunocompetence, sanitary status and growth performance of lambs from birth to two months of age. Animal Microbiome, 2023, 5, .	3.8	1
Variety of Fruit and Vegetables and Alcohol Intake are Associated with Gut Microbial Species and Gene Abundance in Colorectal Cancer Survivors. American Journal of Clinical Nutrition, 2023, 118, 518-529.	4.7	1
Functional response of microbial communities in lab-controlled oil-contaminated marine sediment. Molecular Omics, 0, , .	2.8	1
Toxicity of cadmium on dynamic human gut microbiome cultures and the protective effect of cadmium-tolerant bacteria autochthonous to the gut. Chemosphere, 2023, 338, 139581.	8.2	1
Microbiome convergence and deterministic community assembly along successional biocrust gradients on potash salt heaps. FEMS Microbiology Ecology, 0, , .	2.7	0
Multiomics characterization of the of the zoo-housed gorilla gut microbiome reveals bacterial community compositions shifts, fungal cellulose-degrading, and archaeal methanogenic activity. Gut Microbiome, 0, , 1-25.	3.2	0
Uncovering the dominant role of root metabolism in shaping rhizosphere metabolome under drought in tropical rainforest plants. Science of the Total Environment, 2023, 899, 165689.	8.0	2
Comparing Sediment Microbial Communities of Arctic Beaver Ponds to Tundra Lakes and Streams. Journal of Geophysical Research G: Biogeosciences, 2023, 128, .	3.0	0
Comparison of Gut Microbial Community between Bt-Resistant and Susceptible Strains of Ostrinia furnacalis. Agronomy, 2023, 13, 1923.	3.0	1
RESCUE: a validated Nanopore pipeline to classify bacteria through long-read, 16S-ITS-23S rRNA sequencing. Frontiers in Microbiology, 0, 14, .	3.5	3
Characterizing carotenoids in cyanobacterial cultures – Opportunities and implications for paleolimnological studies. Harmful Algae, 2023, 127, 102481.	4.8	0

#	ARTICLE	IF	CITATIONS
12113	Transplantation of gut microbiota from old mice into young healthy mice reduces lean mass but not bone mass. Gut Microbes, 2023 , 15 , .	9.8	0
12114	Spatial and Sexual Divergence of Gut Bacterial Communities in Field Cricket Teleogryllus occipitalis (Orthoptera: Gryllidae). Microbial Ecology, 2023, 86, 2627-2641.	2.8	O
12115	Within-Host Rhinovirus Evolution in Upper and Lower Respiratory Tract Highlights Capsid Variability and Mutation-Independent Compartmentalization. Journal of Infectious Diseases, 2024, 229, 403-412.	4.0	0
12116	Baseline Gut Microbiome Signatures Correlate with Immunogenicity of SARS-CoV-2 mRNA Vaccines. International Journal of Molecular Sciences, 2023, 24, 11703.	4.1	4
12117	Reciprocal influence of soil, phyllosphere, and aphid microbiomes. Environmental Microbiomes, 2023, 18, .	5.0	3
12118	The composition of the maternal breastmilk microbiota influences the microbiota network structure during early infancy. Journal of Microbiology, Immunology and Infection, 2023, 56, 1084-1097.	3.1	O
12119	Genomic signatures suggesting adaptation to ocean acidification in a coral holobiont from volcanic CO2 seeps. Communications Biology, 2023, 6, .	4.4	2
12120	Diversity and potential plant growth promoting capacity of seed endophytic bacteria of the holoparasite Cistanche phelypaea (Orobanchaceae). Scientific Reports, 2023, 13, .	3.3	1
12121	Identifying macroplastic pathobiomes and antibiotic resistance in a subtropical fish farm. Marine Pollution Bulletin, 2023, 194, 115267.	5.0	2
12124	Interannual dynamics of <i>Tuber melanosporum</i> and fungal communities in productive black truffle orchards amended with truffle nests. FEMS Microbiology Ecology, 2023, 99, .	2.7	2
12125	TRiCit: A High-Throughput Approach to Detect Trichomonas vaginalis from ITS1 Amplicon Sequencing. International Journal of Molecular Sciences, 2023, 24, 11839.	4.1	0
12126	Haplotype-level metabarcoding of freshwater macroinvertebrate species: A prospective tool for population genetic analysis. PLoS ONE, 2023, 18, e0289056.	2.5	O
12127	Variations in the Physical Properties and Microbial Community of Dairy Cow Manureâ€"Implications for Testing and Efficacy of Footbathing Products. Animals, 2023, 13, 2386.	2.3	0
12129	Tumor Microenvironment Can Predict Chemotherapy Response of Patients with Triple-Negative Breast Cancer Receiving Neoadjuvant Chemotherapy. Cancer Research and Treatment, 0, , .	3.0	1
12130	Unique microbial landscape in the human oropharynx during different types of acute respiratory tract infections. Microbiome, 2023, 11 , .	11.1	2
12131	Microbial diversity in Antarctic Dry Valley soils across an altitudinal gradient. Frontiers in Microbiology, 0, 14 , .	3.5	3
12132	Shedding light on the total and active core microbiomes in slow sand filters for drinking water production. Water Research, 2023, 243, 120404.	11.3	1
12133	Metagenomic search of viral coinfections in herpes simplex encephalitis patients. Journal of NeuroVirology, 2023, 29, 588-597.	2.1	1

# ARTICLE	IF	CITATIONS
Microbial communities associated with landfarming amendments during bioremediation of crude oil in Niger Delta soils. Applied Soil Ecology, 2023, 191, 105058.	4.3	1
Exploring the Influence of Small-Scale Geographical and Seasonal Variations Over the Microbial Diversity in a Poly-extreme Athalosaline Wetland. Current Microbiology, 2023, 80, .	2.2	2
An Okinawan-Based Nordic Diet Leads to Profound Effects on Gut Microbiota and Plasma Metabolites Linked to Glucose and Lipid Metabolism. Nutrients, 2023, 15, 3273.	4.1	0
A super sandstorm altered the abundance and composition of airborne bacteria in Beijing. Journal of Environmental Sciences, 2023, , .	6.1	0
Microbial Communities in Ferromanganese Sediments from the Northern Basin of Lake Baikal (Russia). Microorganisms, 2023, 11, 1865.	3.6	1
Gut instinct: Sex differences in the gut microbiome are associated with changes in adolescent nociception following maternal separation in rats. Developmental Neurobiology, 2023, 83, 219-233.	3.0	0
Expanding the range of the respiratory infectome in Australian feedlot cattle with and without respiratory disease using metatranscriptomics. Microbiome, 2023, 11, .	11.1	4
Distribution patterns of benthic bacteria and nematode communities in estuarine sediments. Estuarine Coastal and Shelf Science, 2023, 291, 108448.	2.1	0
Opportunistic feeding habits of two African freshwater clupeid fishes: DNA metabarcoding unravels spatial differences in diet and microbiome, and identifies new prey taxa. Hydrobiologia, 2023, 850, 3777-3796.	2.0	1
Bacterial microbiota management in free-living amoebae (Heterolobosea lineage) isolated from water: 12150 The impact of amoebae identity, grazing conditions, and passage number. Science of the Total Environment, 2023, 900, 165816.	8.0	2
PI3K-CCL2-CCR2-MDSCs axis: A potential pathway for tumor Clostridia-promoted CD 8+ T lymphocyte infiltration in bile tract cancers. Neoplasia, 2023, 43, 100920.	5.3	1
Influence of native and exotic plant diet on the gut microbiome of the Gray's Malayan stick insect, Lonchodes brevipes. Frontiers in Microbiology, 0, 14, .	3.5	1
12158 Influence of soil nutrients on the presence and distribution of CPR bacteria in a long-term crop rotation experiment. Frontiers in Microbiology, 0, 14, .	3.5	0
PGPB and/or AM Fungi Consortia Affect Tomato Native Rhizosphere Microbiota. Microorganisms, 2023 11, 1891.	3.6	0
The impact of respiratory infections and probiotic use on the nasal microbiota of frail residents in long-term care homes. ERJ Open Research, 0, , 00212-2023.	2.6	0
Physicochemical characterization and microbiota modulatory potential of brewer's spent grain and arabinoxylan-derived fractions: A valorization study. LWT - Food Science and Technology, 2023, , 11510	 07. ^{5.2}	0
Aerobic methanotrophy increases the net iron reduction in methanogenic lake sediments. Frontiers in Microbiology, 0, 14, .	3.5	1
Alcohol consumption and oral microbiome composition in a sample of healthy young adults. Alcohol and Alcoholism, 0, , .	1.6	0

#	ARTICLE	IF	Citations
12164	Plant secondary metabolite-dependent plant-soil feedbacks can improve crop yield in the field. ELife, 0 , 12 , .	6.0	11
12167	Mycobiome shifts in Ulmus minor stems after infection with beneficial and pathogenic fungi. Phytobiomes Journal, 0, , .	2.7	0
12168	Effects of Administration of Prebiotics Alone or in Combination with Probiotics on In Vitro Fermentation Kinetics, Malodor Compound Emission and Microbial Community Structure in Swine. Fermentation, 2023, 9, 716.	3.0	0
12169	Characterization of the upper respiratory tract microbiota in Chilean asthmatic children reveals compositional, functional, and structural differences. Frontiers in Allergy, 0, 4, .	2.8	0
12170	The landscape of the immunoglobulin repertoire in endemic pemphigus foliaceus. Frontiers in Immunology, 0, 14 , .	4.8	0
12171	Gut microbiota analyses of inflammatory bowel diseases from a representative Saudi population. BMC Gastroenterology, 2023, 23, .	2.0	0
12172	Divergence and convergence of gut microbiomes of wild insect pollinators. MBio, 0, , .	4.1	1
12173	A blend of medium-chain fatty acids, butyrate, organic acids, and a phenolic compound accelerates microbial maturation in newly weaned piglets. PLoS ONE, 2023, 18, e0289214.	2.5	2
12174	Integration of multi-omics data to elucidate keystone unknown taxa within microbialite-forming ecosystems. Frontiers in Microbiology, $0,14,.$	3.5	0
12175	Recently formed Antarctic lakes host less diverse benthic bacterial and diatom communities than their older counterparts. FEMS Microbiology Ecology, 2023, 99, .	2.7	1
12176	Oral and gut microbial biomarkers of susceptibility to respiratory tract infection in adults: A feasibility study. Heliyon, 2023, 9, e18610.	3.2	0
12177	Sodium levels and grazing pressure shape natural communities of the intracellular pathogen Legionella. Microbiome, 2023, 11, .	11.1	1
12178	Intranasal administration of Lactobacillus johnsonii attenuates hyperoxia-induced lung injury by modulating gut microbiota in neonatal mice. Journal of Biomedical Science, 2023, 30, .	7.0	5
12179	Fiber consumption stimulates the activity of microbial bile salt hydrolases. Journal of Functional Foods, 2023, 107, 105707.	3.4	0
12180	The Bacterial Microbiota of Artisanal Cheeses from the Northern Caucasus. Fermentation, 2023, 9, 719.	3.0	3
12181	Microniches harbor distinct bacterial communities at the soil-plant-earthworm interface. European Journal of Soil Biology, 2023, 118, 103531.	3.2	0
12182	Gut microbiome resilience of green-lipped mussels, Perna canaliculus, to starvation. International Microbiology, 0, , .	2.4	3
12183	Application of Compositional Data Analysis to Study the Relationship between Bacterial Diversity in Human Faeces and Sex, Age, and Weight. Biomedicines, 2023, 11, 2134.	3.2	0

# AI	RTICLE	IF	CITATIONS
12184 m	abitat-specific environmental factors regulate the spatial variability of biological soil crust icrobial communities on the Qinghai-Tibet Plateau. Science of the Total Environment, 2023, 901, 65937.	8.0	4
12185 ha	acterial community trends associated with sea scallop, Placopecten magellanicus, larvae in a atchery system. Aquaculture Reports, 2023, 32, 101693.	1.7	O
12186 co	npact of the fungal pathogen Fusarium oxysporum on the taxonomic and functional diversity of the ommon bean root microbiome. Environmental Microbiomes, 2023, 18, .	5.0	4
	6S rRNA gene primer choice impacts off-target amplification in human gastrointestinal tract biopsies nd microbiome profiling. Scientific Reports, 2023, 13, .	3.3	4
12188 St Fj	tochastic Processes Dominate in the Water Mass–Based Segregation of Diazotrophs in a High Arctic ord (Svalbard). Microbial Ecology, 2023, 86, 2733-2746.	2.8	1
12189 Th	ne intrinsic methane mitigation potential and associated microbes add product value to compost. Vaste Management, 2023, 170, 17-32.	7.4	3
	rought legacy effects on fine-root-associated fungal communities are modulated by root teractions between tree species. Frontiers in Forests and Global Change, 0, 6, .	2.3	1
	nks between regional and depth patterns of microbial communities and enzyme activities in the estern North Atlantic Ocean. Marine Chemistry, 2023, 255, 104299.	2.3	О
	are phylotypes in stone, stool, and urine microbiomes are associated with urinary stone disease. Fontiers in Molecular Biosciences, 0, 10, .	3.5	2
12193 M	licrobial and Metabolite Signatures of Stress Reactivity in Ulcerative Colitis Patients in Clinical emission Predict Clinical Flare Risk. Inflammatory Bowel Diseases, 2024, 30, 336-346.	1.9	1
12195 lm of	npact of Lactobacillus acidophilus—La5 on Composition and Metabolism of the Intestinal Microbiota F Type 2 Diabetics (T2D) and Healthy Individuals Using a Microbiome Model. Fermentation, 2023, 9, 740.	3.0	1
	nteric methane emission of dairy cows supplemented with iodoform in a dose–response study. cientific Reports, 2023, 13, .	3.3	1
	oil chemical and microbial gradients determine accumulation of rootâ€exuded secondary metabolites nd plant–soil feedbacks in the field. , 2023, 2, 173-188.		1
12199 O	ral microbiome and preterm birth. Frontiers in Medicine, 0, 10, .	2.6	О
12202 As	ssessment of prokaryotic communities in Southwestern Atlantic deep-sea sediments reveals revalent methanol-oxidising Methylomirabilales. Scientific Reports, 2023, 13, .	3.3	0
12203 Co	omposition and diversity of bacterial communities associated with honey bee foragers from two ontrasting environments. Bulletin of Entomological Research, 0 , , 1 - 10 .	1.0	О
12204 Ac	ddition of Saccharomyces eubayanus to SCOBY fermentations modulates the chemical and volatile ompound profiles in kombucha. Food Microbiology, 2023, 116, 104357.	4.2	2
12205 D tr	ifferentially abundant bacteria drive the N2-fixation of a widespread moss in the forest-tundra ansition zone. Symbiosis, 0, , .	2.3	О

# ARTICLE	IF	CITATIONS
Salinization and sedimentation drive contrasting assembly mechanisms of planktonic and sedimentâ€bound bacterial communities in agricultural streams. Global Change Biology, 0, , .	9.5	0
Biofloc technology combined with microalgae for improved nitrogen removal at lower C/N ratios using artificial aquaculture wastewater. Aquaculture International, 0, , .	2.2	O
${\it ldentification of robust and generalizable biomarkers for microbiome-based stratification in lifestyle interventions. Microbiome, 2023, 11, .}$	11.1	5
Megapode mound-builders (malleefowl, Leipoa ocellata) enhance soil function through altered bacterial community composition. Applied Soil Ecology, 2023, 192, 105087.	4.3	O
Bacterial community analysis identifies Klebsiella pneumoniae as a native symbiotic bacterium in the newborn Protobothrops mucrosquamatus. BMC Microbiology, 2023, 23, .	e 3.3	2
The impact of protein source and grain inclusion on digestibility, fecal metabolites, and fecal microbiome in adult canines. Journal of Animal Science, 2023, 101, .	0.5	1
The temporal fluctuations and development of faecal microbiota in commercial layer flocks. Animal Nutrition, 2023, 15, 197-209.	5.1	3
Breastfeeding patterns are associated with human milk microbiome composition: The Mother-Infant Microbiomes, Behavior, and Ecology Study (MIMBES). PLoS ONE, 2023, 18, e0287839.	t 2.5	O
12214 <i>Parvimonas micra</i> can translocate from the subgingival sulcus of the human oral cavity to colorectal adenocarcinoma. Molecular Oncology, 0, , .	4.6	0
Activity of root-knot nematodes associated with composition of a nematode-attached microbiome a the surrounding soil microbiota. FEMS Microbiology Ecology, 2023, 99, .	and 2.7	O
Seasonal development of a tidal mixing front drives shifts in community structure and diversity of bacterioplankton. Molecular Ecology, 0, , .	3.9	0
Quantitative Amplicon Sequencing Is Necessary to Identify Differential Taxa and Correlated Taxa Where Population Sizes Differ. Microbial Ecology, 0, , .	2.8	O
Prescribed fire selects for a pyrophilous soil subâ€community in a northern California mixed conifer forest. Environmental Microbiology, 2023, 25, 2498-2515.	3.8	1
Viruses of Freshwater Mussels during Mass Mortality Events in Oregon and Washington, USA. Viruses, 2023, 15, 1719.	3.3	2
lnoculation with Roseovarius increases thermal tolerance of the coral photosymbiont, Breviolum minutum. Frontiers in Ecology and Evolution, 0, 11, .	2.2	5
Grapevine leaf epiphytic fungal and bacterial communities are influenced more by spatial and temporal factors than powdery mildew fungicide spray programs. PhytoFrontiers, 0, , .	oral 1.6	0
A glimpse into the dark – the bacterial and archaeal diversity of tropical anchialine cave sediments Access Microbiology, 2023, 5, .	s. 0.5	0
Metabarcoding approach to identify bacterial community profiling related to nosocomial infection and bacterial trafficking-routes in hospital environments. Journal of Toxicology and Environmental Health - Part A: Current Issues, 0, , 1-13.	2.3	0

#	ARTICLE	IF	CITATIONS
12224	Delayed acquisition of airway commensals in antibiotic $na\tilde{A}$ ve children and its relationship with wheezing in rural Ecuador. Frontiers in Allergy, 0, 4, .	2.8	0
12227	Weighted gene coexpression network analysis and machine learning reveal oncogenome associated microbiome plays an important role in tumor immunity and prognosis in pan-cancer. Journal of Translational Medicine, 2023, 21, .	4.4	1
12228	Biotransformation of Rutin in In Vitro Porcine Ileal and Colonic Fermentation Models. Journal of Agricultural and Food Chemistry, 2023, 71, 12487-12496.	5.2	0
12229	One versus two-stage codigestion of sugarcane vinasse and glycerol: Assessing combinations at mesophilic and (hyper) thermophilic conditions. Science of the Total Environment, 2023, 904, 166294.	8.0	0
12230	Peeling back the layers of coral holobiont multi-omics data. IScience, 2023, 26, 107623.	4.1	0
12231	The rootstock shape microbial diversity and functionality in the rhizosphere of Vitis vinifera L. cultivar Falanghina. Frontiers in Plant Science, 0, 14, .	3.6	2
12232	Changes in the mycobiome structure in response to reduced nitrogen fertilization in two cropping systems of maize. Science of the Total Environment, 2023, 904, 166343.	8.0	1
12234	The Endophytic Microbiome of Wild Grapevines Vitis amurensis Rupr. and Vitis coignetiae Pulliat Growing in the Russian Far East. Plants, 2023, 12, 2952.	3.5	1
12235	Pre- and post-LEEP: analysis of the female urogenital tract microenvironment and its association with sexual dysfunction. Sexual Medicine, 2023, 11 , .	1.6	1
12236	Brief exposure to captivity in a songbird is associated with reduced diversity and altered composition of the gut microbiome. FEMS Microbiology Ecology, 2023, 99, .	2.7	O
12237	Streptomyces cocklensis DSM 42063 and <i>Actinacidiphila bryophytorum</i> DSM 42138 colonize <i>Arabidopsis thaliana </i> and modulate its proteome. PhytoFrontiers, 0, , .	1.6	0
12238	The gut microbiota-induced kynurenic acid recruits GPR35-positive macrophages to promote experimental encephalitis. Cell Reports, 2023, 42, 113005.	6.4	5
12239	Sediment-driven plastisphere community assembly on plastic debris in tropical coastal and marine environments. Environment International, 2023, 179, 108153.	10.0	3
12240	Intravesical <i>Lactobacillus rhamnosus GG</i> Alters Urobiome Composition and Diversity Among People With Neurogenic Lower Urinary Tract Dysfunction. Topics in Spinal Cord Injury Rehabilitation, 2023, 29, 44-57.	1.8	0
12241	The volatilome reveals microcystin concentration, microbial composition, and oxidative stress in a critical Oregon freshwater lake. MSystems, 2023, 8, .	3.8	1
12242	<i>Legionella</i> relative abundance in shower hose biofilms is associated with specific microbiome members. FEMS Microbes, 2023, 4, .	2.1	2
12243	Transcriptomic signature related to poor welfare of sport horses. Comprehensive Psychoneuroendocrinology, 2023, 16, 100201.	1.7	1
12244	Domestication shapes the endophytic microbiome and metabolome of <i>Salicornia europaea</i> Journal of Applied Microbiology, 2023, 134, .	3.1	0

# ARTICLE	IF	CITATIONS
Gill microbiomes accurately predict the geographic origin of bonefish (Albula vulpes) when combin with machine learning models. Environmental Biology of Fishes, 0, , .	ed 1.0	1
Latitudinal variation in the potential activity of Atlantic Ocean bacterioplankton revealed through 16S rRNA and 16S rRNA gene metabarcoding. Frontiers in Marine Science, 0, 10, .	2.5	O
Comparing the transmission of carbapenemase-producing and extended-spectrum beta-lactamase-producing Escherichia coli between broiler chickens. Preventive Veterinary Medicin 2023, 219, 105998.	e, 1.9	0
Comparative assessment of bacterial diversity and composition in arsenic hyperaccumulator, Pteris vittata L. and non-accumulator, Pteris ensiformis Burm. Chemosphere, 2023, 340, 139812.	8.2	1
Genetic Biosignatures of Deep-Subsurface Organisms Preserved in Carbonates Over a 100,000 Yea 12251 Timescale at a Surface-Accessible Mars Analog Site in Southeastern Utah. Astrobiology, 2023, 23, 979-990.	ar 3.0	1
The Alteration of the Gut Microbiome during Ramadan Offers a Novel Perspective on Ramadan Fas A Pilot Study. Microorganisms, 2023, 11, 2106.	ting: 3.6	0
Productivity of Fish and Crop Growth and Characteristics of Bacterial Communities in the FLOCponics System. Fishes, 2023, 8, 422.	1.7	0
Genomic exploration of coral-associated bacteria: identifying probiotic candidates to increase cora bleaching resilience in Galaxea fascicularis. Microbiome, 2023, 11, .	11.1	6
Diversity and assembly of planktonic protist communities in the Jeju Strait, Korea. Frontiers in Mari Science, 0, 10, .	ine 2.5	1
12256 A Study of Sponge Symbionts from Different Light Habitats. Microbial Ecology, 0, , .	2.8	1
Bifidobacterium affects antitumor efficacy of oncolytic adenovirus in a mouse model of melanoma IScience, 2023, 26, 107668.	. 4.1	3
Cattle–compost–soil: The transfer of antibiotic resistance in livestock agriculture. MicrobiologyOpen, 2023, 12, .	3.0	1
Engineering a biofilters microbiome with activated carbon and bioaugmentation to improve stormwater micropollutant removal. Environmental Technology and Innovation, 2023, 32, 103338	6.1	1
The core bacteriobiome of CÃ te dâ \in Mivoire soils across three vegetation zones. Frontiers in Microbiology, 0, 14, .	3.5	1
12262 A study of microbial diversity in a biofertilizer consortium. PLoS ONE, 2023, 18, e0286285.	2.5	1
Gut microbiota and fecal short chain fatty acids differ with adiposity and country of origin: the METS-microbiome study. Nature Communications, 2023, 14 , .	12.8	10
Fiber supplementation protects from antibiotic-induced gut microbiome dysbiosis by modulating g redox potential. Nature Communications, 2023, 14, .	gut 12.8	5
Different trematode parasites in the same snail host: Speciesâ€specific or shared microbiota?. Mole Ecology, 2023, 32, 5414-5428.	ecular 3.9	0

#	ARTICLE	IF	Citations
12267	Soil bacterial community composition is more stable in kiwifruit orchards relative to phyllosphere communities over time. Environmental Microbiomes, 2023, 18, .	5.0	2
12268	Bacterial diversity and network modularity determine alfalfa yield in flood lands. Applied Soil Ecology, 2023, 192, 105101.	4.3	O
12271	Bacillus indicus and Bacillus subtilis as alternative health and colouration promoters to synthetic astaxanthin in cyprinid aquaculture species. Aquaculture, 2024, 578, 740016.	3.5	0
12272	Deterministic Development of Soil Microbial Communities in Disturbed Soils Depends on Microbial Biomass of the Bioinoculum. Microbial Ecology, 0, , .	2.8	0
12273	Recovery of Smelter-Impacted Peat and Sphagnum Moss: a Microbial Perspective. Microbial Ecology, 0, ,	2.8	0
12274	Interactions with alloparents are associated with the diversity of infant skin and fecal bacterial communities in Chicago, United States. American Journal of Human Biology, 0, , .	1.6	1
12275	Occupational exposure to inhalable pathogenic microorganisms in waste sorting. International Journal of Hygiene and Environmental Health, 2023, 253, 114240.	4.3	1
12276	Statistical normalization methods in microbiome data with application to microbiome cancer research. Gut Microbes, 2023, 15, .	9.8	4
12278	Vermicompost Combined with Soil Conditioner Improves the Ecosystem Multifunctionality in Saline-Alkali Land. Water (Switzerland), 2023, 15, 3075.	2.7	1
12279	Neighborhood socioeconomic status is associated with low diversity gut microbiomes and multi-drug resistant microorganism colonization. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	5
12280	The impact of storage buffer and storage conditions on fecal samples for bacteriophage infectivity and metavirome analyses. Microbiome, 2023, 11 , .	11.1	3
12281	Comparative analyses of milk and water kefir: Fermentation temperature, physicochemical properties, sensory qualities, and metagenomic composition. Food Bioscience, 2023, 55, 103079.	4.4	0
12283	Aminoethoxyvinylglycine and low oxygen controlled atmosphere storage shift functional microbiomes of †Gala' apples. Postharvest Biology and Technology, 2023, 206, 112546.	6.0	0
12284	Beneficial microbial consortium improves winter rye performance by modulating bacterial communities in the rhizosphere and enhancing plant nutrient acquisition. Frontiers in Plant Science, $0,14,.$	3.6	1
12285	Sociodemographic Factors and Intestinal Microbiome Development in Preterm, Very Low Birth Weight Infants. American Journal of Perinatology, 0, , .	1.4	0
12286	Drought Shifts Sorghum Root Metabolite and Microbiome Profiles and Enriches for Pipecolic Acid. Phytobiomes Journal, 2023, 7, 449-463.	2.7	2
12287	Coâ€consuming green tea with raloxifene decreases raloxifene systemic exposure in healthy adult participants. Clinical and Translational Science, 2023, 16, 1779-1790.	3.1	1
12288	A perennial living mulch system fosters a more diverse and balanced soil bacterial community. PLoS ONE, 2023, 18, e0290608.	2.5	1

# ARTICLE	IF	CITATIONS
lnitial type and abundance of cyanobacteria determine morphotype development of phototrophic ecosystems. FEMS Microbiology Ecology, 0, , .	2.7	0
Delayed gut microbiota maturation in the first year of life is a hallmark of pediatric allergic disease. Nature Communications, 2023, 14, .	12.8	15
Fine-scale analysis of substrata grazed by parrotfishes (Labridae:Scarini) on the outer-shelf of the Great Barrier Reef, Australia. Marine Biology, 2023, 170, .	1.5	2
Sex hormones, the stool microbiome, and subclinical atherosclerosis in women with and without HIV. Journal of Clinical Endocrinology and Metabolism, 0, , .	3.6	1
Effects of Ramadan intermittent fasting on gut microbiome: is the diet key?. Frontiers in Microbiology, 0, 14, .	3 . 5	1
Assessment of bacterial and viral gut communities in healthy and tumoral colorectal tissue using <scp>RNA</scp> and <scp>DNA</scp> deep sequencing. Cancer Medicine, 2023, 12, 19291-19300.	2.8	1
Targeting oxidation sites on boreal acid sulfate soil macropore surfaces mitigates acid and metal release to recipient water streams. Applied Geochemistry, 2023, 158, 105779.	3.0	1
Gut Microbiota and Cognitive Function Among Women Living with HIV. Journal of Alzheimer's Disease, 2023, , 1-15.	2.6	1
Linking serum vitamin D levels with gut microbiota after 1-year lifestyle intervention with Mediterranean diet in patients with obesity and metabolic syndrome: a nested cross-sectional and prospective study. Gut Microbes, 2023, 15, .	9.8	0
Autonomous eDNA collection using an uncrewed surface vessel over a 4200â€km transect of the eastern Pacific Ocean. Environmental DNA, 2024, 6, .	5.8	3
A comparative methodological approach to studying the diet of a recovering marine predator, the grey seal (Halichoerus grypus). Canadian Journal of Zoology, 0, , .	1.0	0
Longitudinal study across SARS-CoV-2 variants identifies transcriptionally active microbes (TAMs) associated with Delta severity. IScience, 2023, 26, 107779.	4.1	2
A Two Bacteriocinogenic Ligilactobacillus Strain Association Inhibits Growth, Adhesion, and Invasion of Salmonella in a Simulated Chicken Gut Environment. Probiotics and Antimicrobial Proteins, 0, , .	3.9	0
Seasonal fluctuations of hemolymph microbiota and immune parameters in Mytilus galloprovincialis farmed at La Spezia, Italy. Aquaculture, 2024, 578, 740028.	3.5	0
Short-term responses of the soil microbiome and its environment indicate an uncertain future of restored peatland forests. Journal of Environmental Management, 2023, 345, 118879.	7.8	2
Bacterial community responses of the hydrothermal vent crab Xenograpsus testudinatus fed on microplastics. Frontiers in Ecology and Evolution, 0, 11 , .	2.2	0
Inferring potential causative microbial factors of intestinal atrophic disease in the sea cucumber Apostichopus japonicus. Frontiers in Marine Science, $0,10,.$	2.5	0
Precision modulation of dysbiotic adult microbiomes with a human-milk-derived synbiotic reshapes gut microbial composition and metabolites. Cell Host and Microbe, 2023, 31, 1523-1538.e10.	11.0	4

# ARTICLE	IF	CITATIONS
Spatiotemporal diversity and community structure of cyanobacteria and associated bacteria in the large shallow subtropical Lake Okeechobee (Florida, United States). Frontiers in Microbiology, 0, 14, .	3.5	4
Seasonality Is the Main Determinant of Microbial Diversity Associated to Snow/Ice around Concordia Station on the Antarctic Polar Plateau. Biology, 2023, 12, 1193.	2.8	0
Effects of host species on microbiota composition in Phlebotomus and Lutzomyia sand flies. Parasites and Vectors, 2023, 16, .	2.5	1
Detection of fish and mussel <scp>DNA</scp> in lake sediment cores depends on location, species, and molecular method. Environmental DNA, 2023, 5, 1484-1504.	5.8	2
12316 <scp>DNA</scp> metabarcoding of mock communities highlights potential biases when assessing Neotropical fish diversity. Environmental DNA, 2023, 5, 1351-1361.	5.8	3
Molecular transformation and metabolic insights of microbial electrolysis treatment and valorization of post-hydrothermal liquefaction wastewater. Green Chemistry, 0, , .	9.0	0
Bald sea urchin disease shifts the surface microbiome on purple sea urchins in an aquarium. Pathogens and Disease, 2023, 81, .	2.0	1
Bacterial lipopolysaccharide modulates immune response in the colorectal tumor microenvironment. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	2
Methanotrophic potential of Dutch canal wall biofilms is driven by <i>Methylomonadaceae</i> Microbiology Ecology, 2023, 99, .	2.7	0
Antibiotic prophylaxis dysregulates dental implant placement surgeryâ€induced osteoimmune wound 12321 healing and attenuates the alveolar bone–implant interface in mice. Journal of Clinical Periodontology, 2023, 50, 1670-1684.	4.9	O
Microbial metabolomic responses to changes in temperature and salinity along the western Antarctic Peninsula. ISME Journal, 2023, 17, 2035-2046.	9.8	2
A novel SUCNR1 inhibitor alleviates dysbiosis through inhibition of host responses without direct interaction with host microbiota. Molecular Oral Microbiology, 2024, 39, 80-90.	2.7	1
$^{\mbox{\scriptsize 12324}}$	4.1	0
Towards an understanding of the factors controlling bacterial diversity and activity in semi-passive 12325 Fe- and As-oxidizing bioreactors treating arsenic-rich acid mine drainage. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
Host-bacteriome transplants of the schistosome snail host <i>Biomphalaria glabrata</i> reflect species-specific associations. FEMS Microbiology Ecology, 2023, 99, .	2.7	3
Response of Hypolimnetic Water and Bottom Sediment Microbial Communities to Freshwater Salinizationâ€"A Microcosm Experiment. Applied Microbiology, 2023, 3, 915-934.	1.6	0
Steamed broccoli sprouts alleviate DSS-induced inflammation and retain gut microbial biogeography in mice. MSystems, 2023, 8, .	3.8	1
12329 Metaphorâ€"A workflow for streamlined assembly and binning of metagenomes. GigaScience, 2022, 12, .	6.4	3

# ARTICLE	IF	CITATIONS
Influence of soil depth, irrigation, and plant genotype on the soil microbiome, metaphenome, and carbon chemistry. MBio, 2023, 14 , .	4.1	1
12331 Host genomic variation shapes gut microbiome diversity in threespine stickleback fish. MBio, 0, , .	4.1	1
Microbial activity contributes to spatial heterogeneity of wetland methane fluxes. Microbiology Spectrum, 2023, 11, .	3.0	0
Highly divergent CRESS DNA and picorna-like viruses associated with bleached thalli of the green seaweed <i>Ulva</i> . Microbiology Spectrum, 2023, 11, .	3.0	O
Gut microbiota of an Amazonian fish in a heterogeneous riverscape: integrating genotype, environment, and parasitic infections. Microbiology Spectrum, 2023, 11, .	3.0	0
Forage lignocellulose is an important factor in driving the seasonal dynamics of rumen anaerobic fungi in grazing yak and cattle. Microbiology Spectrum, 2023, 11 , .	3.0	0
Pronounced gut microbiota signatures in patients with <i>JAK2V617F-</i> positive essential thrombocythemia. Microbiology Spectrum, 2023, 11, .	3.0	0
Home-field advantage affects the local adaptive interaction between <i>Andropogon gerardii</i> ecotypes and root-associated bacterial communities. Microbiology Spectrum, 2023, 11, .	3.0	O
Celiacâ€"the lone horse? An autoimmune condition without signals of microbiota dysbiosis. Microbiology Spectrum, 2023, 11, .	3.0	2
Long-term benefit of DAAs on gut dysbiosis and microbial translocation in HCV-infected patients with and without HIV coinfection. Scientific Reports, 2023, 13, .	3.3	1
Microaerophilic Activated Sludge System for Ammonia Retention toward Recovery from 12340 High-Strength Nitrogenous Wastewater: Performance and Microbial Communities. Environmental Science & Environm	10.0	3
Household environment and animal fecal contamination are critical modifiers of the gut microbiome and resistome in young children from rural Nicaragua. Microbiome, 2023, 11 , .	11.1	0
Host–microbiome interactions in nicotinamide mononucleotide (NMN) deamidation. FEBS Letters, 2023, 597, 2196-2220.	2.8	2
Microbiome analysis of bile from apparently healthy cats and cats with suspected hepatobiliary disease. Journal of Veterinary Internal Medicine, 2023, 37, 2178-2187.	1.6	O
Pelvic spine reduction affects diet but not gill raker morphology in two polymorphic brook stickleback (<i>Culaea inconstans</i> /i>) populations. Ecology and Evolution, 2023, 13, .	1.9	0
Phyllosphere microbial diversity and specific taxa mediate within-cultivar resistance to <i>Phytophthora palmivora</i> in cacao. MSphere, 2023, 8, .	2.9	O
Plant neopolyploidy and genetic background differentiate the microbiome of duckweed across a variety of natural freshwater sources. Molecular Ecology, 2023, 32, 5849-5863.	3.9	2
Plumbing the depths with environmental <scp>DNA</scp> (<scp>eDNA</scp>): Metabarcoding reveals biodiversity zonation at 45–60 m on mesophotic coral reefs. Molecular Ecology, 2023, 32, 5590-560.	8. ^{3.9}	2

# ARTICLE	IF	CITATIONS
Lifeâ€stage specificity and crossâ€generational climate effects on the microbiome of a tropical sea urchin (Echinodermata: Echinoidea). Molecular Ecology, 2023, 32, 5645-5660.	3.9	0
Three species of axenic mosquito larvae recruit a shared core of bacteria in a common garden experiment. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
Metagenomic Analysis of the Composition of Microbial Consortia Involved in Spruce Degradation over Time in BiaÅ,owieża Natural Forest. Biomolecules, 2023, 13, 1466.	4.0	0
The Effect of a Bacillus Probiotic and Essential Oils Compared to an Ionophore on the Rumen Microbiome Composition of Feedlot Cattle. Animals, 2023, 13, 2927.	2.3	0
The Taxonomic Composition Changes of Bacteria and Fungi in Plant Residue Composts Induced by Biochar and Calcium Carbonate Application. Agronomy, 2023, 13, 2521.	3.0	0
Metataxonomic Characterization of Enriched Consortia Derived from Oil Spill-Contaminated Sites in 12353 Guimaras, Philippines, Reveals Major Role of Klebsiella sp. in Hydrocarbon Degradation. International Journal of Microbiology, 2023, 2023, 1-11.	2.3	0
Effect of Chitosan on Ruminal Fermentation and Microbial Communities, Methane Emissions, and Productive Performance of Dairy Cattle. Animals, 2023, 13, 2861.	2.3	1
The interplay between dietary fatty acids and gut microbiota influences host metabolism and hepatic steatosis. Nature Communications, 2023, 14 , .	12.8	2
Distinct prokaryotic and eukaryotic communities and networks in two agricultural fields of central Japan with different histories of maize–cabbage rotation. Scientific Reports, 2023, 13, .	3.3	0
The microbiome structure of decomposing plant leaves in soil depends on plant species, soil pore sizes, and soil moisture content. Frontiers in Microbiology, 0, 14, .	3.5	0
Diversity Analysis and Biocontrol Potential of Cultivatable Terrestrial Bacterial Streptomyces in Southern China. Agronomy, 2023, 13, 2500.	3.0	0
Functional redundancy in response to runoff input upholds microbial community in hydrocarbon-contaminated land-sea continuum. Environmental Pollution, 2023, 335, 122330.	7.5	0
Geochemical factors impacting nitrifying communities in sandy sediments. Environmental Microbiology, 2023, 25, 3180-3191.	3.8	2
Auricularia auricula polysaccharides attenuate obesity in mice through gut commensal Papillibacter cinnamivorans. Journal of Advanced Research, 2023, 52, 203-218.	9.5	5
Ecogenomics and cultivation reveal distinctive viral-bacterial communities in the surface microlayer of a Baltic Sea slick. ISME Communications, 2023, 3, .	4.2	2
Validation of a minimally-invasive method for sampling epithelial-associated microorganisms on the rumen wall. Frontiers in Animal Science, 0, 4, .	1.9	0
Dynamic genetic adaptation of Bacteroides thetaiotaomicron during murine gut colonization. Cell Reports, 2023, 42, 113009.	6.4	1
Treatment performance and microbial community structure in an aerobic granular sludge sequencing batch reactor amended with diclofenac, erythromycin, and gemfibrozil., $0, 2, .$		1

#	ARTICLE	IF	CITATIONS
12367	Unveiling changes in rhizosphereâ€associated bacteria linked to the genotype and water stress in quinoa. Microbial Biotechnology, 2023, 16, 2326-2344.	4.2	0
12368	Identifying the Microbiome of the Adenoid Surface of Children Suffering from Otitis Media with Effusion and Children without Middle Ear Effusion Using 16S rRNA Genetic Sequencing. Microorganisms, 2023, 11, 1955.	3.6	O
12370	Bacterial microbiota composition in hidradenitis suppurativa differs per skin layer. Journal of Investigative Dermatology, 2023, , .	0.7	0
12372	Mycorrhizal Fungal Diversity Associated with Six Understudied Ectomycorrhizal Trees in the Republic of Korea. Journal of Microbiology, 2023, 61, 729-739.	2.8	0
12373	Chinese Herbal Extracts Mitigate Ammonia Generation in the Cecum of Laying Hens: An In Vitro Study. Animals, 2023, 13, 2969.	2.3	0
12374	Microbiota and Resistome Analysis of Colostrum and Milk from Dairy Cows Treated with and without Dry Cow Therapies. Antibiotics, 2023, 12, 1315.	3.7	0
12375	Effects of cashew nut shell extract and monensin on in vitro ruminal fermentation, methane production, and ruminal bacterial community. Journal of Dairy Science, 2024, 107, 840-856.	3.4	1
12376	Biochar and zero-valent iron sand filtration simultaneously removes contaminants of emerging concern and Escherichia coli from wastewater effluent. Biochar, 2023, 5, .	12.6	2
12377	A novel immune modulator IM33 mediates a glia-gut-neuronal axis that controls lifespan. Neuron, 2023, 111, 3244-3254.e8.	8.1	1
12378	Olive oil-derived endocannabinoid-like mediators inhibit palatable food-induced reward and obesity. Communications Biology, 2023, 6, .	4.4	0
12379	Akkermansia muciniphila exacerbates food allergy in fibre-deprived mice. Nature Microbiology, 2023, 8, 1863-1879.	13.3	14
12380	Evaluation of metagenomic assembly methods for the detection and characterization of antimicrobial resistance determinants and associated mobilizable elements. Journal of Microbiological Methods, 2023, 213, 106815.	1.6	1
12381	Methane Cycling Microbial Community Characteristics: Comparing Natural, Actively Extracted, Restored and Unrestored Boreal Peatlands. Wetlands, 2023, 43, .	1.5	0
12382	Trans-Global Biogeochemistry of Soil to Grain Transport of Arsenic and Cadmium. Exposure and Health, 0, , .	4.9	1
12383	Disentangling the link between zebrafish diet, gut microbiome succession, and Mycobacterium chelonae infection. Animal Microbiome, 2023, 5, .	3.8	1
12384	Contrasting patterns of foraging behavior in neotropical stingless bees using pollen and honey metabarcoding. Scientific Reports, 2023, 13, .	3.3	2
12385	Microbiome Responses to Fecal Microbiota Transplantation in Cats with Chronic Digestive Issues. Veterinary Sciences, 2023, 10, 561.	1.7	0
12386	Effects of oxygen availability on mycobenthic communities of marine coastal sediments. Scientific Reports, 2023, 13, .	3.3	0

# ARTICLE	IF	CITATIONS
Emerging Trends and Focus in Human Skin Microbiome Over the Last Decade: A Bibliometric Analys and Literature Review. Clinical, Cosmetic and Investigational Dermatology, 0, Volume 16, 2153-217		0
Plasmodium falciparum population structure inferred by msp1 amplicon sequencing of parasites collected from febrile patients in Kenya. Malaria Journal, 2023, 22, .	2.3	1
Mesoscale oceanographic meanders influence protist community function and structure in the «scp»southern Indian Ocean«/scp». Environmental Microbiology, 2023, 25, 3161-3179.	3.8	0
Auction market placement and a rest stop during transportation affect the respiratory bacterial microbiota of beef cattle. Frontiers in Microbiology, 0, 14 , .	3.5	1
Microbial growth under drought is confined to distinct taxa and modified by potential future climat conditions. Nature Communications, 2023, 14, .	re 12.8	3
Selection and enrichment of microbial species with an increased lignocellulolytic phenotype from a native soil microbiome by activity-based probing. ISME Communications, 2023, 3, .	4.2	O
Abundance and prevalence of ESBL coding genes in patients undergoing first line eradication therap for Helicobacter pylori. PLoS ONE, 2023, 18, e0289879.	py 2.5	0
Enhancement of Soybean Meal Alters Gut Microbiome and Influences Behavior of Farmed Atlantic Salmon (Salmo salar). Animals, 2023, 13, 2591.	2.3	1
Amplicon-Based Microbiome Profiling: From Second- to Third-Generation Sequencing for Higher Taxonomic Resolution. Genes, 2023, 14, 1567.	2.4	1
Assessment of various standard fish diets on gut microbiome of platyfish <i>Xiphophorus maculatus</i> . Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 0, ,	1.3	1
Chemically Mediated Interactions with Macroalgae Negatively Affect Coral Health but Induce Limite Changes in Coral Microbiomes. Microorganisms, 2023, 11, 2261.	ed 3.6	1
Langerhans cells shape postnatal oral homeostasis in a mechanical-force-dependent but microbiota and IL17-independent manner. Nature Communications, 2023, 14, .	12.8	2
Geochemical, sedimentological and microbial diversity in two thermokarst lakes of far Eastern Siberia. Biogeochemistry, 2023, 165, 239-263.	3.5	0
Protist taxonomic and functional diversity in aquatic ecosystems of the Brazilian Atlantic Forest. Peerl, 0, 11 , e15762.	2.0	O
12404 Intestinal health of broilers challenged with Eimeria spp. using functional oil blends in two physical forms with or without anticoccidials. Scientific Reports, 2023, 13, .	3.3	0
The succession of epiphytic microalgae conditions fungal community composition: how chytrids respond to blooms of dinoflagellates. ISME Communications, 2023, 3, .	4.2	2
Bifidobacteria define gut microbiome profiles of golden lion tamarin (Leontopithecus rosalia) and marmoset (Callithrix sp.) metagenomic shotgun pools. Scientific Reports, 2023, 13, .	3.3	0
Syntrophic entanglements for propionate and acetate oxidation under thermophilic and high-ammo conditions. ISME Journal, 2023, 17, 1966-1978.	onia 9.8	2

# ARTICLE	IF	CITATIONS
COVID-19 alters human microbiomes: a meta-analysis. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	0
Comparison of the Effect of Corn-fermented Protein and Traditional Ingredients on the Fecal Microbiota of Dogs. Veterinary Sciences, 2023, 10, 553.	1.7	1
Microbial Composition of Natural, Agricultural, and Technogenic Soils of Both Forest and Forest-Tundra of the Russian North. Applied Sciences (Switzerland), 2023, 13, 8981.	2.5	1
Built environment microbiomes transition from outdoor to human-associated communities after construction and commissioning. Scientific Reports, 2023, 13, .	3.3	1
Protecting the invisible: Establishing guideline values for copper toxicity to marine microbiomes. Science of the Total Environment, 2023, 904, 166658.	8.0	0
Oligosaccharide feed supplementation reduces plasma insulin in geldings with Equine Metabolic Syndrome. , 0, 2, .		O
Systematic review of cnidarian microbiomes reveals insights into the structure, specificity, and fidelity of marine associations. Nature Communications, 2023, 14, .	12.8	4
Diversity of the Microbiota of Traditional Izmir Tulum and Izmir Brined Tulum Cheeses and Selection of Potential Probiotics. Foods, 2023, 12, 3482.	4.3	1
The effect of sulfadiazine in manure on accumulation of sulfonamide resistance genes in freshly consumable plants. CABI Agriculture and Bioscience, 2023, 4, .	2.4	0
Characterization of Microbial Diversity of Two Tomato Cultivars through Targeted Next-Generation Sequencing 16S rRNA and ITS Techniques. Microorganisms, 2023, 11, 2337.	3.6	O
Antarctic snow algae: unraveling the processes underlying microbial community assembly during blooms formation. Microbiome, 2023, 11, .	11.1	0
Agricultural tillage practice and rhizosphere selection interactively drive the improvement of soybean plant biomass. Plant, Cell and Environment, 2023, 46, 3542-3557.	5.7	2
Environment and Host Genetics Influence the Biogeography of Plant Microbiome Structure. Microbial Ecology, 0, , .	2.8	0
Seeding the Infant Gut in Early Life—Effects of Maternal and Infant Seeding with Probiotics on Strain 12422 Transfer, Microbiota, and Gastrointestinal Symptoms in Healthy Breastfed Infants. Nutrients, 2023, 15, 4000.	4.1	O
Tillage homogenizes soil bacterial communities in microaggregate fractions by facilitating dispersal. Soil Biology and Biochemistry, 2023, 186, 109181.	8.8	4
Profile and potential bioactivity of the miRNome and metabolome expressed in Malva sylvestris L. leaf and flower. BMC Plant Biology, 2023, 23, .	3.6	4
Characterization of microbial communities in seven wetlands with different anthropogenic burden using Next Generation Sequencing in Bogot \tilde{A}_i , Colombia. Scientific Reports, 2023, 13, .	3.3	1
Geographical survey of the mycobiome and microbiome of Southern California glassy-winged sharpshooters. MSphere, 2023, 8, .	2.9	2

# ARTICLE	IF	Citations
12427 Enterotypes of the human gut mycobiome. Microbiome, 2023, 11, .	11.1	6
H2 mediated mixed culture microbial electrosynthesis for high titer acetate production from CO2. Environmental Science and Ecotechnology, 2024, 19, 100324.	13.5	1
Gill-associated bacteria are homogeneously selected in amphibious mangrove crabs to sustain host intertidal adaptation. Microbiome, 2023, 11, .	11.1	2
Defects in microvillus crosslinking sensitize to colitis and inflammatory bowel disease. EMBO Reports, 2023, 24, .	4.5	2
Rhizosphere effects on the microbial community: Specificity and conservatism across geographically disjunct Panax species. Applied Soil Ecology, 2023, 192, 105075.	4.3	0
Human Alcohol-Microbiota Mice have Increased Susceptibility to Bacterial Pneumonia. Cells, 2023, 12 2267.	2, 4.1	0
lmpacts of maternal microbiota and microbial metabolites on fetal intestine, brain, and placenta. BMC Biology, 2023, 21, .	3.8	3
Responses of a soil fungal community to severe windstorm damages in an old silver fir stand. Frontiers in Microbiology, 0, 14, .	3.5	0
12435 Changes in the Gut Microbiota Composition during Implantation of Composite Scaffolds Based on Poly(3-hydroxybutyrate) and Alginate on the Large-Intestine Wall. Polymers, 2023, 15, 3649.	4.5	0
Phylogenetic diversity and functional potential of the microbial communities along the Bay of Bengal coast. Scientific Reports, 2023, 13, .	3.3	0
12437 Quantifying thermal adaptation of soil microbial respiration. Nature Communications, 2023, 14, .	12.8	5
Land use change rather than surrounding vegetation affects fungal endophyte assemblages in the African wild olive. Landscape Ecology, 0 , , .	4.2	0
Evidence supportive of a bacterial component in the etiology for Alzheimer's disease and for a temporal-spatial development of a pathogenic microbiome in the brain. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	4
Potential Environmental Drivers of Fossil Bones Degradation—A Metabarcoding Approach in Two Carpathian Caves. Geomicrobiology Journal, 2023, 40, 654-666.	2.0	0
Another tick bites the dust: exploring the association of microbial composition with a broad transmission competence of tick vector species. Microbiology Spectrum, 0, , .	3.0	0
The secret hidden in dust: Assessing the potential to use biological and chemical properties of the airborne fraction of soil for provenance assignment and forensic casework. Forensic Science International: Genetics, 2023, 67, 102931.	3.1	1
lmpact of Parthenium hysterophorus L. invasion on soil fungal communities in the Yellow River Delta. Annals of Microbiology, 2023, 73, .	2.6	0
16S metabarcoding, total soil DNA content, and functional bacterial genes quantification to 12444 characterize soils under long-term organic and conventional farming systems. Chemical and Biological Technologies in Agriculture, 2023, 10, .	4.6	0

# ARTICLE	IF	CITATIONS
The Impact of Highly Weathered Oil from the Most Extensive Oil Spill in Tropical Oceans (Brazil) on the Microbiome of the Coral Mussismilia harttii. Microorganisms, 2023, 11, 1935.	3.6	0
Experimentally determined traits shape bacterial community composition one and five years following wildfire. Nature Ecology and Evolution, 2023, 7, 1419-1431.	7.8	2
Environmental Drivers of the Moonmilk Microbiome Diversity in Some Temperate and Tropical Caves. Microbial Ecology, 0, , .	2.8	0
Establishment of a transparent soil system to study <i>Bacillus subtilis </i> Communications, 2023, 3, .	4.2	1
12449 Simvastatin induces human gut bacterial cell surface genes. Molecular Microbiology, 0, , .	2.5	0
The social microbiome: gut microbiome diversity and abundance are negatively associated with sociality in a wild mammal. Royal Society Open Science, 2023, 10 , .	2.4	2
Study of the key biotic and abiotic parameters influencing ammonium removal from wastewaters by Fe3+-mediated anaerobic ammonium oxidation (Feammox). Chemosphere, 2023, 339, 139463.	8.2	3
Microbial colonization dynamics of the postnatal digestive tract of <scp><i>Bos indicus</i></scp> <calves. .<="" 2023,="" 94,="" animal="" journal,="" science="" td=""><td>1.4</td><td>1</td></calves.>	1.4	1
Spatial extent of dysbiosis in the branching coral Pocillopora damicornis during an acute disease outbreak. Scientific Reports, 2023, 13, .	3.3	0
Altered Gut Microbiota Composition Is Associated with Difficulty in Explicit Emotion Regulation in Young Children. Microorganisms, 2023, 11, 2245.	3.6	2
Changes in structure and assembly of a species-rich soil natural community with contrasting nutrient availability upon establishment of a plant-beneficial Pseudomonas in the wheat rhizosphere. Microbiome, 2023, 11, .	11.1	3
Biodiversity indices and Random Forests reveal the potential for striped skunk (Mephitis mephitis) fecal microbial communities to function as a biomarker for oral rabies vaccination. PLoS ONE, 2023, 18, e0285852.	2.5	2
ldentification of rare microbial colonizers of plastic materials incubated in a coral reef environment. Frontiers in Microbiology, 0, 14, .	3.5	3
Repurposing Metformin for periodontal disease management as a form of oral-systemic preventive medicine. Journal of Translational Medicine, 2023, 21, .	4.4	1
Silver and Hematite Nanoparticles Had a Limited Effect on the Bacterial Community Structure in Soil Cultivated with Phaseolus vulgaris L Agronomy, 2023, 13, 2341.	3.0	0
Shifts of the soil microbiome composition induced by plant–plant interactions under increasing cover crop densities and diversities. Scientific Reports, 2023, 13, .	3.3	1
Uncovering the relationship between gut microbial dysbiosis, metabolomics, and dietary intake in type 2 diabetes mellitus and in healthy volunteers: a multi-omics analysis. Scientific Reports, 2023, 13, .	3.3	1
Microbial Population Dynamics during Unstable Operation of a Semicontinuous Anaerobic Digester Fed with a Mild-Treated Olive Mill Solid Waste. Processes, 2023, 11, 2724.	2.8	O

#	Article	IF	CITATIONS
12465	Human leukocyte antigen-dependent colonization of Lactobacillus in the early-life gut., 0, 2, .		1
12466	Organic enrichment reduces sediment bacterial and archaeal diversity, composition, and functional profile independent of bioturbator activity. Marine Pollution Bulletin, 2023, 196, 115608.	5.0	O
12467	Gut microbiota of the critically endangered Saiga antelope across two wild populations in a year without mass mortality. Scientific Reports, 2023, 13 , .	3.3	0
12468	Effect of urbanization and parasitism on the gut microbiota of Darwin's finch nestlings. Molecular Ecology, 2023, 32, 6059-6069.	3.9	1
12469	The wild solitary bees Andrena vaga, Anthophora plumipes, Colletes cunicularius, and Osmia cornuta microbiota are host specific and dominated by endosymbionts and environmental microorganisms. Microbial Ecology, 2023, 86, 3013-3026.	2.8	3
12470	Dietary supplementation of zinc oxide modulates intestinal functionality during the post-weaning period in clinically healthy piglets. Journal of Animal Science and Biotechnology, 2023, 14, .	5.3	0
12471	Invasive plant species interact with drought to shift key functions and families in the native rhizosphere. Plant and Soil, 0 , , .	3.7	0
12472	Resource partitioning and amino acid assimilation in a terrestrial geothermal spring. ISME Journal, 2023, 17, 2112-2122.	9.8	O
12473	Changes in the Vaginal Microbiome During Pregnancy and the Postpartum Period in South African Women: a Longitudinal Study. Reproductive Sciences, 2024, 31, 275-287.	2.5	1
12474	Variability of airborne microbiome at different urban sites across seasons: a case study in Rome. Frontiers in Environmental Science, $0,11,.$	3.3	0
12475	Effect of two shampoo formulations on the prokaryotic and eukaryotic microbiota composition of the human scalp. International Journal of Cosmetic Science, 2024, 46, 62-70.	2.6	0
12476	16S rRNA gene-based microbiota profiles from diverse avian faeces are largely independent of DNA preservation and extraction method. Frontiers in Microbiology, 0, 14, .	3.5	O
12477	Anaerobutyricum hallii promotes the functional depletion of a food carcinogen in diverse healthy fecal microbiota. , $0, 2, \ldots$		0
12478	Characterizing the Gut Microbial Communities of Native and Invasive Freshwater Bivalves after Long-Term Sample Preservation. Microorganisms, 2023, 11, 2489.	3.6	O
12479	Compost, plants and endophytes versus metal contamination: choice of a restoration strategy steers the microbiome in polymetallic mine waste. Environmental Microbiomes, 2023, 18, .	5.0	2
12480	Marine viruses disperse bidirectionally along the natural water cycle. Nature Communications, 2023, 14 , .	12.8	2
12481	The airway microbiota of neonates colonized with asthma-associated pathogenic bacteria. Nature Communications, 2023, 14, .	12.8	1
12482	Extracting DNA from soil or directly from isolated nematodes indicate dissimilar community structure for Europe-wide forest soils. Soil Biology and Biochemistry, 2023, 185, 109154.	8.8	1

#	Article	IF	CITATIONS
12483	Environmental distances are more important than geographic distances for predicting earthworm gut bacterial community composition. European Journal of Soil Biology, 2023, 118, 103520.	3.2	1
12484	Microbiome-based study in wild-caught Scomber scombrus fish products at the end of the supply chain. LWT - Food Science and Technology, 2023, 186, 115264.	5.2	1
12485	Gut microbiome correlates with plasma lipids in amyotrophic lateral sclerosis. Brain, 0, , .	7.6	2
12486	Social demographics determinants for resistome and microbiome variation of a multiethnic community in Southern Malaysia. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	0
12487	Influence of oral microbiome on longitudinal patterns of oral mucositis severity in patients with squamous cell carcinoma of the head and neck. Cancer, 2024, 130, 150-161.	4.1	2
12488	Spatial diversity of the skin bacteriome. Frontiers in Microbiology, 0, 14, .	3.5	0
12489	Cooperation and cheating orchestrate Vibrio assemblages and polymicrobial synergy in oysters infected with OsHV-1 virus. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	2
12491	Symbioses of alvinocaridid shrimps from the South West Pacific: No chemosymbiotic diets but conserved gut microbiomes. Environmental Microbiology Reports, 2023, 15, 614-630.	2.4	0
12492	A Gradient of Intestinal Inflammation in Primary Sclerosing Cholangitis. Inflammatory Bowel Diseases, 0, , .	1.9	1
12493	Impact of conservation tillage on wheat performance and its microbiome. Frontiers in Plant Science, 0, 14 , .	3.6	3
12494	Immune checkpoint inhibitor-induced colitis is mediated by polyfunctional lymphocytes and is Âdependent on an ÂlL23/IFN \hat{l}^3 Âaxis. Nature Communications, 2023, 14, .	12.8	0
12496	Community dynamics and co-occurrence relationships of pelagic ciliates and their potential prey at a coastal and an offshore station in the ultra-oligotrophic Eastern Mediterranean Sea. Frontiers in Genetics, 0, 14, .	2.3	0
12497	Shifting pattern of gut microbiota in pregnant women two decades apart $\hat{a} \in \hat{a}$ an observational study. Gut Microbes, 2023, 15, .	9.8	3
12498	Gut microbiota metabolites mediate the interplay between childhood maltreatment and psychopathology in patients with eating disorders. Scientific Reports, 2023, 13, .	3.3	2
12499	ZnO nanoparticles in combination with Zn biofertilizer improve wheat plant growth and grain Zn content without significantly changing the rhizospheric microbiome. Environmental and Experimental Botany, 2023, 213, 105446.	4.2	3
12500	The eukaryome of African children is influenced by geographic location, gut biogeography, and nutritional status. MicroLife, 2023, 4, .	2.1	0
12501	Effects of synbiotic supplementation on intestinal microbiota composition in children and adolescents with exogenous obesity: (Probesity-2 trial). Gut Pathogens, 2023, 15, .	3.4	1
12502	Fecal Microbiota and Diet Composition of Buryatian Horses Grazing Warm- and Cold-Season Grass Pastures. Microorganisms, 2023, 11, 1947.	3.6	1

# ARTICLE	IF	CITATIONS
Exploring Gut Microbiome Variations between Popillia japonica Populations of Azores. Microorganisms, 2023, 11, 1972.	3.6	0
Pilot study on nasal microbiota dynamics and MRSA carriage of a pig cohort housed on straw bedding. Molecular Microbiology, 0, , .	2.5	1
12507 β-mannanase supplemented in diets saved 85 to 100Âkcal of metabolizable energy/kg, supporting growth performance and improving nutrient digestibility in grower pigs. Scientific Reports, 2023, 13, .	3.3	0
12508 Niche and ecosystem preference of earliest diverging fungi in soils. Mycology, 2023, 14, 239-255.	4.4	1
Using environmental DNA to better inform decision making around decommissioning alternatives for offshore oil and gas infrastructure. Science of the Total Environment, 2023, 901, 165991.	8.0	0
Citizen science helps to raise awareness about gut microbiome health in people at risk of developing non-communicable diseases. Gut Microbes, 2023, 15, .	9.8	0
Response of total belowground soil biota in Alhagi sparsifolia monoculture at different soil vertical profiles in desert ecosystem. Science of the Total Environment, 2023, 901, 166027.	8.0	3
12513 Revisiting the intrinsic mycobiome in pancreatic cancer. Nature, 2023, 620, E1-E6.	27.8	12
Impact of active lifestyle on the primary school children saliva microbiota composition. Frontiers in Nutrition, $0,10,$	3.7	0
Experimental Capacity of Human Fecal Microbiota to Degrade Fiber and Produce Short-Chain Fatty 12517 Acids Is Associated with Diet Quality and Anthropometric Parameters. Journal of Nutrition, 2023, 153, 2827-2841.	2.9	0
Microbial fingerprints reveal interaction between museum objects, curators, and visitors. IScience, 2023, 26, 107578.	4.1	1
Mapping the microbial diversity associated with different geochemical regimes in the shallow-water hydrothermal vents of the Aeolian archipelago, Italy. Frontiers in Microbiology, 0, 14, .	3.5	0
Earth to Mars: A Protocol for Characterizing Permafrost in the Context of Climate Change as an Analog for Extraplanetary Exploration. Astrobiology, 2023, 23, 1006-1018.	3.0	1
Marine heatwaves threaten cryptic coral diversity and erode associations among coevolving partners. Science Advances, 2023, 9, .	10.3	4
A multi-attribute approach to evaluating the impact of biostimulants on crop performance. Frontiers in Plant Science, 0, 14 , .	3.6	0
Outcomes Following Acute Severe Colitis at Initial Presentation: A Multi-centre, Prospective, Paediatric Cohort Study. Journal of Crohn's and Colitis, 2024, 18, 233-245.	1.3	1
12527 Intraspecific variation in leaf litter alters fitness metrics and the gut microbiome of consumers. Oecologia, 2023, 202, 769-782.	2.0	0
$_{12529}$ Microbiota is structured by gut regions, life stage, and diet in the Black Soldier Fly (Hermetia) Tj ETQq 110.784	4314 ₃ rgBT /0	Overlock 10 T

#	Article	IF	CITATIONS
12530	Microbiome environmental shifts differ between two co-occurring octocoral hosts. Marine Ecology - Progress Series, 2023, 720, 59-83.	1.9	1
12531	Effects of Different Feeding Systems on Ruminal Fermentation, Digestibility, Methane Emissions, and Microbiota of Hanwoo Steers. Journal of Animal Science and Technology, 0, , .	2.5	O
12532	Within-species variation in the gut microbiome of medaka (Oryzias latipes) is driven by the interaction of light intensity and genetic background. $0, 3, \ldots$		0
12534	Exploring the diversity of microeukaryotic communities in New England tide pools. Aquatic Microbial Ecology, 2023, 89, 143-155.	1.8	0
12536	Treatment with gut-specific nonsteroidal anti-inflammatory drug attenuates metabolic inflammation but not body mass in fattening ground squirrels. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2023, 325, R456-R464.	1.8	0
12540	Fungal and Bacterial Microbiome in Sinus Mucosa of Patients with and without Chronic Rhinosinusitis. Laryngoscope, 2024, 134, 1054-1062.	2.0	2
12541	Signs of aging in midlife: physical function and sex differences in microbiota. GeroScience, 2024, 46, 1477-1488.	4.6	0
12542	Grapevines escaping trunk diseases in New Zealand vineyards have a distinct microbiome structure. Frontiers in Microbiology, $0,14,.$	3.5	0
12544	Contamination of long-term manure-fertilized Indian paddy soils with veterinary antibiotics: Impact on bacterial communities and antibiotics resistance genes. Applied Soil Ecology, 2023, 192, 105106.	4.3	6
12546	<i>Listeria monocytogenes</i> infection in pregnant macaques alters the maternal gut microbiome. Biology of Reproduction, 0, , .	2.7	0
12547	Rumen and cecum bacteria of beef cattle that differ in feed efficiency fed a forage diet. Journal of Animal Science, 2023, 101, .	0.5	0
12549	Particle-attached Microbes in Eelgrass Vegetation Areas Differ in Community Structure Depending on the Distance from the Eelgrass Bed. Microbes and Environments, 2023, 38, n/a.	1.6	O
12552	A discovery down under: decoding the draft genome sequence of Pantoea stewartii from Australia's Critically Endangered western ground parrot/kyloring (Pezoporus flaviventris). Microbial Genomics, 2023, 9, .	2.0	0
12553	Genome-resolved correlation mapping links microbial community structure to metabolic interactions driving methane production from wastewater. Nature Communications, 2023, 14, .	12.8	1
12554	Effects of deterministic assembly of communities caused by global warming on coexistence patterns and ecosystem functions. Journal of Environmental Management, 2023, 345, 118912.	7.8	1
12555	High-throughput DNA metabarcoding for determining the gut microbiome of captive critically endangered Malayan tiger (Panthera tigris jacksoni) during fasting. Biodiversity Data Journal, $0,11,.$	0.8	1
12556	Antibiotic resistance indicator genes in biofilm and planktonic microbial communities after wastewater discharge. Frontiers in Microbiology, 0, 14 , .	3.5	1
12557	Phenotypic associations of common waxbill gut and feather microbiome diversity in a shared environment. Biological Journal of the Linnean Society, 0, , .	1.6	O

# ARTICLE	IF	CITATIONS
A new spike-in-based method for quantitative metabarcoding of soil fungi and bacteria. International Microbiology, 0, , .	2.4	0
Inflammatory response to bacterial lipopolysaccharide drives iron accumulation in human adipocytes. Biomedicine and Pharmacotherapy, 2023, 166, 115428.	5.6	0
Impact of adding tannins or medium-chain fatty acids in a dairy cow diet on variables of in vitro fermentation using a rumen simulation technique (RUSITEC) system. Animal Feed Science and Technology, 2023, 305, 115763.	2.2	1
Effect of stand thinning, former land use and individual tree parameters on wood inhabiting fungal community composition in young living Norway spruce. Fungal Ecology, 2023, 65, 101281.	1.6	1
Effects of blackcurrant extract on indole and ammonia productions in an <i>in vitro </i> human fecal culture model. Bioscience of Microbiota, Food and Health, 2023, , .	1.8	0
Functionally discrete fine roots differ in microbial assembly, microbial functional potential, and produced metabolites. Plant, Cell and Environment, 2023, 46, 3919-3932.	5.7	2
Composition and evolution of the gut microbiota of growing pupples is impacted by their birth weight. Scientific Reports, 2023, 13, .	3.3	0
Studying the microbiome of suppressive soils against vascular wilt, caused by <i>Fusarium oxysporum </i> in cape gooseberry (<i>Physalis peruviana </i>). Environmental Microbiology Reports, 0,	2.4	1
Host phylogeny shapes viral transmission networks in an island ecosystem. Nature Ecology and Evolution, 2023, 7, 1834-1843.	7.8	4
Documenting the microbiome diversity and distribution in selected fleas from South Africa with an emphasis on the cat flea, <i>Ctenocephalides f. felis</i> Parasitology, 0, , 1-11.	1.5	0
Shotgun-metagenomics reveals a highly diverse and communal microbial network present in the drains of three beef-processing plants. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	1
Effect of bovine respiratory disease on the respiratory microbiome: a meta-analysis. Frontiers in Cellular and Infection Microbiology, 0, 13 , .	3.9	0
Fiber deprivation and microbiome-borne curli shift gut bacterial populations and accelerate disease in a mouse model of Parkinson's disease. Cell Reports, 2023, 42, 113071.	6.4	0
The effect of maternal supply of rumen-protected protein to Holstein Friesian cows during the dry period on the transfer of passive immunity and colostral microbial composition. Journal of Dairy Science, 2023, 106, 8723-8745.	3.4	1
Long-term and trimester-specific effects of prenatal stress on the child gut microbiota. Psychoneuroendocrinology, 2023, 158, 106380.	2.7	0
Microbial dynamics in soils of the Damma glacier forefield show succession in the functional genetic potential. Environmental Microbiology, 2023, 25, 3116-3138.	3.8	2
Extended water stagnation in buildings during the COVID-19 pandemic increases the risks posed by opportunistic pathogens. Water Research X, 2023, 21, 100201.	6.1	1
Responses of rhizosphere fungi to the root economics space in grassland monocultures of different age. New Phytologist, 2023, 240, 2035-2049.	7.3	0

#	Article	IF	CITATIONS
12581	Unveiling metabotype clustering in resveratrol, daidzein, and ellagic acid metabolism: Prevalence, associated gut microbiomes, and their distinctive microbial networks. Food Research International, 2023, 173, 113470.	6.2	2
12583	Microbiome analysis of <i>Spodoptera frugiperda</i> (Lepidoptera, Noctuidae) larvae exposed to <i>Bacillus thuringiensis</i> (Bt) endotoxins. PeerJ, 0, 11, e15916.	2.0	1
12585	Relative contribution of season, site, scion and rootstock genotype, and susceptibility to European canker to the variability in bacterial and fungal communities in apple leaf scar tissues. Annals of Applied Biology, 2024, 184, 136-151.	2.5	0
12587	Community Structure and Predicted Functions of Actively Growing Bacteria Responsive to Released Coral Mucus in Surrounding Seawater. Microbes and Environments, 2023, 38, n/a.	1.6	1
12588	Simplification of soil biota communities impairs nutrient recycling and enhances above―and belowground nitrogen losses. New Phytologist, 2023, 240, 2020-2034.	7.3	2
12590	Artificial network inference analysis reveals the impact of biostimulant on bacterial communities in fumigated soil for potato production against common scab. Frontiers in Soil Science, 0, 3, .	2.2	O
12591	An ecological network approach for detecting and validating influential organisms for rice growth. ELife, 0, 12 , .	6.0	0
12592	Metagenomic characterization of the microbiomes in five different body habitats of otherwise healthy individuals with periodontal disease. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	O
12594	Impact of a Powdered Meal Replacement on Metabolism and Gut Microbiota (PREMIUM) in individuals with excessive body weight: a study protocol for a randomised controlled trial. BMJ Open, 2023, 13, e070027.	1.9	0
12596	Feed Regime Slightly Modifies the Bacterial but Not the Fungal Communities in the Intestinal Mucosal Microbiota of Cobia Fish (Rachycentron canadum). Microorganisms, 2023, 11, 2315.	3.6	1
12598	Responses of the gut microbiota to environmental heavy metal pollution in tree sparrow (Passer) Tj ETQq0 0 0 rg	BT/Overlo	ock 10 Tf 50
12600	Evaluating the effects of pH and temperature on sulphate-reducing bacteria and modelling of their effects in stirred bioreactors. Environmental Pollutants and Bioavailability, 2023, 35, .	3.0	O
12601	Digestates from the co-digestion of cattle rumen and manure improve the methane potential of maize silage. Bioresource Technology Reports, 2023, 24, 101625.	2.7	0
12604	Phyllosphere to ferment: Site conditions structures cacao pod and ferment microbiomes in Hawaiâ€~i. PhytoFrontiers, 0, , .	1.6	O
12606	Enteroviral central nervous system infections in patients with Lyme neuroborreliosis. Ticks and Tick-borne Diseases, 2023, 14, 102253.	2.7	0
12607	Batch culture analysis to identify potent organic acids for suppressing ruminal methane production. Animal Science Journal, 2023, 94, .	1.4	O
12608	Sulfur disproportionating microbial communities in a dynamic, microoxicâ€sulfidic karst system. Geobiology, 2023, 21, 791-803.	2.4	1
12610	Potato tuber origin and microbial composition determines resistance against soft rot Pectobacteriaceae. European Journal of Plant Pathology, 0, , .	1.7	2

# Art	TICLE	IF	CITATIONS
	asonal dynamics and tree foliar habit drive the rhizobacterial diversity in congeneric Ficus species m Northern Western Ghats, India. Rhizosphere, 2023, 28, 100790.	3.0	0
12613 Len ran	non flavonoids nutraceutical (Eriomin®) attenuates prediabetes intestinal dysbiosis: A doubleâ€blind domized controlled trial. Food Science and Nutrition, 2023, 11, 7283-7295.	3.4	2
12614 FEN	mparison between the gut bacterial community of laboratory cultured and wild <i>Daphnia</i> . MS Microbiology Ecology, 2023, 99, .	2.7	0
The 12615 1,6	e resuscitation-promoting factor (Rpf) from Micrococcus luteus and its putative reaction product -anhydro-MurNAc increase culturability of environmental bacteria. Access Microbiology, 2023, 5, .	0.5	1
12616 Inve	estigating Biodegradation of 1,4-Dioxane by Groundwater and Soil Microbiomes: Insights into crobial Ecology and Process Prediction. ACS ES&T Water, 2024, 4, 1046-1060.	4.6	1
12619 A to	wo-cohort study on the association between the gut microbiota and bone density, croarchitecture, and strength. Frontiers in Endocrinology, 0, 14, .	3.5	1
	ect of inoculum type, packing material and operational conditions on the biofiltration of a mixture nydrophobic volatile organic compounds in air. Science of the Total Environment, 2023, 904, 167326.	8.0	2
12623 The	e edible plant microbiome: evidence for the occurrence of fruit and vegetable bacteria in the human c. Gut Microbes, 2023, 15, .	9.8	2
Fine 12624 faso	eâ€scale genetic structure in rhizosphere microbial communities associated with <i>Chamaecrista ciculata</i> (Fabaceae). Ecology and Evolution, 2023, 13, .	1.9	1
	atial and temporal variation in the diet of introduced sambar deer (Cervus unicolor) in an alpine dscape. Wildlife Research, 2023, , .	1.4	O
12627 Imp Spe	pacts of biostimulation and bioaugmentation on woodchip bioreactor microbiomes. Microbiology ectrum, 2023, 11 , .	3.0	0
12628 Mic	crobial Community Response to Various Types of Exogenous Organic Matter Applied to Soil. ernational Journal of Molecular Sciences, 2023, 24, 14559.	4.1	O
12630 Arc	tic bacterial diversity and connectivity in the coastal margin of the Last Ice Area. ISME mmunications, 2023, 3, .	4.2	0
	arly variation coupled with social interactions shape the skin microbiome in free-ranging rhesus caques. Microbiology Spectrum, 2023, $11,\dots$	3.0	O
	estigating the cecal microbiota of broilers raised in extensive and intensive production systems. crobiology Spectrum, 2023, 11 , .	3.0	0
12634 Еffе Spe	ects of hydrogeochemistry on the microbial ecology of terrestrial hot springs. Microbiology ectrum, 2023, 11, .	3.0	O
	al fungal profiling and risk of nasopharyngeal carcinoma: a population-based case-control study. oMedicine, 2023, 96, 104813.	6.1	0
12639 Fur Phy	ngal communities associated with corn in a diverse long-term crop rotation in Ohio. vtoFrontiers, 0, , .	1.6	О

# ARTICLE	IF	Citations
Dietâ€related factors strongly shaped the gut microbiota of Japanese macaques. American Journal of Primatology, 2023, 85, .	1.7	1
i»¿Amplicon metagenomics of dung beetles (Coleoptera, Scarabaeidae, Scarabaeinae) as a proxy for lemur (Primates, Lemuroidea) studies in Madagascar. ZooKeys, 0, 1181, 29-39.	. 1.1	1
Skin and gut microbiomes of tadpoles vary differently with host and water environment: a short-term experiment using 16S metabarcoding. Scientific Reports, 2023, 13, .	3.3	0
Select symbionts drive high IgA levels in the mouse intestine. Cell Host and Microbe, 2023, 31, 1620-1638.e7.	11.0	1
Microevolutionary patterns in ecotypes of the symbiotic cyanobacterium UCYN-A revealed from a Northwest Atlantic coastal time series. Science Advances, 2023, 9, .	10.3	1
The resistome and microbiome of wastewater treatment plant workers – The AWARE study. Environment International, 2023, 180, 108242.	10.0	1
Microbiome Metabolome Integration Platform (MMIP): a web-based platform for microbiome and metabolome data integration and feature identification. Briefings in Bioinformatics, 2023, 24, .	6.5	0
Laboratory mice with a wild microbiota generate strong allergic immune responses. Science Immunology, 2023, 8, .	11.9	3
12649 Impact of Leave-on Skin Care Products on the Preservation of Skin Microbiome: An Exploration of Ecobiological Approach. Clinical, Cosmetic and Investigational Dermatology, 0, Volume 16, 2727-2735.	1.8	0
An insight into the functional alterations in the gut microbiome of healthy adults in response to a multi-strain probiotic intake: a single arm open label trial. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	1
Changes in oral health during aging in a novel non-human primate model. GeroScience, 2024, 46, 1909-1926.	4.6	0
Fecal microbiota cooperative metabolism of pectins derived from apple pomace: A functional metagenomic study. LWT - Food Science and Technology, 2023, 187, 115362.	5.2	0
Does ecological drift explain variation in microbiome composition among groups in a social host species?. Journal of Evolutionary Biology, 0, , .	1.7	0
Comparison of exoskeleton microbial communities of co-occurring native and invasive crayfish species. Journal of Invertebrate Pathology, 2023, 201, 107996.	3.2	2
Effect of removal of inhibitors on microbial communities and biogas yield of Jatropha curcas seeds during continuous anaerobic digestion. Journal of Cleaner Production, 2023, 426, 139154.	9.3	1
12658 Effect of recombination on genetic diversity of Caenorhabditis elegans. Scientific Reports, 2023, 13, .	3.3	O
Impact of Oral Administration of Lactiplantibacillus plantarum Strain CNCM Iâ^'4459 on Obesity Induced by High-Fat Diet in Mice. Bioengineering, 2023, 10, 1151.	3.5	0
12660 Similarity in milk microbiota in replicates. MicrobiologyOpen, 2023, 12, .	3.0	0

# ARTICLE		IF	CITATIONS
Smoking, tooth loss and oral hygiene practices have signifi 12661 microbiome of oral mucosal surfaces: a cross-sectional students.	cant and site-specific impacts on the dy. Journal of Oral Microbiology, 2023, 15,	2.7	2
Shifts in the swine nasal microbiota following Bordetella br study. Frontiers in Microbiology, 0, 14, .	onchiseptica challenge in a longitudinal	3.5	0
Trace elements and microbial community composition associated case study in Tablas de Daimiel National Park. Science of the		8.0	0
Stable functional structure despite high taxonomic variabil old-growth montane forests. Microbiome, 2023, 11, .	ity across fungal communities in soils of	11.1	1
Fungal community inside lichen: a curious case of sparse di Environmental Microbiomes, 2023, 18, .	versity and high modularity.	5.0	1
Marine resistome of a temperate zone: Distribution, diversi gradient. Water Research, 2023, 246, 120688.	ty, and driving factors across the trophic	11.3	1
Joining the bacterial conversation: increasing the cultivatio acyl-homoserine lactones and cAMP. Microbiology Spectru	n efficiency of soil bacteria with m, 0, , .	3.0	0
12670 Land use alters bacterial growth dynamics in soil. Environm	ental Microbiology, 2023, 25, 3239-3254.	3.8	1
Characterization of macroalgal-associated microbial comm depths at Manawai, Papahal, naumokual, kea Marine Nation	unities from shallow to mesophotic nal Monument, Hawaiâ€ï. PeerJ, 0, 11, e16114.	2.0	0
Effect of red wheat, aleurone, and testa layers on colon car gut microbiome composition in rats. Food and Function, 0,		4.6	0
Dietary phytosterols supplementation improves the growth fat of broiler chickens by regulating intestinal epithelial struscience and Technology, 2023, 305, 115786.	n performance and decreases the abdominal ucture and microbiota. Animal Feed	2.2	0
Effect of olive cake supplementation on faecal microbiota page cattle. Microbiological Research, 2023, 277, 127510.	profile of Holstein and Modicana dairy	5.3	0
Abrupt permafrost thaw triggers activity of copiotrophs an Microbiology Ecology, 2023, 99, .	d microbiome predators. FEMS	2.7	1
Comprehensive microbiome causal mediation analysis usin Biology Methods and Protocols, 2023, 8, .	g MiMed on user-friendly web interfaces.	2.2	2
Data pre-processing for analyzing microbiome data – A n Biotechnology Journal, 2023, 21, 4804-4815.	nini review. Computational and Structural	4.1	0
Transmission of synthetic seed bacterial communities to ra assembly and plant phenotype. , 0, 3, .	dish seedlings: impact on microbiota		2
Does the urinary microbiome profile change after treatmen Urology, 2023, 41, 3593-3598.	t of bladder cancer?. World Journal of	2.2	1
Soil health, microbial communities, and annual ryegrass yie practices. Agronomy Journal, 2024, 116, 380-393.	ld under contrasting management	1.8	0

# Art	TICLE	IF	CITATIONS
	ne from feeding impacts farmed Atlantic salmon (Salmo salar) gut microbiota and faecal score. uaculture, 2024, 579, 740174.	3.5	0
12684 <sc effe</sc 	cp>16S rRNA geneâ€based metaâ€analysis of the reptile gut microbiota reveals environmental ects, host influences and a limited core microbiota. Molecular Ecology, 2023, 32, 6044-6058.	3.9	2
	okaryotic communities inhabiting a high-radon subterranean ecosystem (Castañar Cave, Spain): vironmental and substrate-driven controls. Microbiological Research, 2023, 277, 127511.	5.3	2
12686 fun	nt species identity and plant-induced changes in soil physicochemistry—but not plant phylogeny or actional traits - shape the assembly of the root-associated soil microbiome. FEMS Microbiology blogy, 2023, 99, .	2.7	O
12687 Sh	gregative Soil Sampling Using Boot Covers Compared to Soil Grabs From Commercial Romaine Fields ows Similar Indicator Organism and Microbial Community Recoveries. Journal of Food Protection, 23, 86, 100177.	1.7	0
12688 Un Rep	cover a microbiota signature of upper respiratory tract in patients with SARS-CoV-2 +. Scientific ports, 2023, 13, .	3.3	1
	ological methane production and accumulation under sulfate-rich conditions at Cape Lookout ht, NC. Frontiers in Microbiology, 0, 14, .	3.5	0
12690 Ou the	tdoor climate drives diversity patterns of dominant microbial taxa in caves worldwide. Science of Total Environment, 2024, 906, 167674.	8.0	3
12691 Ma dist	croalgal microbiome biogeography is shaped by environmental drivers rather than geographical tance. Annals of Botany, 2024, 133, 169-182.	2.9	1
12692 to a	tical review of 16S rRNA gene sequencing workflow in microbiome studies: From primer selection advanced data analysis. Molecular Oral Microbiology, 2023, 38, 347-399.	2.7	5
12695 Mic Aot	crobial signatures of vertebrate visitation in floral nectar: a case study with two endemic tearoa New Zealand plant species. New Zealand Journal of Zoology, 0, , 1-11.	1.1	0
12697 sec	domicrobiome of <i>in vitro</i> and natural plants deciphering the endophytes-associated condary metabolite biosynthesis in <i>Picrorhiza kurrooa</i> , a Himalayan medicinal herb. crobiology Spectrum, 2023, 11, .	3.0	1
	man Breast Tissue Microbiota Reveals Unique Microbial Signatures that Correlate with Prognostic atures in Adult Ethiopian Women with Breast Cancer. Cancers, 2023, 15, 4893.	3.7	1
	ity modulates impact of BMI and gestational weight gain on gut microbiota in human pregnancy. t Microbes, 2023, 15, .	9.8	3
12701 Ma in F	inipulating atmospheric CO2 concentration induces shifts in wheat leaf and spike microbiomes and Fusarium pathogen communities. Frontiers in Microbiology, 0, 14 , .	3.5	0
12702 The	e Microbiomes of Various Types of Abandoned Fallow Soils of South Taiga (Novgorod Region,) Tj ETQq1 1 0.784	314 rgBT (3.0	/Pverlock
	cterial communities in a neotropical full-scale drinking water system including intermittent piped ter supply, from sources to taps. Environmental Science: Water Research and Technology, 0, , .	2.4	0
12705 per	ronic supplementation of a multi-ingredient herbal supplement increases speed of cognitive task formance alongside changes in the urinary metabolism of dopamine and the gut microbiome in gnitively intact older adults experiencing subjective memory decline: a randomized, placebo ntrolled, parallel groups investigation. Frontiers in Nutrition. 0. 10	3.7	0

# ARTICLE	IF	Citations
Ontogeny drives shifts in skin bacterial communities in facultatively paedomorphic salamanders. Microbiology (United Kingdom), 2023, 169, .	1.8	0
Elevated temperature alters microbial communities, but not decomposition rates, during 3 years o i>in situ peat decomposition. MSystems, 0, , .	of 3.8	O
First pelagic fish biodiversity assessment of Cosmonaut Sea based on environmental DNA. Marine Environmental Research, 2023, 192, 106225.	2.5	O
Chronic exposure to pesticides disrupts the bacterial and fungal co-existence and the cross-kingdone network characteristics of honey bee gut microbiome. Science of the Total Environment, 2024, 90 167530.	om 06, 8.0	0
Comprehensive Biodegradation Analysis of Chemically Modified Poly(3-hydroxybutyrate) Materials with Different Crystal Structures. Biomacromolecules, 2023, 24, 4939-4957.	5.4	2
Impact of Chronic Exposure to Arsenate through Drinking Water on the Intestinal Barrier. Chemica Research in Toxicology, 2023, 36, 1731-1744.	al 3.3	2
12714 Characterisation of Milk Microbiota from Subclinical Mastitis and Apparently Healthy Dairy Cattle Free State Province, South Africa. Veterinary Sciences, 2023, 10, 616.	in 1.7	O
Role of Microbiome in the Outcomes Following Surgical Repair of Perianal Fistula: Prospective Cohort Study Design and Preliminary Results. World Journal of Surgery, 2023, 47, 3373-3379.	1.6	1
Juvenile Striped Bass consume diverse prey in Chesapeake Bay tributaries. Marine and Coastal Fish 2023, 15, .	neries, 1.4	0
Tracking succession by means of 3D scans of plant communities in a glacier forefield to infer asser processes. Oikos, 2023, 2023, .	mbly 2.7	O
Maintaining beneficial alga-associated bacterial communities under heat stress: Insights from controlled co-culture experiments using antibiotic-resistant bacterial strains. FEMS Microbiology Ecology, 0, , .	2.7	1
Ethnic endotypes in paediatric atopic dermatitis depend on immunotype, lipid composition and microbiota of the skin. Journal of the European Academy of Dermatology and Venereology, 2024, 365-374.	38, 2.4	1
Host habitat rather than evolutionary history explains gut microbiome diversity in sympatric stickleback species. Frontiers in Microbiology, 0, 14, .	3.5	O
Genotype specific and microbiome effects of hypoxia in the model organism Daphnia magna. Journ Evolutionary Biology, 2023, 36, 1669-1683.	nal of 1.7	O
Capturing drifting species and moleculesâ€"Lessons learned from integrated approaches to assess marine metazoan diversity in highly dynamic waters. Environmental DNA, 2023, 5, 1541-1556.	s 5.8	O
Microbiome depiction through user-adapted bioinformatic pipelines and parameters. Journal of Medical Microbiology, 2023, 72, .	1.8	1
Optimizing Fecal Occult Blood Test (FOBT) Colorectal Cancer Screening Using Gut Bacteriome as Biomarker. Clinical Colorectal Cancer, 2024, 23, 22-34.e2.	a 2.3	1
Species-specific coral microbiome assemblages support host bleaching resistance during an extrer marine heatwave. Science of the Total Environment, 2024, 906, 167803.	me 8. 0	0

#	Article	IF	CITATIONS
12728	Optimization of fermentative parameters to improve hydrogen production: Is the co-fermentation of waste from the citrus agroindustrial an interesting alternative for energy recovery?. Journal of Environmental Chemical Engineering, 2023, 11, 111252.	6.7	4
12729	Hyperimmune bovine colostrum containing lipopolysaccharide antibodies (IMM124-E) has a nondetrimental effect on gut microbial communities in unchallenged mice. Infection and Immunity, 0, , .	2.2	O
12730	Manipulating <i>Agaricus bisporus</i> developmental patterns by passaging microbial communities in complex substrates. Microbiology Spectrum, 2023, 11 ,.	3.0	1
12731	Bacterial networks in Atlantic salmon with Piscirickettsiosis. Scientific Reports, 2023, 13, .	3.3	0
12732	Characteristics of Abdominal Visceral Adipose Tissue, Metabolic Health and the Gut Microbiome in Adults. Journal of Clinical Endocrinology and Metabolism, 2024, 109, 680-690.	3.6	1
12733	Anticancer drugs drive changes in the performance, abundance, diversity, and composition of eukaryotic communities of an aerobic granular sludge system. Chemosphere, 2023, 345, 140374.	8.2	2
12734	Prevalence and diversity of ascarid and strongylid nematodes in Australian Thoroughbred horses using next-generation sequencing and bioinformatic tools. Veterinary Parasitology, 2023, 323, 110048.	1.8	8
12735	Coexistence of specialist and generalist species within mixed plastic derivative-utilizing microbial communities. Microbiome, 2023, 11, .	11.1	0
12736	Monophasic Variant of Salmonella Typhimurium Infection Affects the Serum Metabolome in Swine. Microorganisms, 2023, 11, 2565.	3.6	0
12737	Cultivating Resilience in Dryland Soils: An Assisted Migration Approach to Biological Soil Crust Restoration. Microorganisms, 2023, 11, 2570.	3.6	O
12738	Ecological assessment of combined sewer overflow management practices through the analysis of benthic and hyporheic sediment bacterial assemblages from an intermittent stream. Science of the Total Environment, 2024, 907, 167854.	8.0	1
12739	Seasonal restructuring facilitates compositional convergence of gut microbiota in free-ranging rodents. FEMS Microbiology Ecology, 0, , .	2.7	O
12741	Sulforaphane Bioavailability in Healthy Subjects Fed a Single Serving of Fresh Broccoli Microgreens. Foods, 2023, 12, 3784.	4.3	0
12742	Disturbance frequency directs microbial community succession in marine biofilms exposed to shear. MSphere, 0, , .	2.9	O
12744	Pilot Study: Decoding the Skin microbiome of Bowhead (Balaena mysticetus) and Killer whales (Orcinus orca) in Nunavut, Canada Arctic Science, 0, , .	2.3	0
12745	Optimization of high-throughput 16S rRNA gene amplicon sequencing: an assessment of PCR pooling, mastermix use and contamination. Microbial Genomics, 2023, 9, .	2.0	O
12746	Composition and distribution of diazotrophs in the Baltic Sea. Estuarine, Coastal and Shelf Science, 2023, 294, 108527.	2.1	0
12747	Strain-resolved metagenomics approaches applied to biogas upgrading. Environmental Research, 2024, 240, 117414.	7.5	2

#	ARTICLE	IF	CITATIONS
12748	Microbiome composition and central serotonergic activity in patients with depression and type 1 diabetes. European Archives of Psychiatry and Clinical Neuroscience, 0 , , .	3.2	2
12749	Gut microbiota in adults with moyamoya disease: characteristics and biomarker identification. Frontiers in Cellular and Infection Microbiology, 0, 13 , .	3.9	0
12750	Bacteria associated with ovine gut parasites <i>Trichuris ovis</i> and <i>Haemonchus contortus</i> Journal of Helminthology, 2023, 97, .	1.0	0
12751	Microbial Community Profiling from Natural Whey Starter to Mozzarella among Different Artisanal Dairy Factories in Apulia Region (Italy). Fermentation, 2023, 9, 911.	3.0	0
12752	A crossâ€sectional cohort study on the skin microbiota in patients with different acne durations. Experimental Dermatology, 2023, 32, 2102-2111.	2.9	1
12753	A specific gut microbiota signature is associated with an enhanced GLP-1 and GLP-2 secretion and improved metabolic control in patients with type 2 diabetes after metabolic Roux-en-Y gastric bypass. Frontiers in Endocrinology, 0, 14 , .	3.5	0
12756	Associations between dietary habits, socio-demographics and gut microbial composition in adolescents. British Journal of Nutrition, 2024, 131, 809-820.	2.3	0
12757	What happens to biomass burning-emitted particles in the ocean? A laboratory experimental approach based on their tracers. Science of the Total Environment, 2024, 907, 167770.	8.0	0
12758	Microbial community function and bacterial pathogen composition in pit latrines in peri-urban Malawi., 2023, 2, e0000171.		0
12759	<i>i>Lactococcus lactis</i> <scp>CNCM</scp> lâ€5388 versus <scp>NCDO2118</scp> by its <scp>GABA</scp> hyperproduction ability, counteracts faster stressâ€induced intestinal hypersensitivity in rats. FASEB Journal, 2023, 37, .	0.5	0
12760	Maternal Vertical Microbial Transmission During Skin-to-Skin Care. Advances in Neonatal Care, 0, , .	1.1	0
12761	Holistic integration of omics data reveals the drivers that shape the ecology of microbial meat spoilage scenarios. Frontiers in Microbiology, 0, 14, .	3.5	0
12764	Assessing the contribution of bacteria to the heat tolerance of experimentally evolved coral photosymbionts. Environmental Microbiology, 2023, 25, 3298-3318.	3.8	4
12765	Fungi and bacteria in the beds of rural and urban infants correlate with later risk of atopic diseases. Clinical and Experimental Allergy, 2023, 53, 1268-1278.	2.9	1
12766	Geomicrobiology of the Rincon de Parangueo maar crater: Exploring the link between an evolving extreme environment and its potential metabolic diversity. Freshwater Biology, 2023, 68, 1818-1838.	2.4	0
12768	Saposhnikovia divaricata root and its major components ameliorate inflammation and altered gut microbial diversity and compositions in DSS-induced colitis. Integrative Medicine Research, 2023, , 100998.	1.8	0
12769	Leaf litter decomposition and detrital communities following the removal of two large dams on the Elwha River (Washington, USA). Frontiers in Ecology and Evolution, $0,11,1$	2.2	0
12770	Inadequate Sampling Frequency and Imprecise Taxonomic Identification Mask Results in Studies of Migratory Freshwater Fish Ichthyoplankton. Fishes, 2023, 8, 518.	1.7	1

#	ARTICLE	IF	CITATIONS
12771	Marine sediments are identified as an environmental reservoir for Escherichia coli: comparing signature-based and novel amplicon sequencing approaches for microbial source tracking. Science of the Total Environment, 2024, 907, 167865.	8.0	0
12774	Insight into antimicrobial resistance at a new beef cattle feedlot in western Canada. MSphere, 0, , .	2.9	O
12775	Composition and activity of soil microbial communities in native and non-native vegetation of southern California. Applied Soil Ecology, 2024, 193, 105164.	4.3	0
12776	Sympathetic activity regulates epithelial proliferation and wound healing via adrenergic receptor α2A. Scientific Reports, 2023, 13, .	3.3	1
12778	Associations Between Brain-Gut Axis and Psychological Distress in Fibromyalgia: A Microbiota and Magnetic Resonance Imaging Study. Journal of Pain, 2023, , .	1.4	0
12779	The uselessness of using salivary microbiota in forensic identification purposes of a person with recent antibiotic use. Legal Medicine, 2023, , 102338.	1.3	O
12780	Supplementation of microencapsulated sodium butyrate on the performance, haemato-biochemical profile and intestinal microbiota composition of broiler chickens challenged with <i>Eimeria</i> spp <i>.</i> . Canadian Journal of Animal Science, 2024, 104, 26-39.	1.5	0
12781	Degenerative Cervical Myelopathy induces sex-specific dysbiosis in mice. Frontiers in Microbiology, 0, 14, .	3.5	1
12782	A comprehensive analysis of gut and skin microbiota in canine atopic dermatitis in Shiba Inu dogs. Microbiome, 2023, 11 , .	11.1	2
12783	Secretory IgA impacts the microbiota density in the human nose. Microbiome, 2023, 11, .	11.1	0
12784	Epithelial Dual Oxidase 2 Shapes the Mucosal Microbiome and Contributes to Inflammatory Susceptibility. Antioxidants, 2023, 12, 1889.	5.1	2
12785	Bacillus velezensis ZN-S10 Reforms the Rhizosphere Microbial Community and Enhances Tomato Resistance to TPN. Plants, 2023, 12, 3636.	3.5	1
12786	Variability in lake bacterial growth and primary production under lake ice: Evidence from early winter to spring melt. Limnology and Oceanography, 2023, 68, 2603-2616.	3.1	1
12787	Extracellular polymeric substances are closely related to land cover, microbial communities, and enzyme activity in tropical soils. Soil Biology and Biochemistry, 2023, 187, 109221.	8.8	1
12788	In situ microbial community analysis of container soilless substrates. Acta Horticulturae, 2023, , 725-730.	0.2	0
12789	Inoculating native microorganisms improved soil function and altered the microbial composition of a degraded soil. Restoration Ecology, 2024, 32, .	2.9	O
12790	Endophyte Community Changes in the Seeds of Eight Plant Species following Inoculation with a Multi-Endophytic Bacterial Consortium and an Individual Sphingomonas wittichii Strain Obtained from Noccaea caerulescens. Plants, 2023, 12, 3660.	3.5	0
12791	A comparison of microbiota isolation methods reveals habitat preferences for fermentative yeasts and plant pathogenic fungi in the grape berry. Food Microbiology, 2023, , 104408.	4.2	O

# ARTICLE	IF	CITATIONS
Food desert residence has limited impact on veteran fecal microbiome composition: a U.S. Veteran Microbiome Project study. MSystems, 0, , .	3.8	O
Supragingival mycobiome of HIV-exposed-but-uninfected children reflects a stronger correlation with caries-free-associated taxa compared to HIV-infected or uninfected children. Microbiology Spectrum, 0, , .	3.0	0
Density-dependent effects of exotic brook trout on aquatic communities in mountain lakes revealed by environmental DNA and morphological taxonomy. Hydrobiologia, 2024, 851, 1489-1512.	2.0	1
Unveiling the early life core microbiome of the sea cucumber Apostichopus japonicus and the unexpected abundance of the growth-promoting Sulfitobacter. Animal Microbiome, 2023, 5, .	3.8	1
Metal transporter SLC39A14/ZIP14 modulates regulation between the gut microbiome and host metabolism. American Journal of Physiology - Renal Physiology, 2023, 325, G593-G607.	3.4	1
Fertility islands, keys to the establishment of plant and microbial diversity in a highly alkaline hot desert. Journal of Arid Environments, 2023, 219, 105074.	2.4	1
Microbiota and Nutrient Portraits of European Roe Deer (Capreolus capreolus) Rumen Contents in Characteristic Southern German Habitats. Microbial Ecology, 2023, 86, 3082-3096.	2.8	0
Relationship between the bacterial ocular surface microbiota and outcomes for cats with feline herpesvirus type 1 ocular surface disease. Veterinary Ophthalmology, 0 , , .	1.0	0
Severe Prolonged Drought Favours Stress-Tolerant Microbes in Australian Drylands. Microbial Ecology, 2023, 86, 3097-3110.	2.8	0
Bacterial tolerance to host-exuded specialized metabolites structures the maize root microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	4
12807 Influence of organic plant breeding on the rhizosphere microbiome of common bean (Phaseolus) Tj ETQq0 0	0 rgBT ₃ /Qverlo	ock 10 Tf 50
12808 Direct biological fixation provides a freshwater sink for N2O. Nature Communications, 2023, 14, .	12.8	0
Contaminants from dredged sediments alter the transcriptome of Manila clam and induce shifts in microbiota composition. BMC Biology, 2023, 21, .	3.8	1
Community composition and the environment modulate the population dynamics of type VI secretion in human gut bacteria. Nature Ecology and Evolution, 2023, 7, 2092-2107.	7.8	4
Heterogeneity of gut microbiome compositions in the third decade of life in Japanese women: insights from a comparative analysis. Bioscience of Microbiota, Food and Health, 2023, , .	1.8	1
A pilot study of the use of the oral and faecal microbiota for the diagnosis of ulcerative colitis and Crohn's disease in a paediatric population. Frontiers in Pediatrics, $0,11,10$	1.9	0
Phage therapy minimally affects the water microbiota in an Atlantic salmon (Salmo salar) rearing system while still preventing infection. Scientific Reports, 2023, 13, .	3.3	2
Drivers of plankton community structure in intermittent and continuous coastal upwelling 12814 systems–from microbes and microscale in-situ imaging to large scale patterns. Frontiers in Marine Science, 0, 10, .	2.5	O

# ARTICLE	IF	CITATIONS
lmpact of wastewater treatment upgrade and nitrogen removal on bacterial communities and their interactions in eutrophic prairie streams. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
Microbial hitchhikers harbouring antimicrobial-resistance genes in the riverine plastisphere. Microbiome, 2023, 11, .	11.1	4
Meso―and thermophilic posttreatment of press water coming from a thermophilic municipal solid waste digester. Biotechnology and Bioengineering, 2024, 121, 266-280.	3.3	0
Evaluation of the Immunoprotective Capacity of Five Vaccine Candidate Proteins against Avian Necrotic Enteritis and Impact on the Caecal Microbiota of Vaccinated Birds. Animals, 2023, 13, 3323.	2.3	0
An obesogenic diet increases atherosclerosis through promoting microbiota dysbiosis-induced gut lymphocyte trafficking into the periphery. Cell Reports, 2023, 42, 113350.	6.4	0
Body site microbiota of Magellanic and king penguins inhabiting the Strait of Magellan follow species-specific patterns. Peerl, 0, 11 , e16290.	2.0	0
Smoking and salivary microbiota: a cross-sectional analysis of an Italian alpine population. Scientific Reports, 2023, 13, .	3.3	1
Anionic nanocellulose as competing agent in microbial DNA extraction from mine process samples. Journal of Microbiological Methods, 2023, 215, 106850.	1.6	1
Genomic surveillance reveals early detection and transition of delta to omicron lineages of SARS-CoV-2 variants in wastewater treatment plants of Pune, India. Environmental Science and Pollution Research, 2023, 30, 118976-118988.	5. 3	2
Soil and bark biodiversity forms discrete islands between vineyards that are not affected by distance or management regime. Environmental Microbiology, 2023, 25, 3655-3670.	3.8	0
Widespread and largely unknown prophage activity, diversity, and function in two genera of wheat phyllosphere bacteria. ISME Journal, 2023, 17, 2415-2425.	9.8	0
Earthworm activities change phosphorus mobilization and uptake strategies in deep soil layers. Applied Soil Ecology, 2024, 193, 105168.	4.3	0
Mass-immigration shapes the antibiotic resistome of wastewater treatment plants. Science of the Total Environment, 2024, 908, 168193.	8.0	0
Exploring the influence of climatic variables on mycobiome composition and community diversity in lichens: insights from structural equation modeling analysis. Environmental Microbiomes, 2023, 18, .	5.0	1
Microbial community dynamics and cycling of plutonium and ironÂinÂa seasonally stratified and radiologically contaminated pond. Scientific Reports, 2023, 13, .	3.3	1
Diagnosis of Crohn's disease and ulcerative colitis using the microbiome. BMC Microbiology, 2023, 2	23, 3.3	1
Effects of a stabilized stannous fluoride dentifrice on clinical, immunomodulatory, and microbial outcomes in a human experimental gingivitis model. Journal of Periodontology, 0, , .	3.4	0
Multigenerational effects of elevated temperature on host-microbiota interactions in the marine 12832 water flea Diaphanosoma celebensis exposed to micro- and nanoplastics. Journal of Hazardous Materials, 2024, 465, 132877.	12.4	O

#	ARTICLE	IF	CITATIONS
12833	Convergence of gut microbiota in myrmecophagous amphibians. Proceedings of the Royal Society B: Biological Sciences, 2023, 290, .	2.6	0
12834	Perturbations in lipid metabolism and gut microbiota composition precede cardiac dysfunction in a mouse model of thalassemia. FASEB Journal, 2023, 37, .	0.5	O
12835	Gut microbiota response to in vitro transit time variation is mediated by microbial growth rates, nutrient use efficiency and adaptation to in vivo transit time. Microbiome, $2023,11,1$	11.1	5
12836	Environmental bacteria increase population growth of hydra at low temperature. Frontiers in Microbiology, 0, 14, .	3.5	O
12837	Effects of Lactiplantibacillus plantarum and Lacticaseibacillus paracasei supplementation on the single-cell fecal parasitome in children with celiac disease autoimmunity: a randomized, double-blind placebo-controlled clinical trial. Parasites and Vectors, 2023, 16, .	2.5	O
12838	Domestication shapes the pig gut microbiome and immune traits from the scale of lineage to population. Journal of Evolutionary Biology, 2023, 36, 1695-1711.	1.7	1
12839	Transplantation impacts on the oral microbiome of kidney recipients and donors. , $0, 2, .$		0
12840	Investigating Yeast–Lactobacilli Interactions through Co-Culture Growth and Metabolite Analysis. Fermentation, 2023, 9, 933.	3.0	1
12841	Phylogenetic variation in raw cow milk microbiota and the impact of forage combinations and use of silage inoculants. Frontiers in Microbiology, 0, 14 , .	3.5	0
12842	The Oral Microbiome across Oral Sites in Cats with Chronic Gingivostomatitis, Periodontal Disease, and Tooth Resorption Compared with Healthy Cats. Animals, 2023, 13, 3544.	2.3	1
12843	Soil amendment with insect frass and exuviae affects rhizosphere bacterial community, shoot growth and carbon/nitrogen ratio of a brassicaceous plant. Plant and Soil, 2024, 495, 631-648.	3.7	0
12844	Nanopore-Sequencing Metabarcoding for Identification of Phytopathogenic and Endophytic Fungi in Olive (Olea europaea) Twigs. Journal of Fungi (Basel, Switzerland), 2023, 9, 1119.	3.5	O
12845	Anti-diarrheal drug loperamide induces dysbiosis in zebrafish microbiota via bacterial inhibition. Microbiome, 2023, 11 , .	11.1	0
12846	Copper reduces the virulence of bacterial communities at environmentally relevant concentrations. Environment International, 2023, 182, 108295.	10.0	0
12847	Do regrowth age and microbial inoculant usage affect the microbial diversity and fermentation characteristics of forage peanut silage?. Grass and Forage Science, 2023, 78, 602-621.	2.9	0
12848	Oral lactoferrin administration does not impact the diversity or composition of the infant gut microbiota in a Peruvian cohort. Microbiology Spectrum, 2023, 11 , .	3.0	0
12849	Characterization of bacterial species and antibiotic resistance observed in Seoul, South Korea's popular Gangnam-gu area. Heliyon, 2023, 9, e21751.	3.2	1
12850	Common aquarium antiseptics do not cause long-term shifts in coral microbiota but may impact coral growth rates. Frontiers in Marine Science, 0, 10, .	2.5	O

# ARTICLE	IF	CITATIONS
Concentration-dependent effect of plant secondary metabolites on bacterial and fungal microbiomes in caterpillar guts. Microbiology Spectrum, 0, , .	3.0	1
Biodegradation and sorption of nutrients and endocrine disruptors in a novel concrete-based substrate in vertical-flow constructed wetlands. Chemosphere, 2024, 346, 140531.	8.2	1
12854 A genome catalog of the early-life human skin microbiome. Genome Biology, 2023, 24, .	8.8	0
Environmental filtering along a bathymetric gradient: A metabarcoding metaâ€analysis of freeâ€living nematodes. Molecular Ecology, 2023, 32, 6177-6189.	3.9	3
12856 Characterization of the soil resistome and mobilome in Namib Desert soils. International Microbiology, 0, , .	2.4	0
Strain-resolved metagenomic analysis of the gut as a reservoir for bloodstream infection pathogens among premature infants in Singapore. Gut Pathogens, 2023, 15, .	3.4	0
Combined Dietary Administration of Chlorella fusca and Ethanol-Inactivated Vibrio proteolyticus Modulates Intestinal Microbiota and Gene Expression in Chelon labrosus. Animals, 2023, 13, 3325.	2.3	0
MiTree: A Unified Web Cloud Analytic Platform for User-Friendly and Interpretable Microbiome Data Mining Using Tree-Based Methods. Microorganisms, 2023, 11, 2816.	3.6	1
Evaluation of sequential filtration and centrifugation to capture environmental DNA and survey microbial eukaryotic communities in aquatic environments. Molecular Ecology Resources, 2024, 24, .	4.8	0
Vaccination with an HIV T-Cell Immunogen (HTI) Using DNA Primes Followed by a ChAdOx1-MVA Boost I Immunogenic in Gut Microbiota-Depleted Mice despite Low IL-22 Serum Levels. Vaccines, 2023, 11, 166	ls 3. 4.4	0
Host-microbiota-parasite interactions in two wild sparid fish species, Diplodus annularis and Oblada melanura (Teleostei, Sparidae) over a year: a pilot study. BMC Microbiology, 2023, 23, .	3.3	0
Unveiling the microbiome during post-partum uterine infection: a deep shotgun sequencing approach to characterize the dairy cow uterine microbiome. Animal Microbiome, 2023, 5, .	3.8	0
The Bern Birth Cohort (BeBiCo) to study the development of the infant intestinal microbiota in a high-resource setting in Switzerland: rationale, design, and methods. BMC Pediatrics, 2023, 23, .	1.7	0
Metabolomics and Microbiomics Insights into Differential Surface Fouling of Three Macroalgal Species of Fucus (Fucales, Phaeophyceae) That Co-Exist in the German Baltic Sea. Marine Drugs, 2023, 2 595.	21, 4.6	0
Gallionellaceae in rice root plaque: metabolic roles in iron oxidation, nutrient cycling, and plant interactions. Applied and Environmental Microbiology, 0, , .	3.1	1
Tar patties are hotspots of hydrocarbon turnover and nitrogen fixation during a nearshore pollution event in the oligotrophic southeastern Mediterranean Sea. Marine Pollution Bulletin, 2023, 197, 115747.	5.0	2
Contrasting strengths of eDNA and electrofishing compared to historic records for assessing fish community diversity and composition. Canadian Journal of Fisheries and Aquatic Sciences, 0, , .	1.4	0
Comparative analysis of rhizobial and bacterial communities in experimental cotton fields: Impacts of conventional and conservation soil management in the Texas High Plains. Soil and Tillage Research, 2024, 236, 105920.	5.6	0

# ARTICLE		IF	CITATIONS
Effect of long-term conservation tillage management on microbial divers rainfed conditions. Soil and Tillage Research, 2024, 236, 105923.	ity under Mediterranean	5.6	1
Mycocentric fertilisation of ectomycorrhizae-inoculated <i>Pinus radiata production alters root microbiome and growth outcomes. Australian For</i>	during containerised estry, 2023, 86, 110-128.	0.9	0
Metabolic and fecal microbial changes in adult fetal growth restricted mi 95, 647-659.	ce. Pediatric Research, 2024,	2.3	0
Chicken caecal enterotypes in indigenous Kadaknath and commercial Co with Campylobacter abundance and influenced by farming practices. , 0,			O
Tillandsia landbeckii phyllosphere and laimosphere as refugia for bacteria environment. Microbiome, 2023, 11, .	l life in a hyperarid desert	11.1	1
Oligoagars and microbial agents show potential for Porphyra disease pre $13, \dots$	vention. AMB Express, 2023,	3.0	O
Association between Gut Microbiota and Breast Cancer: Diet as a Potent Nutrients, 2023, 15, 4628.	ial Modulating Factor.	4.1	1
Cyanosphere Dynamic During Dolichospermum Bloom: Potential Roles in Proliferation. Microbial Ecology, 2024, 87, .	Cyanobacterial	2.8	O
Fecal microbiota transplantation promotes reduction of antimicrobial reservable replacement. Science Translational Medicine, 2023, 15, .	sistance by strain	12.4	8
Vaginal microbial dynamics and pathogen colonization in a humanized m Biofilms and Microbiomes, 2023, 9, .	aicrobiota mouse model. Npj	6.4	2
12880 Exploring the microbiome of two uterine sites in cows. Scientific Reports	, 2023, 13, .	3.3	1
Coordination of Root Traits and Rhizosphere Microbial Community in Tea under Drought and Rehydration. Forests, 2023, 14, 2134.	a (Camellia sinensis L.) Plants	2.1	O
Bacterial Community Composition and Presence of Plasmids in the Endo Rhizosphere-Associated Microbiota of Sea Fig (Carpobrotus aequilaterus		1.7	0
eDNA Metabarcoding Analysis as Tool to Assess the Presence of Non-Ind Study in the Bilge Water. Diversity, 2023, 15, 1117.	igenous Species (NIS): A Case	1.7	O
Linking Topographical Ring Features to Geochemical and Geophysical An Journal, 2024, 41, 120-127.	omalies. Geomicrobiology	2.0	0
Metabarcoding read abundances of orchid mycorrhizal fungi are correlat estimated using ddPCR. New Phytologist, 0, , .	ed to copy numbers	7.3	1
Early Colonization of the Intestinal Microbiome of Neonatal Piglets Is Inf Microbiome. Animals, 2023, 13, 3378.	uenced by the Maternal	2.3	1
Persistent effects of intramammary ceftiofur treatment on the gut micro resistance in dairy cattle. Animal Microbiome, 2023, 5 , .	biome and antibiotic	3.8	O

# ARTICLE	IF	CITATIONS
Semi-arid soil bacterial communities are refined by altered plant selection pressure under conservation management practices. Applied Soil Ecology, 2024, 194, 105191.	4.3	0
Metaproteogenomic analysis of saliva samples from Parkinson's disease patients with cognitive impairment. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	0
Interactions between root hairs and the soil microbial community affect the growth of maize seedlings. Plant, Cell and Environment, 2024, 47, 611-628.	5.7	3
The prebiotic potential of RS-3 preparations for pre- and post-weaning piglets. Bioactive Carbohydrate and Dietary Fibre, 2023, 30, 100388.	es <u>2.7</u>	0
The vulvar microbiome in lichen sclerosus and high-grade intraepithelial lesions. Frontiers in Microbiology, 0, 14, .	3.5	1
Host species and habitat shape fish-associated bacterial communities: phylosymbiosis between fish at their microbiome. Microbiome, 2023, 11 , .	nd 11.1	1
Study protocol for FIBROKIT: a new tool for fibromyalgia diagnosis and patient follow-up. Frontiers in Neurology, 0, 14, .	2.4	0
Product-inhibition feedbacks, not microbial population level tradeoffs or soil pH, regulate 12896 decomposition potential under nutrient eutrophication. Soil Biology and Biochemistry, 2024, 189, 109247.	8.8	0
Effect of castration timing and weaning strategy on the taxonomic and functional profile of ruminal bacteria and archaea of beef calves. Animal Microbiome, 2023, 5, .	3.8	0
Shifts in the coral microbiome in response to <i>in situ</i> experimental deoxygenation. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
Tracking the fecal mycobiome through the lifespan of production pigs and a comparison to the feral pig. Applied and Environmental Microbiology, 2023, 89, .	3.1	0
Impacts of Oak Mulch Amendments on Rhizosphere Microbiome of Citrus Trees Grown in Florida Flatwood Soils. Microorganisms, 2023, 11, 2764.	3.6	0
Extended soil surface drying triggered by subsurface drip irrigation decouples carbon and nitrogen cycles and alters microbiome composition. Frontiers in Soil Science, 0, 3, .	2.2	0
The immunostimulatory role of an Enterococcus-dominated gut microbiota in host protection against bacterial and fungal pathogens in Galleria mellonella larvae. Frontiers in Insect Science, 0, 3, .	2.1	0
A multiâ€study analysis of gut microbiome data from the blue mussel (<i>Mytilus edulis</i>) emphasi the impact of depuration on biological interpretation. Environmental Microbiology, 2023, 25, 3435-3449.	ises 3.8	0
Drivers of pelagic and benthic microbial communities on Central Arctic seamounts. Frontiers in Marine Science, 0, 10 , .	2.5	O
Microbe-associated molecular pattern recognition receptors have little effect on endophytic Arabidopsis thaliana microbiome assembly in the field. Frontiers in Plant Science, 0, 14, .	3.6	0
Distinct Microbial Taxa Are Associated with LDL-Cholesterol Reduction after 12 Weeks of Lactobacillus plantarum Intake in Mild Hypercholesterolemia: Results of a Randomized Controlled Study. Probiotics and Antimicrobial Proteins, 0, , .	3.9	0

# ARTICLE	IF	CITATIONS
12907 Influence of Sex and a High-Fiber Diet on the Gut Microbiome of Alentejano Pigs Raised to Heavy Weights. Veterinary Sciences, 2023, 10, 641.	1.7	0
Taxonomic and environmental distribution of bacterial amino acid auxotrophies. Nature Communications, 2023, 14, .	12.8	3
Dietary Patterns Are Associated with the Gut Microbiome and Metabolic Syndrome in Mexican Postmenopausal Women. Nutrients, 2023, 15, 4704.	4.1	0
Effect of Sampling Method on Detection of the Equine Uterine Microbiome during Estrus. Veterinary Sciences, 2023, 10, 644.	1.7	1
Survey of the infant male urobiome and genomic analysis of Actinotignum spp Npj Biofilms and Microbiomes, 2023, 9, .	6.4	0
Dynamics of the Apostichopus californicus-associated flavivirus under suboxic conditions and organic matter amendment. Frontiers in Marine Science, 0, 10, .	2.5	0
TIGIT+ NK cells in combination with specific gut microbiota features predict response to checkpoint inhibitor therapy in melanoma patients. BMC Cancer, 2023, 23, .	2.6	0
Oyster Reefs Are Reservoirs for Potential Pathogens in a Highly Disturbed Subtropical Estuary. Environments - MDPI, 2023, 10, 205.	3.3	1
Environmental Factors and the Symbiont Cardinium Influence the Bacterial Microbiome of Spider Mites Across the Landscape. Microbial Ecology, 2024, 87, .	2.8	0
Lactobacillus from the Altered Schaedler Flora maintain IFNγ homeostasis to promote behavioral stress resilience. Brain, Behavior, and Immunity, 2024, 115, 458-469.	4.1	1
<scp>MuDoGeR</scp> : <scp>Multiâ€Domain</scp> Genome recovery from metagenomes made easy. Molecular Ecology Resources, 0, , .	4.8	2
Associations of Plastic Bottle Exposure with Infant Growth, Fecal Microbiota, and Short-Chain Fatty Acids. Microorganisms, 2023, 11, 2924.	3.6	0
Carbon and Nutrients from Organic Residues Modulate the Dynamics of Prokaryotic and Fungal Communities. Microorganisms, 2023, 11, 2905.	3 . 6	0
Development of a Protocol for Anaerobic Preparation and Banking of Fecal Microbiota 12920 Transplantation Material: Evaluation of Bacterial Richness in the Cultivated Fraction. Microorganisms, 2023, 11, 2901.	3.6	0
Strong chemotaxis by marine bacteria towards polysaccharides is enhanced by the abundant organosulfur compound DMSP. Nature Communications, 2023, 14, .	12.8	2
Bacterial Biomarkers of the Oropharyngeal and Oral Cavity during SARS-CoV-2 Infection. Microorganisms, 2023, 11, 2703.	3. 6	0
12923 Spatial compartmentalisation of bacteria in phoronid microbiomes. Scientific Reports, 2023, 13, .	3.3	0
Bacterial biota composition in gut regions of black soldier fly larvae reared on industrial residual streams: revealing community dynamics along its intestinal tract. Frontiers in Microbiology, 0, 14, .	3.5	0

#	Article	IF	CITATIONS
12925	Effects of low-concentration spinetoram wax-based bait stations on Bactrocera dorsalis (Diptera:) Tj ETQq0 0 0 rg	BŢ./Overlo	ck 10 Tf 50
12926	Addition of soluble fiber to standard purified diets is important for gut morphology in mice. Scientific Reports, 2023, 13, .	3.3	O
12927	<i>Ixodes ricinus</i> tick bacteriome alterations based on a climatically representative survey in Hungary. Microbiology Spectrum, 2023, 11 , .	3.0	2
12928	Volatile methyl jasmonate from roots triggers host-beneficial soil microbiome biofilms. Nature Chemical Biology, 0, , .	8.0	0
12929	Direct contact of fermented rice bran beds promotes food-to-hand transmission of lactic acid bacteria. FEMS Microbiology Letters, 2023, 370, .	1.8	2
12930	Wild bee and pollen microbiomes across an urban-rural divide. FEMS Microbiology Ecology, 0, , .	2.7	0
12931	Distinct microbial communities degrade cellulose diacetate bioplastics in the coastal ocean. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
12932	Gut microbiomes of agropastoral children from the Adadle region of Ethiopia reflect their unique dietary habits. Scientific Reports, 2023, 13, .	3.3	0
12933	Bacterial and Fungal Endophytes of Grapevine Cultivars Growing in Primorsky Krai of Russia. Horticulturae, 2023, 9, 1257.	2.8	0
12934	<i>Potentilla parvifolia</i> strongly influenced soil microbial community and environmental effect along an altitudinal gradient in central Qilian Mountains in western China. Ecology and Evolution, 2023, 13, .	1.9	O
12935	Establishment of plastic-associated microbial community from superworm gut microbiome. Environment International, 2024, 183, 108349.	10.0	0
12936	Freshwater plastispheres as a vector for foodborne bacteria and viruses. Environmental Microbiology, 2023, 25, 2864-2881.	3.8	0
12937	Sequential host-bacteria and bacteria-bacteria interactions determine the microbiome establishment of Nematostella vectensis. Microbiome, 2023, 11 , .	11.1	0
12938	Comparative Analysis of Bacteria, Fungi, and Arbuscular Mycorrhizal Fungi in Medicinal Plants Lippia alba and Petiveria alliacea in Colombia. Diversity, 2023, 15, 1167.	1.7	O
12939	Profiling Prokaryotic Communities and Aaptamines of Sponge Aaptos suberitoides from Tulamben, Bali. Marine Biotechnology, 0, , .	2.4	0
12940	Rhizosphere microbial community structure differs between constant subzero and freeze-thaw temperature regimes in a subarctic soil. FEMS Microbiology Ecology, 2023, 99, .	2.7	1
12941	Long-term continuous cultivation of Kenyan infant fecal microbiota using the host adapted PolyFermS model. Scientific Reports, 2023, 13, .	3.3	0
12942	Dissemination of antibiotic resistance genes through soil-plant-earthworm continuum in the food production environment. Environment International, 2024, 183, 108374.	10.0	0

# A	RTICLE	IF	CITATIONS
12943 N	Molecular interactions in an holobiont-pathogen model: Integromics in gilthead seabream infected vith Sparicotyle chrysophrii. Aquaculture, 2024, 581, 740365.	3.5	0
12944 E	Dynamics of Endophytic Fungal Communities Associated with Cultivated Medicinal Plants in Farmland cosystem. Journal of Fungi (Basel, Switzerland), 2023, 9, 1165.	3.5	O
	Inveiling microbiome changes in Mediterranean octocorals during the 2022 marine heatwaves: uantifying key bacterial symbionts and potential pathogens. Microbiome, 2023, $11,\ldots$	11.1	2
12946 p	NA from non-viable bacteria biases diversity estimates in the corals Acropora loripes and ocillopora acuta. Environmental Microbiomes, 2023, $18, \ldots$	5.0	1
12947 K	dicrobial tapestry of the Shulgan-Tash cave (Southern Ural, Russia): influences of environmental actors on the taxonomic composition of the cave biofilms. Environmental Microbiomes, 2023, 18, .	5.0	0
12948 D	Diversity of heterotrophic picoeukaryotes in the ice of the Kandalaksha Gulf (White Sea, Russia) based n rRNA gene high-throughput sequencing. Marine Biodiversity, 2023, 53, .	1.0	O
12949 b	ntroducing an environmental microbiome to axenic <i>Aedes aegypti</i> mosquitoes documents acterial responses to a blood meal. Applied and Environmental Microbiology, 0, , .	3.1	0
12950 ^{ï»} aı	¿Exploring benthic diatom diversity in the West Antarctic Peninsula: insights from a morphological nd molecular approach. Metabarcoding and Metagenomics, 0, 7, .	0.0	O
12951 H	low pondscapes function: connectivity matters for biodiversity even across small spatial scales in quatic metacommunities. Ecography, 0, , .	4.5	2
12952 d	ermentation of brown seaweeds Alaria esculenta and Saccharina latissima for new product evelopment using Lactiplantbacillus plantarum, Saccharomyces cerevisiae and kombucha SCOBY. Igal Research, 2023, 76, 103322.	4.6	O
12953 B	lend of natural and natural identical essential oil compounds as a strategy to improve the gut ealth of weaning pigs. Animal, 2023, 17, 101031.	3.3	0
12954 C	Connecting thiamine availability to the microbial community composition in Chinook salmon pawning habitats of the Sacramento River basin. Applied and Environmental Microbiology, 0, , .	3.1	O
	apid intestinal and systemic metabolic reprogramming in an immunosuppressed environment. BMC Microbiology, 2023, 23, .	3.3	0
12956 N in	dicrobiota-mediated effects of Parkinson's disease medications on Parkinsonian non-motor symptoms n male transgenic mice. MSphere, 0, , .	2.9	O
	ffect of seaweed canopy disturbance on understory microbial communities on rocky shores. rontiers in Marine Science, $0,10,10$	2.5	1
12958 ln	npact of hydrodynamics on community structure and metabolic production of marine biofouling ormed in a highly energetic estuary. Marine Environmental Research, 2023, 192, 106241.	2.5	0
	arly life gut microbiome in children following spontaneous preterm birth and maternal reeclampsia. IScience, 2023, 26, 108311.	4.1	O
12963 Ex	xploring the role of mobile genetic elements in shaping plant–bacterial interactions for sustainable griculture and ecosystem health. Plants People Planet, 2024, 6, 408-420.	3.3	О

#	ARTICLE	IF	CITATIONS
12964	Consumption of sucralose- and acesulfame-potassium-containing diet soda alters the relative abundance of microbial taxa at the species level: findings of two pilot studies. Applied Physiology, Nutrition and Metabolism, 0, , .	1.9	0
12965	The role of the gut microbiome in hematological cancers. Molecular Cancer Research, 0, , .	3.4	0
12967	A Synthetic Formula Amino Acid Diet Leads to Microbiome Dysbiosis, Reduced Colon Length, Inflammation, and Altered Locomotor Activity in C57BL/6J Mice. Microorganisms, 2023, 11, 2694.	3.6	0
12969	Sequencing and culture-based characterization of the vaginal and uterine microbiota in beef cattle that became pregnant or remained open following artificial insemination. Microbiology Spectrum, 2023, 11, .	3.0	1
12970	Acute pancreatitis is associated with gut dysbiosis in children. Digestive and Liver Disease, 2024, 56, 444-450.	0.9	0
12971	The effects of indigenous microorganisms and water treatment with ion exchange resin on Cu-Ni flotation performance. Minerals Engineering, 2024, 205, 108473.	4.3	0
12979	The effect of sex and dietary crude protein level on nutrient transporter gene expression and cecal microbiota populations in broiler chickens. Poultry Science, 2024, 103, 103268.	3.4	0
12980	Microbial successional pattern along a glacier retreat gradient from Byers Peninsula, Maritime Antarctica. Environmental Research, 2024, 241, 117548.	7.5	1
12981	Association between the skin microbiome and MHC class II diversity in an amphibian. Molecular Ecology, 2024, 33, .	3.9	0
12982	Blockade of IL-6R prevents preterm birth and adverse neonatal outcomes. EBioMedicine, 2023, 98, 104865.	6.1	O
12983	Cross-regulation of antibody responses against the SARS-CoV-2 Spike protein and commensal microbiota via molecular mimicry. Cell Host and Microbe, 2023, 31, 1866-1881.e10.	11.0	1
12986	Proton Pump Inhibitor Use and Complications of Cirrhosis Are Linked With Distinct Gut Microbial Bacteriophage and Eukaryotic Viral-Like Particle Signatures in Cirrhosis. Clinical and Translational Gastroenterology, 2024, 15, e00659.	2.5	0
12989	Gut microbiota and child behavior in early puberty: does child sex play a role?. Gut Microbes, 2023, 15, .	9.8	0
12990	Early life exposure to broccoli sprouts confers stronger protection against enterocolitis development in an immunological mouse model of inflammatory bowel disease. MSystems, 2023, 8, .	3.8	1
12992	Enhancing the dung beetle iDNA tool for mammalian biodiversity monitoring and ecological studies. , 2023, 2, 133-139.		0
12993	Is there a latitudinal diversity gradient for symbiotic microbes? A case study with sensitive partridge peas. Molecular Ecology, 2024, 33, .	3.9	0
12995	Degradation of gaseous hydrocarbons in aerated stirred bioreactors inoculated with Rhodococcus erythropolis: Effect of the carbon source and SIFT-MS method development. Journal of Environmental Sciences, 2023, , .	6.1	0
12997	Genomic characterization of the <i>C. tuberculostearicum</i> species complex, a prominent member of the human skin microbiome. MSystems, 2023, 8, .	3.8	1

# ARTICLE	IF	CITATIONS
Participant-collected household dust for assessing microorganisms and semi-volatile organic compounds in urban homes. Science of the Total Environment, 2024, 908, 168230.	8.0	O
Integrative single-cell meta-analysis reveals disease-relevant vascular cell states and markers in human atherosclerosis. Cell Reports, 2023, 42, 113380.	6.4	4
Unlocking the microbial diversity and the chemical changes throughout the fermentation process of "hákarlâ€; Greenland shark. Heliyon, 2023, 9, e22127.	3.2	0
Degradation, altered microbial community composition, and protein expression in bacterial 13001 consortium/fungus inoculated crude oil contaminated loamy soil. Biocatalysis and Agricultural Biotechnology, 2023, 54, 102940.	3.1	O
Marine nitrogen-fixers in the Canadian Arctic Gateway are dominated by biogeographically distinct noncyanobacterial communities. FEMS Microbiology Ecology, 2023, 99, .	2.7	1
Ready Reckoner for Using Bioinformatics Tools in Fish and Shellfish Microbiome Analysis. , 2023, , 93-120.		O
13004 In situ devices can culture the microbial dark matter of corals. IScience, 2023, 26, 108374.	4.1	0
Comparative diet-gut microbiome analysis in Crohnâ \in [™] s disease and Hidradenitis suppurativa. Frontiers in Microbiology, 0, 14, .	3.5	O
Integrated genomic and functional analyses of human skin–associated <i>Staphylococcus</i> reveal 13008 extensive inter- and intra-species diversity. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	1
Bacteriome analysis of Aggregatibacter actinomycetemcomitans-JP2 genotype-associated Grade C periodontitis in Moroccan adolescents. Frontiers in Oral Health, 0, 4, .	3.0	1
Soil rare microorganisms mediated the plant cadmium uptake: The central role of protists. Science of the Total Environment, 2023, , 168505.	8.0	0
Bacterial microbiome and host inflammatory gene expression in foreskin tissue. Heliyon, 2023, 9, e22145.	3.2	О
Comparison of highâ€throughput sequencing methods for bacterial microbiota profiling in catfish aquaculture. North American Journal of Aquaculture, 0, , .	1.4	0
Longitudinal analysis at three oral sites links oral microbiota to clinical outcomes in allogeneic hematopoietic stem-cell transplant. Microbiology Spectrum, 2023, 11, .	3.0	1
Characterizing microbial communities associated with northern root-knot nematode (Meloidogyne) Tj ETQq0 0	0 rgBJ /Ov	verlock 10 Tf 5
Amorpha canescens and Andropogon gerardii Recruit Comparable Foliar Fungal Communities Across the Steep Precipitation Gradient in Kansas. Transactions of the Kansas Academy of Science, 2023, 126, .	0.1	О
Eating patterns contribute to shaping the gut microbiota in the mucosal simulator of the human intestinal microbial ecosystem. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
Unravelling the importance of cold-adapted bacterial formulations in microbial community dynamics 13021 during in situ lemongrass residue valorization under cold conditions. Biomass Conversion and Biorefinery, 0, , .	4.6	0

# ARTICLE	IF	Citations
PSKR1 balances the plant growth–defence trade-off in the rhizosphere microbiome. Nature Plants, 2023, 9, 2071-2084.	9.3	2
Role of Gut Microbiota in Statin-Associated New-Onset Diabetes—A Cross-Sectional and Prospective 13023 Analysis of the FINRISK 2002 Cohort. Arteriosclerosis, Thrombosis, and Vascular Biology, 2024, 44, 477-487.	2.4	2
Diversity and spatiotemporal variations in bacterial and archaeal communities within Kuwaiti territorial waters of the Northwest Arabian Gulf. PLoS ONE, 2023, 18, e0291167.	2.5	0
Lichen-associated microbial members are prevalent in the snow microbiome of a sub-arctic alpine tundra. FEMS Microbiology Ecology, 2023, 99, .	2.7	2
Ecological and evolutionary inferences from aphid microbiome analyses depend on methods and experimental design. , 2023, 2, 479-488.		0
Spatially-explicit effects of small-scale clear-cutting on soil fungal communities in Pinus sylvestris stands. Science of the Total Environment, 2024, 909, 168628.	8.0	0
Longitudinal study of the interplay between the skin barrier and facial microbiome over $1\hat{a} \in \mathbb{Z}$ Frontiers in Microbiology, 0, 14, .	3 . 5	0
Bacterial community structure of microbial pinnacles in ice-covered Lake Vanda, Antarctica. Arctic, Antarctic, and Alpine Research, 2023, 55, .	1.1	0
13033 Infant gut microbiota and negative and fear reactivity. Development and Psychopathology, 0, , 1-16.	2.3	1
Simultaneous analysis of seven <scp>16S rRNA</scp> hypervariable gene regions increases efficiency in marine bacterial diversity detection. Environmental Microbiology, 2023, 25, 3484-3501.	3.8	1
Global perspective of environmental distribution and diversity of Perkinsea (Alveolata) explored by a meta-analysis of eDNA surveys. Scientific Reports, 2023, 13, .	3.3	0
Microbes within the building envelope—a case study on the patterns of colonization and potential sampling bias. PeerJ, 0, 11, e16355.	2.0	0
The role of the soil microbiome in the colonisation of glacier forefields by Antarctic pearlwort (Colobanthus quitensis) under current and future climate change scenarios. Soil Biology and Biochemistry, 2024, 188, 109249.	8.8	0
Differences in Soil Fungal Communities between Forested Reclamation and Forestry Sites in the Alberta Oil Sands Region. Journal of Fungi (Basel, Switzerland), 2023, 9, 1110.	3.5	0
lmmune activation and inflammation in lactating women on combination antiretroviral therapy: role of gut dysfunction and gut microbiota imbalance. Frontiers in Immunology, 0, 14, .	4.8	0
Bacterial diversity and community structure of some traditional African and European cereal-based fermented foods identified by high-throughput sequencing. Food Bioscience, 2023, 56, 103346.	4.4	0
Associations of gut microbiome richness and diversity with objective and subjective sleep measures in a population sample. Sleep, 0, , .	1.1	3
Why are so many enteric pathogen infections asymptomatic? Pathogen and gut microbiome 13046 characteristics associated with diarrhea symptoms and carriage of diarrheagenic <i>E. coli</i> in northern Ecuador. Gut Microbes, 2023, 15, .	9.8	1

# ARTICLE	IF	Citations
13049 Investigating luxS gene expression in lactobacilli along lab-scale cocoa fermentations. Food Microbiology, 2024, 119, 104429.	4.2	O
Mouse intestinal microbiome modulation by oral administration of a GABA-producing <i>Bifidobacterium adolescentis</i> strain. Microbiology Spectrum, 0, , .	3.0	0
Gut microbiomes of cycad-feeding insects tolerant to \hat{l}^2 -methylamino-L-alanine (BMAA) are rich in siderophore biosynthesis. ISME Communications, 2023, 3, .	4.2	0
Enhancing gut health and performance of grower-finisher pigs: assessing the efficacy of the mixture of microencapsulated essential oils and saponins. Animal Production Science, 2023, , .	1.3	0
Phytobiotic-Prebiotic Feed Additive Containing a Combination of Carob Pulp, Chicory, and Fenugreek Improve Growth Performance, Carcass Traits, and Fecal Microbiota of Fattening Pigs. Animals, 2023, 13, 3621.	2.3	0
Antibiotic prophylaxis and hospitalization of horses subjected to median laparotomy: gut microbiota trajectories and abundance increase of Escherichia. Frontiers in Microbiology, 0, 14 , .	3. 5	0
Alterations to the bovine bacterial ocular surface microbiome in the context of infectious bovine keratoconjunctivitis. Animal Microbiome, 2023, 5, .	3.8	0
In the eye of the ophthalmologist: the corneal microbiome in microbial keratitis. Graefe's Archive for Clinical and Experimental Ophthalmology, 0 , , .	1.9	0
Multi-omics analyses from a single sample: prior metabolite extraction does not alter the 16S rRNA-based characterization of prokaryotic community in a diversity of sample types. FEMS Microbiology Letters, 2023, 370, .	1.8	0
Heat waveâ€induced microbial thermal trait adaptation and its reversal in the Subarctic. Global Change Biology, 2024, 30, .	9.5	1
The microbiome of two strategies for ammonia removal with the sequencing batch moving bed biofilm reactor treating cheese production wastewater. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
Maternal Consumption of Non-Nutritive Sweeteners during Pregnancy Is Associated with Alterations in the Colostrum Microbiota. Nutrients, 2023, 15, 4928.	4.1	1
Complementary yet divergent effects of exercise and an exercise mimetic on microbiome in high-fat diet-induced obesity. Physiological Genomics, 0, , .	2.3	1
Comparison of Fungal and Bacterial Microbiomes of Bats and Their Cave Roosting Environments at El Malpais National Monument, New Mexico, USA. Geomicrobiology Journal, 2024, 41, 82-97.	2.0	0
Oral microbiota analyses of paediatric Saudi population reveals signatures of dental caries. BMC Oral Health, 2023, 23, .	2.3	2
e <scp>DNA</scp> metabarcoding analysis reveals the consequence of creating ecosystemâ€scale refugia from deer grazing for the soil microbial communities. Environmental DNA, 0, , .	5 . 8	0
Enrichment of mixed methanotrophic cultures producing polyhydroxyalkanoates (PHAs) from various environmental sources. Science of the Total Environment, 2024, 912, 168844.	8.0	0
Reduced snow and increased nutrients show enhanced iceâ€associated photoautotrophic growth using a modified experimental underâ€ice design. Limnology and Oceanography, 0, , .	3.1	0

# ARTICLE	IF	CITATIONS
Rapid detection of subterranean fauna from passive sampling of groundwater <scp>eDNA</scp> . Environmental DNA, 2023, 5, 1706-1719.	5.8	0
Analysis of Gut Characteristics and Microbiota Changes with Maternal Supplementation in a Neural Tube Defect Mouse Model. Nutrients, 2023, 15, 4944.	4.1	0
13077 Bacterial biogeography of the Indian Ocean. Limnology and Oceanography, 0, , .	3.1	0
Selective cell lysis pressure on rare and abundant prokaryotic taxa across a shelf-to-slope continuum in the Northern South China Sea. Applied and Environmental Microbiology, $0, \dots$	3.1	O
Combined analysis of cross-population healthy adult human microbiome reveals consistent differences in gut microbial characteristics between Western and non-Western countries. Computational and Structural Biotechnology Journal, 2024, 23, 87-95.	4.1	0
Conspecific versus heterospecific transmission shapes host specialization of the phyllosphere microbiome. Cell Host and Microbe, 2023, 31, 2067-2079.e5.	11.0	1
Too Much of a Good Thing: Extended Duration of Gut Microbiota Depletion Reverses Protection From Experimental Autoimmune Uveitis., 2023, 64, 43.	m	1
The microbial contribution to litter decomposition and plant growth. Environmental Microbiology Reports, 2024, 16 , .	2.4	O
Community assembly of the human piercing microbiome. Proceedings of the Royal Society B: Biolog Sciences, 2023, 290, .	rical 2.6	2
4 <scp>rCRUX 13086 <scp>rCRUX lscp>: A rapid and versatile tool for generating metabarcoding reference libraries in R. Environmental DNA, 2024, 6, .</scp></scp>	5.8	O
A national survey of anthelmintic resistance in ascarid and strongylid nematodes in Australian Thoroughbred horses. International Journal for Parasitology: Drugs and Drug Resistance, 2024, 24, 100517.	3.4	1
$_{13089}$ Effects of maternal type 1 diabetes and confounding factors on neonatal microbiomes. Diabetologia 0, , .	6.3	O
Soil microbiome indicators can predict crop growth response to large-scale inoculation with arbuscular mycorrhizal fungi. Nature Microbiology, 2023, 8, 2277-2289.	13.3	8
Bacterial community and sensory quality from coffee are affected along fermentation under carboni maceration. , 2023, 3, 100554.	c	O
Root-associated microbial community and diversity in napiergrass across radiocesium-contaminated lands after the Fukushima-Daiichi nuclear disaster in Japan. Environmental Pollution, 2024, 342, 123	051. ^{7.5}	0
Carbon amendments in soil microcosms induce uneven response on H2 oxidation activity and microbial community composition. FEMS Microbiology Ecology, 0, , .	2.7	O
Occupational farm work activities influence workers' indoor home microbiome. Environmental Research, 2024, 243, 117819.	7.5	0
Soil enzyme activities and microbial community modulation after addition of poultry litter amendment enriched with Bacillus spp Ciencia E Agrotecnologia, 0, 47, .	1.5	0

# ARTICLE	IF	Citations
Effects of microplastics on microbial community dynamics in sediments from the Volturno River ecosystem, Italy. Chemosphere, 2024, 349, 140872.	8.2	0
A full-length SSU rRNA-based workflow for high-resolution monitoring of nematode communities reveals direct and indirect responses to plant-based manipulations. Soil Biology and Biochemistry, 2024, 189, 109263.	8.8	1
SAD rats: Effects of short photoperiod and carbohydrate consumption on sleep, liver steatosis, and the gut microbiome in diurnal grass rats. Chronobiology International, 2024, 41, 93-104.	2.0	O
Core microbiota play important roles in maintaining soil multiâ€nutrient cycling in lakeshore wetland of plateau lake Caohai. Land Degradation and Development, 2024, 35, 1308-1319.	d 3.9	0
Characterising the gut microbiome of stranded harbour seals (Phoca vitulina) in rehabilitation. PLoS ONE, 2023, 18, e0295072.	2.5	0
Lung microbiome alterations in patients with anti-Jo1 antisynthetase syndrome and interstitial lung disease. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	0
Dynamics of the benthic and planktic microbiomes in a Planktothrix-dominated toxic cyanobacterial bloom in Australia. Water Research, 2024, 249, 120980.	11.3	1
Repeated exposure of wheat to the fungal root pathogen Bipolaris sorokiniana modulates rhizosphere microbiome assembly and disease suppressiveness. Environmental Microbiomes, 2023,	18,.	0
Failure to recover <i>Pseudomonas fluorescens</i> D7 supports claims of ineffectiveness as biocontrol agent of <i>Bromus tectorum</i> Microbiology Spectrum, 0, , .	3.0	0
Association between Dietary Intake and Faecal Microbiota in Children with Cystic Fibrosis. Nutrients 2023, 15, 5013.	4.1	0
Vasoactive Intestinal Polypeptide Plays a Key Role in the Microbial-Neuroimmune Control of Intestinal Motility. Cellular and Molecular Gastroenterology and Hepatology, 2024, 17, 383-398.	al 4.5	1
Sutterella and its metabolic pathways positively correlate with vaccine-elicited antibody responses ir infant rhesus macaques. Frontiers in Immunology, 0, 14, .	n 4.8	0
Host DNA depletion methods and genome-centric metagenomics of bovine hindmilk microbiome. MSphere, 0, , .	2.9	0
<i>Zea mays</i> genotype influences microbial and viral rhizobiome community structure. ISME Communications, 2023, 3, .	4.2	0
Fungal and bacterial gut microbiota differ between <i>Clostridioides difficile</i> colonization and infection., 0, 3, .		0
Presence of digestible starch impacts <i>in vitro</i> fermentation of resistant starch. Food and Function, 0, , .	4.6	1
Waste not, want not: revisiting the analysis that called into question the practice of rarefaction. MSphere, 2024, 9, .	2.9	1
Response of the soil microbial communities to forest ground cover manipulation in a boreal forest. Forest Ecology and Management, 2024, 553, 121615.	3.2	0

#	Article	IF	Citations
	Abundance of Oligoflexales bacteria is associated with algal symbiont density, independent of thermal stress in <i>Aiptasia</i>	1.9	0
13126	Insights into the ecological impact of trout introduction in an oligotrophic lake using sedimentary environmental DNA. Metabarcoding and Metagenomics, 0, 7, .	0.0	O
13127	Diversity and distribution of yeasts in intertidal zones of China. Frontiers in Marine Science, 0, 10, .	2.5	1
13129	Berberine-microbiota interplay: orchestrating gut health through modulation of the gut microbiota and metabolic transformation into bioactive metabolites. Frontiers in Pharmacology, 0, 14 , .	3.5	0
13130	Plumage microorganism communities of tidal marsh sparrows. IScience, 2024, 27, 108668.	4.1	0
13133	Phyllosphere microbial associations improve plant reproductive success. Frontiers in Plant Science, 0, 14, .	3.6	1
	Earthworm co-invasion by Amynthas tokioensis and Amynthas agrestis affects soil microaggregate bacterial communities. Applied Soil Ecology, 2024, 195, 105224.	4.3	1
13135	First insight into strongylid nematode diversity and anthelmintic treatment effectiveness in beef cattle in the Czech Republic explored by HTS metagenomics. Veterinary Parasitology: Regional Studies and Reports, 2024, 47, 100961.	0.5	0
13138	Differential microbial composition in parasitic vs. questing ticks based on 16S next-generation sequencing. Frontiers in Microbiology, 0, 14, .	3.5	0
	Microbial perspective of inhibited carbon turnover in <scp>Tangel</scp> humus of the <scp>Northern Limestone Alps</scp> . Environmental Microbiology Reports, 2024, 16, .	2.4	0
13140	Alkali-buffering effect to increase hydrogen production on co-fermentation of citrus agroindustrial waste. International Journal of Hydrogen Energy, 2024, 53, 364-382.	7.1	0
13141	A case study of the diet-microbiota-parasite interplay in bumble bees. Journal of Applied Microbiology, 0, , .	3.1	O
	Biodiversity in wetland+ system: a passive solution for HCH dump effluents. Water Science and Technology, 2023, 88, 3095-3109.	2.5	2
	The role of diet and host species in shaping the seasonal dynamics of the gut microbiome. FEMS Microbiology Ecology, 0, , .	2.7	1
	Fish gut and skin microbiota dysbiosis induced by exposure to commercial sunscreen formulations. Aquatic Toxicology, 2024, 266, 106799.	4.0	0
13147	Survivability and proliferation of microorganisms in bentonite with implication to radioactive waste geological disposal: strong effect of temperature and negligible effect of pressure. World Journal of Microbiology and Biotechnology, 2024, 40, .	3.6	O
13148	Bacterial microbiota shifts in vacuum-packed beef during storage at different temperatures: Impacts on blown pack spoilage. Food Microbiology, 2024, 119, 104448.	4.2	0
	Process conditions affect microbial diversity and activity in a haloalkaline biodesulfurization system. Applied and Environmental Microbiology, 0, , .	3.1	O

#	Article	IF	Citations
13152	Dietary seaweed (Saccharina latissima) supplementation in pigs induces localized immunomodulatory effects and minor gut microbiota changes during intestinal helminth infection. Scientific Reports, 2023, 13, .	3.3	0
13153	Efficacy of probiotic treatment as post-exposure prophylaxis for COVID-19: A double-blind, Placebo-Controlled Randomized trial. Clinical Nutrition, 2024, 43, 259-267.	5.0	1
13154	Dysbiosis and Associated Stool Features Improve PredictionÂofÂResponse to Biological Therapy in Inflammatory Bowel Disease. Gastroenterology, 2024, 166, 483-495.	1.3	2
13156	Host-related traits influence the microbial diversity of the invasive signal crayfish Pacifastacus leniusculus. Journal of Invertebrate Pathology, 2024, 202, 108039.	3.2	O
13157	Effects of Chlorella fusca-supplemented diet on intestinal microbiota and gene expression related to metabolism, stress, and immune response in Chelon labrosus. Algal Research, 2024, 77, 103362.	4.6	0
13158	Association of Chlamydia trachomatis burden with the vaginal microbiota, bacterial vaginosis, and metronidazole treatment. Frontiers in Cellular and Infection Microbiology, $0,13,13$	3.9	O
13160	The menopause-related gut microbiome: associations with metabolomics, inflammatory protein markers, and cardiometabolic health in women with HIV. Menopause, 2024, 31, 52-64.	2.0	0
13163	Population-level variation in gut bifidobacterial composition and association with geography, age, ethnicity, and staple food. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	O
13164	Microbial shifts associated to ENSO-derived thermal anomalies reveal coral acclimation at holobiont level. Scientific Reports, 2023, 13 , .	3.3	0
13165	A laboratory ice machine as a cold oligotrophic artificial microbial niche for biodiscovery. Scientific Reports, 2023, 13, .	3.3	O
13167	Biodiversity patterns of cyanobacterial oligotypes in lakes and rivers: results of a large-scale metabarcoding survey in the Alpine region. Hydrobiologia, 2024, 851, 1035-1062.	2.0	0
13169	Foliar endophyte diversity in Eastern Asian-Eastern North American disjunct tree species – influences of host identity, environment, phylogeny, and geographic isolation. Frontiers in Plant Science, 0, 14, .	3.6	1
13170	Gut Bacteriomes and Ecological Niche Divergence: An Example of Two Cryptic Gastropod Species. Biology, 2023, 12, 1521.	2.8	1
13171	Longitudinal Analysis of Canine Oral Microbiome Using Whole Genome Sequencing in Aging Companion Dogs. Animals, 2023, 13, 3846.	2.3	0
13172	Optimum ratio of dietary protein and carbohydrate that maximises lifespan is shared among related insect species. Aging Cell, 0 , , .	6.7	1
13173	Insight into the Role of Gut Microbiota in Duchenne Muscular Dystrophy. American Journal of Pathology, 2023, , .	3.8	O
13174	Precision microbial intervention improves social behavior but not autism severity: A pilot double-blind randomized placebo-controlled trial. Cell Host and Microbe, 2023, , .	11.0	1
13175	Interrelation between gut microbiota, SCFA, and fatty acid composition in pigs. MSystems, 2024, 9, .	3.8	1

#	Article	IF	CITATIONS
13176	Gut microbiome dynamics in index patients colonized with extended-spectrum beta-lactamase (ESBL)-producing Enterobacterales after hospital discharge and their household contacts. Microbiology Spectrum, 2023, 11 , .	3.0	0
13177	The influence of diet on gut microbiome and body mass dynamics in a capital-breeding migratory bird. PeerJ, 0, 11, e16682.	2.0	0
13178	Characterization of the Ruminal Microbiome of Water Buffaloes (Bubalus bubalis) Kept in Different Ecosystems in the Eastern Amazon. Animals, 2023, 13, 3858.	2.3	0
13179	Effects of the application of microbiologically activated bio-based fertilizers derived from manures on tomato plants and their rhizospheric communities. Scientific Reports, 2023, 13, .	3.3	1
13180	Benchmarking DNA isolation methods for marine metagenomics. Scientific Reports, 2023, 13, .	3.3	1
13181	Dietary strategies can increase cloacal endotoxin levels and modulate the resident microbiota in broiler chickens. Poultry Science, 2024, 103, 103312.	3.4	0
13182	Molecular responses of sponge larvae exposed to partially weathered condensate oil. Marine Pollution Bulletin, 2024, 199, 115928.	5.0	0
13184	A single dietary factor, daily consumption of a fermented beverage, can modulate the gut bacteria and fecal metabolites within the same ethnic community. MSystems, 2023, 8, .	3.8	O
13185	Evaluation of 16S rRNA gene primer pairs for bacterial community profiling in an across soil and ryegrass plant study., 2023, 2, 500-512.		0
13188	Deep sequencing of extracellular eDNA enables total biodiversity assessment of ecosystems. Ecological Indicators, 2023, 156, 111171.	6.3	1
13189	Fungal Microbiota Composition in Inflammatory Bowel Disease Patients: Characterization in Different Phenotypes and Correlation With Clinical Activity and Disease Course. Inflammatory Bowel Diseases, 0, , .	1.9	0
13191	Surface Properties of Carbonate Speleothems in Karst Caves Changing Under Biofilms. Springer Proceedings in Earth and Environmental Sciences, 2023, , 495-511.	0.4	0
13192	Establishing the link between microbial communities in bovine liver abscesses and the gastrointestinal tract. Animal Microbiome, 2023, 5, .	3.8	0
13194	VIBES: A consensus subtyping of the vaginal microbiota reveals novel classification criteria. Computational and Structural Biotechnology Journal, 2024, 23, 148-156.	4.1	O
13196	Tracking the contamination sources of microbial population and characterizing Listeria monocytogenes in a chicken slaughterhouse by using culture-dependent and -independent methods. Frontiers in Microbiology, 0, 14, .	3.5	0
13197	Understanding temporal and spatial distribution of intestinal nematodes of horses using faecal egg counts and DNA metabarcoding. Veterinary Parasitology, 2024, 325, 110094.	1.8	1
13198	Differential apicomplexan presence predicts thermal stress mortality in the Mediterranean coral <i>Paramuricea clavata </i> Environmental Microbiology, 2024, 26, .	3.8	0
13199	Disease and stage specific alterations of the oral and fecal microbiota in Alzheimer's disease. , 0, , .		1

# ARTICLE	IF	CITATIONS
13200 Microbiological insight into various underground gas storages in Vienna Basin focusing on methanogenic Archaea. Frontiers in Microbiology, 0, 14, .	3.5	0
Exploring the impact of thermal delousing on gill health and microbiome dynamics in farmed Atlantic Salmon. Aquaculture, 2024, 582, 740455.	3.5	0
Associated bacterial communities, confrontation studies, and comparative genomics reveal important interactions between Morchella with Pseudomonas spp Frontiers in Fungal Biology, 0, 4, .	2.0	0
Revealing human impact on natural ecosystems through soil bacterial <scp>DNA</scp> sampled from an archaeological site. Environmental Microbiology, 2024, 26, .	3.8	0
The airway microbiota in siblings with primary ciliary dyskinesia: Related factors and correlation with clinical characteristics. Pediatric Pulmonology, 2024, 59, 695-706.	2.0	0
Interdental oral hygiene interventions elicit varying compositional microbiome changes in naturally 13206 occurring gingivitis: Secondary data analysis from a clinical trial. Journal of Clinical Periodontology, 2024, 51, 309-318.	4.9	0
Nutrient and Microbiome-Mediated Plant–Soil Feedback in Domesticated and Wild Andropogoneae: Implications for Agroecosystems. Microorganisms, 2023, 11, 2978.	3.6	0
Mycobiomes of two distinct clades of ambrosia gall midges (Diptera: Cecidomyiidae) are species-specific in larvae but similar in nutritive mycelia. Microbiology Spectrum, 0, , .	3.0	0
Cotton microbiome profiling and Cotton Leaf Curl Disease (CLCuD) suppression through microbial consortia associated with Gossypium arboreum. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	1
Shotgun metagenomics reveals interkingdom association between intestinal bacteria and fungi involving competition for nutrients. Microbiome, 2023, 11 , .	11.1	O
Effect of rumen-protected choline on dairy cows' metabolism, immunity, lactation performance, and vaginal discharge microbiome. Journal of Dairy Science, 2023, , .	3.4	0
Pulsed dosing and extended daily dosing of oral vancomycin do not facilitate clearance of <i>Clostridioides difficile</i> colonization in mice. Antimicrobial Agents and Chemotherapy, 0, , .	3.2	O
Altering environmental conditions induce shifts in simulated deep terrestrial subsurface bacterial communitiesâ€"Secretion of primary and secondary metabolites. Environmental Microbiology, 2024, 26,	3.8	0
Phylogenetic diversity of functional genes in deep-sea cold seeps: a novel perspective on metagenomics. Microbiome, 2023, 11 , .	11.1	0
13222 Hybrid Filtration Process for Gas Desulfurization. Processes, 2023, 11, 3438.	2.8	0
The infant gut virome is associated with preschool asthma risk independently of bacteria. Nature Medicine, 2024, 30, 138-148.	30.7	1
Gut microbiota in the shortâ€beaked echidnaÂ(<i>Tachyglossus Aculeatus</i>) shows stability across gestation. MicrobiologyOpen, 2023, 12, .	3.0	0
Functional alterations and predictive capacity of gut microbiome in type 2 diabetes. Scientific Reports, 2023, 13 , .	3.3	1

# ARTICLE	IF	CITATIONS
Firmicutes and Bacteroidetes contribute to mass gain variation in female obligate hibernators. Journal of Mammalogy, 0, , .	1.3	0
Interactions between surface properties of pristine coals and the intrinsic microbial communities involved in methane formation. International Journal of Coal Geology, 2024, 282, 104422.	5.0	0
Tasting of traditional Polish fermented cucumbers: Microbiology, morpho-textural features, and volatilome. Food Research International, 2024, 177, 113851.	6.2	0
Neuroblastoma is associated with alterations in gut microbiome composition subsequent to maternal microbial seeding. EBioMedicine, 2024, 99, 104917.	6.1	0
Longitudinal microbial and molecular dynamics in the cystic fibrosis lung after Elexacaftor–Tezacaftor–Ivacaftor therapy. Respiratory Research, 2023, 24, .	3.6	1
Changes in the Murine Microbiome and Bacterial Extracellular Vesicle Production in Response to Antibiotic Treatment and Norovirus Infection. Viruses, 2023, 15, 2443.	3.3	0
Microbiome ecological memory and responses to repeated marine heatwaves clarify variation in coral bleaching and mortality. Global Change Biology, 2024, 30, .	9.5	0
Molecular Characterisation of Faecal Bacterial Assemblages Among Four Species of Syntopic Odonates. Microbial Ecology, 2024, 87, .	2.8	0
A diverse microbial community and common core microbiota associated with the gonad of female Parascaris spp Parasitology Research, 2024, 123, .	1.6	0
Effect of an Alliaceae Encapsulated Extract on Growth Performance, Gut Health, and Intestinal Microbiota in Broiler Chickens Challenged with Eimeria spp Animals, 2023, 13, 3884.	2.3	0
Bacterial community of agricultural soils used for potato cultivation in Sverdlovsk region. Agricultural Science Euro-North-East, 2023, 24, 989-998.	0.7	0
MiscMetabar: an R package to facilitate visualization and reproducibility in metabarcoding analysis. Journal of Open Source Software, 2023, 8, 6038.	4.6	0
Seasonal soil moisture thresholds inhibit bacterial activity and decomposition during drought in a tallgrass prairie. Oikos, 2024, 2024, .	2.7	0
Persistence of location-specific microbial signatures on boats during voyages. Marine Pollution Bulletin, 2024, 199, 115884.	5.0	0
Effects of plant-based proteins and handling stress on intestinal mucus microbiota in rainbow trout. Scientific Reports, 2023, 13, .	3.3	0
Covariation between microeukaryotes and bacteria associated with Planorbidae snails. PeerJ, 0, 11 , e16639.	2.0	1
Seasonality in land–ocean connectivity and local processes control sediment bacterial community structure and function in a High Arctic tidal flat. FEMS Microbiology Ecology, 2024, 100, .	2.7	1
High prevalence of Enterovirus E, Bovine Kobuvirus, and Astrovirus revealed by viral metagenomics in fecal samples from cattle in Central Colombia. Infection, Genetics and Evolution, 2024, 117, 105543.	2.3	0

# ARTICLE	IF	Citations
The probiotic SLAB51 as agent to counteract BPA toxicity on zebrafish gut microbiota -liver-brain axis. Science of the Total Environment, 2024, 912, 169303.	8.0	O
Streptomyces Diversity Maps Reveal Distinct High-Specificity Biogeographical and Environmental Patterns Compared to the Overall Bacterial Diversity. Life, 2024, 14, 11.	2.4	0
Comparative Analysis of Microbial Community Characteristic of Acidic and Neutral Soils in Korean Orchards. Han'guk T'oyang Piryo Hakhoe Chi Han'guk T'oyang Piryo Hakhoe, 2023, 56, 449-462.	0.9	0
Diversidad microbiana en estudios de fertilización mineral de larga duración en caña de azúcar. Revista U D C A Actualidad & Divulgación CientÃfica, 2023, 26, .	0.2	0
lmpact of the gut microbiome on immunological responses to COVID-19 vaccination in healthy controls and people living with HIV. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	0
Microbial ecology and activity of snow algae within a Pacific Northwest snowpack. Arctic, Antarctic, and Alpine Research, 2023, 55 , .	1.1	0
Metabarcoding analysis reveals a differential bacterial community profile associated with â€~Torta del Casar' and â€~Queso de la Serena' PDO cheeses. Food Bioscience, 2024, 57, 103491.	4.4	0
Comparative analysis of fasting effects on the cecum microbiome in three guinea pig breeds: Andina, lnti, and Peru. Frontiers in Microbiology, 0, 14 , .	3.5	0
Comparative analysis of microbial succession and proteolysis focusing on amino acid pathways in Asiago-PDO cheese from two dairies. International Journal of Food Microbiology, 2024, 411, 110548.	4.7	0
Conservation and diversity of the pollen microbiome of Pan-American maize using PacBio and MiSeq. Frontiers in Microbiology, 0, 14 , .	3.5	2
An in-depth investigation of the microbiota and its virulence factors associated 11 with severe udder cleft dermatitis lesions. Journal of Dairy Science, 2023, , .	3.4	0
Intestinal dysbiosis as an intraoperative predictor of septic complications: evidence from human surgical cohorts and preclinical models of peritoneal sepsis. Scientific Reports, 2023, 13, .	3.3	0
Evaluating Metabarcoding Markers for Identifying Zooplankton and Ichthyoplankton Communities to Species in the Salish Sea: Morphological Comparisons and Rare, Threatened or Invasive Species. Dna, 2024, 4, 1-33.	1.3	0
Differential responses of the gut microbiome and resistome to antibiotic exposures in infants and adults. Nature Communications, 2023, 14, .	12.8	1
Selective syngas fermentation to acetate under acidic and psychrophilic conditions using mixed anaerobic culture. Bioresource Technology, 2024, 394, 130235.	9.6	0
Syntrophy between bacteria and archaea enhances methane production in an EGSB bioreactor fed by cheese whey wastewater. Frontiers in Sustainable Food Systems, 0, 7, .	3.9	0
Beneficial Effect of Faecal Microbiota Transplantation on Mild, Moderate and Severe Dextran Sodium Sulphate-Induced Ulcerative Colitis in a Pseudo Germ-Free Animal Model. Biomedicines, 2024, 12, 43.	3.2	0
13267 Enhancing Resistance to Salinity in Wheat by Using Streptomyces sp. HU2014. Agronomy, 2024, 14, 39.	3.0	0

# ARTICLE	IF	CITATIONS
Minimal adverse effects of exogenous phage treatment on soil bacterial communities. Applied Soil Ecology, 2024, 195, 105250.	4.3	0
Alternative amplicon-PCR protocol for maximizing bacterial and fungal sequencing in low-biomass samples. Analytical Biochemistry, 2023, , 115449.	2.4	O
Morpho-molecular characterization of sand-dwelling dinoflagellate communities from the German Wadden Sea and insights into their spatiotemporal distribution. European Journal of Phycology, 0, , 1-22.	2.0	0
Evaluation of short-circuited electrodes in combination with dark fermentation for promoting biohydrogen production process. Bioelectrochemistry, 2024, 157, 108631.	4.6	1
Dietary fibre confers therapeutic effects in a preclinical model of Huntington's disease. Brain, Behavior, and Immunity, 2024, 116, 404-418.	4.1	2
Effects of monensin and cashew nut-shell extract on bacterial community composition in a dual-flow continuous culture system. Translational Animal Science, 0, , .	1.1	O
Effects of early postnatal gastric and colonic microbiota transplantation on piglet gut health. Journal of Animal Science and Biotechnology, 2023, 14, .	5.3	0
Sulforaphane and Sulforaphaneâ€Nitrile Metabolism in Humans Following Broccoli Sprout 13281 Consumption: Interâ€individual Variation, Association with Gut Microbiome Composition, and Differential Bioactivity. Molecular Nutrition and Food Research, 2024, 68, .	3.3	1
Frost Cracks Show a Slight Effect on Fungal Richness in Stem Wood of Hybrid Aspen Trees in Latvia. Diversity, 2024, 16, 14.	1.7	0
Nasopharyngeal Bacterial Prevalence and Microbial Diversity at First Treatment for Bovine 13283 Respiratory Disease (BRD) and Its Associations with Health and Mortality Outcomes in Feedyard Cattle Microorganisms, 2024, 12, 33.	e. 3.6	O
Urinary microbiome community types associated with urinary incontinence severity in women. American Journal of Obstetrics and Gynecology, 2024, 230, 344.e1-344.e20.	1.3	0
Single-cell RNA-Seq reveals intracellular microbial diversity within immune cells during SARS-CoV-2 infection and recovery. IScience, 2023, 26, 108357.	4.1	2
Pilot Study on Gut Microbiota Profile in Indian Children with Type 1 Diabetes. Indian Journal of Endocrinology and Metabolism, 2023, 27, 404-409.	0.4	0
Proton Pump Inhibitors Modulate Gene Expression Profile in Esophageal Mucosa and Microbiome. Journal of Pediatric Pharmacology and Therapeutics, 2023, 28, 504-508.	0.5	O
13289 Bacterial diversity in honey bee environment: Embu County, Kenya. Scientific African, 2024, 23, e0203	36. 1.5	0
Metabonomic Investigation of Penicillium expansum Infection of Apples and Salicylic Acid-Mediated Disease Resistance. Food and Bioprocess Technology, 0, , .	4.7	0
Microbial diversity and oil biodegradation potential of northern Barents Sea sediments. Journal of Environmental Sciences, 2023, , .	6.1	0
Different microbial communities in paddy soils under organic and nonorganic farming. Brazilian Journal of Microbiology, 2024, 55, 777-788.	2.0	0

# ARTICLE	IF	Citations
Biological nitrogen fixation, diversity and community structure of diazotrophs in two mosses in 25 temperate forests. Environmental Microbiology, 2024, 26, .	3.8	0
Preslaughter feed withdrawal time and its effect on rabbit blood measures, gastrointestinal tract parameters and Longissimus lumborum glycolytic potential. World Rabbit Science, 2023, 31, 237-26	51. 0.6	0
Insights into Endophytic and Rhizospheric Bacteria of Five Sugar Beet Hybrids in Terms of Their Diversity, Plant-Growth Promoting, and Biocontrol Properties. Microbial Ecology, 2024, 87, .	2.8	2
13297 Salmo salar Skin and Gill Microbiome during Piscirickettsia salmonis Infection. Animals, 2024, 14, 97	. 2.3	1
Beach sand plastispheres are hotspots for antibiotic resistance genes and potentially pathogenic bacteria even in beaches with good water quality. Environmental Pollution, 2024, 344, 123237.	7.5	0
Changes of the bacterial composition in duodenal fluid from patients with liver cirrhosis and molecular bacterascites. Scientific Reports, 2023, 13, .	3.3	O
Gut microbiome responds to alteration in female sex hormone status and exacerbates metabolic dysfunction. Gut Microbes, 2024, 16 , .	9.8	0
Microbiome pattern and diversity of an anadromous fish, hilsa shad (Tenualosa ilisha). Molecular Biology Reports, 2024, 51, .	2.3	O
Short term antibiotic effects on gut microbiome in Indian preschoolers: A 16S rRNA analysis. Journal of Laboratory Physicians, 0, .	1.1	0
Comparative analysis of HiSeq3000 and BGISEQ-500 sequencing platform over whole genome sequencing metagenomics data. Genomics and Informatics, 2023, 21, e49.	0.8	O
Contaminants of emerging concern reduction and microbial community characterization across a three-barrier advanced water treatment system. Science of the Total Environment, 2024, 912, 16963	37. 8. 0	0
Intestinal microbiota differences associated with physiological health, meat quality, and regulating mineral interactions of Penaeus vannamei fed organic manganese. Aquaculture, 2023, , 740537.	3.5	O
Marsh sediments chronically exposed to nitrogen enrichment contain degraded organic matter that is less vulnerable to decomposition via nitrate reduction. Science of the Total Environment, 2023, , 169681.	8.0	O
Microbial Communities in Model Seawater-Compensated Fuel Ballast Tanks: Biodegradation and Biocorrosion Stimulated by Marine Sediments. Corrosion and Materials Degradation, 2024, 5, 1-26.	2.4	O
Bacteria and bacteriophage consortia are associated with protective intestinal metabolites in patient receiving stem cell transplantation. Nature Cancer, 2024, 5, 187-208.	ts 13.2	1
Spotting disease disrupts the microbiome of infected purple sea urchins, Strongylocentrotus purpuratus. BMC Microbiology, 2024, 24, .	3.3	O
Eukaryotic diversity patterns in the Red Sea: from the surface to the deep. Frontiers in Marine Science $0, 10, .$	ce, 2.5	0
13316 Microbiome changes in Sinularia spp. soft corals relative to health status. Marine Biology, 2024, 171	.,. 1.5	0

#	ARTICLE	IF	CITATIONS
13317	Response of particle-attached and free-living bacterial communities to Microcystis blooms. Applied Microbiology and Biotechnology, 2024, 108, .	3.6	0
13318	Microbial, proteomic, and metabolomic profiling of the estrous cycle in wild house mice. Microbiology Spectrum, 2024, 12, .	3.0	1
13319	Manipulation of the seagrassâ€associated microbiome reduces disease severity. Environmental Microbiology, 2024, 26, .	3.8	0
13320	Turtle species and ecology drive carapace microbiome diversity in three seasonally interconnected wetland habitats. Access Microbiology, 2024, 6, .	0.5	O
13321	Effect of diet supplemented with functional amino acids and polyphenols on gut health in broilers subjected to a corticosterone-induced stress. Scientific Reports, 2024, 14 , .	3.3	0
13322	Efficient chemical and microbial removal of iron and manganese in a rapid sand filter and impact of regular backwash. Applied Geochemistry, 2024, 162, 105904.	3.0	1
13323	Bacterial diversity in arboreal ant nesting spaces is linked to colony developmental stage. Communications Biology, 2023, 6, .	4.4	0
13324	Structural Shifts in the Soil Prokaryotic Communities Marking the Podzol-Forming Process on Sand Dumps. Soil Systems, 2024, 8, 9.	2.6	0
13325	First screening of bacteria assemblages associated with the marine polychaete Melinna palmata Grube, 1870 and adjacent sediments. Frontiers in Marine Science, 0, 10, .	2.5	0
13326	Induced responses contribute to rapid adaptation of Spirodela polyrhiza to herbivory by Lymnaea stagnalis. Communications Biology, 2024, 7, .	4.4	1
13327	Gut microbiome alpha diversity decreases in relation to body weight, antibiotic exposure, and infection with multidrug-resistant organisms. American Journal of Infection Control, 2024, , .	2.3	0
13328	Daily yogurt consumption does not affect bone turnover markers in men and postmenopausal women of Caribbean Latino descent: a randomized controlled trial. BMC Nutrition, 2024, 10, .	1.6	0
13329	Do Microorganisms in Bathing Water in Guadeloupe (French West Indies) Have Resistance Genes?. Antibiotics, 2024, 13, 87.	3.7	0
13330	Microplastic fibres affect soil fungal communities depending on drought conditions with consequences for ecosystem functions. Environmental Microbiology, 2024, 26, .	3.8	0
13331	Functional host-specific adaptation of the intestinal microbiome in hominids. Nature Communications, 2024, 15 , .	12.8	0
13332	No viable bacterial communities reside in the urinary bladder of cats with feline idiopathic cystitis. Research in Veterinary Science, 2024, 168, 105137.	1.9	0
13333	Oxic methane production from methylphosphonate in a large oligotrophic lake: limitation by substrate and organic carbon supply. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
13334	Euglena mutabilis exists in a FAB consortium with microbes that enhance cadmium tolerance. International Microbiology, 0, , .	2.4	O

#	Article	IF	CITATIONS
13335	Disruption of gut barrier integrity and host–microbiome interactions underlie MASLD severity in patients with type-2 diabetes mellitus. Gut Microbes, 2024, 16, .	9.8	0
13336	Genotype Combinations Drive Variability in the Microbiome Configuration of the Rhizosphere of Maize/Bean Intercropping System. International Journal of Molecular Sciences, 2024, 25, 1288.	4.1	1
13337	Exploring the sediment-associated microbiota of the Mar Menor coastal lagoon. Frontiers in Marine Science, $0,11,.$	2.5	0
	Pervasive associations between dark septate endophytic fungi with tree root and soil microbiomes across Europe. Nature Communications, 2024, 15, .	12.8	2
13339	Winged resistance: Storks and gulls increase carriage of antibiotic resistance by shifting from paddy fields to landfills. Science of the Total Environment, 2024, 914, 169946.	8.0	0
13340	An Investigation of Metabolic Risk Factors and Gut Microbiota in Unexplained Syncope. Biomedicines, 2024, 12, 264.	3.2	O
13341	Driving forces shaping the microbial ecology in meat packing plants. Frontiers in Microbiology, 0, 14, .	3.5	0
13342	A grazer's niche edge is associated with increasing diet diversity and poor population performance. Ecology Letters, 2024, 27, .	6.4	0
13343	Nanoscale sulfur alters the bacterial and eukaryotic communities of the tomato rhizosphere and their interactions with a fungal pathogen. NanoImpact, 2024, 33, 100495.	4.5	1
13344	The potential of microbiota information to better predict efficiency traits in growing pigs fed a conventional and a high-fiber diet. Genetics Selection Evolution, 2024, 56, .	3.0	O
13345	The microbiota of long-living and cancer-free blind mole rat \$extit{(Nannospalax xanthodon)}\$ from the edge of its distribution in Northern Anatolia. Communications Faculty of Science University of Ankara Series C Biology Geological Engineering and Geophysical Engineering, 2023, 32, 105-118.	0.1	0
	Pantoea bathycoeliae sp. nov and Sodalis sp. are core gut microbiome symbionts of the two-spotted stink bug. Frontiers in Microbiology, 0, 14 , .	3.5	1
	Viral metagenomics reveals diverse virus-host interactions throughout the soil depth profile. MBio, 2023, 14, .	4.1	0
13348	Exploring Soil Bacterial Diversity in Relation to Edaphic Physicochemical Properties of High-altitude Wetlands from Argentine Puna. Microbial Ecology, 2024, 87, .	2.8	O
13349	Virophages Found in Viromes from Lake Baikal. Biomolecules, 2023, 13, 1773.	4.0	0
13350	The Effectiveness of Co-Inoculation by Consortia of Microorganisms Depends on the Type of Plant and the Soil Microbiome. Plants, 2024, $13,116$.	3.5	1
13352	Land management of formerly subtropical Atlantic Forest reduces soil carbon stocks and alters microbial community structure and function. Applied Soil Ecology, 2024, 195, 105252.	4.3	0
	Effect of fatty acid-enriched black soldier fly larvae meal combined with chitinase on the metabolic processes of Nile tilapia. British Journal of Nutrition, 2024, 131, 1326-1341.	2.3	O

#	ARTICLE	IF	Citations
13354	Pollen Diet Diversity does not Affect Gut Bacterial Communities or Melanization in a Social and Solitary Bee Species. Microbial Ecology, 2024, 87, .	2.8	0
13355	Effect of Fertigation with Struvite and Ammonium Nitrate on Substrate Microbiota and N2O Emissions in a Tomato Crop on Soilless Culture System. Agronomy, 2024, 14, 119.	3.0	O
13357	Analysis of microbial communities in solid and liquid pig manure during the fertilization process. Scientific Reports, 2024, 14, .	3.3	0
13359	A unified compendium of prokaryotic and viral genomes from over 300 anaerobic digestion microbiomes. Environmental Microbiomes, 2024, 19, .	5.0	2
13360	A genus in the bacterial phylum Aquificota appears to be endemic to Aotearoa-New Zealand. Nature Communications, 2024, 15 , .	12.8	0
13363	Major urinary protein ($\langle i \rangle$ Mup $\langle i \rangle$) gene family deletion drives sex-specific alterations in the house-mouse gut microbiota. Microbiology Spectrum, 2024, 12, .	3.0	O
13364	The military gear microbiome: risk factors surrounding the warfighter. Applied and Environmental Microbiology, 2024, 90, .	3.1	0
13365	Influence of overcooking on in vitro digestion and fermentation of ground beef and whole wheat bread. Food Research International, 2024, 178, 113953.	6.2	0
13366	Efficacy of Quadruple-coated Probiotics in Patients With Irritable Bowel Syndrome: A Randomized, Double-blind, Placebo-controlled, Parallel-group Study. Journal of Neurogastroenterology and Motility, 2024, 30, 73-86.	2.4	0
13368	Impact of systemic antimicrobial therapy on the faecal microbiome in symptomatic dairy cows. PLoS ONE, 2024, 19, e0296290.	2.5	0
13370	Microbial associates of the elm leaf beetle: uncovering the absence of resident bacteria and the influence of fungi on insect performance. Applied and Environmental Microbiology, 2024, 90, .	3.1	0
13372	Distinct alterations of gut microbiota between viral- and non-viral-related hepatocellular carcinoma. Applied Microbiology and Biotechnology, 2024, 108, .	3.6	O
13373	Biotic homogenization, lower soil fungal diversity and fewer rare taxa in arable soils across Europe. Nature Communications, 2024, 15, .	12.8	1
13374	Effects of Fishmeal Substitution with Mealworm Meals (Tenebrio molitor and Alphitobius diaperinus) on the Growth, Physiobiochemical Response, Digesta Microbiome, and Immune Genes Expression of Atlantic Salmon (Salmo salar). Aquaculture Nutrition, 2024, 2024, 1-21.	2.7	O
13375	Agricultural land-use legacies affect soil bacterial communities following restoration in a global biodiversity hotspot. Biological Conservation, 2024, 290, 110437.	4.1	0
13377	Bacterial heat shock protein genes during induction chemotherapy in pediatric patients with acute lymphoblastic leukemia. Future Oncology, 2024, 20, 17-23.	2.4	O
13378	A single intranasal dose of essential oil spray confers modulation of the nasopharyngeal microbiota and short-term inhibition of Mannheimia in feedlot cattle: a pilot study. Scientific Reports, 2024, 14, .	3.3	0
13379	Bacterial community composition in the Northern Gulf of Mexico intertidal sediment bioturbated by the ghost shrimp Lepidophthalmus louisianensis. Antonie Van Leeuwenhoek, 2024, 117, .	1.7	0

#	Article	IF	CITATIONS
13381	MiMultiCat: A Unified Cloud Platform for the Analysis of Microbiome Data with Multi-Categorical Responses. Bioengineering, 2024, 11, 60.	3.5	0
13382	Gut microbiota variations in wild yellow baboons (Papio cynocephalus) are associated with sex and habitat disturbance. Scientific Reports, 2024, 14, .	3.3	0
13383	A first report on prokaryotic diversity in northwestern Arafura deep-sea sediments, Indonesia. Scientific Reports, 2024, 14, .	3.3	0
13386	Linking Zetaproteobacterial diversity and substratum type in iron-rich microbial mats from the Lucky Strike hydrothermal field (EMSO-Azores observatory). Applied and Environmental Microbiology, 2024, 90, .	3.1	0
13387	Gut microbiome in atypical depression. Journal of Affective Disorders, 2024, 349, 277-285.	4.1	0
13388	Seafloor incubation experiments at deep-sea hydrothermal vents reveal distinct biogeographic signatures of autotrophic communities. FEMS Microbiology Ecology, 2024, 100, .	2.7	0
13389	Screening of core microorganisms in healthy and diseased peaches and effect evaluation of biocontrol bacteria (Burkholderia sp.). Food Microbiology, 2024, 120, 104465.	4.2	0
13390	New chemical and microbial perspectives on vitamin B1 and vitamer dynamics of a coastal system. ISME Communications, 2024, 4, .	4.2	0
13391	Core microbiota drive multi-functionality of the soil microbiome in the Cinnamomum camphora coppice planting. BMC Microbiology, 2024, 24, .	3.3	1
13392	Unravelling the temporal and spatial variation of fungal phylotypes from embryo to adult stages in Atlantic salmon. Scientific Reports, 2024, 14, .	3.3	0
13394	Soil microbes from conservation agriculture systems reduce growth of Bt-resistant western corn rootworm larvae. Journal of Pest Science, 0, , .	3.7	1
13395	Contrasted host specificity of gut and endosymbiont bacterial communities in alpine grasshoppers and crickets. ISME Communications, 2024, 4, .	4.2	0
13396	Role of indigenous microbial communities in the mobilization of potentially toxic elements and rare-earth elements from alkaline mine waste. Journal of Hazardous Materials, 2024, 466, 133504.	12.4	0
13397	Exploring the effects of transport duration on the fecal microbial communities of surplus dairy calves. Journal of Dairy Science, 2024, , .	3.4	0
13398	The salivary microbiota of patients with acute lower respiratory tract infection–A multicenter cohort study. PLoS ONE, 2024, 19, e0290062.	2.5	0
13400	i»¿Assessing the diversity of nematodes in the Store Mosse National Park (Sweden) using metabarcoding. Metabarcoding and Metagenomics, 0, 8, .	0.0	O
13401	Gut microbiota analyses of cutaneous T-cell lymphoma patients undergoing narrowband ultraviolet B therapy reveal alterations associated with disease treatment. Frontiers in Immunology, 0, 14, .	4.8	0
13402	Severe and mild drought cause distinct phylogenetically linked shifts in the blue grama (Bouteloua) Tj ETQq $1\ 1\ 0$.	784314 rg	ß] /Overloc

# ARTICLE	IF	CITATIONS
13404 Biogeographic survey of soil bacterial communities across Antarctica. Microbiome, 2024, 12, .	11.1	1
Plant-based diets and the gut microbiome: findings from the Baltimore Longitudinal Study of Aging. American Journal of Clinical Nutrition, 2024, $119,628-638$.	4.7	0
Partitioning the effects of coffee-Urochloa intercropping on soil microbial properties at a centimeter-scale. Applied Soil Ecology, 2024, 195, 105264.	4.3	0
Environmental microbiome in the home and daycare settings during the <scp>COVIDâ€19</scp> pandemic, 13409 and potential risk of nonâ€communicable disease in children. Environmental Microbiology Reports, 2024, 16, .	2.4	0
Temperature sensitivity of soil-borne fungal phytopathogens depends on niche breadth and land use types. Fungal Ecology, 2024, 68, 101329.	1.6	0
Soybean microbiome composition and the impact of host plant resistance. Frontiers in Plant Science, 0, 14, .	3.6	0
Exploring Genomics and Microbial Ecology: Analysis of Bidens pilosa L. Genetic Structure and Soil Microbiome Diversity by RAD-Seq and Metabarcoding. Plants, 2024, 13, 221.	3.5	0
Drought legacy interacts with wildfire to alter soil microbial communities in a Mediterranean climate-type forest. Science of the Total Environment, 2024, 915, 170111.	8.0	0
Host- plasmid network structure in wastewater is linked to antimicrobial resistance genes. Nature Communications, 2024, 15, .	12.8	0
Consistent effects of independent domestication events on the plant microbiota. Current Biology, 2024, 34, 557-567.e4.	3.9	1
Long-term conservation tillage with reduced nitrogen fertilization intensity can improve winter wheat health via positive plant–microorganism feedback in the rhizosphere. FEMS Microbiology Ecology, 2024, 100, .	2.7	1
<i>JAK2V617F</i> drives gut microbiota differences in patients with myeloproliferative neoplasms. European Journal of Haematology, 2024, 112, 776-787.	2.2	0
Alterations of rumen and fecal microbiome in growing beef and dairy steers fed rumen-protected <i>Capsicum</i> oleoresin. Journal of Animal Science, 2024, 102, .	0.5	0
Combined omics expose microbial niches of fungi and bacteria correlating with wine volatile profiles in Douro wine region. LWT - Food Science and Technology, 2024, 193, 115769.	5.2	0
13426 Impact of stockpile depth and storage time on soil microbial communities. Applied Soil Ecology, 2024, 196, 105275.	4.3	0
Bacteria involved in the sulfur cycle in tarballs collected from the Alabama Gulf Coast. FEMS Microbiology Letters, 2024, 371, .	1.8	0
Microbial-mediated oxidative dissolution of orpiment and realgar in circumneutral aquatic environments. Water Research, 2024, 251, 121163.	11.3	0
Methanogenic Archaea Quantification in the Human Gut Microbiome with F420 Autofluorescence-Based Flow Cytometry. Applied Microbiology, 2024, 4, 162-180.	1.6	0

# ARTICLE	IF	. (Citations
Pioneering gut health improvements in piglets with phytogenic feed additives. Applied Micro and Biotechnology, 2024, 108 , .	obiology 3.0	6 (O
Impact of salinity and time on structure and functional potential of wastewater treatment b intermittent sand bioreactors. Journal of General and Applied Microbiology, 2024, , .	oiofilms in O.	.7 (0
Metazoan diversity and community assemblages in sediments across a Western Pacific Trench-Arc-Basin system: insights from eDNA metabarcoding. Frontiers in Marine Science, 0,	2.5	.5 (0
Longitudinal gut microbiota composition of South African and Nigerian infants in relation to vaccine responses. Microbiology Spectrum, 2024, 12, .	o tetanus 3.0	.0 (0
Bacterial community dynamics of spineless cactus silage during fermentation and aerobic st Bioresource Technology Reports, 2024, 25, 101762.	tability. 2.:	7 (0
Sponges and their prokaryotic communities sampled from a remote karst ecosystem. Marin Biodiversity, 2024, 54, .	ne 1.0	0 (O
Effects of temperature and microbial disruption on juvenile kelp Ecklonia radiata and its assobacterial community. Frontiers in Marine Science, 0, 10, .	ociated 2.4	.5 (0
High-resolution genomic analysis to investigate the impact of the invasive brushtail possum (Trichosurus vulpecula) and other wildlife on microbial water quality assessments. PLoS ONI 19, e0295529.	E, 2024, 2.:	.5 (0
Consumption of the Non-Nutritive Sweetener Stevia for 12 Weeks Does Not Alter the Comp the Human Gut Microbiota. Nutrients, 2024, 16, 296.	position of 4.3	1 (0
Seasonal temperature dependency of aquatic branched glycerol dialkyl glycerol tetraethers: mesocosm approach. Organic Geochemistry, 2024, 189, 104742.	: A 1.8	8 (0
13443 Microbial diversity in four Mediterranean irciniid sponges. Biodiversity Data Journal, 0, 12, .	0.	.8 (0
Convergent photophysiology and prokaryotic assemblage structure in epilithic cyanobacteri and algal turf communities. Journal of Phycology, 2024, 60, 343-362.	ial tufts 2.:	3 (0
Microbiome Responses to Oral Fecal Microbiota Transplantation in a Cohort of Domestic Doveterinary Sciences, 2024, 11, 42.	ogs. 1.7	7 (0
Exploring the predictive power of jejunal microbiome composition in clinical and subclinical enteritis caused by Clostridium perfringens: insights from a broiler chicken model. Journal of Translational Medicine, 2024, 22, .		.4 1	1
Soil amendment strategies determining microbial community composition and their assembly processes in a continuously cropped soil. Soil Ecology Letters, 2024, 6, .	oly 4.	.5 (0
Divergent morphological and microbiome strategies of two neighbor sponges to cope with Mediterranean CO2 vents. Science of the Total Environment, 2024, 916, 170171.	low pH in 8.	.0 (0
Alkali treatment of maize bran affects utilization of arabinoxylan and other non-digestible carbohydrates by the human gut microbiota in vitro in a dose-dependent manner. Food Hyd 2024, 151, 109764.	rocolloids, 10	0.7 (0
Documenting the diversity of the Namibian Ju \mid $\hat{a} \in \mathbb{N}$ hoansi intestinal microbiome. Cell Reporting 113690.	rts, 2024, 43, 6	.4 (O

#	ARTICLE	IF	CITATIONS
13453	Modeling the limits of detection for antimicrobial resistance genes in agri-food samples: a comparative analysis of bioinformatics tools. BMC Microbiology, 2024, 24, .	3.3	0
13455	A tripartite bacterial-fungal-plant symbiosis in the mycorrhiza-shaped microbiome drives plant growth and mycorrhization. Microbiome, 2024, 12, .	11.1	1
13456	Pre-isolation procedures matter–Comparison of different filtration methods prior to DNA isolation in river microbiome analysis. Ecohydrology and Hydrobiology, 2024, , .	2.3	0
13457	Succession of microbial community composition and secondary metabolism during marine biofilm development. ISME Communications, 2024, 4, .	4.2	0
13458	Multi-species biofilms of environmental microbiota isolated from fruit packing facilities promoted tolerance of Listeria monocytogenes to benzalkonium chloride. Biofilm, 2024, 7, 100177.	3.8	0
13460	Exploring the effects of dietary inulin in rainbow trout fed a high-starch, 100% plant-based diet. Journal of Animal Science and Biotechnology, 2024, 15, .	5.3	O
13461	Metagenomic Characterisation of the Gut Microbiome and Effect of Complementary Feeding on Bifidobacterium spp. in Australian Infants. Microorganisms, 2024, 12, 228.	3.6	0
13462	Sex-specific bacterial microbiome variation in octopus vulgaris skin. Frontiers in Microbiology, 0, 14, .	3.5	0
13463	Impact of Microplastic on Freshwater Sediment Biogeochemistry and Microbial Communities Is Polymer Specific. Water (Switzerland), 2024, 16, 348.	2.7	0
13464	Gut microbial ecology and exposome of a healthy Pakistani cohort. Gut Pathogens, 2024, 16, .	3.4	0
13465	Weather in two climatic regions shapes the diversity and drives the structure of fungal endophytic community of bilberry (Vaccinium myrtillus L.) fruit. Environmental Microbiomes, 2024, 19, .	5.0	0
13467	Gut Biogeography Accentuates Sex-Related Differences in the Murine Microbiome. Microorganisms, 2024, 12, 221.	3.6	0
13468	The Maternal Diet Index and Offspring Microbiota at 1 Month of Life: Insights from the Mediterranean Birth Cohort MAMI. Nutrients, 2024, 16, 314.	4.1	0
13469	Biomonitoring of Dietary Mycotoxin Exposure and Associated Impact on the Gut Microbiome in Nigerian Infants. Environmental Science & Environmental Sci	10.0	O
13470	Moderate variations in the human diet impact the gut microbiota in humanized mice. Acta Physiologica, 2024, 240, .	3.8	0
13472	Elevated methane flux in a tropical peatland post-fire is linked to depth-dependent changes in peat microbiome assembly. Npj Biofilms and Microbiomes, 2024, 10, .	6.4	O
13473	The First Description of the Microbial Diversity in the Amarillo River (La Rioja, Argentina), a Natural Extreme Environment Where the Whole Microbial Community Paints the Landscape Yellow. Microorganisms, 2024, 12, 235.	3.6	0
13474	Study of amino acids absorption and gut microbiome on consumption of pea protein blended with enzymes-probiotics supplement. Frontiers in Nutrition, $0,11,.$	3.7	O

# ARTICLE	IF	Citations
13475 Anaerobic gut fungal communities in marsupial hosts. MBio, 2024, 15, .	4.1	0
Associations of gut microbiota alterations with clinical, metabolic, and immune-inflammatory characteristics of chronic schizophrenia. Journal of Psychiatric Research, 2024, 171, 152-160.	3.1	O
Evolution of the urinary microbiota in spinal cord injury patients with decubitus ulcer: A snapshot study. International Wound Journal, 2024, 21, .	2.9	0
Disturbance–diversity relationships of microbial communities change based on growth substrate. MSystems, 2024, 9, .	3.8	0
Role of Syndiniales parasites in depth-specific networks and carbon flux in the oligotrophic ocean. ISME Communications, 2024, 4, .	4.2	0
Zooming in on the intracellular microbiome composition of bacterivorous <i>Acanthamoeba</i> isolates. ISME Communications, 2024, 4, .	4.2	0
Seed bacterial microbiota in post-submergence tolerant and sensitive barley genotypes. Functional Plant Biology, 2024, 51, .	2.1	0
Unravelling the mechanisms of underweight in Parkinson's disease by investigating into the role of gut microbiome. Npj Parkinson's Disease, 2024, 10, .	5.3	0
Meta-analysis reveals obesity associated gut microbial alteration patterns and reproducible contributors of functional shift. Gut Microbes, 2024, 16, .	9.8	0
Combined pH ratiometry and fluorescence lectin-binding analysis (pH-FLBA) for microscopy-based analyses of biofilm pH and matrix carbohydrates. Applied and Environmental Microbiology, 2024, 90, .	3.1	0
Whole-genome shotgun sequencing unravels the influence of environmental microbial co-infections on the treatment efficacy for severe pediatric infectious diseases. Frontiers in Microbiology, 0, 15, .	3.5	0
Profiling and source tracking of the microbial populations and resistome present in fish products. International Journal of Food Microbiology, 2024, 413, 110591.	4.7	0
The maternal microbiome in pregnancy, delivery, and earlyâ€stage development of neonatal microbiome after cesarean section: A prospective longitudinal study. Acta Obstetricia Et Gynecologica Scandinavica, 2024, 103, 832-841.	2.8	0
Rhizosphere assembly alters along a chronosequence in the HallstÃtter glacier forefield (Dachstein,) Tj E	TQq1 1 0.784314 r	gBT /Overlo
Plastiphily is linked to generic virulence traits of important human pathogenic fungi. Communications Earth & Environment, 2024, 5, .	6.8	0
Biotic interactions outweigh abiotic factors as drivers of bark microbial communities in Central European forests. ISME Communications, 2024, 4, .	4.2	0
Stress and depression-associated shifts in gut microbiota: A pilot study of human pregnancy. Brain, Behavior, & Immunity - Health, 2024, 36, 100730.	2.5	0
A multidisciplinary approach to tackling invasive species: barcoding, morphology, and metataxonomy of the leafhopper Arboridia adanae. Scientific Reports, 2024, 14, .	3.3	O

# ARTICLE	IF	Citations
Microbial decomposition of biodegradable plastics on the deep-sea floor. Nature Communications, 2024, 15, .	12.8	1
Inoculation with adapted bacterial communities promotes development of full scale slow sand filters for drinking water production. Water Research, 2024, 253, 121203.	11.3	0
Skin microbiome disturbance linked to droughtâ€associated amphibian disease. Ecology Letters, 2024, 27, .	6.4	0
Soil carbon mineralization and microbial community dynamics in response to pyrogenic organic matter addition. Soil Biology and Biochemistry, 2024, 191, 109328.	8.8	0
Ceftriaxone alters the gut microbiome composition and reduces alcohol intake in male and female Sprague-Dawley rats. Alcohol, 2024, , .	1.7	0
Addition of (bio)surfactants in the biofiltration of hydrophobic volatile organic compounds in air. Journal of Environmental Management, 2024, 353, 120132.	7.8	0
Effects of a (poly)phenol-rich berry mix on gas production in healthy individuals: An integrated clinical, metagenomic, and metabolomic proof-of-concept study. Journal of Functional Foods, 2024, 113, 106032.	3.4	0
Integrated microbiota–host–metabolome approaches reveal adaptive ruminal changes to prolonged high-grain feeding and phytogenic supplementation in cattle. FEMS Microbiology Ecology, 2024, 100, .	2.7	0
Stratification and summer protist communities in the Arctic influenced coastal systems of Nunavik (Qu \tilde{A} ©bec, Canada). Frontiers in Marine Science, 0, 11, .	2.5	0
Differential Impacts of Road De-icers on Freshwater Bacterial Communities. Water (Switzerland), 2024, 16, 426.	2.7	0
Interspecific interactions facilitate keystone species in a multispecies biofilm that promotes plant growth. ISME Journal, 2024, 18, .	9.8	0
Functional similarity, despite taxonomical divergence in the millipede gut microbiota, points to a common trophic strategy. Microbiome, 2024, 12, .	11.1	1
Stronger deterministic processes shape the plastisphere microbiota of biodegradable microplastics compared to non-biodegradable microplastics in farmland soil. Applied Soil Ecology, 2024, 196, 105312.	4.3	0
Parasitism-Induced Changes in Microbial Eukaryotes of Peruvian Alpaca Gastrointestinal Tract. Life, 2024, 14, 187.	2.4	0
Efficacy of Lactiplantibacillus plantarum PBS067, Bifidobacterium animalis subsp. lactis BL050, and Lacticaseibacillus rhamnosus LRH020 in the Amelioration of Vaginal Microbiota in Post-Menopausal Women: A Prospective Observational Clinical Trial. Nutrients, 2024, 16, 402.	4.1	0
Strategies to Reduce the Environmental Lifetimes of Drinking Straws in the Coastal Ocean. ACS Sustainable Chemistry and Engineering, 2024, 12, 2404-2411.	6.7	0
Stochastic and deterministic assembly processes of microbial communities in relation to natural attenuation of black stains in Lascaux Cave. MSystems, 2024, 9, .	3.8	0
Investigating the outcomes of a threatened gorgonian in situ transplantation: Survival and microbiome diversity in Paramuricea clavata (Risso, 1827). Marine Environmental Research, 2024, 196, 106384.	2.5	0

# /	Article	IF	Citations
13520	Microbiome compositions of nymphal blacklegged ticks (Ixodes scapularis) infected and uninfected with Borrelia burgdorferi in Delaware. Journal of Vector Ecology, 2024, 49, .	1.0	0
13521	Spider webs capture environmental DNA from terrestrial vertebrates. IScience, 2024, 27, 108904.	4.1	0
13522	Characterization of microbial communities in urban subway: connotation for indoor environment quality and public health. Air Quality, Atmosphere and Health, 0, , .	3.3	0
13523	A doubleâ€blind, randomized, placeboâ€controlled study assessing the impact of probiotic supplementation on the symptoms of irritable bowel syndrome in females. Neurogastroenterology and Motility, 2024, 36, .	3.0	0
13524	A conceptual framework for hostâ€associated microbiomes of hybrid organisms. Methods in Ecology and Evolution, 2024, 15, 511-529.	5.2	0
13525	Fecal and vaginal microbiota of vaccinated and non-vaccinated pregnant elk challenged with Brucella abortus. Frontiers in Veterinary Science, $0,11,.$	2.2	0
	Spontaneous fermentation of Mara $\mathring{\rm A}_{ m i}$ tina wines: The correlation between autochthonous mycobiota and phenolic compounds. Food Research International, 2024, 180, 114072.	6.2	0
13527	Falcon gut microbiota is shaped by diet and enriched in Salmonella. PLoS ONE, 2024, 19, e0293895.	2.5	1
13528	Are fecal samples an appropriate proxy for amphibian intestinal microbiota?. Ecology and Evolution, 2024, 14, .	1.9	1
	Identification of synthetic consortia from a set of plantâ€beneficial bacteria. Microbial Biotechnology, 2024, 17, .	4.2	1
13530	Treatment response in rheumatoid arthritis is predicted by the microbiome: a large observational study in UK DMARD-naive patients. Rheumatology, 0, , .	1.9	0
13531	Rat microbial biogeography and age-dependent lactic acid bacteria in healthy lungs. Lab Animal, 2024, 53, 43-55.	0.4	0
13532	Host–gut microbiota interactions shape parasite infections in farmed Atlantic salmon. MSystems, 2024, 9, .	3.8	0
	Coâ€occurring orchid species associated with different lowâ€abundance mycorrhizal fungi from the soil in a highâ€diversity conservation area in Denmark. Ecology and Evolution, 2024, 14, .	1.9	0
13534	Amelioration of the brain structural connectivity is accompanied with changes of gut microbiota in a tuberous sclerosis complex mouse model. Translational Psychiatry, 2024, 14, .	4.8	0
13536	Enteric Dysbiosis in Children With Autism Spectrum Disorder and Associated Response to Stress. Cureus, 2024, , .	0.5	0
13538	lllegal dumping of oil and gas wastewater alters arid soil microbial communities. Applied and Environmental Microbiology, 2024, 90, .	3.1	1
	Gut microbiome and intestinal inflammation in preclinical stages of rheumatoid arthritis. RMD Open, 2024, 10, e003589.	3.8	O

# ARTICLE	IF	CITATIONS
Identification of consensus head and neck cancer-associated microbiota signatures: a systematic review and meta-analysis of 16S rRNA and The Cancer Microbiome Atlas datasets. Journal of Medical Microbiology, 2024, 73, .	1.8	1
<i>Citrobacter rodentium</i> possesses a functional type II secretion system necessary for successful host infection. Gut Microbes, 2024, 16, .	الا	O
Enriching electroactive microorganisms from ferruginous lake waters – Mind the sulfate reducers!. Bioelectrochemistry, 2024, 157, 108661.	4.6	0
Multimodal immune phenotyping reveals microbial-T cell interactions that shape pancreatic cancer. Cell Reports Medicine, 2024, 5, 101397.	6.5	O
Fungal signature differentiates alcohol-associated liver disease from nonalcoholic fatty liver disease. Gut Microbes, 2024, 16, .	9.8	0
Brevibacterium EB3 inoculation enhances rhizobacterial community interactions leading to improved growth of Salicornia europaea. Applied Soil Ecology, 2024, 196, 105306.	4.3	O
Contribution of cryoconite holes in the supraglacial discharge of bioavailable iron in Larsemann Hills, East Antarctica. Polar Science, 2024, , 101052.	1.2	0
TerrANTALife 1.0 Biodiversity data checklist of known Antarctic terrestrial and freshwater life forms. Biodiversity Data Journal, 0, 12, .	0.8	O
Spatial and Temporal Variability of Saxitoxin-Producing Cyanobacteria in U.S. Urban Lakes. Toxins, 2024, 16, 70.	3.4	0
Anticancer drugs impact the performance and prokaryotic microbiome of an aerobic granular sludge system operated in a sequential batch reactor. Journal of Hazardous Materials, 2024, 467, 133674.	12.4	O
Micro-Environmental Variation in Soil Microbial Biodiversity in Forest Frontier Ecosystemsâ€"Implications for Sustainability Assessments. Sustainability, 2024, 16, 1236.	3.2	0
Diversity and community structure of anaerobic gut fungi in the rumen of wild and domesticated herbivores. Applied and Environmental Microbiology, 2024, 90, .	3.1	O
Evaluation of the safety and efficacy of fecal microbiota transplantations in bottlenose dolphins (<i>Tursiops truncatus</i>) using metagenomic sequencing. Journal of Applied Microbiology, 2024, 1.	135, 3.1	0
Human metapneumovirus respiratory infection affects both innate and adaptive intestinal immunity. Frontiers in Immunology, 0, 15 , .	4.8	O
Microbial diversity and soil health parameters associated with turfgrass landscapes. Applied Soil Ecology, 2024, 196, 105311.	4.3	0
Distinct intratumoral microbiome of young-onset and average-onset colorectal cancer. EBioMedicine 2024, 100, 104980.	6.1	1
Bacterial community distribution and functional potentials provide key insights into their role in the ecosystem functioning of a retreating Eastern Himalayan glacier. FEMS Microbiology Ecology, 2024, 100, .	2.7	1
Bacterial diversity in semen from stallions in three European countries evaluated by $16S$ sequencing. Veterinary Research Communications, 0 , , .	1.6	2

# ARTICLE	IF	CITATIONS
The seeds of Plantago lanceolata comprise a stable core microbiome along a plant richness gradient. Environmental Microbiomes, 2024, 19, .	5.0	O
A Murine Model of Maternal Micronutrient Deficiencies and Gut Inflammatory Host-microbe 13561 Interactions in the Offspring. Cellular and Molecular Gastroenterology and Hepatology, 2024, 17, 827-852.	4.5	0
Merging and concatenation of sequencing reads: a bioinformatics workflow for the comprehensive profiling of microbiome from amplicon data. FEMS Microbiology Letters, 2024, 371, .	1.8	0
Impacts of electrochemical disinfection on the viability and structure of the microbiome in secondary effluent water. Frontiers of Environmental Science and Engineering, 2024, 18 , .	6.0	0
Divergent responses of the coral holobiont to deoxygenation and prior environmental stress. Frontiers in Marine Science, 0, 10, .	2.5	0
Early life exposure of infants to benzylpenicillin and gentamicin is associated with a persistent amplification of the gut resistome. Microbiome, 2024, 12 , .	11.1	0
Differential effects of antiretroviral treatment on immunity and gut microbiome composition in people living with HIV in rural versus urban Zimbabwe. Microbiome, 2024, 12, .	11.1	0
Common commercially available parasiticides do not cause fatal changes in the microbiome of the dung beetle <i> Onthophagus binodis < /i> $\hat{a} \in \hat{a}$ pilot study. New Zealand Journal of Zoology, 0, , 1-11.</i>	1.1	0
Pilot study on cultural and metagenomic analysis of bile and biliary stentslead to unveiling the key players in stent occlusion. Scientific Reports, 2024, 14, .	3.3	0
13570 DNA metabarcoding reveals the impact of Cu2+ on soil cercozoan diversity. Protist, 2024, 175, 1260)16. 1.5	0
Improving the efficiency of DNA extraction from iron incrustations and oilfield-produced water. Scientific Reports, 2024, 14, .	3.3	0
Layer chicken microbiota: a comprehensive analysis of spatial and temporal dynamics across all major gut sections. Journal of Animal Science and Biotechnology, 2024, 15, .	r 5.3	0
Soil depths and microhabitats shape soil and root-associated bacterial and archaeal communities more than crop rotation in wheat. , 0, 3, .		0
Evolutionary history influences the microbiomes of a female symbiotic reproductive organ in cephalopods. Applied and Environmental Microbiology, 0, , .	3.1	0
HIV-associated gut microbial alterations are dependent on host and geographic context. Nature Communications, 2024, 15, .	12.8	0
Snowflake: visualizing microbiome abundance tables as multivariate bipartite graphs. Frontiers in Bioinformatics, 0, 4, .	2.1	0
Dissolved organic carbon characteristics are associated with changes in soil microbiome under different plant species. Applied Soil Ecology, 2024, 196, 105313.	4.3	0
Acute gastrointestinal permeability after traumatic brain injury in mice precedes a bloom in Akkermansia muciniphila supported by intestinal hypoxia. Scientific Reports, 2024, 14, .	3.3	0

# ARTICLE	IF	CITATIONS
Fermentation profile and dynamics of bacterial communities in vetch-oat ensiled with a novel spray-dried inoculant. Journal of Agricultural Science, 2023, 161, 835-846.	1.3	O
Glyphosate-based restoration of a degraded grassland threatens soil health and the diversity of nematode communities. Soil Biology and Biochemistry, 2024, 191, 109350.	8.8	0
Changes in Bacterial Gut Composition in Parkinson's Disease and Their Metabolic Contribution to Disease Development: A Gut Community Reconstruction Approach. Microorganisms, 2024, 12, 325.	3.6	0
The role of Helicobacter suis, Fusobacterium gastrosuis, and the pars oesophageal microbiota in gastric ulceration in slaughter pigs receiving meal or pelleted feed. Veterinary Research, 2024, 55, .	3.0	0
Stability of gut microbiome after COVID-19 vaccination in healthy and immuno-compromised individuals. Life Science Alliance, 2024, 7, e202302529.	2.8	0
Geology defines microbiome structure and composition in nunataks and valleys of the Sør Rondane Mountains, East Antarctica. Frontiers in Microbiology, 0, 15, .	3.5	0
13586 Improved 18S rDNA profiling of parasite communities in salmonid tissues using a host blocking primer. Parasitology Research, 2024, 123, .	1.6	0
Exploring the Microbiome in Human Reproductive Tract: High-Throughput Methods for the Taxonomic Characterization of Microorganisms. Seminars in Reproductive Medicine, 2023, 41, 125-143.	1.1	0
Microcystin influence on soil-plant microbiota: Unraveling microbiota modulations and assembly processes in the rhizosphere of Vicia faba. Science of the Total Environment, 2024, 918, 170634.	8.0	0
An artificial intelligence approach of feature engineering and ensemble methods depicts the rumen microbiome contribution to feed efficiency in dairy cows. Animal Microbiome, 2024, 6, .	3.8	2
Microbial interactions among <i>Gardnerella </i> , <i>Prevotella </i> and <i>Fannyhessea </i> prior to incident bacterial vaginosis: protocol for a prospective, observational study. BMJ Open, 2024, 14, e083516.	1.9	0
Preceding crop legacy modulates the early growth of winter wheat by influencing root growth dynamics, rhizosphere processes, and microbial interactions. Soil Biology and Biochemistry, 2024, 191, 109343.	, 8.8	O
Shifts in microbial community composition and metabolism correspond with rapid soil carbon accumulation in response to 20Âyears of simulated nitrogen deposition. Science of the Total Environment, 2024, 918, 170741.	8.0	0
Rebaudioside D decreases adiposity and hepatic lipid accumulation in a mouse model of obesity. Scientific Reports, 2024, 14, .	3.3	0
13595 Impact of Doxycycline Addition on Activated Sludge Microflora and Microbial Communities. Processes, 2024, 12, 350.	2.8	0
Effects of past and present habitat on the gut microbiota of a wild rodent. Proceedings of the Royal Society B: Biological Sciences, 2024, 291, .	2.6	0
Fecal microbiome composition and diversity of cryopreserved canine stool at different duration and storage conditions. PLoS ONE, 2024, 19, e0294730.	2.5	0
Long-read sequencing of metagenomes from wet deposition samples in the Western USA during an elevated precipitation in February 2019. Aerobiologia, 0 , , .	1.7	0

# ARTICLE	IF	Citations
Screening and selection of essential oils for an intranasal spray against bovine respiratory pathogens based on antimicrobial, antiviral, immunomodulatory, and antibiofilm activities. Frontiers in Veterinary Science, 0, 11, .	2.2	О
Preliminary identification of bacterial community on seeds of crown rot symptomatic papaya fruit through Next Generation Sequencing (NGS). AIP Conference Proceedings, 2024, , .	0.4	O
Shallow and deep groundwater moderate methane dynamics in a high Arctic glacial catchment. Frontiers in Earth Science, 0, 12 , .	1.8	0
The source of microbial transmission influences niche colonization and microbiome development. Proceedings of the Royal Society B: Biological Sciences, 2024, 291, .	2.6	O
Divergent maturational patterns of the infant bacterial and fungal gut microbiome in the first year of 13604 life are associated with inter-kingdom community dynamics and infant nutrition. Microbiome, 2024, 12 .	2, 11.1	0
Microbial community and network responses across strong environmental gradients: How do they compare with macroorganisms?. FEMS Microbiology Ecology, 2024, 100, .	2.7	0
Hydraulic retention time drives changes in energy production and the anodic microbiome of a microbial fuel cell (MFC). Journal of Water Process Engineering, 2024, 59, 104966.	5.6	0
Gut microbiota of preterm infants in the neonatal intensive care unit: a study from a tertiary care center in northern India. Frontiers in Microbiology, 0, 15 , .	3.5	O
Characterization of gill bacterial microbiota in wild Arctic char (<i>Salvelinus alpinus </i>) across lakes, rivers, and bays in the Canadian Arctic ecosystems. Microbiology Spectrum, 2024, 12, .	3.0	0
Comparative microbiome analysis of beef cattle, the feedyard environment, and airborne particulate matter as a function of probiotic and antibiotic use, and change in pen environment. Frontiers in Microbiology, 0, 15, .	3.5	O
Soil exposure modulates the immune response to an influenza challenge in a mouse model. Science of the Total Environment, 2024, 922, 170865.	8.0	0
13613 Microbial-derived imidazole propionate links the heart failure-associated microbiome alterations to disease severity. Genome Medicine, 2024, 16 , .	8.2	O
Optimization of the Ex Situ Biomethanation of Hydrogen and Carbon Dioxide in a Novel Meandering Plug Flow Reactor: Start-Up Phase and Flexible Operation. Bioengineering, 2024, 11, 165.	3.5	0
Evaluation of multiple displacement amplification for metagenomic analysis of low biomass samples. ISME Communications, 2024, 4, .	4.2	0
Exploring Microbial Rhizosphere Communities in Asymptomatic and Symptomatic Apple Trees Using Amplicon Sequencing and Shotgun Metagenomics. Agronomy, 2024, 14, 357.	3.0	0
Hepatic granulomas following liver transplantation: A retrospective survey, and analysis of possible microbiological etiology. Pathology Research and Practice, 2024, 255, 155201.	2.3	0
Microbial hotspots in a relict fog-dependent Tillandsia landbeckii dune from the coastal Atacama Desert. Global and Planetary Change, 2024, 234, 104383.	3.5	0
Nutrients or resin? – The relationship between resin and food foraging in stingless bees. Ecology and Evolution, 2024, 14, .	1.9	0

#	ARTICLE	IF	CITATIONS
13622	Effects of seasonality and developed land cover on Culex mosquito abundance and microbiome diversity. Frontiers in Microbiology, $0,15,.$	3.5	0
13624	A zebrafish model to elucidate the impact of host genes on the microbiota. Environmental DNA, 2024, 6, .	5 . 8	O
13625	Dynamics of soil biota and nutrients at varied depths in a Tamarix ramosissima-dominated natural desert ecosystem: Implications for nutrient cycling and desertification management. Journal of Environmental Management, 2024, 354, 120217.	7.8	0
13626	Chicory (Cichorium intybus) reduces cyathostomin egg excretion and larval development in grazing horses. International Journal for Parasitology: Drugs and Drug Resistance, 2024, 24, 100523.	3.4	0
13627	Impact of bacterial and fungal inoculants on the resident rhizosphere microbiome and the volatilome of tomato plants under leaf herbivory stress. FEMS Microbiology Ecology, 2024, 100, .	2.7	0
13628	Insight into planktonic protistan and fungal communities across the nutrient-depleted environment of the South Pacific Subtropical Gyre. Microbiology Spectrum, 2024, 12, .	3.0	0
13629	Preliminary characterization of coral reef diversity using environmental DNA in a hyper-diverse context. Regional Studies in Marine Science, 2024, 71, 103432.	0.7	0
13630	The native distribution of a common legume shrub is limited by the range of its nitrogenâ€fixing mutualist. New Phytologist, 2024, 242, 77-92.	7.3	0
13632	Saccharomyces cerevisiae derived postbiotic alters gut microbiome metabolism in the human distal colon resulting in immunomodulatory potential in vitro. Frontiers in Microbiology, $0,15,15$	3.5	0
13633	Geomicrobiological characterization of the evaporitic ecosystem in the hypersaline lake Laguna Verde (Andean Puna, Northwestern Argentina). Ecology and Evolution, 2024, 14, .	1.9	0
13635	Design of a Remote Time-Restricted Eating and Mindfulness Intervention to Reduce Risk Factors Associated with Early-Onset Colorectal Cancer Development among Young Adults. Nutrients, 2024, 16, 504.	4.1	1
13636	Metagenomic analysis of gut microbiome illuminates the mechanisms and evolution of lignocellulose degradation in mangrove herbivorous crabs. BMC Microbiology, 2024, 24, .	3.3	0
13638	Wildlife fecal microbiota exhibit community stability across a longitudinal semi-controlled non-invasive sampling experiment., 0, 3, .		0
13639	Herptile gut microbiomes: a natural system to study multi-kingdom interactions between filamentous fungi and bacteria. MSphere, 2024, 9, .	2.9	0
13640	Characterizing Chemistry and Microbiomes During Continuous Anaerobic Codigestion of Organics and Cattle Manure Digestate. Energy & Energy & 2024, 38, 4429-4440.	5.1	0
13642	Microbiome composition and dynamics while grapes turn to wine. BIO Web of Conferences, 2023, 68, 02034.	0.2	0
13643	Significant differences in the caecal bacterial microbiota of red and grey squirrels in Britain. Journal of Medical Microbiology, 2024, 73, .	1.8	0
13644	Light–dark cycles may influence inÂsitu soil bacterial networks and diurnallyâ€sensitive taxa. Ecology and Evolution, 2024, 14, .	1.9	0

# ARTICLE	IF	Citations
The invasive legume <i>Lupinus polyphyllus</i> has minor siteâ€specific impacts on the composition of soil bacterial communities. Ecology and Evolution, 2024, 14, .	of 1.9	0
Prokaryote Composition and Structure of Rumen Fluid before and after In Vitro Rumen Fermentation. Fermentation, 2024, 10, 108.	3.0	0
Gut enterotype-dependent modulation of gut microbiota and their metabolism in response to xanthohumol supplementation in healthy adults. Gut Microbes, 2024, 16, .	9.8	0
DNA metabarcoding of gut microbiota reveals considerable taxonomic differences among wild individuals of the dung beetle Trypocopris pyrenaeus (Coleoptera: Geotrupidae). European Journal of Entomology, 0, 121, 40-53.	1.2	O
13649 Temporal changes in ewe vaginal microbiota throughout gestation. Frontiers in Microbiology, 0, 15, .	3.5	0
Longitudinal analysis of microbiome composition in Ghanaians living with HIV-1. Frontiers in Microbiology, 0, 15 , .	3.5	0
High fat intake sustains sorbitol intolerance after antibiotic-mediated Clostridia depletion from the gut microbiota. Cell, 2024, 187, 1191-1205.e15.	28.9	1
Dynamic effects of black soldier fly larvae meal on the cecal bacterial microbiota and prevalence of selected antimicrobial resistant determinants in broiler chickens. Animal Microbiome, 2024, 6, .	3.8	O
Environmental driving forces and phytoplankton diversity across the Ross Sea region during a summer–autumn transition. Limnology and Oceanography, 2024, 69, 772-788.	3.1	0
Enhancing Weaned Piglet Health and Performance: The Role of Autolyzed Yeast (Saccharomyces) Tj E	TQq1 1 0.784314 rg	BT /Overlock
The Eurasian spruce bark beetle Ips typographus shapes the microbial communities of its offspring and the gallery environment. Frontiers in Microbiology, 0, 15, .	nd 3.5	1
Fog caused distinct diversity of airborne bacterial communities enriched with pathogens over central Indo-Gangetic plain in India. Heliyon, 2024, 10, e26370.	3.2	O
Agricultural practices influence foliar endophytic communities in coffee plants of different varieties. , 2024, 7, .		0
Environmental drivers and cryptic biodiversity hotspots define endophytes in Earth's largest terrestrial biome. Current Biology, 2024, 34, 1148-1156.e7.	3.9	0
lmpact of bread diet on intestinal dysbiosis and irritable bowel syndrome symptoms in quiescent ulcerative colitis: A pilot study. PLoS ONE, 2024, 19, e0297836.	2.5	0
Quantification and Characterization of Microbial Emissions over the Northeastern Atlantic Using Mesocosm Experiments. , 2024, 1, 162-174.		0
Profiling of microbial populations present in ground beef and plant-based meat analogues. LWT - Food Science and Technology, 2024, 196, 115845.	d 5.2	0
Association of blood cellâ€based inflammatory markers with gut microbiota and cancer incidence in the Rotterdam study. Cancer Medicine, 2024, 13, .	he 2.8	0

# ARTICLE	IF	CITATIONS
The multispecies microbial cluster of <i>Fusobacterium</i> , <i>Parvimonas</i> , <i>Bacteroides</i> are 13664 <i>Faecalibacterium</i> as a precision biomarker for colorectal cancer diagnosis. Molecular Oncology, 2024, 18, 1093-1122.	nd 4.6	О
Neopolyploidy has variable effects on the diversity and composition of the wild strawberry microbiome. American Journal of Botany, 0, , .	1.7	o
Phosphorus (P) mobilisation from inorganic and organic P sources depends on P-acquisition strategies in dioecious Populus euphratica. Biology and Fertility of Soils, 2024, 60, 393-406.	4.3	0
Beneath the Surface: Investigating soil microbial and metazoa communities at various depths in a natural desert ecosystem inhabited by Karelinia caspia. Ecological Indicators, 2024, 159, 111745.	6.3	O
13668 Influence of host phylogeny and water physicochemistry on microbial assemblages of the fish skin microbiome. FEMS Microbiology Ecology, 2024, 100, .	2.7	0
Horizontal metaproteomics and CAZymes analysis of lignocellulolytic microbial consortia selectively enriched from cow rumen and termite gut. ISME Communications, 2023, 3, .	4.2	О
Etiology and epidemiology of digital dermatitis in Australian dairy herds. Journal of Dairy Science, 2024, , .	3.4	O
The clinical outcome of COVID-19 is strongly associated with microbiome dynamics in the upper respiratory tract. Journal of Infection, 2024, 88, 106118.	3.3	О
Elevated abundance of Komagataeibacter results in a lower pH in kombucha production; insights from microbiomic and chemical analyses. Current Research in Food Science, 2024, 8, 100694.	m 5.8	O
Environmental DNA captures diurnal fluctuations of surface eukaryotes on a tropical coral reef. Environmental DNA, 2024, 6, .	5.8	O
The intestinal digesta microbiota of tropical marine fish is largely uncultured and distinct from surrounding water microbiota. Npj Biofilms and Microbiomes, 2024, 10, .	6.4	0
Effects of Reduced Seawater pH and Oil Contamination on Bacterial Communities and Biochemical Markers of Estuarine Animal Hosts. Environments - MDPI, 2024, 11, 37.	3.3	О
The gut microbiome regulates the clinical efficacy of sulfasalazine therapy for IBD-associated spondyloarthritis. Cell Reports Medicine, 2024, 5, 101431.	6.5	O
The cultivated sea lettuce (Ulva) microbiome: Successional and seasonal dynamics. Aquaculture, 202-585, 740692.	4, 3.5	О
13679 Development of a novel mycobiome diagnostic for fungal infection. BMC Microbiology, 2024, 24, .	3.3	O
Closing the genome of unculturable cable bacteria using a combined metagenomic assembly of long and short sequencing reads. Microbial Genomics, 2024, 10 , .	2.0	0
Conditioner application improves bedding quality and bacterial composition with potential beneficial impacts for dairy cow's health. Microbiology Spectrum, 2024, 12, .	3.0	0
Assessing HCH isomer uptake in Alnus glutinosa: implications for phytoremediation and microbial response. Scientific Reports, 2024, 14, .	3.3	O

# ARTICLE	IF	CITATIONS
Temporal dynamics of volatile fatty acids profile, methane production, and prokaryotic community in an in vitro rumen fermentation system fed with maize silage. Frontiers in Microbiology, 0, 15, .	3.5	0
The path from root input to mineral-associated soil carbon is dictated by habitat-specific microbial traits and soil moisture. Soil Biology and Biochemistry, 2024, 193, 109367.	8.8	0
Fish and coral assemblages of a highly isolated oceanic island: The first e <scp>DNA</scp> survey of the Ogasawara Islands. Environmental DNA, 2024, 6, .	5.8	0
Bacillus amyloliquefaciens Probiotics Mix Supplementation in a Broiler Leaky Gut Model. Microorganisms, 2024, 12, 419.	3.6	O
Decreased skin colonization with Malassezia spp. and increased skin colonization with Candida spp. in patients with severe atopic dermatitis. Frontiers in Medicine, $0,11,1$	2.6	0
13689 Temporal dynamics of gut microbiomes in non-industrialized urban Amazonia. MSystems, 2024, 9, .	3.8	0
Dietary resistant starch supplementation increases gut luminal deoxycholic acid abundance in mice. Gut Microbes, 2024, 16, .	9.8	0
The long and short of it: benchmarking viromics using Illumina, Nanopore and PacBio sequencing technologies. Microbial Genomics, 2024, 10, .	2.0	0
Effect of feeding frequency on the anaerobic digestion of berry fruit waste. Waste Management, 2024, 178, 66-75.	7.4	0
The Influence of Bioclimates and Soil Physicochemical Properties on Bacterial and Archaeal Communities from Forest Ecosystems in CÃte d'Ivoire (West Africa). Forests, 2024, 15, 396.	2.1	0
The Stool Microbiome in African Ruminants: A Comparative Metataxonomic Study Suggests Potential for Biogas Production. Fermentation, 2024, 10, 119.	3.0	0
Lipocalin-2 expression identifies an intestinal regulatory neutrophil population during acute graft-versus-host disease. Science Translational Medicine, 2024, 16, .	12.4	0
Synthetic and natural rubber associated chemicals drive functional and structural changes as well as adaptations to antibiotics in in vitro marine microbiomes. Ecotoxicology and Environmental Safety, 2024, 273, 116134.	6.0	0
Bacterially enhanced plantâ€growing media for controlled environment agriculture. Microbial Biotechnology, 2024, 17, .	4.2	0
Effects of drought-induced stress on nematode communities in aquatic and terrestrial habitats of the Nebraska Sandhills. Frontiers in Ecology and Evolution, 0, 12, .	2.2	0
Informed development of a multiâ€species biofilm in chronic obstructive pulmonary disease. Apmis, 2024, 132, 336-347.	2.0	0
The impact of iron supplementation on the preterm neonatal gut microbiome: A pilot study. PLoS ONE, 2024, 19, e0297558.	2.5	0
A Randomized, Double-Blind, Placebo-Controlled Trial: Efficacy of Opuntia ficus-indica Prebiotic Supplementation in Subjects with Gut Dysbiosis. Nutrients, 2024, 16, 586.	4.1	O

# ARTICLE	IF	CITATIONS
Roadmap for the integration of environmental microbiomes in risk assessments under EFSA's remit. EFSA Supporting Publications, 2024, 21, .	0.7	0
Ecological competition in the oral mycobiome of Hispanic adults living in Puerto Rico associates with periodontitis. Journal of Oral Microbiology, 2024, 16, .	2.7	0
Effect of Ecuadorian natural zeolite on the performance of anaerobic digestion of swine waste in semicontinuous regime. Chemosphere, 2024, 352, 141517.	8.2	0
Diversity of symbiotic cyanobacteria in cycad coralloid roots using a short-read rbcL-X amplicon. Symbiosis, 2024, 92, 271-288.	2.3	0
Finding microbial composition and biological processes as predictive signature to access the ongoing status of mangrove preservation. International Microbiology, 0, , .	2.4	0
Detection of <scp><i>Klebsiella pneumoniae</i></scp> in healthy poultry: Insights and perspectives from culturing and metagenomics. Environmental Microbiology Reports, 2024, 16, .	2.4	0
Fungal Spore Richness and Abundance of Allergenic Taxa: Comparing a Portable Impactor and Passive Trap Indoors and Outdoors in an Urban Setting. Microbial Ecology, 2024, 87, .	2.8	0
Effect of probiotics and prebiotics on the composition of the equine fecal and seminal microbiomes and sperm quality: A pilot study. Journal of Equine Veterinary Science, 2024, 135, 105032.	0.9	0
Multi-omics profiling reveal responses of three major Dendrobium species from different growth years to medicinal components. Frontiers in Plant Science, 0, 15, .	3.6	0
The symbiont <i>Wolbachia</i> alleviates pesticide susceptibility in the twoâ€spotted spider mite <i>Tetranychus urticae</i> through enhanced host detoxification pathways. Insect Science, 0, , .	3.0	0
Robustness of cancer microbiome signals over a broad range of methodological variation. Oncogene, 2024, 43, 1127-1148.	5.9	0
Gut microbiome of the sole surviving member of reptile order Rhynchocephalia reveals biogeographic 13714 variation, influence of host body condition and a substantial core microbiota in tuatara across New Zealand. Ecology and Evolution, 2024, 14, .	1.9	0
13715 Leafhoppers as markers of the impact of climate change on agriculture., 2024, 1, 100029.		0
Metal-oxide precipitation influences microbiome structure in hyporheic zones receiving acid rock drainage. Applied and Environmental Microbiology, 0, , .	3.1	0
Soil warming increases the number of growing bacterial taxa but not their growth rates. Science Advances, 2024, 10, .	10.3	0
Microbiomes of Thalassia testudinum throughout the Atlantic Ocean, Caribbean Sea, and Gulf of 13720 Mexico are influenced by site and region while maintaining a core microbiome. Frontiers in Microbiology, 0, 15, .	3.5	0
Intestinal microbiota composition of children with glycogen storage Type I patients. European Journal of Clinical Nutrition, 2024, 78, 407-412.	2.9	0
Ciliate diversity in rodrigo de freitas lagoon (Rio de Janeiro, Brazil) from an integrative standpoint. Brazilian Journal of Microbiology, 0, , .	2.0	O

#	ARTICLE	IF	CITATIONS
13723	Microplastics affect soil-plant system: Implications for rhizosphere biology and fitness of sage (Salvia) Tj ETQq0 0	0,rgBT/Ov	erlock 10 Tf
13724	Habitat is more important than climate for structuring soil fungal communities associated in truffle sites. Fungal Biology, 2024, 128, 1724-1734.	2.5	O
13725	Dynamics of Gut Bacteria Across Different Zooplankton Genera in the Baltic Sea. Microbial Ecology, 2024, 87, .	2.8	0
13726	Spores of arbuscular mycorrhizal fungi host surprisingly diverse communities of endobacteria. New Phytologist, 2024, 242, 1785-1797.	7.3	O
13727	The microbiomes of five temperate soft corals declining in the Sea of Marmara. Marine Biodiversity, 2024, 54, .	1.0	0
13730	Trichoderma application methods differentially affect the tomato growth, rhizomicrobiome, and rhizosphere soil suppressiveness against Fusarium oxysporum. Frontiers in Microbiology, 0, 15, .	3.5	0
13731	A case study on the application of spore sampling for the monitoring of macrofungi. Molecular Ecology Resources, 2024, 24, .	4.8	0
13734	The Influence of Human Agricultural Activities on the Quality of Selected Fluvisols from the Vistula River Valley, Poland—Preliminary Research. Agronomy, 2024, 14, 480.	3.0	0
13735	Towards eDNA informed biodiversity studies – Comparing water derived molecular taxa with traditional survey methods. Progress in Oceanography, 2024, 222, 103230.	3.2	0
13736	Heterogeneous lineage-specific arginine deiminase expression within dental microbiome species. Microbiology Spectrum, 2024, 12, .	3.0	0
13738	The archaeome in metaorganism research, with a focus on marine models and their bacteria $\hat{\epsilon}$ archaea interactions. Frontiers in Microbiology, 0, 15, .	3.5	0
13739	Fecal DNA metabarcoding reveals seasonal and annual variation in willow ptarmigan diet. Royal Society Open Science, 2024, 11 , .	2.4	0
13740	Comparison of microbial communities and nitrite formation in two different beet sugar extraction systems. LWT - Food Science and Technology, 2024, 197, 115917.	5.2	0
13742	Influence of climatic variation on microbial communities during organic Pinot noir wine production. PLoS ONE, 2024, 19, e0296859.	2.5	O
13743	Inflammation and bacteriophages affect DNA inversion states and functionality of the gut microbiota. Cell Host and Microbe, 2024, 32, 322-334.e9.	11.0	0
13745	Long-term beneficial effect of faecal microbiota transplantation on colonisation of multidrug-resistant bacteria and resistome abundance in patients with recurrent Clostridioides difficile infection. Genome Medicine, 2024, 16, .	8.2	O
13746	Salinity and resource availability as drivers of Baltic benthic fungal diversity. Environmental DNA, 2024, 6, .	5.8	0
13747	Fate of Planktothrix-derived toxins in aquatic food webs: A case study in Lake Mindelsee (Germany). Ecotoxicology and Environmental Safety, 2024, 273, 116154.	6.0	0

#	ARTICLE	IF	CITATIONS
13748	Sedimentary ancient DNA reveals the impact of anthropogenic land use disturbance and ecological shifts on fish community structure in small lowland lake. Science of the Total Environment, 2024, 922, 171266.	8.0	0
13749	Habitat shapes the gut microbiome diversity of Malayan tigers (Panthera tigris jacksoni) as revealed through metabarcoding 16S rRNA profiling. World Journal of Microbiology and Biotechnology, 2024, 40, .	3.6	O
13750	Disentangling the gut bacterial communities of the agave weevil, Scyphophorus acupunctatus (Coleoptera: Curculionidae). Symbiosis, 2024, 92, 381-392.	2.3	0
13751	Host adaptive radiation is associated with rapid virus diversification and cross-species transmission in African cichlid fishes. Current Biology, 2024, 34, 1247-1257.e3.	3.9	0
13752	Annual recurrence of prokaryotic climax communities in shallow waters of the North Mediterranean. Environmental Microbiology, 2024, 26, .	3.8	0
13753	Plant glucosinolate biosynthesis and breakdown pathways shape the rhizosphere bacterial/archaeal community. Plant, Cell and Environment, 2024, 47, 2127-2145.	5.7	0
13754	Metagenomic insight to apprehend the fungal communities associated with leaf blight of Welsh onion in Taiwan. Frontiers in Plant Science, $0,15,.$	3.6	0
13755	Effects of rewatering on soil fungi and soil enzymes in a spruce-beech forest after a 5-year experimental drought. Plant and Soil, 0, , .	3.7	0
13756	Effects of protein concentration and beta-adrenergic agonists on ruminal bacterial communities in finishing beef heifers. PLoS ONE, 2024, 19, e0296407.	2.5	0
13757	Assessment of the Impact of Humic Acids on Intestinal Microbiota, Gut Integrity, Ileum Morphometry, and Cellular Immunity of Turkey Poults Fed an Aflatoxin B1-Contaminated Diet. Toxins, 2024, 16, 122.	3.4	O
13759	A gut microbial signature for combination immune checkpoint blockade across cancer types. Nature Medicine, 2024, 30, 797-809.	30.7	0
13760	Microbial community and antimicrobial resistance niche differentiation in a multistage, surface flow constructed wetland. Water Research, 2024, 254, 121408.	11.3	0
13761	Distinct microbiota assembly and functional patterns in disease-resistant and susceptible varieties of tobacco. Frontiers in Microbiology, $0,15,15$	3.5	0
13762	Seagrass-mediated rhizosphere redox gradients are linked with ammonium accumulation driven by diazotrophs. Microbiology Spectrum, 2024, 12, .	3.0	0
13763	Influence of the gut microbiome on appetite-regulating neuropeptides in the hypothalamus: Insight from conventional, antibiotic-treated, and germ-free mouse models of anorexia nervosa. Neurobiology of Disease, 2024, 193, 106460.	4.4	0
13764	<scp>DNA</scp> â€metabarcoding supports trophic flexibility and reveals new prey species for the Galapagos sea lion. Ecology and Evolution, 2024, 14, .	1.9	0
13765	Soil Fertilization with Palm Oil Mill Effluent Has a Short-Term Effect on the Bacterial Diversity of an Amazonian Agricultural Land Area. Microorganisms, 2024, 12, 507.	3.6	0
13766	16S rRNA Gene-Amplicon-Based Profiling of the Vaginal Microbiome From North African Women. Lecture Notes in Networks and Systems, 2024, , 149-165.	0.7	0

#	ARTICLE	IF	CITATIONS
13767	Unraveling endophytic diversity in dioecious Siraitia grosvenorii: implications for mogroside production. Applied Microbiology and Biotechnology, 2024, 108, .	3.6	0
13768	Bisphenol A exposure affects specific gut taxa and drives microbiota dynamics in childhood obesity. MSystems, 2024, 9, .	3.8	O
13769	Influence of keratinized mucosa width on the resolution of periâ€implant mucositis: A prospective cohort study. Clinical Implant Dentistry and Related Research, 0, , .	3.7	0
13771	Soil Microbiome of Abandoned Plaggic Podzol of Different-Aged Fallow Lands and Native Podzol in South Taiga (Leningrad Region). Agronomy, 2024, 14, 429.	3.0	0
13772	Nav 1.8 -expressing neurons control daily oscillations of food intake, body weight and gut microbiota in mice. Communications Biology, 2024, 7 , .	4.4	0
13773	Thermal fluctuations independently modulate physiological plasticity and the dynamics of the gut microbiome in a tropical rocky shore oyster. Journal of Experimental Marine Biology and Ecology, 2024, 573, 152004.	1.5	O
13774	Periodic Addition of Glucose Suppressed Cyanobacterial Abundance in Additive Lake Water Samples during the Entire Bloom Season. Journal of Water Resource and Protection, 2024, 16, 140-155.	0.8	0
13775	A host-microbial metabolite interaction gut-on-a-chip model of the adult human intestine demonstrates beneficial effects upon inulin treatment of gut microbiome. , 0, 3, .		0
13776	Environmental <scp>DNA</scp> reveals temporal variation in mesophotic reefs of the Humboldt upwelling ecosystems of central Chile: Toward a baseline for biodiversity monitoring of unexplored marine habitats. Ecology and Evolution, 2024, 14, .	1.9	0
13777	Dead in the water – Role of relic DNA and primer choice for targeted sequencing surveys of anaerobic sewage sludge intended for biological monitoring. Water Research, 2024, 253, 121354.	11.3	O
13778	Chemical disinfection as a simple and reliable method to control the amphibian chytrid fungus at breeding points of endangered amphibians. Scientific Reports, 2024, 14, .	3 . 3	0
13779	Microbiome diversity and zoonotic bacterial pathogen prevalence in <i>Peromyscus</i> mice from agricultural landscapes and synanthropic habitat. Molecular Ecology, 2024, 33, .	3.9	O
13780	Arrive and wait: Inactive bacterial taxa contribute to perceived soil microbiome resilience after a multidecadal press disturbance. Ecology Letters, 2024, 27, .	6.4	0
13781	Comparison of environmental DNA and SCUBA diving methods to survey keystone rockfish species on the Central Coast of British Columbia, Canada. Ecological Indicators, 2024, 160, 111830.	6.3	O
13782	Deep sea treasures - Insights from museum archives shed light on coral microbial diversity within deepest ocean ecosystems. Heliyon, 2024, 10, e27513.	3.2	0
13783	Biodiversity of autotrophic euglenids based on the group specific DNA metabarcoding approach. Protist, 2024, 175, 126024.	1.5	O
13784	Bumble bee microbiota shows temporal succession and increase of lactic acid bacteria when exposed to outdoor environments. Frontiers in Cellular and Infection Microbiology, 0, 14, .	3.9	0
13785	<i>Culex pipiens</i> and <i>Culex restuans</i> larval interactions shape the bacterial communities in container aquatic habitats. FEMS Microbes, 2024, 5, .	2.1	O

# ARTICLE	IF	CITATIONS
Macrophyte coverage drives microbial community structure and interactions in a shallow sub-tropical lake. Science of the Total Environment, 2024, 923, 171414.	8.0	0
Combined Genomic and Imaging Techniques Show Intense Arsenic Enrichment Caused by Detoxification in a Microbial Mat of the Dead Sea Shore. Geochemistry, Geophysics, Geosystems, 2024, 25, .	on 2.5	0
Exploring Cereal Metagenomics: Unravelling Microbial Communities for Improved Food Security. Microorganisms, 2024, 12, 510.	3.6	0
Temperature and <scp>CO₂</scp> interactively drive shifts in the compositional and functional structure of peatland protist communities. Global Change Biology, 2024, 30, .	9.5	0
Substrate Matters: Ionic Silver Alters Lettuce Growth, Nutrient Uptake, and Root Microbiome in a Hydroponics System. Microorganisms, 2024, 12, 515.	3.6	0
Can the genetic background modulate the effects of feed additives? Answers from gut microbiome and transcriptome interactions in farmed gilthead sea bream (Sparus aurata) fed with a mix of phytogenics, organic acids or probiotics. Aquaculture, 2024, 586, 740770.	d 3. 5	0
Fecal microbiota colonization dynamics in dairy heifers associated with early-life rumen microbiota modulation and gut health. Frontiers in Microbiology, 0, 15, .	3.5	0
Effects of pectin methyl-esterification on intestinal microbiota and its immunomodulatory properties in naive mice. Carbohydrate Polymers, 2024, 334, 122007.	10.2	0
4) Subacterium rectale (i) is a potential marker of altered gut microbiota in psoriasis and psoriatic arthritis. Microbiology Spectrum, 2024, 12, .	3.0	0
Perspective on intestinal microbiota temporal changes of herbal additives treated shrimp in a natural aquaculture setting. Frontiers in Marine Science, 0, 11, .	2.5	0
An inquiline mosquito modulates microbial diversity and function in an aquatic microecosystem. Molecular Ecology, 2024, 33, .	3.9	0
Paired qualitative and quantitative analysis of bacterial microcolonies in the tonsils of patients with tonsillar hyperplasia. Microbes and Infection, 2024, , 105317.	1.9	0
Exploring the application of signaling compounds and soil amendments to modulate plant–microbe interactions for improved plant salinity tolerance. Plant and Soil, 0, , .	3.7	0
Environmental DNA identifies coastal plant community shift 1,000 years ago in Torrens Island, South Australia. Communications Earth & Environment, 2024, 5, .	6.8	0
Gut diversity and the resistome as biomarkers of febrile neutropenia outcome in paediatric oncology patients undergoing hematopoietic stem cell transplantation. Scientific Reports, 2024, 14, .	3.3	0
Slowing Alzheimerâ \in ^{Ms} disease progression through probiotic supplementation. Frontiers in Neuroscience, 0, 18, .	2.8	0
Composting reduces the risks of resistome in beef cattle manure at the transcriptional level. Applied and Environmental Microbiology, 2024, 90, .	3.1	0
Composition and diversity of rhizosphere microorganisms of Suaeda salsa in the Yellow River Delta. Frontiers in Ecology and Evolution, 0, 12 , .	2.2	0

# ARTICLE	IF	CITATIONS
Snapshot of cyanobacterial toxins in Pakistani freshwater bodies. Environmental Science and Pollution Research, 2024, 31, 24648-24661.	5. 3	0
Bacterial symbionts of the precious coral <i>Corallium rubrum</i> are differentially distributed across colonyâ€specific compartments and differ among colormorphs. Environmental Microbiology Reports, 2024, 16, .	2.4	O
Valuable non-food crops for biochar-assisted phytoremediation of contaminated soils: The case of cardoon, rapeseed and safflower. Applied Soil Ecology, 2024, 198, 105349.	4.3	0
Signatures of disease outcome severity in the intestinal fungal and bacterial microbiome of COVID-19 patients. Frontiers in Cellular and Infection Microbiology, 0, 14, .	3.9	0
Exploring the modulatory role of bovine lactoferrin on the microbiome and the immune response in healthy and Shiga toxin-producing E. coli challenged weaned piglets. Journal of Animal Science and Biotechnology, 2024, 15, .	5.3	0
Host genetics drives differences in cecal microbiota composition and immune traits of laying hens raised in the same environment. Poultry Science, 2024, 103, 103609.	3.4	0
ldentifying environmental factors affecting the microbial community composition on outdoor structural timber. Applied Microbiology and Biotechnology, 2024, 108, .	3.6	0
Biofilms on plastic litter in an urban river: Community composition and activity vary by substrate type. Water Environment Research, 2024, 96, .	2.7	0
High-throughput sequencing reveals the structure and metabolic resilience of desert microbiome confronting climate change. Frontiers in Plant Science, 0, 15, .	3.6	0
Highly heterogeneous mycobiota shape fungal diversity in two globally distributed lichens. Fungal Ecology, 2024, 69, 101331.	1.6	O
A comparison of short-read, HiFi long-read, and hybrid strategies for genome-resolved metagenomics. Microbiology Spectrum, 2024, 12, .	3.0	0
Study of the intestinal microbiota composition and the effect of treatment with intensive chemotherapy in patients recovered from acute leukemia. Scientific Reports, 2024, 14, .	3.3	O
Study of the influence of tributyrin-supplemented diets on the gut bacterial communities of rainbow trout (Oncorhynchus mykiss). Scientific Reports, 2024, 14, .	3.3	0
Assessing anaerobic microbial degradation rates of crude light oil with reverse stable isotope labelling and community analysis. , 0, 3, .		0
Phylometagenomics of cycad coralloid roots reveals shared symbiotic signals. Microbial Genomics, 2024, 10, .	2.0	0
Comparative metabarcoding and biodiversity of gut-associated fungal assemblages of Dendroctonus species (Curculionidae: Scolytinae). Frontiers in Microbiology, 0, 15, .	3.5	O
D genome acquisition and breeding have had a significant impact on interaction of wheat with ACC deaminase producers in soil or ACC deaminase potential activity in the rhizosphere. Soil Biology and Biochemistry, 2024, 193, 109392.	8.8	0
Effects of different long-term fertilization on rhizosphere soil nitrogen mineralization and microbial community composition under the double-cropping rice field. Archives of Agronomy and Soil Science, 2024, 70, 1-16.	2.6	O

# ARTICLE	IF	CITATIONS
Microbial characterization of raw biomasses of Alaria esculenta, Chlorella vulgaris, Lemna minor. , 2024, 2, 100053.		0
Milk replacer feeding once or twice a day did not change the ruminal metabolomic profile and the microbial diversity of dairy calves from birth to weaning. Journal of Dairy Science, 2024, , .	3.4	0
Recovery of microbial biomass and purification performance after scraping of full-scale slow sand filters. Journal of Water Process Engineering, 2024, 60, 105101.	5.6	0
Apis mellifera filamentous virus from a honey bee gut microbiome survey in Hungary. Scientific Reports, 2024, 14, .	3.3	0
Duration of rupture of membranes and microbiome transmission to the newborn: A prospective study. BJOG: an International Journal of Obstetrics and Gynaecology, 0, , .	2.3	0
Environmental filtering governs consistent vertical zonation in sedimentary microbial communities across disconnected mountain lakes. Environmental Microbiology, 2024, 26, .	3.8	0
Reproducible responses of geochemical and microbial successional patterns in the subsurface to carbon source amendment. Water Research, 2024, 255, 121460.	11.3	0
A role for encrusting, endolithic sponges in the feeding of the parrotfish Scarus rubroviolaceus? Evidence of further trophic diversification in Indo-Pacific Scarini. Coral Reefs, 0, , .	2.2	0
Divergent bacterial landscapes: unraveling geographically driven microbiomes in Atlantic cod. Scientific Reports, 2024, 14, .	3.3	0
13841 Cryptic diversity of cellulose-degrading gut bacteria in industrialized humans. Science, 2024, 383, .	12.6	0
Chemical attributes, bacterial community, and antibiotic resistance genes are affected by intensive use of soil in agro-ecosystems of the Atlantic Forest, Southeastern Brazil. Environmental Geochemistry and Health, 2024, 46, .	3.4	0
Enhancing seafood traceability: tracking the origin of seabass and seabream from the tuscan coast area by the analysis of the gill bacterial communities. Animal Microbiome, 2024, 6, .	3.8	0
Ectomycorrhizal fungal communities in natural and urban ecosystems: Quercus humboldtii as a study case in the tropical Andes. Mycorrhiza, 2024, 34, 45-55.	2.8	0
Evaluation of the Impact of Near-Infrared Multiwavelength Locked System Laser Therapy on Skin Microbiome in Atopic Dogs. Animals, 2024, 14, 906.	2.3	0
Early assessment of fungal and oomycete pathogens in greenhouse irrigation water using Oxford nanopore amplicon sequencing. PLoS ONE, 2024, 19, e0300381.	2.5	0
Effect of tetrakis(hydroxymethyl)phosphonium sulfate (THPS) on the microbial community and corrosion of carbon steel in a simulated crude-oil storage tank environment., 2024, 236, 212775.		0
Source-Separated Industrial Wastewater Is a Candidate for Biogas Production through Anaerobic Digestion. Fermentation, 2024, 10, 165.	3.0	0
Symbiosis modulates gene expression of symbionts, but not coral hosts, under thermal challenge. Molecular Ecology, 2024, 33, .	3.9	0

# ARTICLE		IF	Citations
Spatial heterogeneity and oil pollution structured the soil microbial Barataria Bay, Louisiana, USA, eight years after the Deepwater Hori 2024, 160, 111884.	community in salt marshes in zon oil spill. Ecological Indicators,	6.3	0
Oomycete communities are influenced by land use and disease stated Southern Québec, Canada. Environmental DNA, 2024, 6, .	us in Christmas tree production in	5.8	0
Unveiling microbial guilds and symbiotic relationships in Antarctic s Reports, 2024, 14, .	ponge microbiomes. Scientific	3.3	0
The hidden network of biocrust successional stages in the High Arc 13858 factors shaping microbial and metazoan communities. Science of t 171786.		8.0	0
Long-term push–pull cropping system shifts soil and maize-root resilient farming system. BMC Microbiology, 2024, 24, .	nicrobiome diversity paving way to	3.3	0
13860 Effects of relative humidity on dry-aged beef quality. Meat Science,	2024, 213, 109498.	5.5	O
The paradox of spring: Thyroid and glucocorticoid responses to coloravailability in free living Carneddau ponies. Hormones and Behavior		2.1	0
Comprehensive identification of pathogenic microbes and antimicr products using nanopore sequencing-based metagenomics. Food N	obial resistance genes in food Nicrobiology, 2024, 121, 104493.	4.2	0
Bacterial communities associated with an island radiation of licheneo298599.	forming fungi. PLoS ONE, 2024, 19,	2.5	0
Active Microbiota of Penaeus stylirostris Larvae: Partially Shaped vi Transmissions and Larval Ontogeny. Microorganisms, 2024, 12, 60	a Vertical and Horizontal 8.	3.6	O
Comparative Analysis of How the Fecal Microbiota of Green-Winge among Animals Living in Captivity and in Wild Habitats. Animals, 20	d Saltator (Saltator similis) Diverge 124, 14, 937.	2.3	0
Canopy nitrogen deposition enhances soil ecosystem multifunction Change Biology, 2024, 30, .	ality in a temperate forest. Global	9.5	0
Dominant herbaceous plants contribute to the spatial heterogeneit soils by influencing fungal and bacterial diversity. Soil Biology and E		8.8	0
Associations of Early Gut Microbiome and Metabolome with Growt Preterm Infants Within the First 6 Months. Breastfeeding Medicine	n and Body Composition of O, , .	1.7	0
Gastrointestinal Microbiota & Symptoms of Depression and A Re-Analysis of the MICROBIAN Longitudinal Study. Nutrients, 2024		4.1	0
Diet, lifestyle and gut microbiota composition among Malaysian wo mellitus: a prospective cohort study. Scientific Reports, 2024, 14, .	men with gestational diabetes	3.3	O
Responses of vascular plant fine roots and associated microbial cor warming and elevated <scp>CO₂</scp> in northern p 1333-1347.		7.3	0
13876 Interplay of biotic and abiotic factors shapes tree seedling growth a communities. Communications Biology, 2024, 7, .	nd root-associated microbial	4.4	O

# ARTICLE	IF	CITATIONS
Metam sodium fumigation in potato production systems has varying effects on soil health indicators. Field Crops Research, 2024, 310, 109353.	5.1	0
Host population crashes disrupt the diversity of associated marine microbiomes. Environmental Microbiology, 2024, 26, .	3.8	0
13879 Extremophile hypolithic communities in the Vestfold Hills, East Antarctica. Antarctic Science, 0, , 1-17.	0.9	0
Infection and antibiotic-associated changes in the fecal microbiota of <i>C. rodentium</i> i• <i> stx2 _{dact} </i> -infected C57BL/6 mice. Antimicrobial Agents and Chemotherapy, 2024, 68, .	3.2	0
13882 Inflammatory Dietary Potential Is Associated with Vitamin Depletion and Gut Microbial Dysbiosis in Early Pregnancy. Nutrients, 2024, 16, 935.	4.1	0
Plant species within Streptanthoid Complex associate with distinct microbial communities that shift to be more similar under drought. Ecology and Evolution, 2024, 14, .	1.9	0
Evaluating the liver abscess microbiota of beef cattle during a reduction in tylosin supplementation shows differences according to abscess size and fraction. FEMS Microbiology Ecology, 2024, 100, .	2.7	0
Bacterial diversity and chemical ecology of natural product–producing bacteria from Great Salt Lake sediment. ISME Communications, 2024, 4, .	4.2	0
Enhancing soil health and carbon sequestration through phytogenic treatment: insights into microbial functional pathways in pasture dieback affected soil. Plant and Soil, 0, , .	3.7	0
Exploring the biological diversity and source species of medicinal horseflies through metabarcoding. Gene, 2024, 913, 148356.	2.2	0
Core hyphosphere microbiota of Fusarium oxysporum f. sp. niveum. Environmental Microbiomes, 2024, 19, .	5.0	0
Surface Topography, Microbial Adhesion, and Immune Responses in Silicone Mammary Implant-Associated Capsular Fibrosis. International Journal of Molecular Sciences, 2024, 25, 3163.	4.1	0
Rewilding soil and litter invertebrates and fungi increases decomposition rates and alters detritivore communities. Ecology and Evolution, 2024, 14, .	1.9	0
Metataxonomic Identification of Microorganisms during the Coffee Fermentation Process in Colombian Farms (Cesar Department). Foods, 2024, 13, 839.	4.3	0
Unraveling the shift in bacterial communities profile grown in sediments co-contaminated with chlorolignin waste of pulp-paper mill by metagenomics approach. Frontiers in Microbiology, 0, 15, .	3.5	0
Lung microbiota composition, respiratory mechanics, and outcomes in COVID-19-related ARDS. Microbiology Spectrum, 2024, 12, .	3.0	0
Sociobiome - Individual and neighborhood socioeconomic status influence the gut microbiome in a multi-ethnic population in the US. Npj Biofilms and Microbiomes, 2024, 10, .	6.4	0
Fungal endophytes from Thalassia testudinum show bioactivity against the seagrass pathogen, Labyrinthula spp Frontiers in Marine Science, $0,11,1$	2.5	0

# A	RTICLE	IF	Citations
13897 TI	he effect of in vitro simulated colonic pH gradients on microbial activity and metabolite production sing common prebiotics as substrates. BMC Microbiology, 2024, 24, .	3.3	0
13898 a	he prokaryotic and eukaryotic microbiome of Pacific oyster spat is shaped by ocean warming but not cidification. Applied and Environmental Microbiology, 2024, 90, .	3.1	O
13899 Le	egume cover cropping and nitrogen fertilization influence soil prokaryotes and increase carbon ontent in dryland wheat systems. Agriculture, Ecosystems and Environment, 2024, 367, 108959.	5.3	0
	Narine bacteriophages disturb the associated microbiota of Aurelia aurita with a recoverable effect n host morphology. Frontiers in Microbiology, 0, 15, .	3.5	0
	etal Programming Influence on Microbiome Diversity and Ruminal and Cecal Epithelium in Beef Cattle. nimals, 2024, 14, 870.	2.3	0
13902 S	hort impact on soil microbiome of a Bacillus amyloliquefaciens QST713 based product that orrelates with higher potato yield across USA. Frontiers in Plant Science, 0, 15, .	3.6	О
13903 N	laternal obesity increases the risk of hepatocellular carcinoma through the transmission of an tered gut microbiome. JHEP Reports, 2024, 6, 101056.	4.9	0
13904 R	egulation of soil nutrient cycling in the root zone of <i>Pyracantha fortuneana</i> : The role of ore microbiome induced by plant species. Journal of Plant Nutrition and Soil Science, 0, , .	1.9	O
13905 N A	ligratory Shorebird Gut Microbes are not Associated with Bivalve Prey in Monsoon Tropical ustralia. Current Microbiology, 2024, 81, .	2.2	0
13906 Fa	amily shapes microbiome differences in Oklahoma salamanders. , 0, 3, .		О
13907 U	rea amendment decouples nitrification in hydrocarbon contaminated Antarctic soil. Chemosphere, 024, 354, 141665.	8.2	0
13908 G st	eochemical and microbial processes in a deep geothermal well during seven years of production top and their potential impact on the well performance. Geothermics, 2024, 120, 102979.	3.4	O
13909 Li	inking diet switching to reproductive performance across populations of two critically endangered nammalian herbivores. Communications Biology, 2024, 7, .	4.4	0
	igh soil moisture rather than drying-rewetting cycles reduces the effectiveness of nitrification hibitors in mitigating N2O emissions. Biology and Fertility of Soils, 0, , .	4.3	O
13911 G	lycomacropeptide as an Efficient Agent to Fight Pathophysiological Mechanisms of Metabolic yndrome. Nutrients, 2024, 16, 871.	4.1	0
13912 D	rual stressors of infection and warming can destabilize host microbiomes. Philosophical ransactions of the Royal Society B: Biological Sciences, 2024, 379, .	4.0	О
13913 Lo	ose-lose consequences of bacterial community-driven invasions in soil. Microbiome, 2024, 12, .	11.1	0
13914 To	he recovery of soil eukaryotic alpha and beta diversity after wetland restoration. Science of the otal Environment, 2024, 925, 171814.	8.0	О

#	ARTICLE	IF	CITATIONS
13915	Physicochemical Properties and Microbiome of Vineyard Soils from DOP Ribeiro (NW Spain) Are Influenced by Agricultural Management. Microorganisms, 2024, 12, 595.	3.6	0
13917	Exploring associations between the teat apex metagenome and <i>Staphylococcus aureus</i> intramammary infections in primiparous cows under organic directives. Applied and Environmental Microbiology, 2024, 90, .	3.1	O
13918	Transferability of Human and Environmental Microbiome on Clothes as a Tool for Forensic Investigations. Genes, 2024, 15, 375.	2.4	0
13919	Microbial community assembly in engineered bioreactors. Water Research, 2024, 255, 121495.	11.3	O
13921	Diverse winter communities and biogeochemical cycling potential in the under-ice microbial plankton of a subarctic river-to-sea continuum. Microbiology Spectrum, 2024, 12, .	3.0	0
13922	The effect of diet composition on the diversity of active gut bacteria and on the growth of <i>Spodoptera exigua </i> (Lepidoptera: Noctuidae). Journal of Insect Science, 2024, 24, .	1.5	O
13923	Grain versus AIN: Common rodent diets differentially affect health outcomes in adult C57BL/6j mice. PLoS ONE, 2024, 19, e0293487.	2.5	0
13924	High rates of nitrogen removal in aerated VFCWs treating sewage through C-N-S cycle. Bioresource Technology, 2024, 399, 130620.	9.6	O
13925	Capturing the Aerobiome: Application of Polyurethane Foam Disk Passive Samplers for Bioaerosol Monitoring. , 0, , .		0
13926	Uncovering the microbial diversity of Czech Republic archives: A study of metabolically active airborne microbes. Heliyon, 2024, 10, e27930.	3.2	O
13927	Mediterranean pine forest decline: A matter of root-associated microbiota and climate change. Science of the Total Environment, 2024, 926, 171858.	8.0	0
13928	A double-blind, randomized, placebo-controlled study assessing the impact of probiotic supplementation on antibiotic induced changes in the gut microbiome. , 0, 3, .		O
13929	Soil quality reflects microbial resource availability and drives rhizosphere microbiome variation in Ghanaian cocoa farms. Applied Soil Ecology, 2024, 198, 105378.	4.3	0
13930	Shotgun metagenomic analysis of the oral microbiome in gingivitis: a nested case-control study. Journal of Oral Microbiology, 2024, 16, .	2.7	O
13931	Arthropods as Vectors of Grapevine Trunk Disease Pathogens: Quantification of Phaeomoniella chlamydospora on Arthropods and Mycobiome Analysis of Earwig Exoskeletons. Journal of Fungi (Basel, Switzerland), 2024, 10, 237.	3.5	0
13932	Fecal microbiota transplantation stimulates type 2 and tolerogenic immune responses in a mouse model. Anaerobe, 2024, 86, 102841.	2.1	O
13933	Gut microbiota are differentially correlated with blood pressure status in African American collegiate athletes: A pilot study. Physiological Reports, 2024, 12, .	1.7	0
13935	The effect of anaerobic digestate as an organic soil fertilizer on the diversity and structure of the indigenous soil microbial and nematode communities. Environmental Science and Pollution Research, 0, , .	5.3	O

# ARTICLE	IF	CITATIONS
Bioaugmentation and vermicompost facilitated the hydrocarbon bioremediation: scaling up from to field for petroleum-contaminated soils. Environmental Science and Pollution Research, 0, , .	m lab 5.3	0
Out of sight, but not out of season: Nitrifier distributions and population dynamics in a large oligotrophic lake. Environmental Microbiology, 2024, 26, .	3.8	O
Niche availability and competitive loss by facilitation control proliferation of bacterial strains intended for soil microbiome interventions. Nature Communications, 2024, 15, .	12.8	O
Fertilizer regime and cultivar affect barley growth and rhizobiome composition. Applied Soil Eco 2024, 198, 105384.	ology, 4.3	O
Exploring the potential effects of forest urbanization on the interplay between small mammal communities and their gut microbiota. Animal Microbiome, 2024, 6, .	3.8	O
Metabarcoding reveals unique microbial mat communities and evidence of biogeographic influe lowâ€oxygen, highâ€sulfur sinkholes and springs. Ecology and Evolution, 2024, 14, .	ence in 1.9	O
Two intestinal microbiota-derived metabolites, deoxycholic acid and butyrate, synergize to enhal host defense peptide synthesis and alleviate necrotic enteritis. Journal of Animal Science and Biotechnology, 2024, 15, .	ance 5.3	O
Organic farming promotes the abundance of fungi keystone taxa in bacteria-fungi interkingdom networks. World Journal of Microbiology and Biotechnology, 2024, 40, .	3.6	O
Longitudinal profiling of the microbiome at four body sites reveals core stability and individualiz dynamics during health and disease. Cell Host and Microbe, 2024, 32, 506-526.e9.	red 11.0	O
Stratification of Fusobacterium nucleatum by local health status in the oral cavity defines its subspecies disease association. Cell Host and Microbe, 2024, 32, 479-488.e4.	11.0	O
Response of soil bacteria to PUREX chemicals suggests biomarker utility and bioremediation por Journal of Radioanalytical and Nuclear Chemistry, 2024, 333, 1899-1909.	tential. 1.5	O
The impact of reclamation and vegetation removal on compositional and functional attributes of microbial communities in the Athabasca Oil Sands Region. Applied Soil Ecology, 2024, 198, 105	of soil 4.3	O
Differentiation of bacterial communities on five common plastics after six days of exposure to Caribbean coastal waters. Environmental Advances, 2024, 16, 100518.	4.8	O
13951 Impact of rumen microbiome on cattle carcass traits. Scientific Reports, 2024, 14, .	3.3	O
Soil type and moisture content alter soil microbial responses to manure from cattle administere antibiotics. Environmental Science and Pollution Research, 2024, 31, 27259-27272.	5.3	0
13957 Oxygen-dependent biofilm dynamics in leaf decay: an in vitro analysis. Scientific Reports, 2024,	14, . 3.3	O
Xiasangju alleviate metabolic syndrome by enhancing noradrenaline biosynthesis and activating brown adipose tissue. Frontiers in Pharmacology, 0, 15, .	3.5	0
Diet replacement with whole insect larvae affects intestinal morphology and microbiota of broil chickens. Scientific Reports, 2024, 14, .	er 3.3	0