DADA2: High-resolution sample inference from Illumina amplicon data

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#	Paper	IF	Citations
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2207	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. **2016**, 5, 1492		303
2206	Editorial: New Insights into Microbial Ecology through Subtle Nucleotide Variation. **2016**, 7, 1318		9
2205	Piphillin: Improved Prediction of Metagenomic Content by Direct Inference from Human Microbiomes. **2016**, 11, e0166104		203
2204	Host-Microbiome Interaction and Cancer: Potential Application in Precision Medicine. **2016**, 7, 606		24
2203	Synthetic spike-in standards for high-throughput 16S rRNA gene amplicon sequencing. **2017**, 45, e23		66
2202	Quality filtering of Illumina index reads mitigates sample cross-talk. **2016**, 17, 876		75
2201	Resilient microorganisms in dust samples of the International Space Station-survival of the adaptation specialists. **2016**, 4, 65		43
2200	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. **2016**, 1,		55
2199	Emerging Technologies for Gut Microbiome Research. **2016**, 24, 887-901		107
2198	1,2-Dichloroethane Exposure Alters the Population Structure, Metabolism, and Kinetics of a Trichloroethene-Dechlorinating Dehalococcoides mccartyi Consortium. **2016**, 50, 12187-12196		12
2197	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. **2016**, 17, 217		86
2196	Lactobacillus-Deficient Cervicovaginal Bacterial Communities Are Associated with Increased HIV Acquisition in Young South African Women. **2017**, 46, 29-37		320
2195	From Culture to High-Throughput Sequencing and Beyond: A Layperson's Guide to the "Omics" and Diagnostic Potential of the Microbiome. **2017**, 46, 9-17		7
2194	Microbiome Helper: a Custom and Streamlined Workflow for Microbiome Research. **2017**, 2,		266
2193	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. **2017**, 2,		763
2192	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. **2017**, 115, 117-124		17

2191	Ecological dynamics and co-occurrence among marine phytoplankton, bacteria and myoviruses shows microdiversity matters. **2017**, 11, 1614-1629		92
2190	The Landscape Ecology and Microbiota of the Human Nose, Mouth, and Throat. **2017**, 21, 421-432		98
2189	Bayesian Nonparametric Ordination for the Analysis of Microbial Communities. **2017**, 112, 1430-1442		22
2188	Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes. **2018**, 19, 1415-1429		22
2187	Biological Aging and the Human Gut Microbiota. **2017**, 72, 1474-1482		112
2186	Lactobacillus iners: Friend or Foe?. **2017**, 25, 182-191		169
2185	Characterising and predicting cyanobacterial blooms in an 8-year amplicon sequencing time course. **2017**, 11, 1746-1763		46
2184	A quantitative and multiplexed approach to uncover the fitness landscape of tumor suppression in vivo. *Nature Methods*, **2017**, 14, 737-742	21.6	62
2183	Nitrotoga is selected over Nitrospira in newly assembled biofilm communities from a tap water source community at increased nitrite loading. **2017**, 19, 2785-2793		24
2182	The Microbiome and Human Biology. **2017**, 18, 65-86		181
2181	Long-chain fatty acid feeding frequency in anaerobic codigestion impacts syntrophic community structure and biokinetics. **2017**, 117, 218-229		55
2180	Survival of Vinyl Chloride Respiring Dehalococcoides mccartyi under Long-Term Electron Donor Limitation. **2017**, 51, 1635-1642		12
2179	Algorithm for post-clustering curation of DNA amplicon data yields reliable biodiversity estimates. **2017**, 8, 1188		220
2178	Household triclosan and triclocarban effects on the infant and maternal microbiome. **2017**, 9, 1732-1741		52
2177	Wild Mouse Gut Microbiota Promotes Host Fitness and Improves Disease Resistance. **2017**, 171, 1015-1028.e13		365
2176	Secondary compound hypothesis revisited: Selected plant secondary metabolites promote bacterial degradation of cis-1,2-dichloroethylene (cDCE). **2017**, 7, 8406		26
2175	Stool Microbiota at Neutrophil Recovery Is Predictive for Severe Acute Graft vs Host Disease After Hematopoietic Cell Transplantation. **2017**, 65, 1984-1991		88
2174	Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women. **2017**, 114, 9966-9971		182

2173	The salivary microbiome is consistent between subjects and resistant to impacts of short-term hospitalization. **2017**, 7, 11040	22
2172	Community-like genome in single cells of the sulfur bacterium Achromatium oxaliferum. **2017**, 8, 455	16
2171	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. **2017**, 11, 2639-2643	1228
2170	Response of the rhizosphere prokaryotic community of barley (Hordeum vulgare L.) to elevated atmospheric CO concentration in open-top chambers. **2017**, 6, e00462	3
2169	Establishing Causality: Opportunities of Synthetic Communities for Plant Microbiome Research. **2017**, 22, 142-155	219
2168	A clinician’s guide to microbiome analysis. **2017**, 14, 585-595	85
2167	Moving beyond de novo clustering in fungal community ecology. **2017**, 216, 629-634	14
2166	Ecosystem Resilience and Limitations Revealed by Soil Bacterial Community Dynamics in a Bark Beetle-Impacted Forest. **2017**, 8,	9
2165	Multiplexed in vivo homology-directed repair and tumor barcoding enables parallel quantification of Kras variant oncogenicity. **2017**, 8, 2053	44
2164	Methane- and dissolved organic carbon-fueled microbial loop supports a tropical subterranean estuary ecosystem. **2017**, 8, 1835	54
2163	Vertical vs. horizontal transmission of the microbiome in a key disease vector, Ixodes pacificus. **2017**, 26, 6578-6589	39
2162	First Insights into the Diverse Human Archaeome: Specific Detection of Archaea in the Gastrointestinal Tract, Lung, and Nose and on Skin. **2017**, 8,	108
2161	Host-genotype dependent gut microbiota drives zooplankton tolerance to toxic cyanobacteria. **2017**, 8, 1608	65
2160	Intestinal virome changes precede autoimmunity in type I diabetes-susceptible children. **2017**, 114, E6166-E6175	151
2159	Disease Suppressive Soils: New Insights from the Soil Microbiome. **2017**, 107, 1284-1297	219
2158	Comparison of methods for phylogenetic B-cell lineage inference using time-resolved antibody repertoire simulations (AbSim). **2017**, 33, 3938-3946	24
2157	Reconciliation between operational taxonomic units and species boundaries. **2017**, 93,	40
2156	Upper and lower respiratory tract microbiota in horses: bacterial communities associated with health and mild asthma (inflammatory airway disease) and effects of dexamethasone. **2017**, 17, 184	32

2155	Genetic influences on the human oral microbiome. **2017**, 18, 659	44
2154	A comparison of sequencing platforms and bioinformatics pipelines for compositional analysis of the gut microbiome. **2017**, 17, 194	124
2153	Preparing for the crewed Mars journey: microbiota dynamics in the confined Mars500 habitat during simulated Mars flight and landing. **2017**, 5, 129	35
2152	Integrated biomedical data analysis utilizing various types of data for biomarkers identification. **2017**,	2
2151	A ChIP-Seq Data Analysis Pipeline Based on Bioconductor Packages. **2017**, 15, 11-18	6
2150	The Intestinal Eukaryotic and Bacterial Biome of Spotted Hyenas: The Impact of Social Status and Age on Diversity and Composition. **2017**, 7, 262	20
2149	DNA Sequencing as a Tool to Monitor Marine Ecological Status. **2017**, 4,	55
2148	Are Oligotypes Meaningful Ecological and Phylogenetic Units? A Case Study of in Freshwater Lakes. **2017**, 8, 365	43
2147	Spatial Structure of the Mormon Cricket Gut Microbiome and its Predicted Contribution to Nutrition and Immune Function. **2017**, 8, 801	14
2146	Eelgrass Leaf Surface Microbiomes Are Locally Variable and Highly Correlated with Epibiotic Eukaryotes. **2017**, 8, 1312	30
2145	Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. **2017**, 8, 1561	146
2144	High-Resolution Microbiome Profiling for Detection and Tracking of. **2017**, 8, 1587	19
2143	Comparing the Healthy Nose and Nasopharynx Microbiota Reveals Continuity As Well As Niche-Specificity. **2017**, 8, 2372	57
2142	CRISPR Libraries and Screening. **2017**, 152, 69-82	7
2141	Improvement of identification methods for honeybee specific Lactic Acid Bacteria; future approaches. **2017**, 12, e0174614	10
2140	Aquatic environmental DNA detects seasonal fish abundance and habitat preference in an urban estuary. **2017**, 12, e0175186	100
2139	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. **2017**, 13, e1005706	45
2138	Experimental design and quantitative analysis of microbial community multiomics. **2017**, 18, 228	87

2137	The lung microbiome in patients with pneumocystosis. **2017**, 17, 170	6
2136	Predicting the structure of soil communities from plant community taxonomy, phylogeny, and traits. **2018**, 12, 1794-1805	109
2135	Seagrass-associated fungal communities follow Wallace's line, but host genotype does not structure fungal community. **2018**, 45, 762-770	17
2134	Updating the 97% identity threshold for 16S ribosomal RNA OTUs. **2018**, 34, 2371-2375	260
2133	Temporal Variability of Oral Microbiota over 10 Months and the Implications for Future Epidemiologic Studies. **2018**, 27, 594-600	15
2132	The use of larvae or recruits in coral restoration initiatives: Symbiodinium acquisition does not differ between coral life stages in the wild. **2018**, 26, 422-425	2
2131	Sequence clustering threshold has little effect on the recovery of microbial community structure. **2018**, 18, 1064	11
2130	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. **2018**, 3,	181
2129	Microbial rRNA gene expression and co-occurrence profiles associate with biokinetics and elemental composition in full-scale anaerobic digesters. **2018**, 11, 694-709	31
2128	The impact of vegan production on the kimchi microbiome. **2018**, 74, 171-178	16
2127	Guided Protocol for Fecal Microbial Characterization by 16S rRNA-Amplicon Sequencing. **2018**,	6
2126	Estimating the Transfer Range of Plasmids Encoding Antimicrobial Resistance in a Wastewater Treatment Plant Microbial Community. **2018**, 5, 260-265	59
2125	Citric acid as a functional supplement in diets for juvenile turbot, Scophthalmus maximus L.: Effects on phosphorus discharge, growth performance, and intestinal health. **2018**, 495, 643-653	13
2124	Exploring Linkages between Taxonomic and Functional Profiles of the Human Microbiome. **2018**, 3,	42
2123	A 16S rRNA gene sequencing and analysis protocol for the Illumina MiniSeq platform. **2018**, 7, e00611	42
2122	Carrot Juice Fermentations as Man-Made Microbial Ecosystems Dominated by Lactic Acid Bacteria. **2018**, 84,	37
2121	Fecal Microbiota Composition Drives Immune Activation in HIV-infected Individuals. **2018**, 30, 192-202	53
2120	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. **2018**, 9, 681	64

2119	SEED 2: a user-friendly platform for amplicon high-throughput sequencing data analyses. **2018**, 34, 2292-2294	110
2118	A new piece in the microbiome puzzle. **2018**, 16, 186	4
2117	The Madness of Microbiome: Attempting To Find Consensus "Best Practice" for 16S Microbiome Studies. **2018**, 84,	251
2116	Systems biology of the human microbiome. **2018**, 51, 146-153	22
2115	Differential Susceptibility to T Cell-Induced Colitis in Mice: Role of the Intestinal Microbiota. **2018**, 24, 361-379	37
2114	Novel Method Reveals a Narrow Phylogenetic Distribution of Bacterial Dispersers in Environmental Communities Exposed to Low-Hydration Conditions. **2018**, 84,	2
2113	Gut Microbial Diversity in Women With Polycystic Ovary Syndrome Correlates With Hyperandrogenism. **2018**, 103, 1502-1511	113
2112	More bang for the buck? Can arbuscular mycorrhizal fungal communities be characterized adequately alongside other fungi using general fungal primers?. **2018**, 220, 971-976	51
2111	Influence of Pig Farming on the Human Nasal Microbiota: Key Role of Airborne Microbial Communities. **2018**, 84,	45
2110	Assembly and ecological function of the root microbiome across angiosperm plant species. **2018**, 115, E1157-E1165	401
2109	Postmenopausal breast cancer and oestrogen associations with the IgA-coated and IgA-noncoated faecal microbiota. **2018**, 118, 471-479	43
2108	Correlation between gut microbiota and personality in adults: A cross-sectional study. **2018**, 69, 374-385	47
2107	Comammox Nitrospira are abundant ammonia oxidizers in diverse groundwater-fed rapid sand filter communities. **2018**, 20, 1002-1015	115
2106	The gut microbiota as a novel regulator of cardiovascular function and disease. **2018**, 56, 1-15	84
2105	Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis. **2018**, 27, 313-338	140
2104	Hybrid-denovo: a de novo OTU-picking pipeline integrating single-end and paired-end 16S sequence tags. **2018**, 7, 1-7	14
2103	Shifts in spinach microbial communities after chlorine washing and storage at compliant and abusive temperatures. **2018**, 73, 73-84	28
2102	Maturation of the gut microbiome and risk of asthma in childhood. **2018**, 9, 141	216

2101	Bartender: a fast and accurate clustering algorithm to count barcode reads. **2018**, 34, 739-747	29
2100	Identification of Key Bacteria Involved in the Induction of Incident Bacterial Vaginosis: A Prospective Study. **2018**, 218, 966-978	45
2099	SGLT2 inhibition via dapagliflozin improves generalized vascular dysfunction and alters the gut microbiota in type 2 diabetic mice. **2018**, 17, 62	92
2098	Reproducible protocols for metagenomic analysis of human faecal phageomes. **2018**, 6, 68	82
2097	Core microbiomes for sustainable agroecosystems. **2018**, 4, 247-257	328
2096	Diversity, structure and sources of bacterial communities in earthworm cocoons. **2018**, 8, 6632	12
2095	Metabarcoding analysis of strongylid nematode diversity in two sympatric primate species. **2018**, 8, 5933	24
2094	Alterations in the oral microbiome in HIV-infected participants after antiretroviral therapy administration are influenced by immune status. **2018**, 32, 1279-1287	29
2093	Allometry and Ecology of the Bilaterian Gut Microbiome. **2018**, 9,	20
2092	Oral Antibiotic Treatment of Mice Exacerbates the Disease Severity of Multiple Flavivirus Infections. **2018**, 22, 3440-3453.e6	65
2091	Fecal Microbiome Among Nursing Home Residents with Advanced Dementia and Clostridium difficile. **2018**, 63, 1525-1531	17
2090	SeekDeep: single-base resolution de novo clustering for amplicon deep sequencing. **2018**, 46, e21	75
2089	Highlighting Clinical Metagenomics for Enhanced Diagnostic Decision-making: A Step Towards Wider Implementation. **2018**, 16, 108-120	44
2088	LysMD3 is a type II membrane protein without an role in the response to a range of pathogens. **2018**, 293, 6022-6038	5
2087	Tristetraprolin Is Required for Alveolar Bone Homeostasis. **2018**, 97, 946-953	9
2086	Diversity of Entamoeba spp. in African great apes and humans: an insight from Illumina MiSeq high-throughput sequencing. **2018**, 48, 519-530	17
2085	Wastewater treatment plant effluent introduces recoverable shifts in microbial community composition in receiving streams. **2018**, 613-614, 1104-1116	42
2084	DNA-SIP based genome-centric metagenomics identifies key long-chain fatty acid-degrading populations in anaerobic digesters with different feeding frequencies. **2018**, 12, 112-123	54

2083	Soil Microbiomes Associated with Verticillium Wilt-Suppressive Broccoli and Chitin Amendments are Enriched with Potential Biocontrol Agents. **2018**, 108, 31-43	45
2082	Ecological selection of siderophore-producing microbial taxa in response to heavy metal contamination. **2018**, 21, 117-127	58
2081	Identification of probiotic effector molecules: present state and future perspectives. **2018**, 49, 217-223	132
2080	The gut virome of the protochordate model organism, Ciona intestinalis subtype A. **2018**, 244, 137-146	13
2079	Estimating intraspecific genetic diversity from community DNA metabarcoding data. **2018**, 6, e4644	82
2078	Elevated CO Has Little Influence on the Bacterial Communities Associated With the pH-Tolerant Coral, Massive spp. **2018**, 9, 2621	10
2077	Gut microbiome metagenomics to understand how xenobiotics impact human health. **2018**, 11-12, 51-58	13
2076	Phylogeny-Aware Deep 1-Dimensional Convolutional Neural Network for the Classification of Metagenomes. **2018**,	0
2075	Dynamics and Functional Potential of Stormwater Microorganisms Colonizing Sand Filters. **2018**, 10, 1065	8
2074	Assessing the impact of plant genetic diversity in shaping the microbial community structure of Vitis vinifera phyllosphere in the Mediterranean. **2018**, 11, 35-46	14
2073	Denoising the Denoisers: an independent evaluation of microbiome sequence error-correction approaches. **2018**, 6, e5364	129
2072	Is Host Filtering the Main Driver of Phylosymbiosis across the Tree of Life?. **2018**, 3,	64
2071	Full Issue PDF. **2018**, 2, 109-180	
2070	Combination of Principal Component Analysis and Genetic Algorithm for Microbial Biomarker Identification in Obesity. **2018**,	1
2069	An exploration of Prevotella-rich microbiomes in HIV and men who have sex with men. **2018**, 6, 198	64
2068	Dynamics of a Perturbed Microbial Community during Thermophilic Anaerobic Digestion of Chemically Defined Soluble Organic Compounds. **2018**, 6,	6
2067	Microbial Community Changes in a Chlorinated Solvents Polluted Aquifer Over the Field Scale Treatment With Poly-3-Hydroxybutyrate as Amendment. **2018**, 9, 1664	21
2066	Bacteria Associated with Russian Wheat Aphid (Diuraphis noxia) Enhance Aphid Virulence to Wheat. **2018**, 2, 151-164	12

2065	Gut microbiome transition across a lifestyle gradient in Himalaya. **2018**, 16, e2005396	71
2064	Probing the ecological and evolutionary history of a thermophilic cyanobacterial population via statistical properties of its microdiversity. **2018**, 13, e0205396	9
2063	Effect of gastric fluid aspiration on the lung microbiota of laboratory rats. **2018**, 44, 201-210	2
2062	Gut microbiome composition is associated with spatial structuring and social interactions in semi-feral Welsh Mountain ponies. **2018**, 6, 207	43
2061	Effects of Short- and Long-Term Variation in Resource Conditions on Soil Fungal Communities and Plant Responses to Soil Biota. **2018**, 9, 1605	7
2060	Changes in the Drinking Water Microbiome: Effects of Water Treatments Along the Flow of Two Drinking Water Treatment Plants in a Urbanized Area, Milan (Italy). **2018**, 9, 2557	25
2059	Decreased microbial co-occurrence network stability and SCFA receptor level correlates with obesity in African-origin women. **2018**, 8, 17135	15
2058	A Lamina-Associated Domain Border Governs Nuclear Lamina Interactions, Transcription, and Recombination of the Tcrb Locus. **2018**, 25, 1729-1740.e6	24
2057	Dynamic linear models guide design and analysis of microbiota studies within artificial human guts. **2018**, 6, 202	30
2056	Calcite moonmilk of microbial origin in the Etruscan Tomba degli Scudi in Tarquinia, Italy. **2018**, 8, 15839	13
2055	The Composition of Midgut Bacteria in Aedes aegypti (Diptera: Culicidae) That Are Naturally Susceptible or Refractory to Dengue Viruses. **2018**, 18,	5
2054	Enriching Beneficial Microbial Diversity of Indoor Plants and Their Surrounding Built Environment With Biostimulants. **2018**, 9, 2985	13
2053	Bacterial Associates of a Gregarious Riparian Beetle With Explosive Defensive Chemistry. **2018**, 9, 2361	11
2052	Rhizosheath microbial community assembly of sympatric desert speargrasses is independent of the plant host. **2018**, 6, 215	58
2051	Carbon Source and Soil Origin Shape Soil Microbiomes and Tomato Soilborne Pathogen Populations During Anaerobic Soil Disinfestation. **2018**, 2, 138-150	18
2050	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. **2018**, 6, 226	680
2049	Gene probing reveals the widespread distribution, diversity and abundance of isoprene-degrading bacteria in the environment. **2018**, 6, 219	17
2048	The human archaeome: methodological pitfalls and knowledge gaps. **2018**, 2, 469-482	14

2047	Enrichment and Genomic Characterization of a NO-Reducing Chemolithoautotroph From a Deep-Sea Hydrothermal Vent. **2018**, 6, 184	4
2046	A Phylogeny-Regularized Sparse Regression Model for Predictive Modeling of Microbial Community Data. **2018**, 9, 3112	15
2045	Assessment of Microbial Community Dynamics in River Bank Filtrate Using High-Throughput Sequencing and Flow Cytometry. **2018**, 9, 2887	13
2044	Enrichment of Verrucomicrobia, Actinobacteria and Burkholderiales drives selection of bacterial community from soil by maize roots in a traditional milpa agroecosystem. **2018**, 13, e0208852	28
2043	Iron Biofortified Carioca Bean (L.)-Based Brazilian Diet Delivers More Absorbable Iron and Affects the Gut Microbiota In Vivo (). **2018**, 10,	26
2042	GoFish: A versatile nested PCR strategy for environmental DNA assays for marine vertebrates. **2018** , 13, e0198717	14
2041	New Insights into Human Nostril Microbiome from the Expanded Human Oral Microbiome Database (eHOMD): a Resource for the Microbiome of the Human Aerodigestive Tract. **2018**, 3,	184
2040	Disruption of the microbiota affects physiological and evolutionary aspects of insecticide resistance in the German cockroach, an important urban pest. **2018**, 13, e0207985	27
2039	Induced Long-Term Changes in the Upper Intestinal Microflora during the Chronic Stage of Infection. **2018**, 2018, 2308619	4
2038	Host-targeted niclosamide inhibits C. difficile virulence and prevents disease in mice without disrupting the gut microbiota. **2018**, 9, 5233	26
2037	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. **2018**, 3,	104
2036	Identification of Microbial Dark Matter in Antarctic Environments. **2018**, 9, 3165	8
2035	Reproductive and Behavior Dysfunction Induced by Maternal Androgen Exposure and Obesity Is Likely Not Gut Microbiome-Mediated. **2018**, 2, 1363-1380	6
2034	Fungal diversity regulates plant-soil feedbacks in temperate grassland. **2018**, 4, eaau4578	66
2033	Great differences in performance and outcome of high-throughput sequencing data analysis platforms for fungal metabarcoding. **2018**, 29-40	34
2032	Responses of the Endophytic Bacterial Communities of to Pollution With Metals, Emerging Organic Pollutants and to Bioaugmentation With Indigenous Strains. **2018**, 9, 1526	23
2031	Bacterial Diversity Associated With the Rhizosphere and Endosphere of Two Halophytes: and. **2018**, 9, 2878	32
2030	Drying and Rainfall Shape the Structure and Functioning of Nitrifying Microbial Communities in Riverbed Sediments. **2018**, 9, 2794	26

2029	Microbial Community Composition and Predicted Functional Attributes of Antarctic Lithobionts Using Targeted Next-Generation Sequencing and Bioinformatics Tools. **2018**, 243-290	2
2028	Blow Your Nose, Shrimp! Unexpectedly Dense Bacterial Communities Occur on the Antennae and Antennules of Hydrothermal Vent Shrimp. **2018**, 5,	2
2027	A nearly uniform distributional pattern of heterotrophic bacteria in the Mariana Trench interior. **2018**, 142, 116-126	13
2026	Subversion of Systemic Glucose Metabolism as a Mechanism to Support the Growth of Leukemia Cells. **2018**, 34, 659-673.e6	55
2025	Review: The application of omics to rumen microbiota function. **2018**, 12, s233-s245	18
2024	Evolution of the nasopharyngeal bacterial microbiota of beef calves from spring processing to 40 days after feedlot arrival. **2018**, 225, 139-148	19
2023	The gut of the finch: uniqueness of the gut microbiome of the Galþagos vampire finch. **2018**, 6, 167	38
2022	Bifidobacterial Dominance of the Gut in Early Life and Acquisition of Antimicrobial Resistance. **2018** , 3,	42
2021	Monitoring of microbial dynamics in a drinking water distribution system using the culture-free, user-friendly, MYcrobiota platform. **2018**, 8, 14727	8
2020	Metabarcoding of marine environmental DNA based on mitochondrial and nuclear genes. **2018**, 8, 14822	33
2019	Air and waterborne microbiome of a pharmaceutical plant provide insights on spatiotemporal variations and community resilience after disturbance. **2018**, 18, 124	3
2018	Metagenomic analyses highlight the symbiotic association between the glacier stonefly Andiperla willinki and its bacterial gut community. **2018**, 20, 4170-4183	12
2017	Diversity-Function Relationships in Natural, Applied, and Engineered Microbial Ecosystems. **2018**, 105, 131-189	7
2016	PCR-based quantification of taxa-specific abundances in microbial communities: Quantifying and avoiding common pitfalls. **2018**, 153, 139-147	52
2015	Microbiome Analysis. **2018**,	9
2014	Normalization of Microbiome Profiling Data. **2018**, 1849, 143-168	4
2013	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. **2018**, 1849, 169-177	75
2012	16S rRNA Gene Analysis with QIIME2. **2018**, 1849, 113-129	101

2011	Sensitivity of Bacterioplankton to Environmental Disturbance: A Review of Baltic Sea Field Studies and Experiments. **2018**, 5,	15
2010	Planktonic prokaryote and protist communities in a submarine canyon system in the Ligurian Sea (NW Mediterranean). **2018**, 168, 210-221	12
2009	Microbiome composition within a sympatric species complex of intertidal isopods (Jaera albifrons). **2018**, 13, e0202212	5
2008	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. **2018**, 10, 78	69
2007	Intra-host Symbiont Diversity and Extended Symbiont Maintenance in Photosymbiotic Acantharea (Clade F). **2018**, 9, 1998	12
2006	Dosing Regimen of Enrofloxacin Impacts Intestinal Pharmacokinetics and the Fecal Microbiota in Steers. **2018**, 9, 2190	10
2005	Development of Methane-Utilizing Mixed Cultures for the Production of Polyhydroxyalkanoates (PHAs) from Anaerobic Digester Sludge. **2018**, 52, 12376-12387	22
2004	Genotype-Environment Interaction Shapes the Microbial Assemblage in Grapevine's Phyllosphere and Carposphere: An NGS Approach. **2018**, 6,	24
2003	Biology and Taxonomy of crAss-like Bacteriophages, the Most Abundant Virus in the Human Gut. **2018**, 24, 653-664.e6	119
2002	A comprehensive analysis of the faecal microbiome and metabolome of Strongyloides stercoralis infected volunteers from a non-endemic area. **2018**, 8, 15651	29
2001	Community profiling of the urinary microbiota: considerations for low-biomass samples. **2018**, 15, 735-749	52
2000	Phylogenetic Diversity and Single-Cell Genome Analysis of "Melainabacteria", a Non-Photosynthetic Cyanobacterial Group, in the Termite Gut. **2018**, 33, 50-57	20
1999	Community dynamics in a nitrate-reducing microbial consortium cultivated with p-alkylated vs. non-p-alkylated aromatic compounds. **2019**, 95,	2
1998	Microbiome-assisted carrion preservation aids larval development in a burying beetle. **2018**, 115, 11274-11279	51
1997	Daylight exposure modulates bacterial communities associated with household dust. **2018**, 6, 175	40
1996	Species-level bacterial community profiling of the healthy sinonasal microbiome using Pacific Biosciences sequencing of full-length 16S rRNA genes. **2018**, 6, 190	64
1995	Lack of detection of a human placenta microbiome in samples from preterm and term deliveries. **2018**, 6, 196	142
1994	Over 2.5 million COI sequences in GenBank and growing. **2018**, 13, e0200177	66

1993	Comparing the bacterial communities of wild and captive golden mantella frogs: Implications for amphibian conservation. **2018**, 13, e0205652	4
1992	Bleaching-Associated Changes in the Microbiome of Large Benthic Foraminifera of the Great Barrier Reef, Australia. **2018**, 9, 2404	9
1991	Impact of DNA Sequencing and Analysis Methods on 16S rRNA Gene Bacterial Community Analysis of Dairy Products. **2018**, 3,	30
1990	TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution. **2018**, 3,	37
1989	Dichotomous development of the gut microbiome in preterm infants. **2018**, 6, 157	35
1988	Fecal microbiota and bile acid interactions with systemic and adipose tissue metabolism in diet-induced weight loss of obese postmenopausal women. **2018**, 16, 244	44
1987	Protocols for Investigating the Leaf Mycobiome Using High-Throughput DNA Sequencing. **2018**, 1848, 39-51	8
1986	High-resolution ISR amplicon sequencing reveals personalized oral microbiome. **2018**, 6, 153	18
1985	Quantification of variation and the impact of biomass in targeted 16S rRNA gene sequencing studies. **2018**, 6, 155	27
1984	Genetic and Functional Diversity of Bacterial Microbiome in Soils With Long Term Impacts of Petroleum Hydrocarbons. **2018**, 9, 1923	52
1983	Root exudates drive the soil-borne legacy of aboveground pathogen infection. **2018**, 6, 156	163
1982	Sponge-microbe partnerships are stable under eutrophication pressure from mariculture. **2018**, 136, 125-134	10
1981	Autophagy proteins suppress protective type I interferon signalling in response to the murine gut microbiota. **2018**, 3, 1131-1141	51
1980	Dysbiosis and early mortality in zebrafish larvae exposed to subclinical concentrations of streptomycin. **2018**, 365,	28
1979	The microbiota of hematophagous ectoparasites collected from migratory birds. **2018**, 13, e0202270	11
1978	Advantages and Limitations of Environmental DNA/RNA Tools for Marine Biosecurity: Management and Surveillance of Non-indigenous Species. **2018**, 5,	43
1977	Environmental temperature alters the digestive performance and gut microbiota of a terrestrial amphibian. **2018**, 221,	48
1976	Best practices for analysing microbiomes. **2018**, 16, 410-422	668

1975	Impact of the griffithsin anti-HIV microbicide and placebo gels on the rectal mucosal proteome and microbiome in non-human primates. **2018**, 8, 8059	22
1974	Probiotic supplementation and associated infant gut microbiome and health: a cautionary retrospective clinical comparison. **2018**, 8, 8283	40
1973	Cold adaptation and replicable microbial community development during long-term low-temperature anaerobic digestion treatment of synthetic sewage. **2018**, 94,	18
1972	Comparison of the oral microbiome in mouthwash and whole saliva samples. **2018**, 13, e0194729	21
1971	The cotton stainer's gut microbiota suppresses infection of a cotransmitted trypanosomatid parasite. **2018**, 27, 3408	12
1970	Phosphorus addition shifts the microbial community in the rhizosphere of blueberry (Vaccinium corymbosum L.). **2018**, 7, 1-7	14
1969	Variations in activities of sewer biofilms due to ferrous and ferric iron dosing. **2018**, 2017, 845-858	2
1968	Comparing Sanger sequencing and high-throughput metabarcoding for inferring photobiont diversity in lichens. **2018**, 8, 8624	31
1967	Distinct bacterial metacommunities inhabit the upper and lower respiratory tracts of healthy feedlot cattle and those diagnosed with bronchopneumonia. **2018**, 221, 105-113	43
1966	Why We Need Sustainable Networks Bridging Countries, Disciplines, Cultures and Generations for Aquatic Biomonitoring 2.0: A Perspective Derived From the DNAqua-Net COST Action. **2018**, 58, 63-99	75
1965	Microbial community adaptability to altered temperature conditions determines the potential for process optimisation in biogas production. **2018**, 226, 838-848	60
1964	Effects of Substance Use and Sex Practices on the Intestinal Microbiome During HIV-1 Infection. **2018**, 218, 1560-1570	28
1963	Exploring the diversity-stability paradigm using sponge microbial communities. **2018**, 8, 8425	23
1962	Tucum□Oil Shifted Ruminal Fermentation, Reducing Methane Production and Altering the Microbiome but Decreased Substrate Digestibility Within a RUSITEC Fed a Mixed Hay - Concentrate Diet. **2018**, 9, 1647	18
1961	From hairballs to hypotheses-biological insights from microbial networks. **2018**, 42, 761-780	187
1960	Emergent simplicity in microbial community assembly. **2018**, 361, 469-474	348
1959	Propionibacterium acnes Abundance Correlates Inversely with Staphylococcus aureus: Data from Atopic Dermatitis Skin Microbiome. **2018**, 98, 490-495	35
1958	Selection of Appropriate Metagenome Taxonomic Classifiers for Ancient Microbiome Research. **2018**, 3,	18

1957	WHAM!: a web-based visualization suite for user-defined analysis of metagenomic shotgun sequencing data. **2018**, 19, 493	6
1956	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. **2018**, 16, e2006352	130
1955	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. **2017**, 8, 2241	10
1954	Do we treat our patients or rather periodontal microbes with adjunctive antibiotics in periodontal therapy? A 16S rDNA microbial community analysis. **2018**, 13, e0195534	23
1953	Impact of Edible Cricket Consumption on Gut Microbiota in Healthy Adults, a Double-blind, Randomized Crossover Trial. **2018**, 8, 10762	91
1952	The Microbial Landscape of Sea Stars and the Anatomical and Interspecies Variability of Their Microbiome. **2018**, 9, 1829	13
1951	Uses and Misuses of Environmental DNA in Biodiversity Science and Conservation. **2018**, 49, 209-230	113
1950	Time Course-Dependent Methanogenic Crude Oil Biodegradation: Dynamics of Fumarate Addition Metabolites, Biodegradative Genes, and Microbial Community Composition. **2017**, 8, 2610	33
1949	Linking Associations of Rare Low-Abundance Species to Their Environments by Association Networks. **2018**, 9, 297	8
1948	Comparing Microbiome Sampling Methods in a Wild Mammal: Fecal and Intestinal Samples Record Different Signals of Host Ecology, Evolution. **2018**, 9, 803	114
1947	Comparison of Channel Catfish and Blue Catfish Gut Microbiota Assemblages Shows Minimal Effects of Host Genetics on Microbial Structure and Inferred Function. **2018**, 9, 1073	15
1946	Sediment Microbial Communities Influenced by Cool Hydrothermal Fluid Migration. **2018**, 9, 1249	8
1945	Exposure to Arsenic Alters the Microbiome of Larval Zebrafish. **2018**, 9, 1323	31
1944	Predictive Modeling of Microbiome Data Using a Phylogeny-Regularized Generalized Linear Mixed Model. **2018**, 9, 1391	21
1943	CasPER, a method for directed evolution in genomic contexts using mutagenesis and CRISPR/Cas9. **2018**, 48, 288-296	42
1942	Human Microbiome Acquisition and Bioinformatic Challenges in Metagenomic Studies. **2018**, 19,	25
1941	Meanings, measurements, and musings on the significance of patterns in human microbiome variation. **2018**, 53, 43-52	4
1940	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. **2018**, 6, 90	1227

1939	Network hubs in root-associated fungal metacommunities. **2018**, 6, 116	58
1938	Coral Bacterial-Core Abundance and Network Complexity as Proxies for Anthropogenic Pollution. **2018**, 9, 833	29
1937	microbial communities: a potential mechanism for the initial acquisition of gut microbiota among oviparous birds and lizards. **2018**, 14,	26
1936	The cecal microbiome of commercial broiler chickens varies significantly by season. **2018**, 97, 3635-3644	16
1935	Ten reasons why a sequence-based nomenclature is not useful for fungi anytime soon. **2018**, 9, 177-183	27
1934	Robust Microbial Markers for Non-Invasive Inflammatory Bowel Disease Identification. **2019**, 16, 2078-2088	6
1933	Real-Time Imaging Revealed That Exoelectrogens from Wastewater Are Selected at the Center of a Gradient Electric Field. **2018**, 52, 8939-8946	38
1932	Opportunities and limitations for DNA metabarcoding in Australasian plant-pathogen biosecurity. **2018**, 47, 467-474	12
1931	Stochastic processes govern invasion success in microbial communities when the invader is phylogenetically close to resident bacteria. **2018**, 12, 2748-2756	25
1930	Taxon Disappearance from Microbiome Analysis Reinforces the Value of Mock Communities as a Standard in Every Sequencing Run. **2018**, 3,	34
1929	Effect of the Synthetic Bile Salt Analog CamSA on the Hamster Model of Clostridium difficile Infection. **2018**, 62,	12
1928	Oral microbiota in youth with perinatally acquired HIV infection. **2018**, 6, 100	18
1927	A horizontal permeable reactive barrier stimulates nitrate removal and shifts microbial ecology during rapid infiltration for managed recharge. **2018**, 144, 274-284	18
1926	Attachment between heterotrophic bacteria and microalgae influences symbiotic microscale interactions. **2018**, 20, 4385-4400	25
1925	Age and fecal microbial strain-specific differences in patients with spondyloarthritis. **2018**, 20, 14	36
1924	Combining 16S rRNA gene variable regions enables high-resolution microbial community profiling. **2018**, 6, 17	91
1923	Microbiota inoculum composition affects holobiont assembly and host growth in Daphnia. **2018**, 6, 56	43
1922	Near full-length 16S rRNA gene next-generation sequencing revealed Asaia as a common midgut bacterium of wild and domesticated Queensland fruit fly larvae. **2018**, 6, 85	39

1921	Multilevel social structure and diet shape the gut microbiota of the gelada monkey, the only grazing primate. **2018**, 6, 84	30
1920	Incidence and taxonomic richness of mosquitoes in the diets of little brown and big brown bats. **2018**, 99, 668-674	19
1919	EukRef-Ciliophora: a manually curated, phylogeny-based database of small subunit rRNA gene sequences of ciliates. **2018**, 20, 2218-2230	18
1918	Exploring the Root Microbiome: Extracting Bacterial Community Data from the Soil, Rhizosphere, and Root Endosphere. **2018**,	15
1917	Biodiversity estimates and ecological interpretations of meiofaunal communities are biased by the taxonomic approach. **2018**, 1, 112	19
1916	Fungal communities in organic and mineral soil horizons in an industrially polluted boreal forest. **2018**, 19, 161-171	1
1915	Breast Cancer and Its Relationship with the Microbiota. **2018**, 15,	128
1914	MicroPheno: predicting environments and host phenotypes from 16S rRNA gene sequencing using a k-mer based representation of shallow sub-samples. **2018**, 34, i32-i42	33
1913	Hyperactivated PI3K□promotes self and commensal reactivity at the expense of optimal humoral immunity. **2018**, 19, 986-1000	54
1912	Assessing and Interpreting the Within-Body Biogeography of Human Microbiome Diversity. **2018**, 9, 1619	4
1911	Effects of transportation to and co-mingling at an auction market on nasopharyngeal and tracheal bacterial communities of recently weaned beef cattle. **2018**, 223, 126-133	20
1910	Impact of lincosamides antibiotics on the composition of the rat gut microbiota and the metabolite profile of plasma and feces. **2018**, 296, 139-151	14
1909	Stationary and portable sequencing-based approaches for tracing wastewater contamination in urban stormwater systems. **2018**, 8, 11907	18
1908	Comparative evaluation of a new magnetic bead-based DNA extraction method from fecal samples for downstream next-generation 16S rRNA gene sequencing. **2018**, 13, e0202858	5
1907	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. **2018**, 24, 1842-1851	52
1906	Fecal microbiota transplantation in a kidney transplant recipient with recurrent urinary tract infection. **2018**, 46, 871-874	19
1905	Bacteria and Competing Herbivores Weaken Top-Down and Bottom-Up Aphid Suppression. **2018**, 9, 1239	13
1904	Effects of Sub-Chronic MPTP Exposure on Behavioral and Cognitive Performance and the Microbiome of Wild-Type and mGlu8 Knockout Female and Male Mice. **2018**, 12, 140	17

1903	Effect of Antibiotic-Mediated Microbiome Modulation on Rotavirus Vaccine Immunogenicity: A Human, Randomized-Control Proof-of-Concept Trial. **2018**, 24, 197-207.e4	59
1902	Broadscale Ecological Patterns Are Robust to Use of Exact Sequence Variants versus Operational Taxonomic Units. **2018**, 3,	95
1901	An anaerobic hybrid bioreactor for biologically enhanced primary treatment of domestic wastewater under low temperatures. **2018**, 4, 1851-1866	8
1900	Chloroplast sequence variation and the efficacy of peptide nucleic acids for blocking host amplification in plant microbiome studies. **2018**, 6, 144	34
1899	The gut microbiome of nonhuman primates: Lessons in ecology and evolution. **2018**, 80, e22867	62
1898	Gut microbiome and magnetic resonance spectroscopy study of subjects at ultra-high risk for psychosis may support the membrane hypothesis. **2018**, 53, 37-45	54
1897	Does universal 16S rRNA gene amplicon sequencing of environmental communities provide an accurate description of nitrifying guilds?. **2018**, 151, 28-34	7
1896	Assessing Cat Flea Microbiomes in Northern and Southern California by 16S rRNA Next-Generation Sequencing. **2018**, 18, 491-499	9
1895	Dynamics and interactions of highly resolved marine plankton via automated high-frequency sampling. **2018**, 12, 2417-2432	35
1894	Deficiency of BrpA in Streptococcus mutans reduces virulence in rat caries model. **2018**, 33, 353-363	12
1893	Evaluation of milk sample fractions for characterization of milk microbiota from healthy and clinical mastitis cows. **2018**, 13, e0193671	38
1892	Endospores and other lysis-resistant bacteria comprise a widely shared core community within the human microbiota. **2018**, 12, 2403-2416	22
1891	The colonic epithelium plays an active role in promoting colitis by shaping the tissue cytokine profile. **2018**, 16, e2002417	26
1890	Microbiome niche modification drives diurnal rumen community assembly, overpowering individual variability and diet effects. **2018**, 12, 2446-2457	32
1889	A novel mouse model of Campylobacter jejuni enteropathy and diarrhea. **2018**, 14, e1007083	37
1888	Wild Bee Pollen Usage and Microbial Communities Co-vary Across Landscapes. **2019**, 77, 513-522	28
1887	Finding flies in the mushroom soup: Host specificity of fungus-associated communities revisited with a novel molecular method. **2019**, 28, 190-202	11
1886	Seasonality of the gut microbiota of free-ranging white-faced capuchins in a tropical dry forest. **2019**, 13, 183-196	36

1885	Links between environment, diet, and the hunter-gatherer microbiome. **2019**, 10, 216-227	66
1884	Assessment of urinary 3-indoxyl sulfate as a marker for gut microbiota diversity and abundance of Clostridiales. **2019**, 10, 133-141	10
1883	Initial description of the core ocular surface microbiome in dogs: Bacterial community diversity and composition in a defined canine population. **2019**, 22, 337-344	17
1882	Effect of Intentional Weight Loss on Mortality Biomarkers in Older Adults With Obesity. **2019**, 74, 1303-1309	4
1881	Terrestriality and bacterial transfer: a comparative study of gut microbiomes in sympatric Malagasy mammals. **2019**, 13, 50-63	33
1880	Elucidating Syntrophic Butyrate-Degrading Populations in Anaerobic Digesters Using Stable-Isotope-Informed Genome-Resolved Metagenomics. **2019**, 4,	12
1879	Metagenomic analysis of drinking water samples collected from treatment plants of Hyderabad City and Mehran University Employees Cooperative Housing Society. **2019**, 26, 29052-29064	4
1878	Microbiome-driven identification of microbial indicators for postharvest diseases of sugar beets. **2019**, 7, 112	20
1877	Align to Define: Ecologically Meaningful Populations from Genomes. **2019**, 178, 767-768	2
1876	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. **2019**, 95,	18
1875	Vancomycin relieves mycophenolate mofetil-induced gastrointestinal toxicity by eliminating gut bacterial glucuronidase activity. **2019**, 5, eaax2358	40
1874	Contamination Is Not Linked to the Gestational Microbiome. **2019**, 85,	0
1873	Variations in Vaginal, Penile, and Oral Microbiota After Sexual Intercourse: A Case Report. **2019**, 6, 178	7
1872	rpoB, a promising marker for analyzing the diversity of bacterial communities by amplicon sequencing. **2019**, 19, 171	28
1871	in saliva associates with chronic and aggressive periodontitis. **2019**, 11, 1653123	21
1870	Genetic risk for autoimmunity is associated with distinct changes in the human gut microbiome. **2019**, 10, 3621	59
1869	Reproducible changes in the gut microbiome suggest a shift in microbial and host metabolism during spaceflight. **2019**, 7, 113	29
1868	Geomicrobiology of a seawater-influenced active sulfuric acid cave. **2019**, 14, e0220706	17

1867	Gut microbiota, dietary phytochemicals and benefits to human health. **2019**, 5, 332-344	24
1866	Assessment of a metabarcoding approach for the characterisation of vector-borne bacteria in canines from Bangkok, Thailand. **2019**, 12, 394	15
1865	Oral vancomycin treatment does not alter markers of postprandial inflammation in lean and obese subjects. **2019**, 7, e14199	4
1864	Diversity and structure of the bacterial microbiome of the American dog tick, Dermacentor variabilis, is dominated by the endosymbiont Francisella. **2019**, 79, 239-250	10
1863	Amplicon sequencing provides more accurate microbiome information in healthy children compared to culturing. **2019**, 2, 291	29
1862	Potential roles of gut microbiome and metabolites in modulating ALS in mice. **2019**, 572, 474-480	240
1861	Effect of sulfite addition and pied de cuve inoculation on the microbial communities and sensory profiles of Chardonnay wines: dominance of indigenous Saccharomyces uvarum at a commercial winery. **2019**, 19,	10
1860	Stable Isotope Probing. **2019**,	7
1859	Profiling of Active Microorganisms by Stable Isotope Probing-Metagenomics. **2019**, 2046, 151-161	3
1858	Microdiversity ensures the maintenance of functional microbial communities under changing environmental conditions. **2019**, 13, 2969-2983	48
1857	Non-symbiotic soil microbes are more strongly influenced by altered tree biodiversity than arbuscular mycorrhizal fungi during initial forest establishment. **2019**, 95,	
1856	Impact of hydraulic retention time and organic matter concentration on side-stream aerobic granular membrane bioreactor. **2019**, 693, 133525	6
1855	Microbiomes of Velloziaceae from phosphorus-impoverished soils of the campos rupestres, a biodiversity hotspot. **2019**, 6, 140	3
1854	Laboratory mice born to wild mice have natural microbiota and model human immune responses. **2019**, 365,	189
1853	Plant-driven changes in soil microbial communities influence seed germination through negative feedbacks. **2019**, 9, 9298-9311	10
1852	Co-digestion of blackwater with kitchen organic waste: Effects of mixing ratios and insights into microbial community. **2019**, 236, 117703	35
1851	Post-exercise hypotension and skeletal muscle oxygenation is regulated by nitrate-reducing activity of oral bacteria. **2019**, 143, 252-259	14
1850	High bacterial diversity in pioneer biofilms colonizing ceramic roof tiles. **2019**, 144, 104745	7

1849	Non-specific amplification compromises environmental DNA metabarcoding with COI. **2019**, 10, 1985-2001	95
1848	Fecal Microbiotas of Indonesian and New Zealand Children Differ in Complexity and Bifidobacterial Taxa during the First Year of Life. **2019**, 85,	14
1847	Consumer Safety Considerations of Skin and Oral Microbiome Perturbation. **2019**, 32,	8
1846	Characterization of fungal biodiversity and communities associated with the reef macroalga Sargassum ilicifolium reveals fungal community differentiation according to geographic locality and algal structure. **2019**, 49, 2601-2608	13
1845	Dysbiosis associated with acute helminth infections in herbivorous youngstock - observations and implications. **2019**, 9, 11121	15
1844	Influence of Environment and Host Plant Genotype on the Structure and Diversity of the Brassica napus Seed Microbiota. **2019**, 3, 326-336	17
1843	Baseline microbiota composition modulates antibiotic-mediated effects on the gut microbiota and host. **2019**, 7, 111	24
1842	Can Targeting Non-Contiguous V-Regions With Paired-End Sequencing Improve 16S rRNA-Based Taxonomic Resolution of Microbiomes?: An Evaluation. **2019**, 10, 653	4
1841	Soil bacterial and fungal response to wildfires in the Canadian boreal forest across a burn severity gradient. **2019**, 138, 107571	47
1840	A hierarchy of environmental covariates control the global biogeography of soil bacterial richness. **2019**, 9, 12129	10
1839	Archaeal nitrification is a key driver of high nitrous oxide emissions from arctic peatlands. **2019**, 137, 107539	18
1838	Seasonal Changes of Airborne Bacterial Communities Over Tokyo and Influence of Local Meteorology. **2019**, 10, 1572	40
1837	Experimental Inoculation of Coral Recruits With Marine Bacteria Indicates Scope for Microbiome Manipulation in and. **2019**, 10, 1702	23
1836	Nitrate addition stimulates microbial decomposition of organic matter in salt marsh sediments. **2019**, 25, 3224-3241	29
1835	Approaches to metagenomic classification and assembly. **2019**,	0
1834	Short communication: Intra- and inter-individual milk microbiota variability in healthy and infected water buffalo udder quarters. **2019**, 102, 7476-7482	1
1833	Population Genetic Divergence and Environment Influence the Gut Microbiome in Oregon Threespine Stickleback. **2019**, 10,	14
1832	Enhanced biomethane recovery from fat, oil, and grease through co-digestion with food waste and addition of conductive materials. **2019**, 236, 124362	33

1831	Molecular Diagnosis of Vaginitis: Comparing Quantitative PCR and Microbiome Profiling Approaches to Current Microscopy Scoring. **2019**, 57,	6
1830	Fecal microbiota of different reproductive stages of the central population of the lesser-long nosed bat, Leptonycteris yerbabuenae. **2019**, 14, e0219982	7
1829	Molecular techniques and their limitations shape our view of the holobiont. **2019**, 137, 125695	4
1828	The effect of levofloxacin on the lung microbiota of laboratory rats. **2019**, 45, 200-208	1
1827	Developmental exposure to polychlorinated biphenyls (PCBs) in the maternal diet causes host-microbe defects in weanling offspring mice. **2019**, 253, 708-721	32
1826	TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. **2019** , 35, i31-i40	4
1825	A sparse covarying unit that describes healthy and impaired human gut microbiota development. **2019**, 365,	74
1824	DAIRYdb: a manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products. **2019**, 20, 560	20
1823	Spatial and temporal dynamics of Antarctic shallow soft-bottom benthic communities: ecological drivers under climate change. **2019**, 19, 27	12
1822	Detection of low-density Plasmodium falciparum infections using amplicon deep sequencing. **2019**, 18, 219	22
1821	The application of high-throughput sequencing technology to analysis of amoA phylogeny and environmental niche specialisation of terrestrial bacterial ammonia-oxidisers. **2019**, 14, 3	31
1820	Predicting provenance of forensic soil samples: Linking soil to ecological habitats by metabarcoding and supervised classification. **2019**, 14, e0202844	20
1819	Dust-Associated Airborne Microbes Affect Primary and Bacterial Production Rates, and Eukaryotes Diversity, in the Northern Red Sea: A Mesocosm Approach. **2019**, 10, 358	10
1818	Does the endometrial cavity have a molecular microbial signature?. **2019**, 9, 9905	55
1817	Evaluation of the impact of in ovo administered bacteria on microbiome of chicks through 10 days of age. **2019**, 98, 5949-5960	15
1816	Changes in the composition and function of bacterial communities during vermicomposting may explain beneficial properties of vermicompost. **2019**, 9, 9657	38
1815	Contrasting microbial community responses to salinization and straw amendment in a semiarid bare soil and its wheat rhizosphere. **2019**, 9, 9795	12
1814	Early-Onset Preeclampsia Is Associated With Gut Microbial Alterations in Antepartum and Postpartum Women. **2019**, 9, 224	50

1813	Impacts of Continuous Inflow of Low Concentrations of Silver Nanoparticles on Biological Performance and Microbial Communities of Aerobic Heterotrophic Wastewater Biofilm. **2019**, 53, 9148-9159	4
1812	Spatiotemporal Controls on the Urban Aerobiome. **2019**, 7,	30
1811	Ammonia Oxidation by the Arctic Terrestrial Thaumarchaeote Nitrosocosmicus arcticus Is Stimulated by Increasing Temperatures. **2019**, 10, 1571	21
1810	Human gut microbiome changes during a 10 week Randomised Control Trial for micronutrient supplementation in children with attention deficit hyperactivity disorder. **2019**, 9, 10128	34
1809	The effect of having Christmas dinner with in-laws on gut microbiota composition. **2019**, 13, 100058	
1808	Microbiome dynamics and phaC synthase genes selected in a pilot plant producing polyhydroxyalkanoate from the organic fraction of urban waste. **2019**, 689, 765-773	16
1807	Bacterial biofilm composition in healthy subjects with and without caries experience. **2019**, 11, 1633194	24
1806	Homogeneous selection dominates the microbial community assembly in the sediment of the Three Gorges Reservoir. **2019**, 690, 50-60	43
1805	Making the Most of Trait-Based Approaches for Microbial Ecology. **2019**, 27, 814-823	22
1804	Vertical transmission of sponge microbiota is inconsistent and unfaithful. **2019**, 3, 1172-1183	31
1803	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. **2019**, 7, 100	42
1802	Nontuberculous Mycobacteria in Two Drinking Water Distribution Systems and the Role of Residual Disinfection. **2019**, 53, 8563-8573	24
1801	Community analysis of gut microbiota in hornets, the largest eusocial wasps, Vespa mandarinia and V. simillima. **2019**, 9, 9830	17
1800	Disentangling the complex microbial community of coral reefs using standardized Autonomous Reef Monitoring Structures (ARMS). **2019**, 28, 3496-3507	16
1799	Metabarcoding reveals differences in fungal communities between unflooded versus tidal flat soil in coastal saline ecosystem. **2019**, 690, 911-922	11
1798	Characterizing symbiont inheritance during host-microbiota evolution: Application to the great apes gut microbiota. **2019**, 19, 1659-1671	9
1797	Amazon fish bacterial communities show structural convergence along widespread hydrochemical gradients. **2019**, 28, 3612-3626	9
1796	Genomic and Seasonal Variations among Aquatic Phages Infecting the Baltic Sea Gammaproteobacterium sp. Strain BAL341. **2019**, 85,	10

1795	Facultative Anaerobes Shape Multispecies Biofilms Composed of Meat Processing Surface Bacteria and Escherichia coli O157:H7 or Salmonella enterica Serovar Typhimurium. **2019**, 85,	6
1794	Modelling approaches for studying the microbiome. **2019**, 4, 1253-1267	56
1793	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. **2019**, 6, 129	13
1792	Treatment-Specific Composition of the Gut Microbiota Is Associated With Disease Remission in a Pediatric Crohn's Disease Cohort. **2019**, 25, 1927-1938	11
1791	Salinity drives meiofaunal community structure dynamics across the Baltic ecosystem. **2019**, 28, 3813-3829	14
1790	Nexus of Stochastic and Deterministic Processes on Microbial Community Assembly in Biological Systems. **2019**, 10, 1536	17
1789	Temporal Variation in the Microbiome of Coral Species Does Not Reflect Seasonality. **2019**, 10, 1775	7
1788	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. **2019**, 37, 852-857	4050
1787	Chronic obstructive pulmonary disease upper airway microbiome is associated with select clinical characteristics. **2019**, 14, e0219962	9
1786	Engineered in situ biogeochemical transformation as a secondary treatment following ISCO - A field test. **2019**, 237, 124460	4
1785	Jellyfish summer outbreaks as bacterial vectors and potential hazards for marine animals and humans health? The case of Rhizostoma pulmo (Scyphozoa, Cnidaria). **2019**, 692, 305-318	17
1784	Analysis of proximal bone margins in diabetic foot osteomyelitis by conventional culture, DNA sequencing and microscopy. **2019**, 127, 660-670	10
1783	Decoding Wheat Endosphere-Rhizosphere Microbiomes in -Infested Soils Challenged by Biocontrol Agents. **2019**, 10, 1038	22
1782	The role of inoculum dispersal and plant species identity in the assembly of leaf endophytic fungal communities. **2019**, 14, e0219832	10
1781	Gut Microbiota and Risk of Persistent Nonalcoholic Fatty Liver Diseases. **2019**, 8,	24
1780	Non-sterile heterotrophic cultivation of native wastewater yeast and microalgae for integrated municipal wastewater treatment and bioethanol production. **2019**, 151, 107319	35
1779	Effects of Hardwood Biochar on Methane Production, Fermentation Characteristics, and the Rumen Microbiota Using Rumen Simulation. **2019**, 10, 1534	23
1778	The relative importance of ecological drivers of arbuscular mycorrhizal fungal distribution varies with taxon phylogenetic resolution. **2019**, 224, 936-948	8

1777	Effects of Chestnut Tannin Extract, Vescalagin and Gallic Acid on the Dimethyl Acetals Profile and Microbial Community Composition in Rumen Liquor: An In Vitro Study. **2019**, 7,	11
1776	Insights into the Potential of the Atlantic Cod Gut Microbiome as Biomarker of Oil Contamination in the Marine Environment. **2019**, 7,	12
1775	Developing Gut Microbiota Exerts Colonisation Resistance to syn. in Piglets. **2019**, 7,	10
1774	Analysis of Soil Properties, Bacterial Community Composition, and Metabolic Diversity in Fluvisols of a Floodplain Area. **2019**, 11, 3929	7
1773	Visualization of microbes by 16S in situ hybridization in term and preterm placentas without intraamniotic infection. **2019**, 221, 146.e1-146.e23	60
1772	Short communication: Surface charring from prescribed burning has minimal effects on soil bacterial community composition two weeks post-fire in jack pine barrens. **2019**, 144, 134-138	4
1771	Enhancing biomethane recovery from source-diverted blackwater through hydrogenotrophic methanogenesis dominant pathway. **2019**, 378, 122258	31
1770	Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. **2019**, 8,	56
1769	Improving eDNA-based protist diversity assessments using networks of amplicon sequence variants. **2019**, 21, 4109-4124	24
1768	Microbial Similarity between Students in a Common Dormitory Environment Reveals the Forensic Potential of Individual Microbial Signatures. **2019**, 10,	18
1767	Microbiota and gut ultrastructure of Anisakis pegreffii isolated from stranded cetaceans in the Adriatic Sea. **2019**, 12, 381	4
1766	On the Role of Bioinformatics and Data Science in Industrial Microbiome Applications. **2019**, 10, 721	7
1765	Trait-based life-history strategies explain succession scenario for complex bacterial communities under varying disturbance. **2019**, 21, 3751-3764	12
1764	Deciphering Microbiome Related to Rusty Roots of and Evaluation of Antagonists Against Pathogenic. **2019**, 10, 1350	23
1763	Anthropogenic remediation of heavy metals selects against natural microbial remediation. **2019**, 286, 20190804	6
1762	Longitudinal microbiome profiling reveals impermanence of probiotic bacteria in domestic pigeons. **2019**, 14, e0217804	7
1761	Effects of thermal hydrolytic pre-treatment on biogas process efficiency and microbial community structure in industrial- and laboratory-scale digesters. **2019**, 95, 150-160	21
1760	Short-term impact of sucralose consumption on the metabolic response and gut microbiome of healthy adults. **2019**, 122, 856-862	19

1759	Supplementation with Akkermansia muciniphila in overweight and obese human volunteers: a proof-of-concept exploratory study. **2019**, 25, 1096-1103	650
1758	Monitored Indoor Environmental Quality of a Mass Timber Office Building: A Case Study. **2019**, 9, 142	7
1757	Full Issue PDF. **2019**, 3, 82-157	
1756	Microbial community structure associated with submarine groundwater discharge in northern Java (Indonesia). **2019**, 689, 590-601	25
1755	Pathogenic Autoreactive T and B Cells Cross-React with Mimotopes Expressed by a Common Human Gut Commensal to Trigger Autoimmunity. **2019**, 26, 100-113.e8	63
1754	High-throughput amplicon sequencing of the full-length 16S rRNA gene with single-nucleotide resolution. **2019**, 47, e103	155
1753	Translating Recent Microbiome Insights in Otitis Media into Probiotic Strategies. **2019**, 32,	15
1752	iMAP: an integrated bioinformatics and visualization pipeline for microbiome data analysis. **2019**, 20, 374	16
1751	Comparative evaluation of a biotrickling filter and a tubular photobioreactor for the continuous abatement of toluene. **2019**, 380, 120860	19
1750	Pooled clone collections by multiplexed CRISPR-Cas12a-assisted gene tagging in yeast. **2019**, 10, 2960	10
1749	Altered Stool Microbiota of Infants with Cystic Fibrosis Shows a Reduction in Genera Associated with Immune Programming from Birth. **2019**, 201,	25
1748	Organic Soils Control Beetle Survival While Competitors Limit Aphid Population Growth. **2019**, 48, 1323-1330	3
1747	Surviving onshore soil microbial communities differ among the Qing-Tibetan lakes with different salinity. **2019**, 95,	1
1746	Identifying the mechanisms that shape fungal community and metacommunity patterns in Yunnan, China. **2019**, 42, 100862	6
1745	Tradeoffs in hyphal traits determine mycelium architecture in saprobic fungi. **2019**, 9, 14152	10
1744	Bacterial and Fungal Diversity Inside the Medieval Building Constructed with Sandstone Plates and Lime Mortar as an Example of the Microbial Colonization of a Nutrient-Limited Extreme Environment (Wawel Royal Castle, Krakow, Poland). **2019**, 7,	5
1743	Changes in the Bacterioplankton Community Structure from Southern Gulf of Mexico During a Simulated Crude Oil Spill at Mesocosm Scale. **2019**, 7,	14
1742	Putative Mixotrophic Nitrifying-Denitrifying Gammaproteobacteria Implicated in Nitrogen Cycling Within the Ammonia/Oxygen Transition Zone of an Oil Sands Pit Lake. **2019**, 10, 2435	21

1741	Characterization of the Spoilage Microbiota of Hake Fillets Packaged Under a Modified Atmosphere (MAP) Rich in CO (50% CO/50% N) and Stored at Different Temperatures. **2019**, 8,	9
1740	Inter-correlated gut microbiota and SCFAs changes upon antibiotics exposure links with rapid body-mass gain in weaned piglet model. **2019**, 74, 108246	15
1739	Alterations to the Gastrointestinal Microbiome Associated with Methamphetamine Use among Young Men who have Sex with Men. **2019**, 9, 14840	19
1738	Yeasts of Burden: Exploring the Mycobiome-Bacteriome of the Piglet GI Tract. **2019**, 10, 2286	18
1737	Metformin alters the duodenal microbiome and decreases the incidence of pancreatic ductal adenocarcinoma promoted by diet-induced obesity. **2019**, 317, G763-G772	17
1736	Gut microbiome diversity is associated with sleep physiology in humans. **2019**, 14, e0222394	84
1735	Looking at the Origin: Some Insights into the General and Fermentative Microbiota of Vineyard Soils. **2019**, 5, 78	7
1734	CD109 Restrains Activation of Cutaneous IL-17-Producing □T Cells by Commensal Microbiota. **2019**, 29, 391-405.e5	10
1733	A Bioinformatics Guide to Plant Microbiome Analysis. **2019**, 10, 1313	22
1732	Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal Escherichia coli, and the microbiome of steers. **2019**, 14, e0223378	5
1731	Parasite microbiome project: Grand challenges. **2019**, 15, e1008028	22
1730	How should we store avian faecal samples for microbiota analyses? Comparing efficacy and cost-effectiveness. **2019**, 165, 105689	3
1729	Gastrointestinal Tract Dysbiosis Enhances Distal Tumor Progression through Suppression of Leukocyte Trafficking. **2019**, 79, 5999-6009	16
1728	Evaluation of the bacterial ocular surface microbiome in clinically normal cats before and after treatment with topical erythromycin. **2019**, 14, e0223859	8
1727	Copper-Induced Stimulation of Nitrification in Biological Rapid Sand Filters for Drinking Water Production by Proliferation of spp. **2019**, 53, 12433-12441	5
1726	Species abundance information improves sequence taxonomy classification accuracy. **2019**, 10, 4643	22
1725	Changes in soil bacterial community diversity following the removal of invasive feral pigs from a Hawaiian tropical montane wet forest. **2019**, 9, 14681	4
1724	Mystifying mass in the right ventricle. **2020**, 21, 281	

1723	Supply of Methionine During Late-Pregnancy Alters Fecal Microbiota and Metabolome in Neonatal Dairy Calves Without Changes in Daily Feed Intake. **2019**, 10, 2159	19
1722	Bacterial Communities from Extreme Environments: Vulcano Island. **2019**, 11, 140	2
1721	Relationships among wood-boring beetles, fungi, and the decomposition of forest biomass. **2019**, 28, 4971-4986	24
1720	Floral organs act as environmental filters and interact with pollinators to structure the yellow monkeyflower (Mimulus guttatus) floral microbiome. **2019**, 28, 5155-5171	18
1719	Angiosperm to Gymnosperm host-plant switch entails shifts in microbiota of the Welwitschia bug, Probergrothius angolensis (Distant, 1902). **2019**, 28, 5172-5187	9
1718	Seagrass-associated fungal communities show distance decay of similarity that has implications for seagrass management and restoration. **2019**, 9, 11288-11297	19
1717	Large-scale distribution of bacterial communities in the Qaidam Basin of the Qinghai-Tibet Plateau. **2019**, 8, e909	7
1716	An examination of data from the American Gut Project reveals that the dominance of the genus Bifidobacterium is associated with the diversity and robustness of the gut microbiota. **2019**, 8, e939	12
1715	Community structure and distribution of benthic Bacteria and Archaea in a stratified coastal lagoon in the Southern Gulf of Mexico. **2019**, 230, 106433	4
1714	Selection imposed by local environmental conditions drives differences in microbial community composition across geographically distinct groundwater aquifers. **2019**, 95,	16
1713	A comparative assessment of conventional and molecular methods, including MinION nanopore sequencing, for surveying water quality. **2019**, 9, 15726	30
1712	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. **2019**, 20, 219	41
1711	Rapid Bacterial Community Changes during Vermicomposting of Grape Marc Derived from Red Winemaking. **2019**, 7,	13
1710	Impacts of Maize Domestication and Breeding on Rhizosphere Microbial Community Recruitment from a Nutrient Depleted Agricultural Soil. **2019**, 9, 15611	37
1709	Agricultural management and plant selection interactively affect rhizosphere microbial community structure and nitrogen cycling. **2019**, 7, 146	99
1708	The -Regulated Microbiome Enhances Experimental Allergic Asthma. **2019**, 203, 3113-3125	8
1707	Guidelines for Transparency on Gut Microbiome Studies in Essential and Experimental Hypertension. **2019**, 74, 1279-1293	24
1706	Microbial communities of the house fly Musca domestica vary with geographical location and habitat. **2019**, 7, 147	33

1705	"Bowel on the Bench": Proof of Concept of a Three-Stage, Fermentation Model of the Equine Large Intestine. **2019**, 86,	3
1704	Regional biogeography of microbiota composition in the Chagas disease vector Rhodnius pallescens. **2019**, 12, 504	11
1703	Influence of pig gut microbiota on Mycoplasma hyopneumoniae susceptibility. **2019**, 50, 86	8
1702	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. **2019**, 7,	4
1701	Temporal and spatial dynamics of Bacteria, Archaea and protists in equatorial coastal waters. **2019**, 9, 16390	14
1700	The role of multiple global change factors in driving soil functions and microbial biodiversity. **2019**, 366, 886-890	169
1699	Recovery of the Gut Microbiota after Antibiotics Depends on Host Diet, Community Context, and Environmental Reservoirs. **2019**, 26, 650-665.e4	80
1698	Distinct Polysaccharide Utilization Profiles of Human Intestinal Prevotella copri Isolates. **2019**, 26, 680-690.e5	53
1697	Reductionist synthetic community approaches in root microbiome research. **2019**, 49, 97-102	39
1696	Changes in human gut microbiota composition are linked to the energy metabolic switch during 10 d of Buchinger fasting. **2019**, 8, e36	29
1695	Longitudinal profiling of gut microbiome among tuberculosis patients under anti-tuberculosis treatment in China: protocol of a prospective cohort study. **2019**, 19, 211	1
1694	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. **2019**, 10, 5029	406
1693	Tracing the evolutionary routes of plant-microbiota interactions. **2019**, 49, 34-40	31
1692	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. **2019**, 20, 581	26
1691	Soil sterilization leads to re-colonization of a healthier rhizosphere microbiome. **2019**, 12, 100176	14
1690	Cross-kingdom analysis of nymphal-stage Ixodes scapularis microbial communities in relation to Borrelia burgdorferi infection and load. **2019**, 95,	13
1689	Diatom DNA Metabarcoding for Biomonitoring: Strategies to Avoid Major Taxonomical and Bioinformatical Biases Limiting Molecular Indices Capacities. **2019**, 7,	27
1688	Microbiota Analysis Using Two-step PCR and Next-generation 16S rRNA Gene Sequencing. **2019**,	9

1687	Variations in the microbiome due to storage preservatives are not large enough to obscure variations due to factors such as host population, host species, body site, and captivity. **2019**, 81, e23045	3
1686	Pembrolizumab for anaplastic thyroid cancer: a case study. **2019**, 68, 1921-1934	10
1685	Microbial Community Shifts Associated With the Ongoing Stony Coral Tissue Loss Disease Outbreak on the Florida Reef Tract. **2019**, 10, 2244	62
1684	Reduced Gut Microbiome Diversity and Metabolome Differences in Rhinoceros Species at Risk for Iron Overload Disorder. **2019**, 10, 2291	8
1683	The Effect of Milk Replacer Composition on the Intestinal Microbiota of Pre-ruminant Dairy Calves. **2019**, 6, 371	7
1682	An Association of Gut Microbiota with Different Phenotypes in Chinese Patients with Rheumatoid Arthritis. **2019**, 8,	30
1681	Scales of persistence: transmission and the microbiome. **2019**, 50, 42-49	14
1680	Storage media and not extraction method has the biggest impact on recovery of bacteria from the oral microbiome. **2019**, 9, 14968	13
1679	Antigen-Specific Mucosal Immunity Regulates Development of Intestinal Bacteria-Mediated Diseases. **2019**, 157, 1530-1543.e4	11
1678	Temperature dependence of parasitic infection and gut bacterial communities in bumble bees. **2019**, 21, 4706-4723	15
1677	Application of Environmental DNA Metabarcoding to Spatiotemporal Finfish Community Assessment in a Temperate Embayment. **2019**, 6,	7
1676	Metagenomics Reveals Bacterial and Archaeal Adaptation to Urban Land-Use: N Catabolism, Methanogenesis, and Nutrient Acquisition. **2019**, 10, 2330	6
1675	Late-Night Eating-Induced Physiological Dysregulation and Circadian Misalignment Are Accompanied by Microbial Dysbiosis. **2019**, 63, e1900867	11
1674	Mastiha (Pistacia lentiscus) Improves Gut Microbiota Diversity, Hepatic Steatosis, and Disease Activity in a Biopsy-Confirmed Mouse Model of Advanced Non-Alcoholic Steatohepatitis and Fibrosis. **2019**, 63, e1900927	12
1673	Defining the Distinct Skin and Gut Microbiomes of the Northern Pike (). **2019**, 10, 2118	10
1672	MAIT cells are imprinted by the microbiota in early life and promote tissue repair. **2019**, 366,	162
1671	High-throughput DNA sequencing technologies for water and wastewater analysis. **2019**, 102, 351-376	8
1670	Associations between dietary micronutrient intake and molecular-Bacterial Vaginosis. **2019**, 16, 151	15

1669	Formulation and Evaluation of Slow-Release Fertilizer from Agricultural and Industrial Wastes for Remediation of Crude Oil-Polluted Soils. **2019**,	2
1668	Therapeutic Potential of an Endolysin Derived from Kayvirus S25-3 for Staphylococcal Impetigo. **2019**, 11,	19
1667	Monitoring of marine nematode communities through 18S rRNA metabarcoding as a sensitive alternative to morphology. **2019**, 107, 105554	8
1666	A commercial seaweed extract structured microbial communities associated with tomato and pepper roots and significantly increased crop yield. **2019**, 12, 1346-1358	23
1665	Accurate estimation of microbial sequence diversity with Distanced. **2020**, 36, 728-734	2
1664	Successional Dynamics in the Gut Microbiome Determine the Success of Infection in Adult Pig Models. **2019**, 9, 271	4
1663	TreeCluster: Clustering biological sequences using phylogenetic trees. **2019**, 14, e0221068	33
1662	Biological pretreatment with Trametes versicolor to enhance methane production from lignocellulosic biomass: A metagenomic approach. **2019**, 140, 111659	32
1661	Exploring interactions between Blastocystis sp., Strongyloides spp. and the gut microbiomes of wild chimpanzees in Senegal. **2019**, 74, 104010	11
1660	Highly Reproducible 16S Sequencing Facilitates Measurement of Host Genetic Influences on the Stickleback Gut Microbiome. **2019**, 4,	5
1659	Evaluation of the effects of four media on human intestinal microbiota culture in vitro. **2019**, 9, 69	7
1658	Intestinal Microbial Products From Alcohol-Fed Mice Contribute to Intestinal Permeability and Peripheral Immune Activation. **2019**, 43, 2122-2133	10
1657	Maturation of the infant rhesus macaque gut microbiome and its role in the development of diarrheal disease. **2019**, 20, 173	19
1656	Gut microbiota features associated with Clostridioides difficile colonization in puppies. **2019**, 14, e0215497	10
1655	Vaginal Microbiome Signature Is Associated With Spontaneous Preterm Delivery. **2019**, 6, 201	29
1654	A novel metabarcoding diagnostic tool to explore protozoan haemoparasite diversity in mammals: a proof-of-concept study using canines from the tropics. **2019**, 9, 12644	15
1653	Early life determinants induce sustainable changes in the gut microbiome of six-year-old children. **2019**, 9, 12675	16
1652	Genetic determinants of gut microbiota composition and bile acid profiles in mice. **2019**, 15, e1008073	32

1651	Space Station conditions are selective but do not alter microbial characteristics relevant to human health. **2019**, 10, 3990	33
1650	Identification of Initial Colonizing Bacteria in Dental Plaques from Young Adults Using Full-Length 16S rRNA Gene Sequencing. **2019**, 4,	11
1649	Microbiomic differences at cancer-prone oral mucosa sites with marijuana usage. **2019**, 9, 12697	7
1648	Opportunistic pathogens and large microbial diversity detected in source-to-distribution drinking water of three remote communities in Northern Australia. **2019**, 13, e0007672	6
1647	Effects of Regular Kefir Consumption on Gut Microbiota in Patients with Metabolic Syndrome: A Parallel-Group, Randomized, Controlled Study. **2019**, 11,	39
1646	Cadmium and Selenate Exposure Affects the Honey Bee Microbiome and Metabolome, and Bee-Associated Bacteria Show Potential for Bioaccumulation. **2019**, 85,	27
1645	Differential dynamics of microbial community networks help identify microorganisms interacting with residue-borne pathogens: the case of Zymoseptoria tritici in wheat. **2019**, 7, 125	16
1644	Drivers of human gut microbial community assembly: coadaptation, determinism and stochasticity. **2019**, 13, 3080-3092	12
1643	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. **2019**, 25, 1442-1452	125
1642	Almond Snacking for 8 wk Increases Alpha-Diversity of the Gastrointestinal Microbiome and Decreases Abundance Compared with an Isocaloric Snack in College Freshmen. **2019**, 3, nzz079	21
1641	Aerosol Microbiome over the Mediterranean Sea Diversity and Abundance. **2019**, 10, 440	15
1640	Dairy farm soil presents distinct microbiota and varied prevalence of antibiotic resistance across housing areas. **2019**, 254, 113058	14
1639	The microbiome of the invertebrate model host Galleria mellonella is dominated by Enterococcus. **2019**, 1, 7	14
1638	MITRE: inferring features from microbiota time-series data linked to host status. **2019**, 20, 186	10
1637	Meta-taxonomic analysis of prokaryotic and eukaryotic gut flora in stool samples from visceral leishmaniasis cases and endemic controls in Bihar State India. **2019**, 13, e0007444	16
1636	Effect of dried oregano (Origanum vulgare L.) plant material in feed on methane production, rumen fermentation, nutrient digestibility, and milk fatty acid composition in dairy cows. **2019**, 102, 9902-9918	16
1635	Next-generation sequencing of whole saliva from patients with primary Sjögren's syndrome and non-Sjögren's sicca reveals comparable salivary microbiota. **2019**, 11, 1660566	19
1634	Natural groundwater nutrient fluxes exceed anthropogenic inputs in an ecologically impacted estuary: lessons learned from Mobile Bay, Alabama. **2019**, 145, 1-33	11

1633	Microbiological Profile and Bioactive Properties of Insect Powders Used in Food and Feed Formulations. **2019**, 8,	17
1632	Changes in the Substrate Source Reveal Novel Interactions in the Sediment-Derived Methanogenic Microbial Community. **2019**, 20,	4
1631	Complex interactions between the microbiome and cancer immune therapy. **2019**, 56, 567-585	17
1630	Successful strategies for human microbiome data generation, storage and analyses. **2019**, 44, 1	
1629	Gut microbiome comparability of fresh-frozen versus stabilized-frozen samples from hospitalized patients using 16S rRNA gene and shotgun metagenomic sequencing. **2019**, 9, 13351	9
1628	Transformation of raw ewes' milk applying "Grana" type pressed cheese technology: Development of extra-hard "Gran Ovino" cheese. **2019**, 307, 108277	5
1627	Full Issue PDF. **2019**, 3, 1-81	
1626	Sputum microbiota and inflammation at stable state and during exacerbations in a cohort of chronic obstructive pulmonary disease (COPD) patients. **2019**, 14, e0222449	13
1625	Temporal Dynamics of the Sap Microbiome of Grapevine Under High Pierce's Disease Pressure. **2019**, 10, 1246	25
1624	Discrepant gut microbiota markers for the classification of obesity-related metabolic abnormalities. **2019**, 9, 13424	99
1623	Benchmarking urine storage and collection conditions for evaluating the female urinary microbiome. **2019**, 9, 13409	19
1622	Microbiome data science. **2019**, 44, 1	11
1621	Microbiota adaptation after an alkaline pH perturbation in a full-scale UASB anaerobic reactor treating dairy wastewater. **2019**, 42, 2035-2046	10
1620	Gut microbiota adaptation after weight loss by Roux-en-Y gastric bypass or sleeve gastrectomy bariatric surgeries. **2019**, 15, 1888-1895	35
1619	Remission in Crohn's disease is accompanied by alterations in the gut microbiota and mucins production. **2019**, 9, 13263	17
1618	Bacteria isolated from Bengal cat (Felis catus Prionailurus bengalensis) anal sac secretions produce volatile compounds potentially associated with animal signaling. **2019**, 14, e0216846	4
1617	Dietary Bioactive Lipid Compounds Rich in Menthol Alter Interactions Among Members of Ruminal Microbiota in Sheep. **2019**, 10, 2038	13
1616	Microbial characterization and fermentative characteristics of crop maize ensiled with unsalable vegetables. **2019**, 9, 13183	4

1615	Bacterial community structure and response to nitrogen amendments in Lake Shenandoah (VA, USA). **2019**, 80, 675-684	3
1614	Gut microbiota regulates cardiac ischemic tolerance and aortic stiffness in obesity. **2019**, 317, H1210-H1220	15
1613	A Pine Enhanced Biochar Does Not Decrease Enteric CH Emissions, but Alters the Rumen Microbiota. **2019**, 6, 308	19
1612	Transgenerational inheritance of shuffled symbiont communities in the coral Montipora digitata. **2019**, 9, 13328	24
1611	Phyllosphere Fungal Communities of Plum and Antifungal Activity of Indigenous Phenazine-Producing Against. **2019**, 10, 2287	8
1610	Amplicon sequencing dataset of soil fungi and associated environmental variables collected in karst and non-karst sites across Yunnan province, southwest China. **2019**, 27, 104575	1
1609	A fiber-deprived diet disturbs the fine-scale spatial architecture of the murine colon microbiome. **2019**, 10, 4366	34
1608	A Metabarcoding Analysis of the Mycobiome of Wheat Ears Across a Topographically Heterogeneous Field. **2019**, 10, 2095	7
1607	Food Preservatives Induce Dysbiosis in Human-Microbiota Associated -Deficient Mice. **2019**, 7,	14
1606	Lactulose drives a reversible reduction and qualitative modulation of the faecal microbiota diversity in healthy dogs. **2019**, 9, 13350	7
1605	Comparison of the microbial composition of African fermented foods using amplicon sequencing. **2019**, 9, 13863	27
1604	Evaluation of the Nasopharyngeal Microbiota in Beef Cattle Transported to a Feedlot, With a Focus on Lactic Acid-Producing Bacteria. **2019**, 10, 1988	11
1603	Partially Hydrolyzed Guar Gum Attenuates d-Galactose-Induced Oxidative Stress and Restores Gut Microbiota in Rats. **2019**, 20,	6
1602	The Impact of Bioinformatics Pipelines on Microbiota Studies: Does the Analytical "Microscope" Affect the Biological Interpretation?. **2019**, 7,	9
1601	N2 fixation, and the relative contribution of fixed N, in corals from Cura�o and Hawaii. **2019**, 38, 1145-1158	4
1600	Current practice in plankton metabarcoding: optimization and error management. **2019**, 41, 571-582	18
1599	Biodegradation, Photo-oxidation, and Dissolution of Petroleum Compounds in an Arctic Fjord during Summer. **2019**, 53, 12197-12206	11
1598	Metagenomic Signatures of Gut Infections Caused by Different Pathotypes. **2019**, 85,	16

1597	Altered Middle Ear Microbiome in Children With Chronic Otitis Media With Effusion and Respiratory Illnesses. **2019**, 9, 339	12
1596	Understanding the phyllosphere microbiome assemblage in grape species (Vitaceae) with amplicon sequence data structures. **2019**, 9, 14294	22
1595	Horizontal gene transfer overrides mutation in colonizing the mammalian gut. **2019**, 116, 17906-17915	52
1594	Limited changes in the fecal microbiome composition of laying hens after oral inoculation with wild duck feces. **2019**, 98, 6542-6551	4
1593	Disease Specific Bacterial Communities in a Coralline Algae of the Northwestern Mediterranean Sea: A Combined Culture Dependent and -Independent Approach. **2019**, 10, 1850	8
1592	Host availability drives distributions of fungal endophytes in the imperilled boreal realm. **2019**, 3, 1430-1437	49
1591	Core gut microbial communities are maintained by beneficial interactions and strain variability in fish. **2019**, 4, 2456-2465	42
1590	Effects of Habitat Partitioning on the Distribution of Bacterioplankton in Deep Lakes. **2019**, 10, 2257	8
1589	Fecal Microbiome Characteristics and the Resistome Associated With Acquisition of Multidrug-Resistant Organisms Among Elderly Subjects. **2019**, 10, 2260	8
1588	Bark and Grape Microbiome of : Influence of Geographic Patterns and Agronomic Management on Bacterial Diversity. **2018**, 9, 3203	39
1587	Changes in arbuscular mycorrhizal fungi between young and old Vitis roots. **2019**, 78, 33-42	4
1586	Microbial consumption of organophosphate esters in seawater under phosphorus limited conditions. **2019**, 9, 233	28
1585	Rare Taxa Exhibit Disproportionate Cell-Level Metabolic Activity in Enriched Anaerobic Digestion Microbial Communities. **2019**, 4,	13
1584	Pilose antler polypeptides ameliorate inflammation and oxidative stress and improves gut microbiota in hypoxic-ischemic injured rats. **2019**, 64, 93-108	15
1583	Urogenital schistosomiasis is associated with signatures of microbiome dysbiosis in Nigerian adolescents. **2019**, 9, 829	14
1582	A longitudinal assessment of host-microbe-parasite interactions resolves the zebrafish gut microbiome's link to Pseudocapillaria tomentosa infection and pathology. **2019**, 7, 10	34
1581	The Microbial Communities of Leaves and Roots Associated with Turtle Grass () and Manatee Grass () are Distinct from Seawater and Sediment Communities, but Are Similar between Species and Sampling Sites. **2018**, 7,	30
1580	Archaea dominate the microbial community in an ecosystem with low-to-moderate temperature and extreme acidity. **2019**, 7, 11	24

1579	A Pilot-Scale Field Study: In Situ Treatment of PCB-Impacted Sediments with Bioamended Activated Carbon. **2019**, 53, 2626-2634	33
1578	Fecal Microbiota of Toxigenic -Associated Diarrhea. **2018**, 9, 3331	15
1577	Effects of Dietary Supplementation With and , Either Alone or in Combination, on Growth and Fecal Microbiota Composition of Post-weaning Pigs at a Commercial Farm. **2019**, 6, 26	10
1576	The Purple Sea Urchin Demonstrates a Compartmentalization of Gut Bacterial Microbiota, Predictive Functional Attributes, and Taxonomic Co-Occurrence. **2019**, 7,	14
1575	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. **2019** , 8, 617-628	33
1574	Reductive metabolism of the important atmospheric gas isoprene by homoacetogens. **2019**, 13, 1168-1182	10
1573	Snow algae communities in Antarctica: metabolic and taxonomic composition. **2019**, 222, 1242-1255	35
1572	Unicellular Cyanobacteria Are Important Components of Phytoplankton Communities in Australia's Northern Oceanic Ecoregions. **2018**, 9, 3356	5
1571	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. **2019**, 21, 1331-1343	36
1570	Use of a Fluorescent Analog of Glucose (2-NBDG) To Identify Uncultured Rumen Bacteria That Take Up Glucose. **2019**, 85,	8
1569	Suppression of arbuscular mycorrhizal fungal activity in a diverse collection of non-cultivated soils. **2019**, 95,	13
1568	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. **2019**, 597, 2361-2378	64
1567	Diversity of the oral microbiome between dentate and edentulous individuals. **2019**, 25, 911-918	13
1566	Cheatgrass-associated AMF community negatively affects sagebrush root production but not C transfer to the soil. **2019**, 436, 381-396	3
1565	Microbial biofilm formation and community structure on low-density polyethylene microparticles in lake water microcosms. **2019**, 252, 94-102	62
1564	Biological composition and microbial dynamics of sinking particulate organic matter at abyssal depths in the oligotrophic open ocean. **2019**, 116, 11824-11832	69
1563	Modular Assembly of Polysaccharide-Degrading Marine Microbial Communities. **2019**, 29, 1528-1535.e6	69
1562	The Impact of DNA Polymerase and Number of Rounds of Amplification in PCR on 16S rRNA Gene Sequence Data. **2019**, 4,	50

1561	Triclosan Alters Microbial Communities in Freshwater Microcosms. **2019**, 11, 961	7
1560	Shifts in Ectomycorrhizal Fungal Communities and Exploration Types Relate to the Environment and Fine-Root Traits Across Interior Douglas-Fir Forests of Western Canada. **2019**, 10, 643	25
1559	Advancing integration of data on food microbiome studies: FoodMicrobionet 3.1, a major upgrade of the FoodMicrobionet database. **2019**, 305, 108249	15
1558	Association between the oral microbiome and brain resting state connectivity in smokers. **2019**, 200, 121-131	11
1557	Controlling for Contaminants in Low-Biomass 16S rRNA Gene Sequencing Experiments. **2019**, 4,	93
1556	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. **2019**, 4, 1826-1831	71
1555	Microbiota of Telenomus tridentatus (Platygastroidea: Scelionidae): An unwanted parasitoid. **2019**, 143, 834-841	2
1554	Gestation alters the gut microbiota of an oviparous lizard. **2019**, 95,	10
1553	An Enrichment Strategy for Formulating Synergistic Synbiotics. **2019**, 85,	7
1552	Bacterial alkylquinolone signaling contributes to structuring microbial communities in the ocean. **2019**, 7, 93	13
1551	Metagenomic Insights into the Bacterial Functions of a Diesel-Degrading Consortium for the Rhizoremediation of Diesel-Polluted Soil. **2019**, 10,	40
1550	IL-33 drives group 2 innate lymphoid cell-mediated protection during Clostridium difficile infection. **2019**, 10, 2712	57
1549	Longitudinal 16S rRNA data derived from limb regenerative tissue samples of axolotl Ambystoma mexicanum. **2019**, 6, 70	6
1548	Outbreaks of an Emerging Viral Disease Covary With Differences in the Composition of the Skin Microbiome of a Wild United Kingdom Amphibian. **2019**, 10, 1245	13
1547	The detection of aquatic macroorganisms using environmental DNA analysisA review of methods for collection, extraction, and detection. **2019**, 1, 99-108	90
1546	Sexually Dimorphic Influence of Neonatal Antibiotics on Bone. **2019**, 37, 2122-2129	1
1545	Characterisation of coral-associated bacterial communities in an urbanised marine environment shows strong divergence over small geographic scales. **2019**, 38, 1097-1106	18
1544	Probing the active fraction of soil microbiomes using BONCAT-FACS. **2019**, 10, 2770	53

1543	Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. **2019**, 25, 1104-1109	242
1542	Quantitative and qualitative evaluation of the impact of the G2 enhancer, bead sizes and lysing tubes on the bacterial community composition during DNA extraction from recalcitrant soil core samples based on community sequencing and qPCR. **2019**, 14, e0200979	12
1541	Kelp beds and their local effects on seawater chemistry, productivity, and microbial communities. **2019**, 100, e02798	36
1540	Metagenomic assessment of the Cebus apella gut microbiota. **2019**, 81, e23023	3
1539	Bacterial communities differ between plant species and soil type, and differentially influence seedling establishment on serpentine soils. **2019**, 441, 423-437	11
1538	16S rDNA high-throughput sequencing and MALDI-TOF MS are complementary when studying psychrotrophic bacterial diversity of raw cows' milk. **2019**, 97, 86-91	17
1537	Specific inhibitors of lysozyme and peptidases inhibit the growth of the rumen protozoan Entodinium caudatum without decreasing feed digestion or fermentation in vitro. **2019**, 127, 670-682	7
1536	Correlation between Disease Severity and the Intestinal Microbiome in Mycobacterium tuberculosis-Infected Rhesus Macaques. **2019**, 10,	14
1535	Pelleted-hay alfalfa feed increases sheep wether weight gain and rumen bacterial richness over loose-hay alfalfa feed. **2019**, 14, e0215797	7
1534	Ground beef microbiome changes with antimicrobial decontamination interventions and product storage. **2019**, 14, e0217947	9
1533	Microbial Communities in Aquaculture Ecosystems. **2019**,	3
1532	Microbial community dynamics in anaerobic digesters treating conventional and vacuum toilet flushed blackwater. **2019**, 160, 249-258	47
1531	Unveiled feather microcosm: feather microbiota of passerine birds is closely associated with host species identity and bacteriocin-producing bacteria. **2019**, 13, 2363-2376	16
1530	Pyrethroid exposure alters internal and cuticle surface bacterial communities in Anopheles albimanus. **2019**, 13, 2447-2464	22
1529	Total RNA Analysis of Bacterial Community Structural and Functional Shifts Throughout Vertebrate Decomposition. **2019**, 64, 1707-1719	6
1528	Chronic obstructive pulmonary disease upper airway microbiota alpha diversity is associated with exacerbation phenotype: a case-control observational study. **2019**, 20, 114	18
1527	Host-Microbiota Interactions and Their Importance in Promoting Growth and Resistance to Opportunistic Diseases in Salmonids. **2019**, 21-50	0
1526	Effects of Agricultural Management on Rhizosphere Microbial Structure and Function in Processing Tomato Plants. **2019**, 85,	11

1525	Microbial Networks in SPRING - Semi-parametric Rank-Based Correlation and Partial Correlation Estimation for Quantitative Microbiome Data. **2019**, 10, 516	27
1524	Novel Strategies for Soil-Borne Diseases: Exploiting the Microbiome and Volatile-Based Mechanisms Toward Controlling -Based Disease Complexes. **2019**, 10, 1296	18
1523	Single Fragment or Bulk Soil DNA Metabarcoding: Which is Better for Characterizing Biological Taxa Found in Surface Soils for Sample Separation?. **2019**, 10,	5
1522	Host selection and stochastic effects influence bacterial community assembly on the microalgal phycosphere. **2019**, 40, 101489	21
1521	Crop-based composting of lignocellulosic digestates: Focus on bacterial and fungal diversity. **2019**, 288, 121549	36
1520	Improved yield and accuracy for DNA extraction in microbiome studies with variation in microbial biomass. **2019**, 66, 285-289	7
1519	Characterization of ocular and nasopharyngeal microbiome in allergic rhinoconjunctivitis. **2019**, 30, 624-631	12
1518	Restoration of belowground fungal communities in reclaimed landscapes of the Canadian boreal forest. **2019**, 27, 1369-1380	3
1517	The piglet mycobiome during the weaning transition: a pilot study1. **2019**, 97, 2889-2900	17
1516	Faecal microbiota shift during weaning transition in piglets and evaluation of AO blood types as shaping factor for the bacterial community profile. **2019**, 14, e0217001	19
1515	Anacapa Toolkit: An environmental DNA toolkit for processing multilocus metabarcode datasets. **2019**, 10, 1469-1475	39
1514	World Workshop on Oral Medicine VII: Targeting the microbiome for oral medicine specialists-Part 1. A methodological guide. **2019**, 25 Suppl 1, 12-27	8
1513	Fecal Microbiota Transplantation Controls Murine Chronic Intestinal Inflammation by Modulating Immune Cell Functions and Gut Microbiota Composition. **2019**, 8,	31
1512	Sex-specific association between gut microbiome and fat distribution. **2019**, 10, 2408	40
1511	Bacterial community changes with granule size in cryoconite and their susceptibility to exogenous nutrients on NW Greenland glaciers. **2019**, 95,	8
1510	Dynamic Modulation of the Gut Microbiota and Metabolome by Bacteriophages in a Mouse Model. **2019**, 25, 803-814.e5	165
1509	Role of Vertical Transmission of Shoot Endophytes in Root-Associated Microbiome Assembly and Heavy Metal Hyperaccumulation in Sedum alfredii. **2019**, 53, 6954-6963	51
1508	Understanding microbial community dynamics to improve optimal microbiome selection. **2019**, 7, 85	61

1507	Antibiotic treatment in feedlot cattle: a longitudinal study of the effect of oxytetracycline and tulathromycin on the fecal and nasopharyngeal microbiota. **2019**, 7, 86	26
1506	Low-Dose Stevia (Rebaudioside A) Consumption Perturbs Gut Microbiota and the Mesolimbic Dopamine Reward System. **2019**, 11,	32
1505	Biogeography of the Oral Microbiome: The Site-Specialist Hypothesis. **2019**, 73, 335-358	73
1504	Identification of Salivary Microbiota and Its Association With Host Inflammatory Mediators in Periodontitis. **2019**, 9, 216	46
1503	A Review and Tutorial of Machine Learning Methods for Microbiome Host Trait Prediction. **2019**, 10, 579	71
1502	Distribution of potentially pathogenic bacteria in the groundwater of the Jianghan Plain, central China. **2019**, 143, 104711	6
1501	Soil biota composition and the performance of a noxious weed across its invaded range. **2019**, 42, 1671-1681	4
1500	Optimizing the Production of Nursery-Based Biological Soil Crusts for Restoration of Arid Land Soils. **2019**, 85,	13
1499	Anaerobic methane oxidation is an important sink for methane in the ocean's largest oxygen minimum zone. **2019**, 64, 2569-2585	22
1498	Gut microbiota in ALS: possible role in pathogenesis?. **2019**, 19, 785-805	21
1497	A novel metabarcoding approach to investigate Fusarium species composition in soil and plant samples. **2019**, 95,	10
1496	Microbiomes of stony and soft deep-sea corals share rare core bacteria. **2019**, 7, 90	21
1495	Multi-year dynamics of fine-scale marine cyanobacterial populations are more strongly explained by phage interactions than abiotic, bottom-up factors. **2019**, 21, 2948-2963	21
1494	Stoichiometric controls of soil carbon and nitrogen cycling after long-term nitrogen and phosphorus addition in a mesic grassland in South Africa. **2019**, 135, 294-303	37
1493	Nutrient Sensing in CD11c Cells Alters the Gut Microbiota to Regulate Food Intake and Body Mass. **2019**, 30, 364-373.e7	17
1492	Sources and drivers of contamination along an urban tropical river (Ciliwung, Indonesia): Insights from microbial DNA, isotopes and water chemistry. **2019**, 682, 382-393	6
1491	The development and ecology of the Japanese macaque gut microbiome from weaning to early adolescence in association with diet. **2019**, 81, e22980	9
1490	A longitudinal big data approach for precision health. **2019**, 25, 792-804	183

1489	Bacterial Insights into the Formation of Opaline Stromatolites from the Chimalacatepec Lava Tube System, Mexico. **2019**, 36, 694-704	1
1488	Evaluating the Effect of QIIME Balanced Default Parameters on Metataxonomic Analysis Workflows With a Mock Community. **2019**, 10, 1084	4
1487	Habitat fragmentation is associated with dietary shifts and microbiota variability in common vampire bats. **2019**, 9, 6508-6523	29
1486	Influence of operation mode and wastewater strength on aerobic granulation at pilot scale: Startup period, granular sludge characteristics, and effluent quality. **2019**, 160, 81-96	34
1485	Spatial Gradients of Fungal Abundance and Ecology throughout a Damp Building. **2019**, 6, 329-333	11
1484	Bacterial succession and functional diversity during vermicomposting of the white grape marc Vitis vinifera v. Albariô. **2019**, 9, 7472	18
1483	Vaginal microbiota and mucosal pharmacokinetics of tenofovir in healthy women using tenofovir and tenofovir/levonorgestrel vaginal rings. **2019**, 14, e0217229	9
1482	Composition and stability of the vervet monkey milk microbiome. **2019**, 81, e22982	3
1481	Use of a filter cartridge combined with intra-cartridge bead-beating improves detection of microbial DNA from water samples. **2019**, 10, 1142-1156	13
1480	Fecal microbiota dysbiosis in macaques and humans within a shared environment. **2019**, 14, e0210679	4
1479	Development of a Blocking Primer to Inhibit the PCR Amplification of the 18S rDNA Sequences of and Its Efficacy in. **2019**, 10, 830	4
1478	Rethinking gut microbiome residency and the Enterobacteriaceae in healthy human adults. **2019**, 13, 2306-2318	40
1477	Bioinformatics matters: The accuracy of plant and soil fungal community data is highly dependent on the metabarcoding pipeline. **2019**, 41, 23-33	82
1476	Source Environments of the Microbiome in Perennially Ice-Covered Lake Untersee, Antarctica. **2019** , 10, 1019	14
1475	Comparison of Two Process Schemes Combining Hydrothermal Treatment and Acidogenic Fermentation of Source-Separated Organics. **2019**, 24,	6
1474	Comparative genomics of Bifidobacterium species isolated from marmosets and humans. **2019**, 81, e983	11
1473	Differences in resource use lead to coexistence of seed-transmitted microbial populations. **2019**, 9, 6648	5
1472	Bacterial succession and co-occurrence patterns of an enriched marine microbial community during light crude oil degradation in a batch reactor. **2019**, 127, 495-507	12

1471	The Water Microbiome Through a Pilot Scale Advanced Treatment Facility for Direct Potable Reuse. **2019**, 10, 993	18
1470	Small to modest impact of social group on the gut microbiome of wild Costa Rican capuchins in a seasonal forest. **2019**, 81, e22985	6
1469	Microbiome: Current Status and Future Applications. **2019**, 213-232	0
1468	Periodontal Health and Oral Microbiota in Patients with Rheumatoid Arthritis. **2019**, 8,	38
1467	Sex-specific effects of microbiome perturbations on cerebral A□amyloidosis and microglia phenotypes. **2019**, 216, 1542-1560	93
1466	Amphibian skin fungal communities vary across host species and do not correlate with infection by a pathogenic fungus. **2019**, 21, 2905-2920	7
1465	Tree diversity is not always a strong driver of soil microbial diversity: a 7-yr-old diversity experiment with trees. **2019**, 10, e02685	7
1464	No guts, no glory: Gut content metabarcoding unveils the diet of a flower-associated coastal sage scrub predator. **2019**, 10, e02712	4
1463	The immune response of the scallop Argopecten purpuratus is associated with changes in the host microbiota structure and diversity. **2019**, 91, 241-250	5
1462	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. **2019**, 10, 2200	151
1461	Effects of H:CO ratio and H supply fluctuation on methane content and microbial community composition during in-situ biological biogas upgrading. **2019**, 12, 104	45
1460	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. **2019**, 20,	19
1459	Airway response to respiratory syncytial virus has incidental antibacterial effects. **2019**, 10, 2218	19
1458	Skin Microbiome Differences in Atopic Dermatitis and Healthy Controls in Egyptian Children and Adults, and Association with Serum Immunoglobulin E. **2019**, 23, 247-260	9
1457	Household composition and the infant fecal microbiome: The INSPIRE study. **2019**, 169, 526-539	15
1456	Bacterial communities protect the alga Microchloropsis salina from grazing by the rotifer Brachionus plicatilis. **2019**, 40, 101500	9
1455	Spatial vs. temporal controls over soil fungal community similarity at continental and global scales. **2019**, 13, 2082-2093	22
1454	Parallel sequencing of porA reveals a complex pattern of Campylobacter genotypes that differs between broiler and broiler breeder chickens. **2019**, 9, 6204	8

1453	Bacterial and Fungal Endophytic Microbiomes of. **2019**, 85,	31
1452	Data of metal and microbial analyses from anaerobic co-digestion of organic and mineral wastes. **2019**, 24, 103934	5
1451	Diesel uptake by an indigenous microbial consortium isolated from sediments of the Southern Gulf of Mexico: Emulsion characterisation. **2019**, 250, 849-855	9
1450	Bacterial community structure and function distinguish gut sites in captive red-shanked doucs (Pygathrix nemaeus). **2019**, 81, e22977	6
1449	A Forward Chemical Genetic Screen Reveals Gut Microbiota Metabolites That Modulate Host Physiology. **2019**, 177, 1217-1231.e18	134
1448	Exploring the emerging role of the microbiome in cancer immunotherapy. **2019**, 7, 108	134
1447	Extracellular DNA in Monochloraminated Drinking Water and Its Influence on DNA-Based Profiling of a Microbial Community. **2019**, 6, 306-312	13
1446	Variations in microbiome composition of sewer biofilms due to ferrous and ferric iron dosing. **2019**, 5, 1595293	2
1445	Microbiomes in Ground Water and Alternative Irrigation Water, and Spinach Microbiomes Impacted by Irrigation with Different Types of Water. **2019**, 3, 137-147	10
1444	Does exercise impact gut microbiota composition in men receiving androgen deprivation therapy for prostate cancer? A single-blinded, two-armed, randomised controlled trial. **2019**, 9, e024872	6
1443	Microbial community shifts in the oxic-settling-anoxic process in response to changes to sludge interchange ratio. **2019**, 5, e01517	9
1442	Age-related analysis of the gut microbiome in a purebred dog colony. **2019**, 366,	9
1441	Metagenomic analysis of isolation methods of a targeted microbe, Campylobacter jejuni, from chicken feces with high microbial contamination. **2019**, 7, 67	10
1440	Success in Academic Surgery: Basic Science. **2019**,	0
1439	One-locus-several-primers: A strategy to improve the taxonomic and haplotypic coverage in diet metabarcoding studies. **2019**, 9, 4603-4620	29
1438	New Insights Into Nematode DNA-metabarcoding as Revealed by the Characterization of Artificial and Spiked Nematode Communities. **2019**, 11, 52	19
1437	Novel insights into plant-associated archaea and their functioning in arugula (Mill.). **2019**, 19, 39-48	26
1436	Impact of Warming on Greenhouse Gas Production and Microbial Diversity in Anoxic Peat From a -Dominated Bog (Grand Rapids, Minnesota, United States). **2019**, 10, 870	27

1435	Man against machine: Do fungal fruitbodies and eDNA give similar biodiversity assessments across broad environmental gradients?. **2019**, 233, 201-212	29
1434	Controlling intestinal colonization of high-risk haematology patients with ESBL-producing Enterobacteriaceae: a randomized, placebo-controlled, multicentre, Phase II trial (CLEAR). **2019**, 74, 2065-2074	5
1433	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. **2019**, 4,	11
1432	Magnetite doped granular activated carbon as an additive for high-performance anaerobic digestion. **2019**, 2, 377-384	8
1431	Growth Characteristics and Thermodynamics of Syntrophic Acetate Oxidizers. **2019**, 53, 5512-5520	32
1430	ANCHOR: a 16S rRNA gene amplicon pipeline for microbial analysis of multiple environmental samples. **2019**, 21, 2440-2468	15
1429	Invasion genetics from eDNA and thousands of larvae: A targeted metabarcoding assay that distinguishes species and population variation of zebra and quagga mussels. **2019**, 9, 3515-3538	22
1428	Less biomass and intracellular glutamate in anodic biofilms lead to efficient electricity generation by microbial fuel cells. **2019**, 12, 72	10
1427	Coupling growth kinetics modeling with machine learning reveals microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process. **2019**, 7, 65	13
1426	Integrated Analysis of Human Milk Microbiota With Oligosaccharides and Fatty Acids in the CHILD Cohort. **2019**, 6, 58	42
1425	Soil microbiome analysis in an ESCA diseased vineyard. **2019**, 135, 60-70	13
1424	Exposure to a Healthy Gut Microbiome Protects Against Reproductive and Metabolic Dysregulation in a PCOS Mouse Model. **2019**, 160, 1193-1204	31
1423	Habitat-dependent composition of bacterial and fungal communities in biological soil crusts from Oman. **2019**, 9, 6468	16
1422	Oral probiotics reduce halitosis in patients wearing orthodontic braces: a randomized, triple-blind, placebo-controlled trial. **2019**, 13, 036010	25
1421	Identification and Characterization of the Core Rice Seed Microbiome. **2019**, 3, 148-157	23
1420	The bumble bee microbiome increases survival of bees exposed to selenate toxicity. **2019**, 21, 3417	19
1419	Colonization of the human gut by bovine bacteria present in Parmesan cheese. **2019**, 10, 1286	26
1418	A different suite: The assemblage of distinct fungal communities in water-damaged units of a poorly-maintained public housing building. **2019**, 14, e0213355	11

1417	Cervicovaginal microbiota and local immune response modulate the risk of spontaneous preterm delivery. **2019**, 10, 1305	130
1416	PHAGE Study: Effects of Supplemental Bacteriophage Intake on Inflammation and Gut Microbiota in Healthy Adults. **2019**, 11,	59
1415	Recruit symbiosis establishment and Symbiodiniaceae composition influenced by adult corals and reef sediment. **2019**, 38, 405-415	12
1414	Molecular Heterogeneity in Large-Scale Biological Data: Techniques and Applications. **2019**, 2, 39-67	0
1413	Using a soil bacterial species balance index to estimate potato crop productivity. **2019**, 14, e0214089	14
1412	New Insights into Sediment Transport in Interconnected River-Lake Systems Through Tracing Microorganisms. **2019**, 53, 4099-4108	21
1411	Vaginal Glycogen, Not Estradiol, Is Associated With Vaginal Bacterial Community Composition in Black Adolescent Women. **2019**, 65, 130-138	8
1410	Fate of CMY-2-Encoding Plasmids Introduced into the Human Fecal Microbiota by Exogenous. **2019**, 63,	10
1409	Environmental filtering determines family-level structure of sulfate-reducing microbial communities in subsurface marine sediments. **2019**, 13, 1920-1932	24
1408	Biotic filtering of endophytic fungal communities in Bromus tectorum. **2019**, 189, 993-1003	7
1407	Understanding and overcoming the pitfalls and biases of next-generation sequencing (NGS) methods for use in the routine clinical microbiological diagnostic laboratory. **2019**, 38, 1059-1070	74
1406	Disease Incidence in Sugar Beet Fields Is Correlated with Microbial Diversity and Distinct Biological Markers. **2019**, 3, 22-30	18
1405	Microbial communities in hummingbird feeders are distinct from floral nectar and influenced by bird visitation. **2019**, 286, 20182295	7
1404	Calour: an Interactive, Microbe-Centric Analysis Tool. **2019**, 4,	20
1403	Pilot Study of Vaginal Microbiome Using QIIME 2□in Women With Gynecologic Cancer Before and After Radiation Therapy. **2019**, 46, E48-E59	7
1402	Intestinal Serum amyloid A suppresses systemic neutrophil activation and bactericidal activity in response to microbiota colonization. **2019**, 15, e1007381	32
1401	'RA and the microbiome: do host genetic factors provide the link?. **2019**, 99, 104-115	28
1400	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. **2019**, 10, 69	23

1399	Production of Naturally Aminobutyric Acid-Enriched Cheese Using the Dairy Strains 84C and DSM 32386. **2019**, 10, 93	15
1398	Host genetics and diet composition interact to modulate gut microbiota and predisposition to metabolic syndrome in spontaneously hypertensive stroke-prone rats. **2019**, 33, 6748-6766	9
1397	Relative stability of the Pocillopora acuta microbiome throughout a thermal stress event. **2019**, 38, 373-386	20
1396	Airborne microbial transport limitation to isolated Antarctic soil habitats. **2019**, 4, 925-932	51
1395	The Indoor-Air Microbiota of Pig Farms Drives the Composition of the Pig Farmers' Nasal Microbiota in a Season-Dependent and Farm-Specific Manner. **2019**, 85,	15
1394	Crop Residues in Wheat-Oilseed Rape Rotation System: a Pivotal, Shifting Platform for Microbial Meetings. **2019**, 77, 931-945	21
1393	The Potential Role of spp. in Sulfur Oxidation and Acid Generation in Circum-Neutral Mine Tailings Reservoirs. **2019**, 10, 297	14
1392	Metformin-induced changes of the gut microbiota in healthy young men: results of a non-blinded, one-armed intervention study. **2019**, 62, 1024-1035	79
1391	Linking nano-ZnO contamination to microbial community profiling in sanitary landfill simulations. **2019**, 26, 13580-13591	2
1390	Incorporating microbial community data with machine learning techniques to predict feed substrates in microbial fuel cells. **2019**, 133, 64-71	32
1389	A review on the plant microbiome: Ecology, functions, and emerging trends in microbial application. **2019**, 19, 29-37	444
1388	Long-term seasonal and interannual variability of marine aerobic anoxygenic photoheterotrophic bacteria. **2019**, 13, 1975-1987	12
1387	Heritable variation in bleaching responses and its functional genomic basis in reef-building corals (Orbicella faveolata). **2019**, 28, 2238-2253	23
1386	Species-specific enhancement of enterohemorrhagic E. coli pathogenesis mediated by microbiome metabolites. **2019**, 7, 43	64
1385	Invasion genetics of the silver carp Hypophthalmichthys molitrix across North America: Differentiation of fronts, introgression, and eDNA metabarcode detection. **2019**, 14, e0203012	19
1384	Chemical Dispersant Enhances Microbial Exopolymer (EPS) Production and Formation of Marine Oil/Dispersant Snow in Surface Waters of the Subarctic Northeast Atlantic. **2019**, 10, 553	8
1383	Gut microbiota dysbiosis in a cohort of patients with psoriasis. **2019**, 181, 1287-1295	59
1382	A Risky Business? Habitat and Social Behavior Impact Skin and Gut Microbiomes in Caribbean Cleaning Gobies. **2019**, 10, 716	13

1381	What is new and relevant for sequencing-based microbiome research? A mini-review. **2019**, 19, 105-112	58
1380	Characterization of the Blood Microbiota in Korean Females with Rosacea. **2019**, 235, 255-259	5
1379	Shifts in Soil Bacterial Communities as a Function of Carbon Source Used During Anaerobic Soil Disinfestation. **2019**, 6,	18
1378	Longitudinal tracking and quantification of individual Plasmodium falciparum clones in complex infections. **2019**, 9, 3333	17
1377	Intensity of Nosema ceranae infection is associated with specific honey bee gut bacteria and weakly associated with gut microbiome structure. **2019**, 9, 3820	42
1376	Identification of Nitrogen-Fixing Associated With Roots of Field-Grown Sorghum by Metagenome and Proteome Analyses. **2019**, 10, 407	35
1375	Patterns of community assembly in the developing chicken microbiome reveal rapid primary succession. **2019**, 8, e00821	42
1374	Ultrahigh-Throughput Multiplexing and Sequencing of >500-Base-Pair Amplicon Regions on the Illumina HiSeq 2500 Platform. **2019**, 4,	54
1373	Microbial community composition and network analyses in arid soils of the Patagonian Monte under grazing disturbance reveal an important response of the community to soil particle size. **2019**, 138, 223-232	19
1372	Bioinformatics applied to biotechnology: A review towards bioenergy research. **2019**, 123, 195-224	14
1371	Prokaryotic Community Structure of Long-Term Fertilization Field Andisols in Central Japan. **2019**, 8,	
1370	A census-based estimate of Earth's bacterial and archaeal diversity. **2019**, 17, e3000106	78
1369	16S rRNA sequence embeddings: Meaningful numeric feature representations of nucleotide sequences that are convenient for downstream analyses. **2019**, 15, e1006721	12
1368	Fungal Biodiversity of the Most Common Types of Polish Soil in a Long-Term Microplot Experiment. **2019**, 10, 6	23
1367	Urbanization Altered Bacterial and Archaeal Composition in Tidal Freshwater Wetlands Near Washington DC, USA, and Buenos Aires, Argentina. **2019**, 7,	2
1366	Species identity dominates over environment in shaping the microbiota of small mammals. **2019**, 22, 826-837	45
1365	Impact of a bathing tradition on shared gut microbe among Japanese families. **2019**, 9, 4380	10
1364	Effect of Dietary Carbohydrate-to-Protein Ratio on Gut Microbiota in Atlantic Salmon (). **2019**, 9,	14

1363	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. **2019**, 7, 50	77
1362	A New Method to Correct for Habitat Filtering in Microbial Correlation Networks. **2019**, 10, 585	11
1361	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of Clostridioides (Clostridium) difficile, despite cellular susceptibility to its toxins. **2019**, 58, 53-72	13
1360	Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. **2019**, 9, 5821	240
1359	Antibiotic-resistant bacteria on personal devices in hospital intensive care units: Molecular approaches to quantifying and describing changes in the bacterial community of personal mobile devices. **2019**, 40, 717-720	4
1358	Exploring the microbiota and metabolites of traditional rice beer varieties of Assam and their functionalities. **2019**, 9, 174	11
1357	Combined Deterministic and Stochastic Processes Control Microbial Succession in Replicate Granular Biofilm Reactors. **2019**, 53, 4912-4921	22
1356	Evaluation of the bacterial ocular surface microbiome in clinically normal horses before and after treatment with topical neomycin-polymyxin-bacitracin. **2019**, 14, e0214877	10
1355	Influence of Urbanization on Epiphytic Bacterial Communities of the Tree Leaves in a Biennial Study. **2019**, 10, 675	21
1354	Comprehensive biodiversity analysis via ultra-deep patterned flow cell technology: a case study of eDNA metabarcoding seawater. **2019**, 9, 5991	46
1353	Bioremediation of chlorophenol-contaminated sawmill soil using pilot-scale bioreactors under consecutive anaerobic-aerobic conditions. **2019**, 227, 670-680	20
1352	Comammox Nitrospira are the dominant ammonia oxidizers in a mainstream low dissolved oxygen nitrification reactor. **2019**, 157, 396-405	104
1351	Submerged aerobic granular sludge membrane bioreactor (AGMBR): Organics and nutrients (nitrogen and phosphorus) removal. **2019**, 6, 260-267	19
1350	Bacterial colonization and antimicrobial resistance genes in neonatal enteral feeding tubes. **2019**, 95,	3
1349	What's Normal? Microbiomes in Human Milk and Infant Feces Are Related to Each Other but Vary Geographically: The INSPIRE Study. **2019**, 6, 45	84
1348	Microbiome dynamics during cast ageing in the earthworm Aporrectodea caliginosa. **2019**, 139, 56-63	20
1347	Combined Effects of Three High-Energy Charged Particle Beams Important for Space Flight on Brain, Behavioral and Cognitive Endpoints in B6D2F1 Female and Male Mice. **2019**, 10, 179	30
1346	A place for taxonomic profiling in the study of the coral prokaryotic microbiome. **2019**, 366,	5

1345	Sediment microbial assemblage structure is modified by marine polychaete gut passage. **2019**, 95,	5
1344	A guide to the application of Hill numbers to DNA-based diversity analyses. **2019**, 19, 804-817	51
1343	Intestinal Epithelial Cells and the Microbiome Undergo Swift Reprogramming at the Inception of Colonic Citrobacter rodentium Infection. **2019**, 10,	26
1342	Marker genes as predictors of shared genomic function. **2019**, 20, 268	1
1341	Wildfire severity reduces richness and alters composition of soil fungal communities in boreal forests of western Canada. **2019**, 25, 2310-2324	34
1340	Darkening of the Greenland Ice Sheet: Fungal Abundance and Diversity Are Associated With Algal Bloom. **2019**, 10, 557	32
1339	Priority effects of wheat seed endophytes on a rhizosphere symbiosis. **2019**, 78, 19-31	16
1338	16S rRNA amplicon sequencing characterization of caecal microbiome composition of broilers and free-range slow-growing chickens throughout their productive lifespan. **2019**, 9, 2506	54
1337	Wastewater microbial community structure and functional traits change over short timescales. **2019**, 662, 779-785	21
1336	Comparison of Small Gut and Whole Gut Microbiota of First-Degree Relatives With Adult Celiac Disease Patients and Controls. **2019**, 10, 164	46
1335	Environmental DNA metabarcoding of wild flowers reveals diverse communities of terrestrial arthropods. **2019**, 9, 1665-1679	49
1334	Adaptive signatures in thermal performance of the temperate coral. **2019**, 222,	16
1333	Offspring Microbiomes Differ Across Breeding Sites in a Panmictic Species. **2019**, 10, 35	22
1332	Denitrification performance and microbial versatility in response to different selection pressures. **2019**, 281, 72-83	94
1331	Compositional changes to the ileal microbiome precede the onset of spontaneous ileitis in SHIP deficient mice. **2019**, 10, 578-598	21
1330	Potential biomarkers to predict outcome of faecal microbiota transfer for recurrent Clostridioides difficile infection. **2019**, 51, 944-951	6
1329	Rare gut microbiota associated with breeding success, hormone metabolites and ovarian cycle phase in the critically endangered eastern black rhino. **2019**, 7, 27	35
1328	Impact of routine sanitation on the microbiomes in a fresh produce processing facility. **2019**, 294, 31-41	13

1327	Microbial basis of Fusarium wilt suppression by Allium cultivation. **2019**, 9, 1715	14
1326	Helminth-Based Product and the Microbiome of Mice with Lupus. **2019**, 4,	13
1325	Performance of Microbiome Sequence Inference Methods in Environments with Varying Biomass. **2019**, 4,	60
1324	Longitudinal Microbiome Composition and Stability Correlate with Increased Weight and Length of Very-Low-Birth-Weight Infants. **2019**, 4,	29
1323	Metabarcoding free-living marine nematodes using curated 18S and CO1 reference sequence databases for species-level taxonomic assignments. **2019**, 9, 1211-1226	39
1322	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. **2019**, 231, 56-62	18
1321	Interactions in self-assembled microbial communities saturate with diversity. **2019**, 13, 1602-1617	26
1320	Effects of a Saccharomyces cerevisiae fermentation product on liver abscesses, fecal microbiome, and resistome in feedlot cattle raised without antibiotics. **2019**, 9, 2559	13
1319	The tea leaf microbiome shows specific responses to chemical pesticides and biocontrol applications. **2019**, 667, 33-40	26
1318	Equine Fecal Microbiota Changes Associated With Anthelmintic Administration. **2019**, 77, 98-106	13
1317	Differences in Soil Bacterial Community Compositions in Paddy Fields under Organic and Conventional Farming Conditions. **2019**, 34, 108-111	6
1316	Successional Dynamics and Seascape-Level Patterns of Microbial Communities on the Canopy-Forming Kelps and. **2019**, 10, 346	34
1315	Lupus nephritis is linked to disease-activity associated expansions and immunity to a gut commensal. **2019**, 78, 947-956	126
1314	SLIM: a flexible web application for the reproducible processing of environmental DNA metabarcoding data. **2019**, 20, 88	29
1313	Composition and Variation of the Human Milk Microbiota Are Influenced by Maternal and Early-Life Factors. **2019**, 25, 324-335.e4	214
1312	The Relationship between Platelet Count and Host Gut Microbiota: A Population-Based Retrospective Cross-Sectional Study. **2019**, 8,	3
1311	Co-digestion of organic and mineral wastes for enhanced biogas production: Reactor performance and evolution of microbial community and function. **2019**, 87, 313-325	18
1310	Prebiotic effect of two grams of lactulose in healthy Japanese women: a randomised, double-blind, placebo-controlled crossover trial. **2019**, 10, 629-639	11

1309	-fermented rice bran and rice bran supplementation affects the gut microbiome and metabolome. **2019**, 10, 823-839	10
1308	Association between blood omega-3 polyunsaturated fatty acids and the gut microbiota among breast cancer survivors. **2019**, 10, 751-758	13
1307	The neuroactive potential of the human gut microbiota in quality of life and depression. **2019**, 4, 623-632	651
1306	and increased gut microbiota diversity and functionality, and mitigated , in a mouse model. **2019**, 10, 413-424	10
1305	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. **2019**, 4,	11
1304	Impaired glucose metabolism and altered gut microbiome despite calorie restriction of ob/ob mice. **2019**, 1, 11	5
1303	Rectal Microbiome Alterations Associated With Oral Human Immunodeficiency Virus Pre-Exposure Prophylaxis. **2019**, 6, ofz463	4
1302	Augmentation of Granular Anaerobic Sludge with Algalytic Bacteria Enhances Methane Production from Microalgal Biomass. **2019**, 5, 88	2
1301	Microbial Diversity of the Red Sea Urchin Loxechinus albus during Controlled Farming in Puerto Montt, Chile, Using 16S rRNA Gene Amplicon Sequencing. **2019**, 8,	2
1300	Therapeutic Effect of Bifidobacterium Administration on Experimental Autoimmune Myasthenia Gravis in Lewis Rats. **2019**, 10, 2949	7
1299	Anterior Nares Diversity and Pathobionts Represent Sinus Microbiome in Chronic Rhinosinusitis. **2019**, 4,	27
1298	The Impact of Soil-Applied Biochars From Different Vegetal Feedstocks on Durum Wheat Plant Performance and Rhizospheric Bacterial Microbiota in Low Metal-Contaminated Soil. **2019**, 10, 2694	13
1297	Impact of Sample Preservation and Manipulation on Insect Gut Microbiome Profiling. A Test Case With Fruit Flies (Diptera, Tephritidae). **2019**, 10, 2833	12
1296	Exploring the Archaeome: Detection of Archaeal Signatures in the Human Body. **2019**, 10, 2796	44
1295	Looking like the locals - gut microbiome changes post-release in an endangered species. **2019**, 1, 8	21
1294	Global Comparison of the Bacterial Communities of Bilge Water, Boat Surfaces, and External Port Water. **2019**, 85,	4
1293	Butyrogenic bacteria after acute graft-versus-host disease (GVHD) are associated with the development of steroid-refractory GVHD. **2019**, 3, 2866-2869	21
1292	Methods in microbiome research: Past, present, and future. **2019**, 33, 101498	6

1291	The Critical Importance of Rhodoliths in the Life Cycle Completion of Both Macro- and Microalgae, and as Holobionts for the Establishment and Maintenance of Marine Biodiversity. **2019**, 5,	21
1290	Not all birds have a single dominantly expressed MHC-I gene: Transcription suggests that siskins have many highly expressed MHC-I genes. **2019**, 9, 19506	8
1289	Microbiome profiling of the onion thrips, Thrips tabaci Lindeman (Thysanoptera: Thripidae). **2019**, 14, e0223281	5
1288	Uncovering the Diversity and Activity of Methylotrophic Methanogens in Freshwater Wetland Soils. **2019**, 4,	12
1287	Prokaryotic taxa play keystone roles in the soil microbiome associated with woody perennial plants in the genus. **2019**, 9, 11102-11111	3
1286	Comparative analysis of microbiota along the length of the gastrointestinal tract of two tree squirrel species (and) living in sympatry. **2019**, 9, 13344-13358	4
1285	Mixed-Cropping Between Field Pea Varieties Alters Root Bacterial and Fungal Communities. **2019**, 9, 16953	6
1284	Enzymatically Digested Food Waste Altered Fecal Microbiota But Not Meat Quality and Carcass Characteristics of Growing-Finishing Pigs. **2019**, 9,	1
1283	Geography, seasonality, and host-associated population structure influence the fecal microbiome of a genetically depauparate Arctic mammal. **2019**, 9, 13202-13217	8
1282	Characterization and comprehensive analysis of the ecological interaction networks of bacterial communities in Paullinia cupana var. sorbilis by 16S rRNA gene metabarcoding. **2019**, 35, 182	2
1281	Intracellular Infection of Diverse Diatoms by an Evolutionary Distinct Relative of the Fungi. **2019**, 29, 4093-4101.e4	12
1280	Temporal evolution of the microbiome, immune system and epigenome with disease progression in ALS mice. **2019**, 13,	32
1279	The effects of soil phosphorus content on plant microbiota are driven by the plant phosphate starvation response. **2019**, 17, e3000534	58
1278	Whole-Virome Analysis Sheds Light on Viral Dark Matter in Inflammatory Bowel Disease. **2019**, 26, 764-778.e5	120
1277	Sulfide level in municipal sludge digesters affects microbial community response to long-chain fatty acid loads. **2019**, 12, 259	10
1276	Characteristics of Wetting-Induced Bacteriophage Blooms in Biological Soil Crust. **2019**, 10,	23
1275	Quantitative stable isotope probing with H218O to measure taxon-specific microbial growth. **2019**, 4, 1503	2
1274	High-resolution micro-epidemiology of parasite spatial and temporal dynamics in a high malaria transmission setting in Kenya. **2019**, 10, 5615	7

1273	Microbiome differences in disease-resistant vs. susceptible Acropora corals subjected to disease challenge assays. **2019**, 9, 18279	24
1272	Effects of disease, antibiotic treatment and recovery trajectory on the microbiome of farmed seabass (Dicentrarchus labrax). **2019**, 9, 18946	27
1271	Tailings microbial community profile and prediction of its functionality in basins of tungsten mine. **2019**, 9, 19596	14
1270	ROR�Treg to Th17 ratios correlate with susceptibility to Giardia infection. **2019**, 9, 20328	10
1269	Annual replication is essential in evaluating the response of the soil microbiome to the genetic modification of maize in different biogeographical regions. **2019**, 14, e0222737	3
1268	Linking the effects of helminth infection, diet and the gut microbiota with human whole-blood signatures. **2019**, 15, e1008066	11
1267	Characteristics of Bacterial Community and Function in Paddy Soil Profile around Antimony Mine and Its Response to Antimony and Arsenic Contamination. **2019**, 16,	10
1266	Grapevine Phyllosphere Community Analysis in Response to Elicitor Application against Powdery Mildew. **2019**, 7,	9
1265	Exogenous and endogenous microbiomes of wild-caught Phormia regina (Diptera: Calliphoridae) flies from a suburban farm by 16S rRNA gene sequencing. **2019**, 9, 20365	9
1264	Distinct cellular roles for PDCD10 define a gut-brain axis in cerebral cavernous malformation. **2019**, 11,	25
1263	AMON: annotation of metabolite origins via networks to integrate microbiome and metabolome data. **2019**, 20, 614	16
1262	Environmental Filtering Drives the Assembly of Habitat Generalists and Specialists in the Coastal Sand Microbial Communities of Southern China. **2019**, 7,	11
1261	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. **2019**, 7,	4
1260	Human Endometrial Microbiota at Term of Normal Pregnancies. **2019**, 10,	22
1259	Compositional homogeneity in the pathobiome of a new, slow-spreading coral disease. **2019**, 7, 139	20
1258	Of microbes and mange: consistent changes in the skin microbiome of three canid species infected with Sarcoptes scabiei mites. **2019**, 12, 488	11
1257	Early exposure to antibiotics in the neonatal intensive care unit alters the taxonomic and functional infant gut microbiome. **2021**, 34, 3335-3343	3
1256	Characterization of the Mycobiome of the Seagrass, , Reveals Putative Associations With Marine Chytrids. **2019**, 10, 2476	16

1255	Resolution and Cooccurrence Patterns of Gardnerella leopoldii, G. swidsinskii, G. piotii, and G. vaginalis within the Vaginal Microbiome. **2019**, 87,	28
1254	Suppression treatment differentially influences the microbial community and the occurrence of broad host range plasmids in the rhizosphere of the model cover crop Avena sativa L. **2019**, 14, e0223600	5
1253	Inhibition of Rumen Protozoa by Specific Inhibitors of Lysozyme and Peptidases. **2019**, 10, 2822	4
1252	Crop Sorghum Ensiled With Unsalable Vegetables Increases Silage Microbial Diversity. **2019**, 10, 2599	6
1251	Early-life programming of mesenteric lymph node stromal cell identity by the lymphotoxin pathway regulates adult mucosal immunity. **2019**, 4,	15
1250	A Comparison of Biopsy and Mucosal Swab Specimens for Examining the Microbiota of Upper Gastrointestinal Carcinoma. **2019**, 28, 2030-2037	8
1249	Urinary Microbiome Evaluation in Patients Presenting with Hematuria with a Focus on Exposure to Tobacco Smoke. **2019**, 11, 359-367	5
1248	Diversity-Stability Dynamics of the Amphibian Skin Microbiome and Susceptibility to a Lethal Viral Pathogen. **2019**, 10, 2883	18
1247	Intestinal Flora Disruption and Novel Biomarkers Associated With Nasopharyngeal Carcinoma. **2019** , 9, 1346	8
1246	The subway microbiome: seasonal dynamics and direct comparison of air and surface bacterial communities. **2019**, 7, 160	20
1245	Associations of prenatal exposure to polybrominated diphenyl ethers and polychlorinated biphenyls with long-term gut microbiome structure: a pilot study. **2019**, 3,	14
1244	Applying indirect open-circuit calorimetry to study energy expenditure in gnotobiotic mice harboring different human gut microbial communities. **2019**, 7, 158	2
1243	Enteral Nutrition in Pediatric Patients Undergoing Hematopoietic SCT Promotes the Recovery of Gut Microbiome Homeostasis. **2019**, 11,	33
1242	The Effect of Hops (L.) Extract Supplementation on Weight Gain, Adiposity and Intestinal Function in Ovariectomized Mice. **2019**, 11,	10
1241	Systematic processing of ribosomal RNA gene amplicon sequencing data. **2019**, 8,	26
1240	Impact of occupational exposure on human microbiota. **2019**, 19, 86-91	5
1239	Changes in Microbiota Across Developmental Stages of , an Invasive Mosquito Vector in Europe: Indications for Microbiota-Based Control Strategies. **2019**, 10, 2832	16
1238	Synergistic Effects of Probiotics and Phytobiotics on the Intestinal Microbiota in Young Broiler Chicken. **2019**, 7,	27

1237	Selection of microbial biomarkers with genetic algorithm and principal component analysis. **2019**, 20, 413	5
1236	Examining transmission of gut bacteria to preserved carcass via anal secretions in Nicrophorus defodiens. **2019**, 14, e0225711	6
1235	Physiologic intestinal F-FDG uptake is associated with alteration of gut microbiota and proinflammatory cytokine levels in breast cancer. **2019**, 9, 18273	2
1234	Disruption of the Gut Microbiome Increases the Risk of Periprosthetic Joint Infection in Mice. **2019**, 477, 2588-2598	14
1233	Host-mediated microbiome engineering (HMME) of drought tolerance in the wheat rhizosphere. **2019**, 14, e0225933	37
1232	Culture-Dependent and -Independent Analyses Reveal the Diversity, Structure, and Assembly Mechanism of Benthic Bacterial Community in the Ross Sea, Antarctica. **2019**, 10, 2523	6
1231	Profiling the Oral Microbiome and Plasma Biochemistry of Obese Hyperglycemic Subjects in Qatar. **2019**, 7,	7
1230	Effects of HIV viremia on the gastrointestinal microbiome of young MSM. **2019**, 33, 793-804	17
1229	From Genes to Nitrogen Removal: Determining the Impacts of Poultry Industry Wastewater on Tidal Creek Denitrification. **2020**, 54, 146-157	8
1228	Microbial Community Predicts Functional Stability of Microbial Fuel Cells. **2020**, 54, 427-436	14
1227	Hermetia illucens in diets for zebrafish (Danio rerio): A study of bacterial diversity by using PCR-DGGE and metagenomic sequencing. **2019**, 14, e0225956	21
1226	Discordant transmission of bacteria and viruses from mothers to babies at birth. **2019**, 7, 156	35
1225	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. **2019**, 14, e0219235	7
1224	Differences in the intestinal microbiome of healthy children and patients with newly diagnosed Crohn's disease. **2019**, 9, 18880	43
1223	Bile acid metabolites control T17 and T cell differentiation. **2019**, 576, 143-148	310
1222	Modulation of JNK-1/ □catenin signaling by , inulin and their combination in 1,2-dimethylhydrazine-induced colon cancer in mice.. **2019**, 9, 29368-29383	12
1221	Rapid and Concomitant Gut Microbiota and Endocannabinoidome Response to Diet-Induced Obesity in Mice. **2019**, 4,	22
1220	Long-term impact of fecal transplantation in healthy volunteers. **2019**, 19, 312	24

1219	Sexual practices have a significant impact on the vaginal microbiota of women who have sex with women. **2019**, 9, 19749	14
1218	Soil Bacterial and Fungal Communities Exhibit Distinct Long-Term Responses to Disturbance in Temperate Forests. **2019**, 10, 2872	20
1217	Estimation of Fungal Diversity and Identification of Major Abiotic Drivers Influencing Fungal Richness and Communities in Northern Temperate and Boreal Quebec Forests. **2019**, 10, 1096	9
1216	In Silico and Experimental Evaluation of Primer Sets for Species-Level Resolution of the Vaginal Microbiota Using 16S Ribosomal RNA Gene Sequencing. **2019**, 219, 305-314	13
1215	The effects of metabolic syndrome, obesity, and the gut microbiome on load-induced osteoarthritis. **2019**, 27, 129-139	43
1214	Biological As(III) oxidation in biofilters by using native groundwater microorganisms. **2019**, 651, 93-102	31
1213	Alcohol consumption increases susceptibility to pneumococcal pneumonia in a humanized murine HIV model mediated by intestinal dysbiosis. **2019**, 80, 33-43	10
1212	The effect of rhizosphere microbes outweighs host plant genetics in reducing insect herbivory. **2019**, 28, 1801-1811	32
1211	High diversity of benthic bacterial and archaeal assemblages in deep-Mediterranean canyons and adjacent slopes. **2019**, 171, 154-161	8
1210	Gut microbial compositions mirror caste-specific diets in a major lineage of social insects. **2019**, 11, 196-205	13
1209	Microcosm experiments and kinetic modeling of glyphosate biodegradation in soils and sediments. **2019**, 658, 105-115	19
1208	Ectosymbiotic bacterial microbiota densely colonize the surface of thelastomatid nematodes in the gut of the wood-feeding cockroach Panesthia angustipennis. **2019**, 95,	6
1207	Distribution of antibiotic resistance genes in soils and crops. A field study in legume plants (Vicia faba L.) grown under different watering regimes. **2019**, 170, 16-25	48
1206	The Role of the Gut Microbiota in Sustained Weight Loss Following Roux-en-Y Gastric Bypass Surgery. **2019**, 29, 1259-1267	26
1205	Ecological impact evaluation by constructing in situ microcosm with porous ceramic arrowhead. **2019**, 219, 202-208	1
1204	The Vaginal Microbiome of Transgender Men. **2019**, 65, 199-207	10
1203	Planctomycetes in boreal and subarctic wetlands: diversity patterns and potential ecological functions. **2019**, 95,	55
1202	Initial microbial community of the neonatal stomach immediately after birth. **2019**, 10, 289-297	7

1201	Detecting Associations Between Ciliated Protists and Prokaryotes with Culture-Independent Single-Cell Microbiomics: a Proof-of-Concept Study. **2019**, 78, 232-242	10
1200	Extensive studies on the treatment of pulp mill wastewater using aerobic granular sludge (AGS) technology. **2019**, 359, 1175-1194	27
1199	Considerations When Designing a Microbiome Study: Implications for Nursing Science. **2019**, 21, 125-141	12
1198	The use of next generation sequencing for improving food safety: Translation into practice. **2019**, 79, 96-115	130
1197	Are We Overestimating Protistan Diversity in Nature?. **2019**, 27, 197-205	35
1196	Bacterial diversity in the marine sponge Halichondria panicea from Icelandic waters and host-specificity of its dominant symbiont "Candidatus Halichondribacter symbioticus". **2019**, 95,	13
1195	Composition of gut microbiota and its association with body mass index and lifestyle factors in a cohort of 7-18 years old children from the American Gut Project. **2019**, 14, e12480	63
1194	Mycobiome diversity: high-throughput sequencing and identification of fungi. **2019**, 17, 95-109	296
1193	Influence of the early bacterial biofilms developed on vats made with seven wood types on PDO Vastedda della valle del Bel�e cheese characteristics. **2019**, 291, 91-103	18
1192	The microbiome of Escherichia coli and culture-negative nonsevere clinical mastitis: Characterization and associations with linear score and milk production. **2019**, 102, 578-594	6
1191	Genome-wide association studies on the phyllosphere microbiome: Embracing complexity in host-microbe interactions. **2019**, 97, 164-181	43
1190	Responses of foraminifera communities to aquaculture-derived organic enrichment as revealed by environmental DNA metabarcoding. **2019**, 28, 1138-1153	13
1189	Bulk tank raw milk microbiota differs within and between farms: A moving goalpost challenging quality control. **2019**, 102, 1959-1971	39
1188	The Impact of Cholecystectomy on the Gut Microbiota: A Case-Control Study. **2019**, 8,	26
1187	Enzyme-Identified Phosphorus Limitation Linked to More Rapid Headloss Accumulation in Drinking Water Biofilters. **2019**, 53, 2027-2035	10
1186	Pollution from azithromycin-manufacturing promotes macrolide-resistance gene propagation and induces spatial and seasonal bacterial community shifts in receiving river sediments. **2019**, 123, 501-511	36
1185	Bioreactivity and Microbiome of Biodeposits from Filter-Feeding Bivalves. **2019**, 77, 343-357	12
1184	A great-ape view of the gut´microbiome. **2019**, 20, 195-206	30

1183	Impact of intramammary inoculation of inactivated Lactobacillus rhamnosus and antibiotics on the milk microbiota of water buffalo with subclinical mastitis. **2019**, 14, e0210204	6
1182	T Cell Acute Lymphoblastic Leukemia as a Consequence of Thymus Autonomy. **2019**, 202, 1137-1144	13
1181	Earthworms and cadmium - Heavy metal resistant gut bacteria as indicators for heavy metal pollution in soils?. **2019**, 171, 843-853	43
1180	Bacterial Dispersers along Preferential Flow Paths of a Clay Till Depth Profile. **2019**, 85,	4
1179	Fungal bioaugmentation of anaerobic digesters fed with lignocellulosic biomass: What to expect from anaerobic fungus Orpinomyces sp. **2019**, 277, 1-10	34
1178	Community dynamics of free-living and particle-attached bacteria following a reservoir Microcystis bloom. **2019**, 660, 501-511	49
1177	Using BEAN-counter to quantify genetic interactions from multiplexed barcode sequencing experiments. **2019**, 14, 415-440	8
1176	Longitudinal changes during pregnancy in gut microbiota and methylmercury biomarkers, and reversal of microbe-exposure correlations. **2019**, 172, 700-712	14
1175	Coupled virus - bacteria interactions and ecosystem function in an engineered microbial system. **2019**, 152, 264-273	16
1174	Invited Commentary: Improving the Accessibility of Human Microbiome Project Data Through Integration With R/Bioconductor. **2019**, 188, 1027-1030	2
1173	Antarctic Relic Microbial Mat Community Revealed by Metagenomics and Metatranscriptomics. **2019**, 7,	24
1172	Optimization of organics to nutrients (COD:N:P) ratio for aerobic granular sludge treating high-strength organic wastewater. **2019**, 650, 3168-3179	36
1171	Do soil bacterial communities respond differently to abrupt or gradual additions of copper?. **2019**, 95,	5
1170	High-throughput identification and diagnostics of pathogens and pests: Overview and practical recommendations. **2019**, 19, 47-76	47
1169	Promises and pitfalls of using high-throughput sequencing for diet analysis. **2019**, 19, 327-348	77
1168	Antibiotic resistance genes distribution in microbiomes from the soil-plant-fruit continuum in commercial Lycopersicon esculentum fields under different agricultural practices. **2019**, 652, 660-670	37
1167	The Interior Surfaces of Wooden Barrels Are an Additional Microbial Inoculation Source for Lambic Beer Production. **2019**, 85,	18
1166	Sputum Microbiome Is Associated with 1-Year Mortality after Chronic Obstructive Pulmonary Disease Hospitalizations. **2019**, 199, 1205-1213	62

1165	Gut bacterial and fungal communities in ground-dwelling beetles are associated with host food habit and habitat. **2019**, 13, 676-685	29
1164	Chlortetracycline Enhances Tonsil Colonization and Fecal Shedding of Multidrug-Resistant Serovar Typhimurium DT104 without Major Alterations to the Porcine Tonsillar and Intestinal Microbiota. **2019**, 85,	6
1163	Floral and Foliar Source Affect the Bee Nest Microbial Community. **2019**, 78, 506-516	26
1162	Towards Quantitative Microbiome Community Profiling Using Internal Standards. **2019**, 85,	27
1161	Bacterial diversity in the waterholes of the Kruger National Park: an eDNA metabarcoding approach. **2019**, 62, 229-242	2
1160	DiTaxa: nucleotide-pair encoding of 16S rRNA for host phenotype and biomarker detection. **2019**, 35, 2498-2500	8
1159	Analysis of the gut and gill microbiome of resistant and susceptible lines of rainbow trout (Oncorhynchus mykiss). **2019**, 86, 497-506	53
1158	Larger plants promote a greater diversity of symbiotic nitrogen-fixing soil bacteria associated with an Australian endemic legume. **2019**, 107, 977-991	29
1157	Glucomannan Hydrolysate Promotes Gut Proliferative Homeostasis and Extends Life Span in Drosophila melanogaster. **2019**, 74, 1549-1556	4
1156	Microbiota of sliced cooked ham packaged in modified atmosphere throughout the shelf life: Microbiota of sliced cooked ham in MAP. **2019**, 289, 200-208	23
1155	Rhythmicity of coastal marine picoeukaryotes, bacteria and archaea despite irregular environmental perturbations. **2019**, 13, 388-401	37
1154	Haloalkaliphilic microorganisms assist sulfide removal in a microbial electrolysis cell. **2019**, 363, 197-204	18
1153	Novel Cardinium strains in non-marine ostracod (Crustacea) hosts from natural populations. **2019**, 130, 406-415	7
1152	Potentials and pitfalls in the analysis of bipartite networks to understand plantmicrobe interactions in changing environments. **2019**, 33, 107-117	13
1151	The effect of sulfur dioxide addition at crush on the fungal and bacterial communities and the sensory attributes of Pinot gris wines. **2019**, 290, 1-14	19
1150	Genome analyses of uncultured TG2/ZB3 bacteria in 'Margulisbacteria' specifically attached to ectosymbiotic spirochetes of protists in the termite gut. **2019**, 13, 455-467	17
1149	Characterization of the skin and gill microbiomes of the farmed seabass (Dicentrarchus labrax) and seabream (Sparus aurata). **2019**, 500, 57-64	31
1148	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. **2019**, 13, 468-481	22

1147	An improved method for utilizing high-throughput amplicon sequencing to determine the diets of insectivorous animals. **2019**, 19, 176-190	49
1146	A review of methods and databases for metagenomic classification and assembly. **2019**, 20, 1125-1136	209
1145	Microbiome profiling reveals gut dysbiosis in a transgenic mouse model of Huntington's disease. **2020**, 135, 104268	70
1144	OBSOLETE: Bioinformatic Platforms for Metagenomics. **2020**,	
1143	Does birth mode modify associations of maternal pre-pregnancy BMI and gestational weight gain with the infant gut microbiome?. **2020**, 44, 23-32	19
1142	Associations among diet, the gastrointestinal microbiota, and negative emotional states in adults. **2020**, 23, 983-992	28
1141	Impact of chemotherapy on the association between fear of cancer recurrence and the gut microbiota in breast cancer survivors. **2020**, 85, 186-191	13
1140	Using Data Science for Medical Decision Making Case: Role of Gut Microbiome in Multiple Sclerosis. **2020**, 349-356	1
1139	Dynamic immunoglobulin responses to gut bacteria during inflammatory bowel disease. **2020**, 11, 405-420	24
1138	Elucidating the ecological networks in stone-dwelling microbiomes. **2020**, 22, 1467-1480	18
1137	Belowground microbial communities respond to water deficit and are shaped by decades of maize hybrid breeding. **2020**, 22, 889-904	6
1136	Modulation of cytokine patterns and microbiome during pregnancy in IBD. **2020**, 69, 473-486	31
1135	Effects of oral probiotic supplements on vaginal microbiota during pregnancy: a randomised, double-blind, placebo-controlled trial with microbiome analysis. **2020**, 127, 275-284	36
1134	Specific class of intrapartum antibiotics relates to maturation of the infant gut microbiota: a prospective cohort study. **2020**, 127, 217-227	43
1133	Diverse respiratory capacity among Thermus strains from US Great Basin hot springs. **2020**, 24, 71-80	2
1132	Impact of oral metronidazole treatment on the vaginal microbiota and correlates of treatment failure. **2020**, 222, 157.e1-157.e13	26
1131	Effects of a novel three-step sous-vide cooking and subsequent chilled storage on the microbiota of beef steaks. **2020**, 159, 107938	10
1130	Removal of three proteinaceous antinutrients from soybean does not mitigate soybean-induced enteritis in Atlantic salmon (Salmo salar, L). **2020**, 514, 734495	13

1129	The effect of salt concentrations on the fermentation of doenjang, a traditional Korean fermented soybean paste. **2020**, 86, 103329	34
1128	Nonoptimal Vaginal Microbiota After Azithromycin Treatment for Chlamydia trachomatis Infection. **2020**, 221, 627-635	17
1127	Biodiversity analyses in freshwater meiofauna through DNA sequence data. **2020**, 847, 2597-2611	10
1126	Niche partitioning of methane-oxidizing bacteria along the oxygen-methane counter gradient of stratified lakes. **2020**, 14, 274-287	22
1125	In Planta Colonization and Role of T6SS in Two Rice Endophytes. **2020**, 33, 349-363	17
1124	Comparison of gut bacterial communities and their associations with host diets in four fruit borers. **2020**, 76, 1353-1362	16
1123	Metabarcoding of eukaryotic parasite communities describes diverse parasite assemblages spanning the primate phylogeny. **2020**, 20, 204-215	9
1122	A case of 'blown pack' spoilage of vacuum-packaged pork likely associated with Clostridium estertheticum in Canada. **2020**, 70, 13-20	9
1121	Persistence of a mixed lactic acid bacterial starter culture during lysine fortification of sourdough breads by addition of pistachio powder. **2020**, 86, 103349	18
1120	phylogenize: correcting for phylogeny reveals genes associated with microbial distributions. **2020**, 36, 1289-1290	0
1119	Anaerobically digested blackwater treatment by simultaneous denitrification and anammox processes: Feeding loading affects reactor performance and microbial community succession. **2020**, 241, 125101	17
1118	Diatom metabarcoding applied to large scale monitoring networks: Optimization of bioinformatics strategies using Mothur software. **2020**, 109, 105775	25
1117	Culture-independent analysis of an endophytic core microbiome in two species of wheat: Triticum aestivum L. (cv. 'Hondia') and the first report of microbiota in Triticum spelta L. (cv. 'Rokosz'). **2020**, 43, 126025	34
1116	Consecutive lactate formation and chain elongation to reduce exogenous chemicals input in repeated-batch food waste fermentation. **2020**, 169, 115215	53
1115	Early Life Stages of a Common Broadcast Spawning Coral Associate with Specific Bacterial Communities Despite Lack of Internalized Bacteria. **2020**, 79, 706-719	16
1114	Each Additional Day of Antibiotics Is Associated With Lower Gut Anaerobes in Neonatal Intensive Care Unit Patients. **2020**, 70, 2553-2560	13
1113	Exploration of the Vaginal and Gut Microbiome in African American Women by Body Mass Index, Class of Obesity, and Gestational Weight Gain: A Pilot Study. **2020**, 37, 1160-1172	5
1112	Variation in the Microbiota Associated with Daphnia magna Across Genotypes, Populations, and Temperature. **2020**, 79, 731-742	15

1111	What Goes Up Might Come Down: the Spectacular Spread of an Endosymbiont Is Followed by Its Decline a Decade Later. **2020**, 79, 482-494	11
1110	Soil Microbial Community Responses After Amendment with Thermally Altered Pinus radiata Needles. **2020**, 79, 409-419	
1109	Structured exercise alters the gut microbiota in humans with overweight and obesity-A randomized controlled trial. **2020**, 44, 125-135	34
1108	Culture-independent and dependent evaluation of the equine paranasal sinus microbiota in health and disease. **2020**, 52, 455-463	6
1107	Early Colonization of Weathered Polyethylene by Distinct Bacteria in Marine Coastal Seawater. **2020**, 79, 517-526	36
1106	Effects of a multispecies synbiotic on glucose metabolism, lipid marker, gut microbiome composition, gut permeability, and quality of life in diabesity: a randomized, double-blind, placebo-controlled pilot study. **2020**, 59, 2969-2983	19
1105	No evidence for phylosymbiosis in western chipmunk species. **2020**, 96,	10
1104	Hysteretic response of Microbial Eukaryotic Communities to Gradually Decreased Nutrient Concentrations in Eutrophic Water. **2020**, 79, 815-822	5
1103	Salivary dysbiosis and the clinical spectrum in anti-Ro positive mothers of children with neonatal lupus. **2020**, 107, 102354	6
1102	Influences of melatonin and endotoxin lipopolysaccharide on goose productive performance and gut microbiota. **2020**, 61, 217-224	4
1101	pime: A package for discovery of novel differences among microbial communities. **2020**, 20, 415-428	12
1100	Germ-free mice exhibit profound gut microbiota-dependent alterations of intestinal endocannabinoidome signaling. **2020**, 61, 70-85	32
1099	Spatial and temporal axes impact ecology of the gut microbiome in juvenile European lobster (Homarus gammarus). **2020**, 14, 531-543	18
1098	From metabarcoding to metaphylogeography: separating the wheat from the chaff. **2020**, 30, e02036	36
1097	Co-dynamics of Symbiodiniaceae and bacterial populations during the first year of symbiosis with Acropora tenuis juveniles. **2020**, 9, e959	18
1096	Bacterial succession in oil-contaminated soil under phytoremediation with poplars. **2020**, 243, 125242	13
1095	Emergence and fate of volatile iodinated organic compounds during biological treatment of oil and gas produced water. **2020**, 699, 134202	13
1094	Phylogenetic signature of fungal response to long-term chemical pollution. **2020**, 140, 107644	7

1093	Red Wine Consumption Associated With Increased Gut Microbiota Diversity in 3 Independent Cohorts. **2020**, 158, 270-272.e2	31
1092	Natural compulsive-like behaviour in the deer mouse (Peromyscus maniculatus bairdii) is associated with altered gut microbiota composition. **2020**, 51, 1419-1427	11
1091	Methods in Lung Microbiome Research. **2020**, 62, 283-299	36
1090	Molecular mechanisms of acclimation to long-term elevated temperature exposure in marine symbioses. **2020**, 26, 1271-1284	3
1089	Metabolic Analysis of Regionally Distinct Gut Microbial Communities Using an Platform. **2020**, 68, 13056-13067	3
1088	Genetic basis for the cooperative bioactivation of plant lignans by Eggerthella lenta and other human gut bacteria. **2020**, 5, 56-66	29
1087	The Evolution of Microbial Community during Acclimation for High Sodium Food Waste Anaerobic digestion. **2020**, 11, 6057-6063	4
1086	Mixed-mode bacterial transmission in the common brooding coral Pocillopora acuta. **2020**, 22, 397-412	17
1085	High-throughput DNA sequencing of microbiota at interproximal sites. **2020**, 12, 1687397	6
1084	Fish Gut Microbiome: A Primer to an Emerging Discipline in the Fisheries Sciences. **2020**, 45, 271-282	4
1083	Different and diverse anaerobic microbiota were seen in women living with HIV with unsuppressed HIV viral load and in women with recurrent bacterial vaginosis: a cohort study. **2020**, 127, 250-259	2
1082	Population-level inferences from environmental DNA-Current status and future perspectives. **2020**, 13, 245-262	33
1081	Stream Algal Biofilm Community Diversity Along An Acid Mine Drainage Recovery Gradient Using Multimarker Metabarcoding. **2020**, 56, 11-22	2
1080	Symbiodiniaceae probiotics for use in bleaching recovery. **2020**, 28, 282-288	16
1079	Complex associations between cross-kingdom microbial endophytes and host genotype in ash dieback disease dynamics. **2020**, 108, 291-309	18
1078	Bacterial communities of the reproductive organs of virgin and mated common bedbugs, Cimex lectularius. **2020**, 45, 142-154	11
1077	The interaction between microbiome and pig efficiency: A review. **2020**, 137, 4-13	21
1076	Monoacylglycerol Lipase Inhibition Protects From Liver Injury in Mouse Models of Sclerosing Cholangitis. **2020**, 71, 1750-1765	10

1075	Analysis of bacterial microbiome associated with nylon and copper nets in an aquaculture context. **2020**, 516, 734540	2
1074	Analysis of the Microbiota in the Fecal Material of Painted Turtles (Chrysemys picta). **2020**, 77, 11-14	6
1073	Insect-associated bacterial communities in an alpine stream. **2020**, 847, 331-344	6
1072	Anaerobic digestion of mixed urban biowaste: The microbial community shift towards stability. **2020**, 55, 108-117	14
1071	The impact of elevated temperature and drought on the ecology and evolution of plant–soil microbe interactions. **2020**, 108, 337-352	26
1070	Evaluating Bioinformatic Pipeline Performance for Forensic Microbiome Analysis. **2020**, 65, 513-525	3
1069	Bacterial communities of plum phyllosphere and characterization of indigenous antagonistic Bacillus thuringiensis R3/3 isolate. **2020**, 128, 528-543	5
1068	Analysis of leaf microbiome composition of near-isogenic maize lines differing in broad-spectrum disease resistance. **2020**, 225, 2152-2165	19
1067	Transient exposure to novel high temperatures reshapes coastal phytoplankton communities. **2020**, 14, 413-424	15
1066	Soil hydrology drives ecological niche differentiation in a native prairie microbiome. **2020**, 96,	4
1065	Western Diet Promotes Intestinal Colonization by Collagenolytic Microbes and Promotes Tumor Formation After Colorectal Surgery. **2020**, 158, 958-970.e2	25
1064	Inoculum Source Determines Acetate and Lactate Production during Anaerobic Digestion of Sewage Sludge and Food Waste. **2019**, 7,	20
1063	Evaluation of primer pairs for studying arbuscular mycorrhizal fungal community compositions using a MiSeq platform. **2020**, 56, 853-858	8
1062	Biomethane recovery from source-diverted household blackwater: Impacts from feed sulfate. **2020**, 136, 28-38	18
1061	Disparate effects of antibiotic-induced microbiome change and enhanced fitness in ́Daphnia magna. **2020**, 15, e0214833	12
1060	Characterization of black patina from the Tiber River embankments using Next-Generation Sequencing. **2020**, 15, e0227639	13
1059	Temporal Responses of Microbial Communities to Anaerobic Soil Disinfestation. **2020**, 80, 191-201	4
1058	Variation of soil microbial and earthworm communities along an agricultural transect with tree windbreak. **2020**, 94, 1639-1649	4

1057	Panel 3: Genomics, precision medicine and targeted therapies. **2020**, 130 Suppl 1, 109835	1
1056	Evidence for phylogenetically and catabolically diverse active diazotrophs in deep-sea sediment. **2020**, 14, 971-983	16
1055	CAMITAX: Taxon labels for microbial genomes. **2020**, 9,	4
1054	Impact of Antibiotic-Resistant Bacteria on Immune Activation and Clostridioides difficile Infection in the Mouse Intestine. **2020**, 88,	4
1053	Salivary microbiota and inflammation-related proteins in patients with psoriasis. **2020**, 26, 677-687	11
1052	Unique bacterial assembly, composition, and interactions in a parasitic plant and its host. **2020**, 71, 2198-2209	5
1051	Microbial imbalance in inflammatory bowel disease patients at different taxonomic levels. **2020**, 12, 1	98
1050	The impact of food additives, artificial sweeteners and domestic hygiene products on the human gut microbiome and its fibre fermentation capacity. **2020**, 59, 3213-3230	27
1049	Development of microbial communities in organochlorine pesticide contaminated soil: A post-reclamation perspective. **2020**, 150, 103467	13
1048	Effects of rearing density on growth, digestive conditions, welfare indicators and gut bacterial community of gilthead sea bream (Sparus aurata, L. 1758) fed different fishmeal and fish oil dietary levels. **2020**, 518, 734854	10
1047	Greywater treatment using an oxygen-based membrane biofilm reactor: Formation of dynamic multifunctional biofilm for organics and nitrogen removal. **2020**, 386, 123989	24
1046	DNA metabarcoding reveals organisms contributing to particulate matter flux to abyssal depths in the North East Pacific ocean. **2020**, 173, 104708	17
1045	Superchilling in combination with modified atmosphere packaging resulted in long shelf-life and limited microbial growth in Atlantic cod (Gadus morhua L.) from capture-based-aquaculture in Greenland. **2020**, 88, 103405	7
1044	Multiannual variations in Microcystis bloom episodes - Temperature drives shift in species composition. **2020**, 92, 101710	10
1043	Effect of a bioactive cement on the microbial community in carious dentin after selective caries removal - An in-vivo study. **2020**, 92, 103264	4
1042	Effect of dimethyl disulfide on the sulfur formation and microbial community composition during the biological HS removal from sour gas streams. **2020**, 386, 121916	16
1041	Bioinformatic strategies to address limitations of 16rRNA short-read amplicons from different sequencing platforms. **2020**, 169, 105811	6
1040	Microbiome changes and oxidative capability of an anaerobic PCB dechlorinating enrichment culture after oxygen exposure. **2020**, 56, 96-102	8

1039	Effects of a Companion Plant on the Formation of Mycorrhizal Propagules in Artemisia tridentata Seedlings. **2020**, 73, 138-146	
1038	Microbial responses to perfluoroalkyl substances and perfluorooctanesulfonate (PFOS) desulfurization in the Antarctic marine environment. **2020**, 171, 115434	16
1037	Fecal Metabolomics as a Novel Noninvasive Method for Short-Term Stress Monitoring in Beef Cattle. **2020**, 19, 845-853	3
1036	Design of novel primer sets for easy detection of species from seawater. **2020**, 84, 854-864	2
1035	Microbial indicators are better predictors of wheat yield and quality than N fertilization. **2020**, 96,	15
1034	Microbiome-Guided Exploration of the Microbial Assemblage of the Exotic Beverage "Insect Tea" Native to Southwestern China. **2019**, 10, 3087	1
1033	The composition characteristics of arbuscular mycorrhizal fungal communities associated with barley in saline-alkaline soils in Central Anatolia. **2020**, 66, 268-274	2
1032	Evaluation of accuracy and precision in an amplicon sequencing workflow for marine protist communities. **2020**, 18, 20-40	5
1031	Assessing passive rehabilitation for carbon gains in rain-filled agricultural wetlands. **2020**, 256, 109971	4
1030	A survey of the oral cavity microbiome of New Zealand fur seal pups (Arctocephalus forsteri). **2020**, 36, 334-343	1
1029	Using vertebrate environmental DNA from seawater in biomonitoring of marine habitats. **2020**, 34, 697-710	33
1028	Evaluating intraspecific genetic diversity using environmental DNA and denoising approach: A case study using tank water. **2020**, 2, 42-52	26
1027	Performance of extraction methods for extracellular DNA from sediments across marine habitats. **2020**, 2, 91-98	0
1026	Microbial biomass, marine invertebrate meals and feed restriction influence the biological and gut microbiota response of shrimp Penaeus monodon. **2020**, 520, 734679	16
1025	Characteristics of microbial eukaryotic community recovery in eutrophic water by using ecological floating beds. **2020**, 711, 134551	15
1024	Steps towards a more efficient use of chironomids as bioindicators for freshwater bioassessment: Exploiting eDNA and other genetic tools. **2020**, 110, 105868	10
1023	Comparing Approaches for Capturing Bacterial Assemblages Associated with Symptomatic (Bacterial Blotch) and Asymptomatic Mushroom (Agaricus bisporus) Caps. **2020**, 4, 90-99	2
1022	High-resolution mycobiota analysis reveals dynamic intestinal translocation preceding invasive candidiasis. **2020**, 26, 59-64	81

1021	Diversity and structure of bacterial community in rhizosphere of lima bean. **2020**, 150, 103490	11
1020	Impacts of morphological-controlled ZnO nanoarchitectures on aerobic microbial communities during real wastewater treatment in an aerobic-photocatalytic system. **2020**, 259, 113867	4
1019	Commensal Bacteroidetes protect against Klebsiella pneumoniae colonization and transmission through IL-36 signalling. **2020**, 5, 304-313	30
1018	Infliximab Does Not Promote the Presence of Collagenolytic Bacteria in a Mouse Model of Colorectal Anastomosis. **2020**, 24, 2637-2642	1
1017	Comparative analysis of the midgut microbiota of two natural tick vectors of Rickettsia rickettsii. **2020**, 106, 103606	10
1016	Bacterial diversity and microbial functional responses to organic matter composition and persistent organic pollutants in deltaic lagoon sediments. **2020**, 233, 106508	8
1015	Gut microbiota structure differs between honeybees in winter and summer. **2020**, 14, 801-814	78
1014	Influence of terminal electron-accepting conditions on the soil microbial community and degradation of organic contaminants of emerging concern. **2020**, 706, 135327	8
1013	Reproductive Senescence and Ischemic Stroke Remodel the Gut Microbiome and Modulate the Effects of Estrogen Treatment in Female Rats. **2020**, 11, 812-830	20
1012	RNA-based spatial community analysis revealed intra-reactor variation and expanded collection of direct interspecies electron transfer microorganisms in anaerobic digestion. **2020**, 298, 122534	27
1011	Protist Interactions and Community Structure During Early Autumn in the Kerguelen Region (Southern Ocean). **2020**, 171, 125709	11
1010	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. **2020**, 150, 806-817	24
1009	Soil exposed to silver nanoparticles reveals significant changes in community structure and altered microbial transcriptional profiles. **2020**, 258, 113816	13
1008	The Effect of Burn Resuscitation Volumes on the Gut Microbiome in a Swine Model. **2020**, 54, 368-376	7
1007	Host determinants of among-species variation in microbiome composition in drosophilid flies. **2020**, 14, 217-229	12
1006	Depth-dependent detritus production in the sponge, Halisarca caerulea. **2020**, 65, 1200-1216	13
1005	The effects of glyphosate and AMPA on the mediterranean mussel Mytilus galloprovincialis and its microbiota. **2020**, 182, 108984	17
1004	Microbiota associated with the skin, gills, and gut of the fish Parachondrostoma toxostoma from the Rh□e basin. **2020**, 65, 446-459	2

1003	Microbiome convergence following sanitizer treatment and identification of sanitizer resistant species from spinach and lettuce rinse water. **2020**, 318, 108458	9
1002	Bioelectrochemical remediation of phenanthrene in a microbial fuel cell using an anaerobic consortium enriched from a hydrocarbon-contaminated site. **2020**, 389, 121845	19
1001	Quantification of toluene phytoextraction rates and microbial biodegradation functional profiles at a fractured bedrock phytoremediation site. **2020**, 707, 135890	5
1000	Network analysis reveals succession of Microcystis genotypes accompanying distinctive microbial modules with recurrent patterns. **2020**, 170, 115326	22
999	Ear mite infection is associated with altered microbial communities in genetically depauperate Santa Catalina Island foxes (Urocyon littoralis catalinae). **2020**, 29, 1463-1475	7
998	Long-term decomposition captures key steps in microbial breakdown of seagrass litter. **2020**, 705, 135806	18
997	Unexpected mitochondrial genome diversity revealed by targeted single-cell genomics of heterotrophic flagellated protists. **2020**, 5, 154-165	23
996	Bacterial and algal symbiont dynamics in early recruits exposed to two adult coral species. **2020**, 39, 189-202	9
995	The Missing Metric: An Evaluation of Fungal Importance in Wetland Assessments. **2020**, 40, 825-838	2
994	Genotype and soil water availability shape the composition of AMF communities at chickpea early growth stages. **2020**, 150, 103443	8
993	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. **2020**, 9, 797-806	19
992	Improvements in Metabolic Syndrome by Xanthohumol Derivatives Are Linked to Altered Gut Microbiota and Bile Acid Metabolism. **2020**, 64, e1900789	19
991	Development of a multi-assay approach for monitoring coral diversity using eDNA metabarcoding. **2020**, 39, 159-171	18
990	Towards centralized biogas plants: Co-digestion of sewage sludge and pig manure maintains process performance and active microbiome diversity. **2020**, 297, 122442	12
989	Diarrhea as a Potential Cause and Consequence of Reduced Gut Microbial Diversity Among Undernourished Children in Peru. **2020**, 71, 989-999	18
988	Gut Microbiota Features Associated With Campylobacter Burden and Postnatal Linear Growth Deficits in a Peruvian Birth Cohort. **2020**, 71, 1000-1007	12
987	Distinguishing nutrient-dependent plant driven bacterial colonization patterns in alfalfa. **2020**, 12, 70-77	4
986	A succession of marine bacterial communities in batch reactor experiments during the degradation of five different petroleum types. **2020**, 150, 110775	9

985	Prenatal low-dose penicillin results in long-term sex-specific changes to murine behaviour, immune regulation, and gut microbiota. **2020**, 84, 154-163	13
984	Depletion of Foxp3 regulatory T cells is accompanied by an increase in the relative abundance of Firmicutes in the murine gut microbiome. **2020**, 159, 344-353	12
983	Arbuscular mycorrhizal fungal community differentiation along a post-coal mining reclamation chronosequence in South Africa: A potential indicator of ecosystem recovery. **2020**, 147, 103429	16
982	Under temperate climate, the conversion of grassland to arable land affects soil nutrient stocks and bacteria in a short term. **2020**, 703, 135494	6
981	Analysis of Flagellin-Specific Adaptive Immunity Reveals Links to Dysbiosis in Patients With Inflammatory Bowel Disease. **2020**, 9, 485-506	10
980	Detection of sentinel bacteria in mangrove sediments contaminated with heavy metals. **2020**, 150, 110701	20
979	Soil microbial community responses to labile organic carbon fractions in relation to soil type and land use along a climate gradient. **2020**, 141, 107692	42
978	Pyrogenic organic matter effects on soil bacterial community composition. **2020**, 141, 107678	14
977	Investigation of direct and indirect transfer of microbiomes between individuals. **2020**, 45, 102212	17
976	A practical guide to DNA metabarcoding for entomological ecologists. **2020**, 45, 373-385	32
975	Combined effects of HIV and obesity on the gastrointestinal microbiome of young men who have sex with men. **2020**, 21, 365-377	1
974	Human airway construct model is suitable for studying transcriptome changes associated with indoor air particulate matter toxicity. **2020**, 30, 433-444	6
973	Effects of nebulized dexamethasone on the respiratory microbiota and mycobiota and relative equine herpesvirus-1, 2, 4, 5 in an equine model of asthma. **2020**, 34, 307-321	6
972	Rhizosphere modelling reveals spatiotemporal distribution of daidzein shaping soybean rhizosphere bacterial community. **2020**, 43, 1036-1046	28
971	Structural and Functional Dynamics of Soil Microbes following Spruce Beetle Infestation. **2020**, 86,	8
970	Tissue- and Population-Level Microbiome Analysis of the Wasp Spider Identified a Novel Dominant Bacterial Symbiont. **2019**, 8,	13
969	The Effect of Thermal Stress on the Bacterial Microbiome of. **2019**, 8,	6
968	Switching to a Healthy Diet Prevents the Detrimental Effects of Western Diet in a Colitis-Associated Colorectal Cancer Model. **2019**, 12,	5

967	Associated Keratoconjunctivitis in Norwegian Muskox (). **2020**, 56, 489-491	5
966	Attenuation of immune-mediated bone marrow damage in conventionally housed mice. **2020**, 59, 237-245	4
965	Anaerobic digestion of co-ensiled cover crop and barley straw: Effect of co-ensiling ratios, manure addition and impact on microbial community structure. **2020**, 144, 112025	5
964	Tomato Genotype Modulates Selection and Responses to Root Microbiota. **2020**, 4, 314-326	8
963	Duodenal microbiome in patients with or without Helicobacter pylori infection. **2020**, 25, e12753	3
962	Gut microbiota degrades toxic isothiocyanates in a flea beetle pest. **2020**, 29, 4692-4705	11
961	Migration, pathogens and the avian microbiome: A comparative study in sympatric migrants and residents. **2020**, 29, 4706-4720	6
960	Butterflies Host Characteristic and Phylogenetically Structured Adult-Stage Microbiomes. **2020**, 86,	5
959	Chloroflexi Dominate the Deep-Sea Golf Ball Sponges Craniella zetlandica and Craniella infrequens Throughout Different Life Stages. **2020**, 7,	8
958	Assessment of Inter-Laboratory Variation in the Characterization and Analysis of the Mucosal Microbiota in Crohn’s Disease and Ulcerative Colitis. **2020**, 11, 2028	3
957	Effects of Sulfamethoxazole on the Microbial Community Dynamics During the Anaerobic Digestion Process. **2020**, 11, 537783	6
956	Large Enrichment of Anthropogenic Organic Matter Degrading Bacteria in the Sea-Surface Microlayer at Coastal Livingston Island (Antarctica). **2020**, 11, 571983	7
955	The Microbiome of Neotropical Water Striders and Its Potential Role in Codiversification. **2020**, 11,	4
954	An Overview of Bioinformatics Tools for DNA Meta-Barcoding Analysis of Microbial Communities of Bioaerosols: Digest for Microbiologists. **2020**, 10,	0
953	Improvement in Uncontrolled Eating Behavior after Laparoscopic Sleeve Gastrectomy Is Associated with Alterations in the Brain-Gut-Microbiome Axis in Obese Women. **2020**, 12,	12
952	Root-Secreted Coumarins and the Microbiota Interact to Improve Iron Nutrition in Arabidopsis. **2020**, 28, 825-837.e6	58
951	Effects of hybrid, kernel maturity, and storage period on the bacterial community in high-moisture and rehydrated corn grain silages. **2020**, 43, 126131	12
950	A Diet-Dependent Microbiota Profile Associated with Incident Type 2 Diabetes: From the CORDIOPREV Study. **2020**, 64, e2000730	1

949	Functional attributes and response of bacterial communities to nature-based fertilization during hydrocarbon remediation. **2020**, 154, 105084	5
948	Effect of dietary n-3 polyunsaturated fatty acids on the composition of cecal microbiome of Lohmann hens. **2020**, 162, 102182	0
947	Geographic partitioning or environmental selection: What governs the global distribution of bacterial communities inhabiting floral nectar?. **2020**, 749, 142305	8
946	Anthropogenic impact on the historical phytoplankton community of Lake Constance reconstructed by multimarker analysis of sediment-core environmental DNA. **2021**, 30, 3040-3056	6
945	Trichomes form genotype-specific microbial hotspots in the phyllosphere of tomato. **2020**, 15, 17	2
944	Metagenomic Characterization of the Microbiome and Resistome of Retail Ground Beef Products. **2020**, 11, 541972	6
943	Enhanced lactic acid production from the anaerobic co-digestion of swine manure with apple or potato waste via ratio adjustment. **2020**, 318, 124237	7
942	The community compositions of three nitrogen removal wastewater treatment plants of different configurations in Victoria, Australia, over a 12-month operational period. **2020**, 104, 9839-9852	12
941	Characterization of the Aedes albopictus (Diptera: Culicidae) holobiome: bacterial composition across land use type and mosquito sex in Malaysia. **2020**, 212, 105683	2
940	Robustness of fermented carrot juice against Listeria monocytogenes, Salmonella Typhimurium and Escherichia coli O157:H7. **2020**, 335, 108854	5
939	Progression of nasopharyngeal and tracheal bacterial microbiotas of feedlot cattle during development of bovine respiratory disease. **2020**, 248, 108826	7
938	Lactobacillus spp. attenuate antibiotic-induced immune and microbiota dysregulation in honey bees. **2020**, 3, 534	13
937	Multiomic features associated with mucosal healing and inflammation in paediatric Crohn's disease. **2020**, 52, 1491-1502	4
936	Review article: how the intestinal microbiota may reflect disease activity and influence therapeutic outcome in inflammatory bowel disease. **2020**, 52, 1453-1468	15
935	Monitoring the ecological status of rivers with diatom eDNA metabarcoding: A comparison of taxonomic markers and analytical approaches for the inference of a molecular diatom index. **2021**, 30, 2959-2968	9
934	Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. **2020**, 183, 666-683.e17	74
933	A possible universal role for mRNA secondary structure in bacterial translation revealed using a synthetic operon. **2020**, 11, 4827	3
932	Ureteral Stent Microbiota Is Associated with Patient Comorbidities but Not Antibiotic Exposure. **2020**, 1, 100094	6

931	A single bacterial genus maintains root growth in a complex microbiome. **2020**, 587, 103-108	70
930	Understanding the impact of antibiotic perturbation on the human microbiome. **2020**, 12, 82	48
929	Microplastic-associated biofilms in lentic Italian ecosystems. **2020**, 187, 116429	31
928	Strain-Level Analysis of spp. from Gut Microbiomes of Adults with Differing Lactase Persistence Genotypes. **2020**, 5,	5
927	The Znt7-null mutation has sex dependent effects on the gut microbiota and goblet cell population in the mouse colon. **2020**, 15, e0239681	2
926	Evaluation of Two Primer Sets for Amplification of Comammox Genes in Wetland Soils. **2020**, 11, 560942	5
925	Fecal microbiota transplantation from warthog to pig confirms the influence of the gut microbiota on African swine fever susceptibility. **2020**, 10, 17605	4
924	Gut Microbiome Changes in Patients with Active Left-Sided Ulcerative Colitis after Fecal Microbiome Transplantation and Topical 5-aminosalicylic Acid Therapy. **2020**, 9,	18
923	Effects of chronic exposure to water accommodated fraction (WAF) of light crude oil on gut microbiota composition of the lined sole (Achirus lineatus). **2020**, 161, 105116	4
922	A Potential Role for Stress-Induced Microbial Alterations in IgA-Associated Irritable Bowel Syndrome with Diarrhea. **2020**, 1,	8
921	Parameters influencing the development of highly conductive and efficient biofilm during microbial electrosynthesis: the importance of applied potential and inorganic carbon source. **2020**, 6, 40	18
920	Environmental Factors Driving Spatial Heterogeneity in Desert Halophile Microbial Communities. **2020**, 11, 578669	2
919	Preserving Microbial Community Integrity in Oilfield Produced Water. **2020**, 11, 581387	2
918	Environmental DNA metabarcoding reveals estuarine benthic community response to nutrient enrichment - Evidence from an in-situ experiment. **2020**, 267, 115472	9
917	Postprandial factor VII activation does not increase plasma concentrations of prothrombin fragment 1´+´2 in patients with morbid obesity. **2020**, 196, 260-267	3
916	A systematic review on bacterial community changes after periodontal therapy with and without systemic antibiotics: An analysis with a wider lens. **2020**, 55, 785-800	5
915	Diversity of gut microbiomes in marine fishes is shaped by host-related factors. **2020**, 29, 5019-5034	15
914	Immune Response and Microbiota Profiles during Coinfection with Plasmodium vivax and Soil-Transmitted Helminths. **2020**, 11,	2

913	The intestinal microbiome, weight, and metabolic changes in women treated by adjuvant chemotherapy for breast and gynecological malignancies. **2020**, 18, 281	3
912	Interpretations of Environmental Microbial Community Studies Are Biased by the Selected 16S rRNA (Gene) Amplicon Sequencing Pipeline. **2020**, 11, 550420	37
911	Accelerated consolidation of oil sands tailings using an anaerobic bioreactor. **2020**, 11, 100547	3
910	Stimulation of methanogenesis in bituminous coal from the upper Silesian coal basin. **2020**, 231, 103609	4
909	Effects of increasing dietary level of organic acids and nature-identical compounds on growth, intestinal cytokine gene expression and gut microbiota of rainbow trout (Oncorhynchus mykiss) reared at normal and high temperature. **2020**, 107, 324-335	10
908	Comparative analysis of rhizosphere soil physiochemical characteristics and microbial communities between rusty and healthy ginseng root. **2020**, 10, 15756	17
907	Physical Activity Shapes the Intestinal Microbiome and Immunity of Healthy Mice but Has No Protective Effects against Colitis in MUC2 Mice. **2020**, 5,	5
906	Diet composition analysis provides new management insights for a highly specialized endangered small mammal. **2020**, 15, e0240136	2
905	Delayed Establishment of Gut Microbiota in Infants Delivered by Cesarean Section. **2020**, 11, 2099	17
904	Phragmites australis Associates with Belowground Fungal Communities Characterized by High Diversity and Pathogen Abundance. **2020**, 12, 363	2
903	The microbiota of the surface, dermis and subcutaneous tissue of dog skin. **2020**, 2, 34	3
902	From Sea Surface to Seafloor: A Benthic Allochthonous eDNA Survey for the Abyssal Ocean. **2020**, 7,	6
901	A New Business as Usual Climate Scenario and the Stress Response of the Caribbean Coral Montastraea cavernosa. **2020**, 7,	1
900	Spirotrichonymphea (Parabasalia) symbionts of the termite Paraneotermes simplicicornis. **2020**, 76, 125742	1
899	Nematodes as bioindicators of polluted sediments using metabarcoding and microscopic taxonomy. **2020**, 143, 105922	12
898	Co-infection of With Bacterial Pathobionts or Leads to Distinct Sinonasal Inflammatory Responses in a Murine Acute Sinusitis Model. **2020**, 10, 472	4
897	Dataset supporting the use of nematodes as bioindicators of polluted sediments. **2020**, 32, 106087	1
896	Effects of nitrogen and phosphorus addition on microbial community composition and element cycling in a grassland soil. **2020**, 151, 108041	23

895	Roles of host genetics and sperm microbiota in reproductive success in healthy rabbit. **2020**, 158, 416-423	3
894	Microbial therapeutics for acute colitis based on genetically modified Lactococcus lactis hypersecreting IL-1Ra in mice. **2020**, 52, 1627-1636	15
893	Impact of a resistance gene against a fungal pathogen on the plant host residue microbiome: The case of the Leptosphaeria maculans-Brassica napus pathosystem. **2020**, 21, 1545-1558	5
892	Performance and community structure dynamics of microbial electrolysis cells operated on multiple complex feedstocks. **2020**, 13, 169	2
891	The aging mouse microbiome has obesogenic characteristics. **2020**, 12, 87	3
890	Fungal Community, Metabolic Diversity, and Glomalin-Related Soil Proteins (GRSP) Content in Soil Contaminated With Crude Oil After Long-Term Natural Bioremediation. **2020**, 11, 572314	10
889	Grow - Store - Steam - Re-peat: Reuse of spent growing media for circular cultivation of Chrysanthemum. **2020**, 276, 124128	10
888	52´years of ecological restoration following a major disturbance by opencast lignite mining does not reassemble microbiome structures of the original arable soils. **2020**, 745, 140955	5
887	Laboratory and Field Testing Assessment of Next Generation Biocide-Free, Fouling-Resistant Slippery Coatings. **2020**, 2, 5147-5162	4
886	Temporal dynamics of bacterial communities during seed development and maturation. **2020**, 96,	14
885	Faecal microbiota and antimicrobial resistance gene profiles of healthy foals. **2021**, 53, 806-816	2
884	(Nano)microplastics promote the propagation of antibiotic resistance genes in landfill leachate. **2020**, 7, 3536-3546	23
883	Identification of microbial interaction network: zero-inflated latent Ising model based approach. **2020**, 13, 16	1
882	Taxonomic profiling of individual nematodes isolated from copse soils using deep amplicon sequencing of four distinct regions of the 18S ribosomal RNA gene. **2020**, 15, e0240336	6
881	Bioaminergic Responses in an In Vitro System Studying Human Gut Microbiota-Kiwifruit Interactions. **2020**, 8,	1
880	Pet-Human Gut Microbiome Host Classifier Using Data from Different Studies. **2020**, 8,	0
879	Gut Microbiome in Children from Indigenous and Urban Communities in Mxico: Different Subsistence Models, Different Microbiomes. **2020**, 8,	4
878	Vaginal microbiota and human papillomavirus infection among young Swedish women. **2020**, 6, 39	17

877	Pan-regional marine benthic cryptobiome biodiversity patterns revealed by metabarcoding Autonomous Reef Monitoring Structures. **2020**, 29, 4882-4897	5
876	Is a Central Sediment Sample Sufficient? Exploring Spatial and Temporal Microbial Diversity in a Small Lake. **2020**, 12,	3
875	Clostridioides difficile carriage in animals and the associated changes in the host fecal microbiota. **2020**, 66, 102279	5
874	Profiling of bacterial assemblages in the marine cage farm environment, with implications on fish, human and ecosystem health. **2020**, 118, 106785	3
873	Belowground changes to community structure alter methane-cycling dynamics in Amazonia. **2020**, 145, 106131	9
872	Use of the synbiotic VSL#3 and yacon-based concentrate attenuates intestinal damage and reduces the abundance of Candidatus Saccharimonas in a colitis-associated carcinogenesis model. **2020**, 137, 109721	9
871	Evaluating quality indicators through the quantification of histamine and bacterial communities. **2020**, 6, e04461	6
870	Unravelling the composition of tap and mineral water microbiota: Divergences between next-generation sequencing techniques and culture-based methods. **2020**, 334, 108850	9
869	Determining groundwater inflow and Si behavior in a wetland using 222Rn mass balance and multidisciplinary approach. **2020**, 591, 125575	
868	Alterations in the gut-associated microbiota of juvenile Caribbean spiny lobsters Panulirus argus (Latreille, 1804) infected with PaV1. **2020**, 176, 107457	2
867	Dietary supplementation with fermented defatted "alperujo" induces modifications of the intestinal mucosa and cecal microbiota of broiler chickens. **2020**, 99, 5308-5315	2
866	A reasonable correlation between cloacal and cecal microbiomes in broiler chickens. **2020**, 99, 6062-6070	4
865	Changes in soil microbial communities in post mine ecological restoration: Implications for monitoring using high throughput DNA sequencing. **2020**, 749, 142262	10
864	Soil-microorganism-mediated invasional meltdown in plants. **2020**, 4, 1612-1621	10
863	Dental black plaque: metagenomic characterization and comparative analysis with white-plaque. **2020**, 10, 15962	4
862	The complete chloroplast genome of Gleditsia sinensis and Gleditsia japonica: genome organization, comparative analysis, and development of taxon specific DNA mini-barcodes. **2020**, 10, 16309	2
861	Loss of bacterial diversity in the sinuses is associated with lower smell discrimination scores. **2020**, 10, 16422	1
860	Food Resource Sharing of Alder Leaf Beetle Specialists (Coleoptera: Chrysomelidae) as Potential Insect-Plant Interface for Horizontal Transmission of Endosymbionts. **2020**, 49, 1402-1414	4

859	Enhanced microbial degradation of irradiated cellulose under hyperalkaline conditions. **2020**, 96,	7
858	Temporal dynamics in the taxonomic and functional profile of the Sphagnum-associated fungi (mycobiomes) in a Sphagnum farming field site in Northwestern Germany. **2020**, 96,	0
857	Dysbiosis, gut barrier dysfunction and inflammation in dementia: a pilot study. **2020**, 20, 248	28
856	The gut microbiome and its potential role in paradoxical anaerobism in pupfishes of the Mojave Desert. **2020**, 2, 20	7
855	Large Overlap Between the Intestinal and Reproductive Tract Microbiomes of Chickens. **2020**, 11, 1508	9
854	The Urinary Tract Microbiome in Older Women Exhibits Host Genetic and Environmental Influences. **2020**, 28, 298-305.e3	14
853	The microbiome: An emerging key player in aging and longevity. **2020**, 4, 103-116	31
852	Initial butyrate producers during infant gut microbiota development are endospore formers. **2020**, 22, 3909-3921	18
851	Impaired Hypothalamic Microglial Activation in Offspring of Antibiotic-Treated Pregnant/Lactating Rats Is Attenuated by Prebiotic Oligofructose Co-Administration. **2020**, 8,	3
850	Microglia Require CD4 T Cells to Complete the Fetal-to-Adult Transition. **2020**, 182, 625-640.e24	77
849	Epigenetic landscape links upper airway microbiota in infancy with allergic rhinitis at 6 years of age. **2020**, 146, 1358-1366	14
848	Metagenome analysis of gut microbial in both the caged and non-caged ducks. **2020**, 1524, 012076	
847	Methane oxidation and methylotroph population dynamics in groundwater mesocosms. **2020**, 22, 1222-1237	9
846	Community assembly of the native C. elegans microbiome is influenced by time, substrate and individual bacterial taxa. **2020**, 22, 1265-1279	12
845	Revealing changes in the microbiome of Symbiodiniaceae under thermal stress. **2020**, 22, 1294-1309	14
844	Sponge microbiome stability during environmental acquisition of highly specific photosymbionts. **2020**, 22, 3593-3607	5
843	Environmental plasticity and colonisation history in the Atlantic salmon microbiome: A translocation experiment. **2020**, 29, 886-898	23
842	A database for ITS2 sequences from nematodes. **2020**, 21, 74	10

841	Gut microbiota maturation during early human life induces enterocyte proliferation via microbial metabolites. **2020**, 20, 205	7
840	The effect of short-course antibiotics on the resistance profile of colonizing gut bacteria in the ICU: a prospective cohort study. **2020**, 24, 404	1
839	Microbiota in Waterlogged Archaeological Wood: Use of Next-Generation Sequencing to Evaluate the Risk of Biodegradation. **2020**, 10, 4636	6
838	The Effects of Prebiotic Supplementation with OMNi-LOGiC FIBRE on Fecal Microbiome, Fecal Volatile Organic Compounds, and Gut Permeability in Murine Neuroblastoma-Induced Tumor-Associated Cachexia. **2020**, 12,	9
837	The sources and transmission routes of microbial populations throughout a meat processing facility. **2020**, 6, 26	18
836	Laboratory colonization by Dirofilaria immitis alters the microbiome of female Aedes aegypti mosquitoes. **2020**, 13, 349	
835	Combined eDNA and Acoustic Analysis Reflects Diel Vertical Migration of Mixed Consortia in the Gulf of Mexico. **2020**, 7,	5
834	Effects of Zinc Pollution and Compost Amendment on the Root Microbiome of a Metal Tolerant Poplar Clone. **2020**, 11, 1677	26
833	The Intestinal Microbiome Restricts Alphavirus Infection and Dissemination through a Bile Acid-Type I IFN Signaling Axis. **2020**, 182, 901-918.e18	42
832	Long-term diverse rotation alters nitrogen cycling bacterial groups and nitrous oxide emissions after nitrogen fertilization. **2020**, 149, 107917	22
831	Reclamation with organic amendments and plants remodels the diversity and structure of bacterial community in ion-adsorption rare earth element mine tailings. **2020**, 20, 3669-3680	6
830	Conventional seed coating reduces prevalence of proteobacterial endophytes in Nicotiana tabacum. **2020**, 155, 112784	4
829	The bacterioplankton community composition and a host genotype dependent occurrence of taxa shape the Daphnia magna gut bacterial community. **2020**, 96,	13
828	Gut microbiota in a host-brood parasite system: insights from common cuckoos raised by two warbler species. **2020**, 96,	4
827	Using molecular and crowd-sourcing methods to assess breeding ground diet of a migratory brood parasite of conservation concern. **2020**, 51,	1
826	CeMbio - The Microbiome Resource. **2020**, 10, 3025-3039	29
825	The Effects of In Vivo Exposure to Copper Oxide Nanoparticles on the Gut Microbiome, Host Immunity, and Susceptibility to a Bacterial Infection in Earthworms. **2020**, 10,	10
824	Sex-Specific Differences in the Gut Microbiome in Response to Dietary Fiber Supplementation in IL-10-Deficient Mice. **2020**, 12,	7

823	Lythrum salicaria L. herb and gut microbiota of healthy post-weaning piglets. Focus on prebiotic properties and formation of postbiotic metabolites in ex vivo cultures. **2020**, 261, 113073	7
822	Host Genotype and Colonist Arrival Order Jointly Govern Plant Microbiome Composition and Function. **2020**, 30, 3260-3266.e5	22
821	Tasting the differences: Microbiota analysis of different insect-based novel food. **2020**, 137, 109426	5
820	Etifoxine reverses weight gain and alters the colonic bacterial community in a mouse model of obesity. **2020**, 180, 114151	6
819	Gram-negative Microbiota Blooms in Premature Twins Discordant for Parenteral Nutrition-associated Cholestasis. **2020**, 70, 640-644	1
818	Reconstructing marine plankton food web interactions using DNA metabarcoding. **2020**, 29, 3380-3395	15
817	Evaluation of fecal DNA extraction protocols for human gut microbiome studies. **2020**, 20, 212	6
816	Nutrient and microbial water quality of the upper Ganga River, India: identification of pollution sources. **2020**, 192, 533	9
815	Body-size Scaling is Related to Gut Microbial Diversity, Metabolism and Dietary Niche of Arboreal Folivorous Flying Squirrels. **2020**, 10, 7809	3
814	Impact of land use history on the arbuscular mycorrhizal fungal diversity in arid soils of Argentinean farming fields. **2020**, 367,	5
813	Oral or Topical Exposure to Glyphosate in Herbicide Formulation Impacts the Gut Microbiota and Survival Rates of Honey Bees. **2020**, 86,	33
812	Influence of Green Tuff Fertilizer Application on Soil Microorganisms, Plant Growth, and Soil Chemical Parameters in Green Onion (Allium fistulosum L.) Cultivation. **2020**, 10, 929	6
811	Effects of the soil microbiome on the demography of two annual prairie plants. **2020**, 10, 6208-6222	0
810	Macroinvertebrate community diversity and habitat quality relationships along a large river from targeted eDNA metabarcode assays. **2020**, 2, 572-586	7
809	Impacts of dibenzopyrenes on bacterial community isolated from Gulf of Mexico sediment. **2020**, 9, e1039	1
808	Next-Generation Omics Technologies for Exploring Complex Metabolic Regulation During Plant-Microbe Interaction. **2020**, 123-138	2
807	Distinct Distribution of Archaea From Soil to Freshwater to Estuary: Implications of Archaeal Composition and Function in Different Environments. **2020**, 11, 576661	6
806	Co-infection of Chicken Layers With and Avian Pathogenic Is Associated With Dysbiosis, Cecal Colonization and Translocation of the Bacteria From the Gut Lumen. **2020**, 11, 586437	6

805	The Transition From Stochastic to Deterministic Bacterial Community Assembly During Permafrost Thaw Succession. **2020**, 11, 596589	6
804	Microbial Species-Area Relationships in Antarctic Cryoconite Holes Depend on Productivity. **2020**, 8,	3
803	Demography and Adhesion Determinants in the Oral Cavity of Healthy Individuals. **2020**, 8,	3
802	Jumping the green wall: The use of PNA-DNA clamps to enhance microbiome sampling depth in wildlife microbiome research. **2020**, 10, 11779-11786	3
801	Environmental DNA metabarcoding of cow dung reveals taxonomic and functional diversity of invertebrate assemblages. **2021**, 30, 3374-3389	7
800	Spatial heterogeneity of bacterial colonization across different gut segments following inter-species microbiota transplantation. **2020**, 8, 161	24
799	Data-Driven Modeling for Species-Level Taxonomic Assignment From 16S rRNA: Application to Human Microbiomes. **2020**, 11, 570825	4
798	Functional Seasonality of Free-Living and Particle-Associated Prokaryotic Communities in the Coastal Adriatic Sea. **2020**, 11, 584222	5
797	Obesity-Related Metabolome and Gut Microbiota Profiles of Juvenile Göttingen Minipigs-Long-Term Intake of Fructose and Resistant Starch. **2020**, 10,	4
796	Bacterial Respiration Used as a Proxy to Evaluate the Bacterial Load in Cooling Towers. **2020**, 20,	
795	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. **2020**, 11, 5886	55
794	Exploring the Microbiota of East African Indigenous Leafy Greens for Plant Growth, Health, and Resilience. **2020**, 11, 585690	3
793	A Richer Community of Botryosphaeriaceae Within a Less Diverse Community of Fungal Endophytes in Grapevines than in Adjacent Forest Trees Revealed by a Mixed Metabarcoding Strategy. **2020**, 4, 252-267	5
792	Changes in Activity and Community Composition Shape Bacterial Responses to Size-Fractionated Marine DOM. **2020**, 11, 586148	2
791	Symbiosis between river and dry lands: Phycobiont dynamics on river gravel bars. **2020**, 51, 102062	5
790	Parasites of an Arctic scavenger; the wolverine ( ). **2020**, 13, 178-185	0
789	Environmental Nutrients Alter Bacterial and Fungal Gut Microbiomes in the Common Meadow Katydid,. **2020**, 11, 557980	1
788	Can toxin warfare against fungal parasitism influence short-term Dolichospermum bloom dynamics? - A field observation. **2020**, 99, 101915	2

787	FAM3D is essential for colon homeostasis and host defense against inflammation associated carcinogenesis. **2020**, 11, 5912	6
786	Microbial function and genital inflammation in young South African women at high risk of HIV infection. **2020**, 8, 165	4
785	Host Defense Effectors Expressed by Hemocytes Shape the Bacterial Microbiota From the Scallop Hemolymph. **2020**, 11, 599625	0
784	Microbial Signatures in Deep CO-Saturated Miocene Sediments of the Active Hartoušov Mofette System (NW Czech Republic). **2020**, 11, 543260	0
783	Gut Microbiomes Differ Among Dietary Types and Stool Consistency in the Captive Red Wolf (). **2020**, 11, 590212	9
782	Selective Bacterial Colonization of the Murine Larynx in a Gnotobiotic Model. **2020**, 11, 594617	2
781	Microbial Shifts Following Five Years of Cover Cropping and Tillage Practices in Fertile Agroecosystems. **2020**, 8,	4
780	VALENCIA: a nearest centroid classification method for vaginal microbial communities based on composition. **2020**, 8, 166	45
779	Perinatal environment shapes microbiota colonization and infant growth: impact on host response and intestinal function. **2020**, 8, 167	20
778	Resource Partitioning Between Phytoplankton and Bacteria in the Coastal Baltic Sea. **2020**, 7,	2
777	Metabolic Responses to Butyrate Supplementation in LF- and HF-Fed Mice Are Cohort-Dependent and Associated with Changes in Composition and Function of the Gut Microbiota. **2020**, 12,	2
776	A haplotype-led approach to increase the precision of wheat breeding. **2020**, 3, 712	31
775	Enduring neurobehavioral effects induced by microbiota depletion during the adolescent period. **2020**, 10, 382	15
774	The microbiota of farmed mink (Neovison vison) follows a successional development and is affected by early life antibiotic exposure. **2020**, 10, 20434	1
773	The Response of Estuarine Ammonia-Oxidizing Communities to Constant and Fluctuating Salinity Regimes. **2020**, 11, 574815	0
772	Distinct Stage Changes in Early-Life Colonization and Acquisition of the Gut Microbiota and Its Correlations With Volatile Fatty Acids in Goat Kids. **2020**, 11, 584742	3
771	Behind Taxonomic Variability: The Functional Redundancy in the Tick Microbiome. **2020**, 8,	9
770	Anti-Tick Microbiota Vaccine Impacts Performance during Feeding. **2020**, 8,	21

769	The gut microbiota is associated with immune cell dynamics in humans. **2020**, 588, 303-307	99
768	Dietary Ginsenoside T19 Supplementation Regulates Glucose and Lipid Metabolism via AMPK and PI3K Pathways and Its Effect on Intestinal Microbiota. **2020**, 68, 14452-14462	12
767	Wild black bears harbor simple gut microbial communities with little difference between the jejunum and colon. **2020**, 10, 20779	3
766	The Epidome - a species-specific approach to assess the population structure and heterogeneity of Staphylococcus epidermidis colonization and infection. **2020**, 20, 362	2
765	Temporal changes in water temperature and salinity drive the formation of a reversible plastic-specific microbial community. **2020**, 96,	6
764	Estimation of Full-Length TprK Diversity in Treponema pallidum subsp.. **2020**, 11,	3
763	Ozone Decreased Enteric Methane Production by 20% in an Rumen Fermentation System. **2020**, 11, 571537	3
762	Prokaryotic Diversity and Distribution Along Physical and Nutrient Gradients in the Tunisian Coastal Waters (South Mediterranean Sea). **2020**, 11, 593540	4
761	Enhancing Phenol Conversion Rates in Saline Anaerobic Membrane Bioreactor Using Acetate and Butyrate as Additional Carbon and Energy Sources. **2020**, 11, 604173	3
760	Shinshu N-07 isolated from fermented L. attenuates visceral fat accumulation induced by high-fat diet in mice. **2020**, 11, 655-667	2
759	Anaerobic Respiration of NOX1-Derived Hydrogen Peroxide Licenses Bacterial Growth at the Colonic Surface. **2020**, 28, 789-797.e5	11
758	Insights into community of photosynthetic microorganisms from permafrost. **2020**, 96,	3
757	Delivery mode and gut microbial changes correlate with an increased risk of childhood asthma. **2020**, 12,	33
756	Critical Factors Facilitating Nitrotoga To Be Prevalent Nitrite-Oxidizing Bacteria in Activated Sludge. **2020**, 54, 15414-15423	14
755	No Tangible Effects of Field-Grown Cisgenic Potatoes on Soil Microbial Communities. **2020**, 8, 603145	4
754	Migratory Zooplankton Excreta and Its Influence on Prokaryotic Communities. **2020**, 7,	7
753	Conversion of Rutin, a Prevalent Dietary Flavonol, by the Human Gut Microbiota. **2020**, 11, 585428	17
752	Identification of Plant DNA in Adults of the Phytoplasma Vector Helps Understanding Its Feeding Behavior. **2020**, 11,	0

751	Clinical and Microbiological Efficacy of Pyrophosphate Containing Toothpaste: A Double-Blinded Placebo-Controlled Randomized Clinical Trial. **2020**, 8,	2
750	A Role for the Microbiota in the Immune Phenotype Alteration Associated with the Induction of Disease Tolerance and Persistent Asymptomatic Infection of in the Chicken. **2020**, 8,	1
749	Multi-modal Single-Cell Analysis Reveals Brain Immune Landscape Plasticity during Aging and Gut Microbiota Dysbiosis. **2020**, 33, 108438	17
748	Fermentation Product Did Not Attenuate Clinical Signs, but Psyllium Husk Has Protective Effects in a Murine Dextran Sulfate Sodium-Induced Colitis Model. **2020**, 4, nzaa159	3
747	Characterizing the cirri and gut microbiomes of the intertidal barnacle Semibalanus balanoides. **2020**, 2, 41	1
746	Soil Microbial Community Profiling and Bacterial Metabolic Activity of Technosols as an Effect of Soil Properties following Land Reclamation: A Case Study from the Abandoned Iron Sulphide and Uranium Mine in Rudki (South-Central Poland). **2020**, 10, 1795	5
745	Determining Soil Microbial Communities and Their Influence on Disease Incidences in Oil Palm () via High-Throughput Sequencing. **2020**, 9,	7
744	New Insights into the Microbial Profiles of Infected Root Canals in Traumatized Teeth. **2020**, 9,	3
743	A Multi-Omics Protocol for Swine Feces to Elucidate Longitudinal Dynamics in Microbiome Structure and Function. **2020**, 8,	3
742	Combinatorial Glycomic Analyses to Direct CAZyme Discovery for the Tailored Degradation of Canola Meal Non-Starch Dietary Polysaccharides. **2020**, 8,	3
741	Cage bedding modifies metabolic and gut microbiota profiles in mouse studies applying dietary restriction. **2020**, 10, 20835	1
740	The Aromatic Plant Clary Sage Shaped Bacterial Communities in the Roots and in the Trace Element-Contaminated Soil More Than Mycorrhizal Inoculation - A Two-Year Monitoring Field Trial. **2020**, 11, 586050	9
739	Bioaugmented Sand Filter Columns Provide Stable Removal of Pesticide Residue From Membrane Retentate. **2020**, 2,	1
738	Hydrogeological Behaviour and Geochemical Features of Waters in Evaporite-Bearing Low-Permeability Successions: A Case Study in Southern Sicily, Italy. **2020**, 10, 8177	2
737	Activity and Diversity of Microorganisms in Root Zone of Plant Species Spontaneously Inhabiting Smelter Waste Piles. **2020**, 25,	3
736	Analysis of microbial compositions: a review of normalization and differential abundance analysis. **2020**, 6, 60	33
735	Distinct gut microbiotas between southern elephant seals and Weddell seals of Antarctica. **2020**, 58, 1018-1026	3
734	Space and Vine Cultivar Interact to Determine the Arbuscular Mycorrhizal Fungal Community Composition. **2020**, 6,	2

733	A multi-disciplinary comparison of great ape gut microbiota in a central African forest and European zoo. **2020**, 10, 19107	5
732	The absence of murine cathelicidin-related antimicrobial peptide impacts host responses enhancing Salmonella enterica serovar Typhimurium infection. **2020**, 12, 53	1
731	Study on the Salivary Microbial Alteration of Men With Head and Neck Cancer and Its Relationship With Symptoms in Southwest China. **2020**, 10, 514943	4
730	Prokaryotic and Fungal Characterization of the Facilities Used to Assemble, Test, and Launch the OSIRIS-REx Spacecraft. **2020**, 11, 530661	2
729	Changes in Microbiota Composition Along the Metamorphosis Developmental Stages of. **2020**, 11, 586678	4
728	Exercise and/or Genistein Treatment Impact Gut Microbiota and Inflammation after 12 Weeks on a High-Fat, High-Sugar Diet in C57BL/6 Mice. **2020**, 12,	3
727	Renewable energy from the solid-state anaerobic digestion of grape marc and cheese whey at high treatment capacity. **2020**, 143, 105880	5
726	Cardiorespiratory performance capacity and airway microbiome in patients following primary repair of esophageal atresia. **2021**, 90, 66-73	2
725	Arsenic mobilization by anaerobic iron-dependent methane oxidation. **2020**, 1,	9
724	Urban Aerobiomes are Influenced by Season, Vegetation, and Individual Site Characteristics. **2021**, 18, 331-344	7
723	Natrix: a Snakemake-based workflow for processing, clustering, and taxonomically assigning amplicon sequencing reads. **2020**, 21, 526	5
722	Fine Particulate Matter Exposure Alters Pulmonary Microbiota Composition and Aggravates Pneumococcus-Induced Lung Pathogenesis. **2020**, 8, 570484	5
721	New Frontiers of Anaerobic Hydrocarbon Biodegradation in the Multi-Omics Era. **2020**, 11, 590049	12
720	Prebiotic Maltose Gel Can Promote the Vaginal Microbiota From BV-Related Bacteria Dominant to in Rhesus Macaque. **2020**, 11, 594065	3
719	Effect of Mycorrhizal Inoculation and Irrigation on Biological Properties of Sweet Pepper Rhizosphere in Organic Field Cultivation. **2020**, 10, 1693	5
718	Rumen epithelial transcriptome and microbiome profiles of rumen epithelium and contents of beef cattle with and without liver abscesses. **2020**, 98,	1
717	Parasite-host ecology: the limited impacts of an intimate enemy on host microbiomes. **2020**, 2, 42	1
716	A Cross-Sectional Study of the Gut Microbiota Composition in Moscow Long-Livers. **2020**, 8,	2

715	Influence of invasive earthworms (Amynthas spp.) on Wisconsin forest soil microbial communities and soil chemistry. **2020**, 149, 107955	6
714	A large-scale assessment of lakes reveals a pervasive signal of land use on bacterial communities. **2020**, 14, 3011-3023	19
713	Chronic G signaling in AgRP neurons does not cause obesity. **2020**, 117, 20874-20880	7
712	Blind assessment of vertebrate taxonomic diversity across spatial scales by clustering environmental DNA metabarcoding sequences. **2020**, 43, 1779-1790	12
711	Host plants and shape the population genetics of sympatric herbivore populations. **2020**, 13, 2740-2753	3
710	: An Overlooked Human Skin Colonizer. **2020**, 8,	7
709	Distinct mechanisms underlying the assembly of microeukaryotic generalists and specialists in an anthropogenically impacted river. **2020**, 748, 141434	14
708	Unravelling microalgal-bacterial interactions in aquatic ecosystems through 16S rRNA gene-based co-occurrence networks. **2023**, 13,	0
707	Co-cultivation is a powerful approach to produce a robust functionally designed synthetic consortium as a live biotherapeutic product (LBP). **2023**, 15,	0
706	Using fecal immmunochemical cartridges for gut microbiome analysis within a colorectal cancer screening program. **2023**, 15,	0
705	Gut Microbiome Composition Reveals the Distinctiveness between the Bengali people and the Indigenous Ethnicities in Bangladesh.	0
704	First insights into the gut microbiome of Diatraea saccharalis: From a sugarcane pest to a reservoir of new bacteria with biotechnological potential. 11,	0
703	Root and rhizosphere fungi associated with the yield of diverse Brassica napus genotypes. **2023**, 25, 100677	0
702	Metagenomic mapping of cyanobacteria and potential cyanotoxin producing taxa in large rivers of the United States. **2023**, 13,	0
701	The role of long-term mineral and manure fertilization on P species accumulation and phosphate-solubilizing microorganisms in paddy red soils. **2023**, 9, 101-116	0
700	Comprehensive elucidation of the terroir of Korean kimchi through the study of recipes, metabolites, microbiota, and sensory characteristics. **2023**, 166, 112614	0
699	Contribution of preoperative gut microbiota in postoperative neurocognitive dysfunction in elderly patients undergoing orthopedic surgery. 15,	0
698	Interleukin-23 receptor signaling impairs the stability and function of colonic regulatory T´cells. **2023**, 42, 112128	0

697	Epilithic Bacterial Assemblages on Subtidal Rocky Reefs: Variation Among Alternative Habitats at Ambient and Enhanced Nutrient Levels.	0
696	Biological CH4 production from H2/CO2 streams: Influence of trace metals concentration on the hydrogenotrophic process. **2023**, 11, 109528	0
695	Active dry yeast supplementation benefits ruminal fermentation, bacterial community, blood immunoglobulins, and growth performance in young dairy goats, but not for intermittent supplementation. **2023**,	0
694	Dynamic changes of the gut microbial colonization in preterm infants with different time points after birth. 14,	0
693	A needle in a haystack: A new metabarcoding approach to survey diversity at the species level of Arcellinida (Amoebozoa: Tubulinea).	0
692	Tree-distance and tree-species effects on soil biota in a temperate agroforestry system.	0
691	Chironomus riparius Larval Gut Bacteriobiota and Its Potential in Microplastic Degradation.	0
690	Moss and Liverwort Covers Structure Soil Bacterial and Fungal Communities Differently in the Icelandic Highlands.	0
689	Within-species variation in the gut microbiome of fish is driven by the interaction of light intensity and genetic background.	0
688	Effects of feeding Saccharomyces cerevisiae fermentation postbiotic on the fecal microbial community of Holstein dairy calves. **2023**, 5,	0
687	Impact of Molasses on Ruminal Volatile Fatty Acid Production and Microbiota Composition In Vitro. **2023**, 13, 728	0
686	Crosstalk between microbiome, regulatory T cells and HCA2 orchestrates the inflammatory response in a murine psoriasis model. 14,	0
685	Hazardous potential evaluation of biochar exposure on mice through analyses of gut-microbiome and fatty acids in brain. **2023**, 461, 142006	0
684	Strong restructuration of skin microbiota during captivity challenges ex-situ conservation of amphibians. 14,	0
683	Assessing the Effects of Rotifer Feed Enrichments on Turbot (Scophthalmus maximus) Larvae and Post-Larvae Gut-Associated Bacterial Communities. **2023**, 11, 520	0
682	Best practices for generating and analyzing 16S rRNA amplicon data to track coral microbiome dynamics. 13,	0
681	Sputum bacterial load and bacterial composition correlate with lung function and are altered by long-term azithromycin treatment in children with HIV-associated chronic lung disease. **2023**, 11,	0
680	Awaking the dormant virome in the rhizosphere.	0

679	Comparison of genomic and transcriptional microbiome analysis in gastric cancer patients and healthy individuals. 29, 1202-1218	0
678	Co-localization of antibiotic resistance genes is widespread in the infant gut microbiome and associates with an immature gut microbial composition.	0
677	Gut microbiome composition is associated with long-term disability worsening in multiple sclerosis. **2023**, 15,	0
676	Targeting the gut-lung axis by synbiotic feeding to infants in a randomized controlled trial. **2023**, 21,	0
675	The Effects of Probiotics on Small Intestinal Microbiota Composition, Inflammatory Cytokines and Intestinal Permeability in Patients with Non-Alcoholic Fatty Liver Disease. **2023**, 11, 640	1
674	A new competitive strategy to unveil the antibiotic-producing Actinobacteria.	0
673	Randomized controlled trial demonstrates response to a probiotic intervention for metabolic syndrome that may correspond to diet. **2023**, 15,	0
672	Microbial Diversity, Community Turnover, and Putative Functions in Submarine Canyon Sediments under the Action of Sedimentary Geology. **2023**, 11,	0
671	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. **2023**, 24,	0
670	Saliva microbiome alterations in dental fluorosis population. **2023**, 15,	0
669	Metataxonomic insights in the distribution of Lactobacillaceae in foods and food environments. **2023**, 391-393, 110124	0
668	Metagenomics and metabarcoding experimental choices and their impact on microbial community characterization in freshwater recirculating aquaculture systems. **2023**, 18,	1
667	Detecting and validating influential organisms for rice growth: An ecological network approach.	0
666	Effect of in vitro cultivation on human gut microbiota composition using 16S rDNA amplicon sequencing and metabolomics approach. **2023**, 13,	0
665	Community Characteristics of Soil Ectomycorrhizal Fungi under Different Forests in the Sandy Areas of Northeastern China.	0
664	Elevated atmospheric CO2 concentrations caused a shift of the metabolically active microbiome in vineyard soil. **2023**, 23,	0
663	The Long-Term Straw Returning to Paddy Land Altered the Soil Phosphate Fractions and Composition of Microbial Communities.	0
662	HIV, asymptomatic STI, and the rectal mucosal immune environment among young men who have sex with men.	0

661	Calcium promotes persistent soil organic matter by altering microbial transformation of plant litter.	0
660	Bacterial community structure in the alcyoniid Lobophytum pauciflorum.	0
659	The Impact of Sewage-Sludge- and Olive-Mill-Waste-Derived Biochar Amendments to Tomato Cultivation. **2023**, 15, 3879	0
658	Passion fruit plants alter the soil microbial community with continuous cropping and improve plant disease resistance by recruiting beneficial microorganisms. **2023**, 18, e0281854	0
657	Life stage and vaccination shape the gut microbiome of hatchery-reared Atlantic salmon (Salmo salar).	0
656	Community composition and the environment modulate the population dynamics of type VI secretion in human gut bacteria.	0
655	Short-chain fatty acids improve inflamm-aging and acute lung injury in old mice. **2023**, 324, L480-L492	0
654	The use of different 16S rRNA gene variable regions in biogeographical studies.	0
653	The vaginal microbiota among the different status of human papillomavirus infection and bacterial vaginosis. **2023**, 95,	0
652	Taxonomic composition, community structure and molecular novelty of microeukaryotes in a temperate oligomesotrophic lake as revealed by metabarcoding. **2023**, 13,	0
651	Multi-scale Investigation of Ammonia-Oxidizing Microorganisms in Biofilters Used for Drinking Water Treatment. **2023**, 57, 3833-3842	0
650	Spatial and Sexual Divergence of Gut Microbial Communities in Field Cricket Teleogryllus occipitalis (Orthoptera: Gryllidae).	0
649	Machined silicon traps for capturing novel bacterial communities and strainsin-situ.	0
648	Malaria Molecular Surveillance in the Peruvian Amazon with a Novel Highly Multiplexed Plasmodium falciparum AmpliSeq Assay. **2023**, 11,	0
647	Fecal Microbiota, Forage Nutrients, and Metabolic Responses of Horses Grazing Warm- and Cool-Season Grass Pastures. **2023**, 13, 790	0
646	Microbiome diversity, composition and assembly in a California citrus orchard. 14,	0
645	Invasion by an ecosystem engineer changes biotic interactions between native and non-native taxa. **2023**, 13,	0
644	Oral mucosal breaks trigger anti-citrullinated bacterial and human protein antibody responses in rheumatoid arthritis. **2023**, 15,	0

643	Effects of dielectric barrier discharge plasma and plasma-activated water on the surface microbial diversity of fresh goji berries during storage. **2023**, 313, 111920	0
642	The waxy mutation in sorghum and other cereal grains reshapes the gut microbiome by reducing levels of multiple beneficial species. **2023**, 15,	0
641	Composition and biodiversity of soil and root-associated microbiome in Vitis vinifera cultivar Lambrusco distinguish the microbial terroir of the Lambrusco DOC protected designation of origin area on a local scale. 14,	0
640	Effect of fabric mulch ground covers on lemon trees rhizosphere microbiome in Florida flatwood soils. 3,	0
639	Do antimicrobial peptide levels alter performance of insect-based aquaculture feeds □a study using genetic models of insect immune activation. 1-16	0
638	Association Studies on Gut and Lung Microbiomes in Patients with Lung Adenocarcinoma. **2023**, 11, 546	0
637	Shifts from conventional horticulture to agroecology impacts soil fungal diversity in Central Argentina. **2023**, 22,	0
636	Persistence and Potential Atmospheric Ramifications of Ice-Nucleating Particles Released from Thawing Permafrost. **2023**, 57, 3505-3515	0
635	Microbial methane cycling in sediments of Arctic thermokarst lagoons. **2023**, 29, 2714-2731	0
634	Comparing the transmission of carbapenemase-producing and extended-spectrum beta-lactamase-producingEscherichia colibetween broiler chickens.	0
633	Microbiota-derived 3-IAA influences chemotherapy efficacy in pancreatic cancer. **2023**, 615, 168-174	0
632	Distinct Ecological Processes Mediate Domain-Level Differentiation in Microbial Spatial Scaling. **2023**, 89,	0
631	Drought-induced recruitment of specific root-associated bacteria enhances adaptation of alfalfa to drought stress. 14,	0
630	Upper respiratory tract microbiota dynamics following COVID-19 in adults. **2023**, 9,	0
629	Metabolic and microbial changes in light-vented bulbul during recent northward range expansion.	0
628	The spatial patterns of diversity and their relationships with environments in rhizosphere microorganisms and host plants differ along elevational gradients. 14,	0
627	Key soil physicochemical properties regulating microbial community structure under vegetation restoration in a karst region.	0
626	Diet and high altitude strongly drive convergent adaptation of gut microbiota in wild macaques, humans, and dogs to high altitude environments. 14,	0

625	Fine-scale evaluation of two standard 16S rRNA gene amplicon primer pairs for analysis of total prokaryotes and archaeal nitrifiers in differently managed soils. 14,	0
624	Persistent flocks of diverse motile bacteria in long-term incubations of electron-conducting cable bacteria, Candidatus Electronema aureum. 14,	0
623	Maximizing the reliability and the number of species assignments in metabarcoding studies using a curated regional library and a public repository. 7,	0
622	Biophotoelectrochemical process co-driven by dead microalgae and live bacteria. **2023**, 17, 712-719	0
621	Influence of Sex on Respiratory Syncytial Virus Genotype Infection Frequency and Nasopharyngeal Microbiome. **2023**, 97,	0
620	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N2O cycling. **2023**, 6,	0
619	When phytoplankton do not bloom: the case of the dinoflagellate Lepidodinium chlorophorum in southern Brittany (France) assessed by environmental DNA. **2023**, 212, 102999	0
618	Tail fell syndrome impacts intestinal microbiota in porcupinefish (Diodon hystrix). 10,	0
617	Correlation Between Microbial Community and Hatching Failure in Loggerhead Sea Turtle Caretta caretta.	1
616	Data on lung and intestinal microbiome after air pollution exposure in ageing rats. **2023**, 47, 109004	0
615	Diversity and Distribution of Harmful Algal Bloom Species from Seamount to Coastal Waters in the South China Sea. **2023**, 11,	0
614	Crop rotations increased soil ecosystem multifunctionality by improving keystone taxa and soil properties in potatoes. 14,	0
613	Cover Crops Modulate the Response of Arbuscular Mycorrhizal Fungi to Water Supply: A Field Study in Corn. **2023**, 12, 1015	1
612	Three-Dimensional Humanized Model of the Periodontal Gingival Pocket to Study Oral Microbiome. 2205473	0
611	Matrine alleviates depressive-like behaviors via modulating microbiota□gut□brain axis in CUMS-induced mice. **2023**, 21,	0
610	A Distinct Nasal Microbiota Signature in Peritoneal Dialysis Patients.	0
609	Spatial and Temporal Dynamics at an Actively Silicifying Hydrothermal System.	0
608	The Taxonomic Structure of the Prokaryotic Biome of the Rhizosphere Triticum Aestivum L. Depending on the Variety and Application of Associative Bacteria. **2023**, 1878-1887	0

607	Microbiota of Urine, Glans and Prostate Biopsies in Patients with Prostate Cancer Reveals a Dysbiosis in the Genitourinary System. **2023**, 15, 1423	0
606	Comparing the gut microbiome of obese, African American, older adults with and without mild cognitive impairment. **2023**, 18, e0280211	0
605	Avian Malaria Parasites Modulate Gut Microbiome Assembly in Canaries. **2023**, 11, 563	0
604	Concentrations of dissolved dimethyl sulfide (DMS), methanethiol and other trace gases in context of microbial communities from the temperate Atlantic to the Arctic Ocean. **2023**, 20, 851-867	1
603	Reprogramming of the gut microbiota following feralization in Sus scrofa. **2023**, 5,	0
602	Estuarine Sediment Microbiomes from a Chronosequence of Restored Urban Salt Marshes.	0
601	Anthropogenic Nitrate Contamination Impacts Nitrous Oxide Emissions and Microbial Communities in the Marchica Lagoon (Morocco). **2023**, 15, 4077	0
600	Prebiotic Consumption Alters Microbiota but Not Biological Markers of Stress and Inflammation or Mental Health Symptoms in Healthy Adults: A Randomized, Controlled, Crossover Trial. **2023**, 153, 1283-1296	0
599	Rise and metabolic roles of Vibrio during the fermentation of crab paste. 10,	0
598	Characterization of Gut Microbiome Composition in Patients with Triple-Negative Breast Cancer Treated with Neoadjuvant Chemotherapy.	0
597	Biostimulation ofSalicornia europaeaL. crops with plant growth-promoting bacteria in laboratory and field conditions: effects on growth and metabolite profile. **2023**, 134,	0
596	Age-Dependent and Body Composition–Dependent Association of Child Gut Microbial Enterotype With Puberty Timing: A Chinese Cohort.	0
595	The bacterial communities in vagina of different Candida species-associated vulvovaginal candidiasis. **2023**, 177, 106037	0
594	Responses of Nitrous Oxide Emissions and Bacterial Communities to Experimental Freeze–Thaw Cycles in Contrasting Soil Types. **2023**, 11, 593	0
593	Benchmarking and Validation of a Bioinformatics Workflow for Meat Species Identification Using 16S rDNA Metabarcoding. **2023**, 12, 968	0
592	Thermal Selection of Microbial Communities and Preservation of Microbial Function in Guaymas Basin Hydrothermal Sediments. **2023**, 89,	0
591	Breed and ruminal fraction effects on bacterial and archaeal community composition in sheep. **2023**, 13,	0
590	Homogeneous Environmental Selection Structures the Bacterial Communities of Benthic Biofilms in Proglacial Floodplain Streams. **2023**, 89,	0

589	Soil Properties Correlate with Microbial Community Structure in Qatari Arid Soils. **2023**, 11,	0
588	100 years of anthropogenic impact causes changes in freshwater functional biodiversity.	0
587	Compositional Alteration of Gut Microbiota in Psoriasis Treated with IL-23 and IL-17 Inhibitors. **2023**, 24, 4568	0
586	Alteration of the Gut Microbiota in Missed Abortion.	0
585	Short-Term Impact of Oxytetracycline Administration on the Fecal Microbiome, Resistome and Virulome of Grazing Cattle. **2023**, 12, 470	0
584	The vaginal microbiota of pregnant women varies with gestational age, maternal age, and parity.	0
583	Longitudinal study of the short- and long-term effects of hospitalisation and oral trimethoprim-sulfadiazine administration on the equine faecal microbiome and resistome. **2023**, 11,	0
582	Diversity of Microbial Communities Associated with Epilithic Macroalgae in Different Coral Reef Conditions and Damselfish Territories of the Gulf of Thailand. **2023**, 11, 514	0
581	Distinct Growth Responses of Tundra Soil Bacteria to Short-Term and Long-Term Warming. **2023**, 89,	0
580	Red Meat Intake, Indole-3-Acetate, and Dorea longicatena Together Affect Insulin Resistance after Gastric Bypass. **2023**, 15, 1185	0
579	Bacterial communities in the nasal passage of postviral olfactory dysfunction patients.	0
578	Successful invasions to freshwater systems double with climate warming. **2023**, 68, 953-962	0
577	The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. **2023**, 8,	1
576	Particle Size Matters: Distribution, Source, and Seasonality Characteristics of Airborne and Pathogenic Bacteria in Wastewater Treatment Plants. **2023**, 14, 465	0
575	Nutrients strengthen density dependence of per-capita growth and mortality rates in the soil bacterial community. **2023**, 201, 771-782	0
574	Estimating number of European eel (Anguilla anguilla) individuals using environmental DNA and haplotype count in small rivers. **2023**, 13,	0
573	Root exudate concentrations of indole-3-acetic acid (IAA) and abscisic acid (ABA) affect maize rhizobacterial communities at specific developmental stages. **2023**, 99,	0
572	Keystone taxa responsible for the microbial community stability and performance of activated sludges.	0

571	Comparison of carbon sources in a partial denitrification/anammox MBBR using glycerol, acetate, and methanol. **2023**, 9, 1041-1052	○
570	Inhibitory mechanisms on dry anaerobic digestion: Ammonia, hydrogen and propionic acid relationship. **2023**, 161, 29-42	○
569	Comparing environmental DNA collection methods for sampling community composition on marine infrastructure. **2023**, 283, 108283	○
568	Changes in Bacterial Communities and Their Effects on Soil Carbon Storage in Spartina alterniflora Invasion Areas, Coastal Wetland Bare Flats, and Sueada salsa Areas. **2023**, 20, 4308	○
567	SCRAPT:an iterative algorithm for clustering large 16S rRNA gene data sets.	○
566	Secretory IgM (sIgM) is an ancient master regulator of microbiota homeostasis and metabolism.	○
565	Disturbed rhythmicity of intestinal hydrogen peroxide alters gut microbial oscillations in BMAL1-deficient monkeys. **2023**, 42, 112183	○
564	Microbial community shift on artificial biological reef structures (ABRs) deployed in the South China Sea. **2023**, 13,	○
563	Composition and evolution of the gut microbiota of growing puppies is impacted by their birth weight.	○
562	Spatiotemporal dynamics of benthic bacterial communities in the Perdido Fold Belt, Northwestern Gulf of Mexico. 10,	○
561	Dietary protein to starch metabolizable energy ratios alter growth performance and gastrointestinal microbiota of calves. 14,	○
560	Global Meta-analysis of Urine Microbiome: Colonization of Polycyclic Aromatic Hydrocarbon-degrading Bacteria Among Bladder Cancer Patients. **2023**, 6, 190-203	○
559	Amplicons, Metagenomes, and Metatranscriptomes from Sediment and Water. **2023**, 12,	○
558	Microbial community profiling and culturing reveal functional groups of bacteria associated with Thai commercial stingless worker bees (Tetragonula pagdeni). **2023**, 18, e0280075	○
557	Leaf Microbiome Data for European Cultivated Grapevine (Vitis vinifera) During Downy Mildew (Plasmopara viticola) Epidemics in Three Wine-Producing Regions in France.	○
556	Study on the correlation between microbial communities with physicochemical properties and flavor substances in the Xiasha round of cave-brewed sauce-flavor Baijiu. 14,	○
555	The endometrial microbiota of women with or without a live birth within 12´months after a first failed IVF/ICSI cycle. **2023**, 13,	○
554	Intestine microbiota and SCFAs response in naturally Cryptosporidium-infected plateau yaks. 13,	○

553	Diversity and function of soybean rhizosphere microbiome under nature farming. 14,	0
552	The Microbiome of Complicated Diverticulitis: An Imbalance of Sulfur-Metabolizing Bacteria. **2023**, 66, 707-715	0
551	Geographic characteristics and environmental variables determine the diversities and assembly of the algal communities in interconnected river-lake system. **2023**, 233, 119792	0
550	Divergent TLR2 and TLR4 Activation by Fungal Spores and Species Diversity in Dust from Waste Sorting Plants. **2023**, 89,	0
549	Potential Exposure to Respiratory and Enteric Bacterial Pathogens among Wastewater Treatment Plant Workers, South Africa. **2023**, 20, 4338	0
548	Composition and variability of core phyllosphere fungal mycobiota on field-grown broccoli. **2023**, 18,	0
547	Evaluation of the rbcL marker for metabarcoding of marine diatoms and inference of population structure of selected genera. 14,	0
546	Neighboring plant community attributes drive rhizobiome assemblages of a focal plant in a Kobresia meadow. **2023**, 432, 116409	0
545	Changes in upper airways microbiota in ventilator-associated pneumonia. **2023**, 11,	0
544	Analysis of an Indian colorectal cancer faecal microbiome collection demonstrates universal colorectal cancer-associated patterns, but closest correlation with other Indian cohorts. **2023**, 23,	0
543	Soil and tree phyllosphere microbial communities differ between coniferous and broadleaf deciduous boreal forests.	0
542	Loss of soil carbon and nitrogen indicates climate change-induced alterations in a temperate forest ecosystem. **2023**, 148, 110055	0
541	Bulk soil microbial reservoir or plant recruitment dominates rhizosphere microbial community assembly: Evidence from the rare, endangered Lauraceae species Cinmaomum migao. **2023**, 148, 110071	0
540	Australian soil microbiome: A first sightseeing regional prediction driven by cycles of soil temperature and pedogenic variations.	0
539	Winners and Losers of Atlantification: The Degree of Ocean Warming Affects the Structure of Arctic Microbial Communities. **2023**, 14, 623	0
538	Temporal dynamics of the cecal and litter microbiome of chickens raised in two separate broiler houses. 14,	0
537	Variety of rumen microbial populations involved in biohydrogenation related to individual milk fat percentage of dairy cows. 10,	0
536	Microbiome analysis revealed distinct microbial communities occupying different sized nodules in field-grown peanut. 14,	0

535	Prokaryotic community dynamics and nitrogen-cycling genes in an oxygen-deficient upwelling system during La Niâ and El Niê conditions.	o
534	A bacterial sulfoglycosidase highlights mucin O-glycan breakdown in the gut ecosystem.	o
533	Microbiomes of a disease-resistant genotype of Acropora cervicornis are resistant to acute, but not chronic, nutrient enrichment. **2023**, 13,	o
532	Unraveling Key Features of Microbial Alpha-Diversity Metrics and Their Practical Applications.	o
531	Exploring the mycobiome and arbuscular mycorrhizal fungi associated with the rizosphere of the genus Inga in the pristine Ecuadorian Amazon. 4,	o
530	Gut microbiome is linked to functions of peripheral immune cells in transition cows during excessive lipolysis. **2023**, 11,	o
529	Holo-omics analysis reveals the influence of gut microbiota on obesity indicators in Jinhua pigs.	o
528	Participants in the Trans-Antarctic Winter Traverse Expedition Showed Increased Bacterial Load and Diversity in Saliva but Maintained Individual Differences within Stool Microbiota and Across Metabolite Fingerprints. **2023**, 24, 4850	o
527	Development and validation of an experimental life support system to study the impact of ultraviolet B radiation and temperature on coral reef microbial communities.	o
526	Bacterial Communities in Lanna Fermented Soybeans from Three Different Ethnolinguistic Groups in Northern Thailand. **2023**, 11, 649	o
525	Decoupling Fe0 Application and Bioaugmentation in Space and Time Enables Microbial Reductive Dechlorination of Trichloroethene to Ethene: Evidence from Soil Columns. **2023**, 57, 4167-4179	o
524	First morphological and molecular investigation of the mycobiota associated with Astragalus nebrodensis in its natural environment (Madonie mountains, Sicily). 1-11	o
523	Disparate population and holobiont structure of pocilloporid corals across the Red Sea gradient demonstrate species-specific evolutionary trajectories.	o
522	Local environment drives rapid shifts in composition and phylogenetic clustering of seagrass microbiomes. **2023**, 13,	o
521	Manipulation in grazing, viral pressure and resource availability leads to success in the isolation of abundant marine bacteria.	o
520	Effects of compound prebiotics as prophylactic and therapeutic supplementation in a mouse model of acute colitis. **2023**, 107, 2597-2609	o
519	Influence of adrenalectomy on the gut microbiome and MDMA-induced hyperthermia. **2023**, 945, 175643	o
518	Metatranscriptomics and metabarcoding reveal spatiotemporal shifts in fungal communities and their activities in Chinese coastal waters.	o

517	Soil Inoculation and Blocker-Mediated Sequencing Show Effects of the Antibacterial T6SS on Agrobacterial Tumorigenesis and Gallobiome.	0
516	Encouraging news for in situ conservation: Translocation of salamander larvae has limited impacts on their skin microbiota.	0
515	Predicting Neurodegenerative Disease Using Prepathology Gut Microbiota Composition: a Longitudinal Study in Mice Modeling Alzheimer□ Disease Pathologies. **2023**, 11,	0
514	Habitat and tree species identity shape aboveground and belowground fungal communities in central European forests. 14,	0
513	Alterations in Fecal Microbiota Linked to Environment and Sex in Red Deer (Cervus elaphus). **2023**, 13, 929	0
512	Microbial Populations in Ruminal Liquid Samples from Young Beefmaster Bulls at Both Extremes of RFI Values. **2023**, 11, 663	0
511	Core endophytic mycobiome in Ulmus minor and its relation to Dutch elm disease resistance. 14,	0
510	Lactobacillus gasseri LG-G12 Restores Gut Microbiota and Intestinal Health in Obesity Mice on Ceftriaxone Therapy. **2023**, 12, 1092	0
509	Rhizosphere Microbiomes of Amaranthus spp. Grown in Soils with Anthropogenic Polyelemental Anomalies. **2023**, 13, 759	0
508	Endogenous small intestinal microbiome determinants of transient colonisation efficiency by bacteria from fermented dairy products: a randomised controlled trial. **2023**, 11,	0
507	Nested PCR Approach for petB Gene Metabarcoding of Marine Synechococcus Populations. **2023**, 11,	0
506	Periodontitis salivary microbiota exacerbates nonalcoholic fatty liver disease in high-fat diet-induced obese mice. **2023**, 26, 106346	0
505	Giardia duodenalis Colonization Slightly Affects Gut Microbiota and Hematological Parameters in Clinically Healthy Dogs. **2023**, 13, 958	0
504	Comparative analysis of two nonlethal methods for the study of the gut bacterial communities in wild lizards.	0
503	The commensal protistTritrichomonas musculusexhibits a dynamic life cycle that induces B cell-modulated remodeling of the gut microbiota.	0
502	Roles of microbiota in autoimmunity in Arabidopsis.	0
501	Moss and underlying soil bacterial community structures are linked to moss functional traits. **2023**, 14,	0
500	Positive response of host root-associated bacterial community and soil nutrients to inhibitory parasitism of dodder.	0

499	Core and conditionally rare taxa as indicators of agricultural drainage ditch and stream health and function. **2023**, 23,	O
498	Fine characterization and microbiota assessment as keys to understanding the positive effect of standardized natural citrus extract on broiler chickens. **2023**, 101,	O
497	Productive and physiological implications of top-dress addition of branched-chain amino acids and arginine on lactating sows and offspring. **2023**, 14,	O
496	Environmental DNA phylogeography: Successful reconstruction of phylogeographic patterns of multiple fish species from cups of water.	O
495	Effects of paraprobiotics on bile acid metabolism and liver health in largemouth bass (Micropterus salmoides) fed a cottonseed protein concentrate-based diet. **2023**,	O
494	Earthworm-Driven Changes in Soil Chemico-Physical Properties, Soil Bacterial Microbiota, Tree/Tea Litter Decomposition, and Plant Growth in a Mesocosm Experiment with Two Plant Species. **2023**, 12, 1216	O
493	Stay in the loop: lessons learned about the microbial water quality in pipe loops transitioned from conventional to direct potable reuse water.	O
492	Nasal Bacteriomes of Patients with Asthma and Allergic Rhinitis Show Unique Composition, Structure, Function and Interactions. **2023**, 11, 683	O
491	Age-Related Rhizosphere Analysis of Coffea arabica Plants. **2023**, 80,	O
490	Antibiotic Resistance Gene Variant Sequencing is Necessary to Reveal the Complex Dynamics of Immigration from Sewers to Activated Sludge.	O
489	Eelgrass (Zosteraspp.) associated phytomyxids are host-specific congeneric parasites and predominant eukaryotes in the eelgrass rhizosphere on a global scale.	O
488	Multiplexed Amplicon Sequencing Reveals High Sequence Diversity of Antibiotic Resistance Genes in Qubec Sewers.	O
487	Microclimate is a strong predictor of the native and invasive plant-associated soil microbiome on San Cristóbal Island, Galápagos archipelago.	O
486	Climate Change Factors Interact to Shift Functional Microbial Composition in Peatlands.	O
485	Mother-to-infant microbiota transmission and infant microbiota development across multiple body sites. **2023**, 31, 447-460.e6	O
484	Litter Matters: The Importance of Decomposition Products for Soil Bacterial Diversity and abundance of key groups of the N cycle in Tropical Areas.	O
483	Sample Collection, DNA Extraction, and Library Construction Protocols of the Human Microbiome Studies in the International Human Phenome Project.	O
482	Captive and urban environments are associated with distinct gut microbiota in deer mice (Peromyscus maniculatus). **2023**, 19,	O

481	Synergistic effect of biotic and abiotic factors drives microbiota succession and assembly in medium-temperature Daqu.	0
480	Decreased Paneth cell □defensins promote fibrosis in a choline-deficient L-amino acid-defined high-fat diet-induced mouse model of nonalcoholic steatohepatitis via disrupting intestinal microbiota. **2023**, 13,	0
479	External and internal microbiomes of Antarctic nematodes are distinct, but more similar to each other than the surrounding environment. **2023**, 55,	0
478	Analysis of the effect of hyaluronic acid on intestinal flora and its metabolites in diabetic mice via high-throughput sequencing and nontargeted metabolomics. **2023**, 103, 105496	0
477	Leaf microbiome data for European beech (Fagus sylvatica) at the leaf and canopy scales collected in a gallery forest in South-West France. **2023**, 80,	0
476	Succession Patterns of Microbial Composition and Activity following the Diesel Spill in an Urban River. **2023**, 11, 698	0
475	Alterations in bacterial community dynamics from noncancerous to Gastric cancer. 14,	0
474	Body Metrics and the Gut Microbiome in Response to Macronutrient Limitation in the Zebrafish Danio rerio. **2023**, 7, 100065	0
473	IL-22 alters gut microbiota composition and function to increase aryl hydrocarbon receptor activity in mice and humans. **2023**, 11,	0
472	Biotic interactions contribute more than environmental factors and geographic distance to biogeographic patterns of soil prokaryotic and fungal communities. 14,	0
471	Identification of the intestinal microbes associated with muscle strength.	0
470	Water chlorination increases the relative abundance of an antibiotic resistance marker in developing sourdough starters.	0
469	□Glucan attenuates cognitive impairment of APP / PS1 mice via regulating intestinal flora and its metabolites.	0
468	Reciprocal influence of soil, phyllosphere and aphid microbiomes.	0
467	Trophic interactions in microbiomes influence plant host population size and ecosystem function.	0
466	Characterization of the Lower Airways and Oral Microbiota in Healthy Young Persons in the Community. **2023**, 11, 841	0
465	Bacterial aerobic methane cycling by the marine sponge-associated microbiome. **2023**, 11,	0
464	Changes in the bacterial community colonizing extracted and non-extracted tannin-rich plants in the rumen of dromedary camels. **2023**, 18, e0282889	0

463	Characterization of skin- and intestine microbial communities in migrating high Arctic lake whitefish and cisco.	1
462	Microbiome–Metabolome Reveals the Contribution of the Gut–Testis Axis to Sperm Motility in Sheep (Ovis aries). **2023**, 13, 996	0
461	Prolonged Antibiotic Exposure during Adolescence Dysregulates Liver Metabolism and Promotes Adiposity in Mice. **2023**,	0
460	Basal Diet Fed to Recipient Mice Was the Driving Factor for Colitis and Colon Tumorigenesis, despite Fecal Microbiota Transfer from Mice with Severe or Mild Disease. **2023**, 15, 1338	0
459	Uncovering the link between gut microbiome, highly processed food consumption and diet quality through bioinformatics methods.	0
458	Tillage homogenizes soil bacterial communities in microaggregate fractions by facilitating dispersal.	0
457	Association of aberrant brain network dynamics with gut microbial composition uncovers disrupted brain–gut–microbiome interactions in irritable bowel syndrome: Preliminary findings.	0
456	Differential contribution of nitrifying prokaryotes to nitrification in groundwater.	0
455	Individual variation in the avian gut microbiota: The influence of host state and environmental heterogeneity.	0
454	Spinach (Spinacia oleracea) as green manure modifies the soil nutrients and microbiota structure for enhanced pepper productivity. **2023**, 13,	0
453	The impact of diet and ethnicity on gut microbiota variation in irritable bowel syndrome: A multi-center study.	0
452	16S Amplicon Metabarcoding of the Nest Materials of Native Australian Stingless Bees. **2023**, 12,	0
451	Predicting metabolomic profiles from microbial composition through neural ordinary differential equations. **2023**, 5, 284-293	0
450	Evaluation of DNA metabarcoding for identifying fish eggs: a case study on the West Florida Shelf. 11, e15016	0
449	Bacterial Diversity Analysis of Chaozhou Sauerkraut Based on High-Throughput Sequencing of Different Production Methods. **2023**, 9, 282	0
448	Integrated multiomic wastewater-based epidemiology can elucidate population-level dietary behaviour and inform public health nutrition assessments. **2023**, 4, 257-266	0
447	Microbial Composition on Abandoned and Reclaimed Mining Sites in the Komi Republic (North Russia). **2023**, 11, 720	0
446	Facilitation of non-indigenous ascidian by marine eco-engineering interventions at an urban site. **2023**, 39, 80-93	0

445	Fish eDNA detections in ports mirror fishing fleet activities and highlight the spread of non-indigenous species in the Mediterranean Sea. **2023**, 189, 114792	0
444	Thrive or survive: prokaryotic life in hypersaline soils. **2023**, 18,	0
443	Tumor bacterial markers diagnose the initiation and four stages of colorectal cancer. 13,	0
442	Assessment of multidimensional healthcare parameters in Japanese adults for developing a virtual human generative model: protocol for an observational study (Preprint).	0
441	The Oral Microbiome as Mediator between Oral Hygiene and Its Impact on Nasopharyngeal Carcinoma. **2023**, 11, 719	0
440	Vaginal and neonatal microbiota in pregnant women with preterm premature rupture of membranes and consecutive early onset neonatal sepsis. **2023**, 21,	1
439	Beyond purified dietary fibre supplements: Compositional variation between cell wall fibre from different plants influences human faecal microbiota activity and growth in vitro.	0
438	Environmental factors and host genotype control foliar epiphytic microbial community of wild soybeans across China. 14,	0
437	From a cell model to a fish trial: Immunomodulatory effects of heat-killed Lactiplantibacillus plantarum as a functional ingredient in aquafeeds for salmonids. 14,	0
436	Postbiotics from Pichia kudriavzevii promote intestinal health performance through regulation of Limosilactobacillus reuteri in weaned piglets.	0
435	The tropical cookbook: Termite diet and phylogenetics□over geographical origin□drive the microbiome and functional genetic structure of nests. 14,	0
434	Assessment of fungal spores and spore-like diversity in environmental samples by targeted lysis. **2023**, 23,	0
433	Trophic diversification and parasitic invasion as ecological niche modulators for gut microbiota of whitefish. 14,	0
432	Acetoclastic archaea adaptation under increasing temperature in lake sediments and wetland soils from Alaska.	0
431	The climate-driven distribution and response to global change of soil-borne pathogens in agroecosystems. **2023**, 32, 766-779	0
430	Transition of an estuarine benthic meiofauna assemblage 1.7 and 2.8 years after a mining disaster. 11, e14992	0
429	Fibre fermentation and pig faecal microbiota composition are affected by the interaction between sugarcane fibre and (poly)phenols in vitro. **2023**, 74, 219-233	0
428	Different and unified responses of soil bacterial and fungal community composition and predicted functional potential to 3 years□drought stress in a semiarid alpine grassland. 14,	0

427	A Longitudinal Characterization of the Seminal Microbiota and Antibiotic Resistance in Yearling Beef Bulls Subjected to Different Rates of Gain. **2023**, 11,	0
426	Dietary fibre supplementation enhances radiotherapy tumour control and alleviates intestinal radiation toxicity.	0
425	Trade-Offs between Competitive Ability and Resistance to Top-Down Control in Marine Microbes.	0
424	Epilepsy and Giardia intestinalis infection impact the gut microbiome of canine species..	0
423	Ubiquitous, B12-dependent virioplankton utilizing ribonucleotide triphosphate reductase demonstrate interseasonal dynamics and associate with a diverse range of bacterial hosts in the pelagic ocean.	0
422	The dietary sweetener sucralose is a negative modulator of T cell-mediated responses. **2023**, 615, 705-711	0
421	Microbial and Viral Genome and Proteome Nitrogen Demand Varies across Multiple Spatial Scales within a Marine Oxygen Minimum Zone.	0
420	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. 14,	0
419	Deciphering the gut microbiome of grass carp through multi-omics approach.	0
418	NEMoE: a nutrition aware regularized mixture of experts model to identify heterogeneous diet-microbiome-host health interactions. **2023**, 11,	0
417	Early Probiotic Supplementation of Healthy Term Infants with Bifidobacterium longum subsp. infantis M-63 Is Safe and Leads to the Development of Bifidobacterium-Predominant Gut Microbiota: A Double-Blind, Placebo-Controlled Trial. **2023**, 15, 1402	0
416	Gut microbiota in a mouse model of obesity and peripheral neuropathy associated with plasma and nerve lipidomics and nerve transcriptomics. **2023**, 11,	0
415	Congruent downy mildew-associated microbiomes reduce plant disease and function as transferable resistobiomes.	0
414	Soluble TNF mediates amyloid-independent, diet-induced alterations to immune and neuronal functions in an Alzheimer’s disease mouse model. 17,	0
413	Mycorrhizal-based inoculants in the root microbiome enhanced phytocannabinoid production in medical Cannabis cultivars.	0
412	A Pilot Study Exploring Temporal Development of Gut Microbiome/Metabolome in Breastfed Neonates during the First Week of Life. **2023**, 26, 99	0
411	Dopamine receptor D2 confers colonization resistance via gut microbial metabolites.	0
410	Spatially-resolved metabolomic identifies colibactin-specific principles of reprogrammed lipid metabolism to promote cancer progression.	0

409	Revived Amplicon Sequence Variants Monitoring in Closed Systems Identifies More Dormant Microorganisms. **2023**, 11, 757	0
408	Contamination source modeling with SCRuB improves cancer phenotype prediction from microbiome data.	0
407	Diseased-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. 14,	0
406	Fly iDNA suggests strict reliance of the causative agent of sylvatic anthrax on rainforest ecosystems.	0
405	Neoadjuvant chemotherapy plus nivolumab with or without ipilimumab in operable non-small cell lung cancer: the phase 2 platform NEOSTAR trial. **2023**, 29, 593-604	0
404	Arctic nekton uncovered by e DNA metabarcoding: Diversity, potential range expansions, and pelagic-benthic coupling.	0
403	Internal Transcribed Spacer and 16S Amplicon Sequencing Identifies Microbial Species Associated with Asbestos in New Zealand. **2023**, 14, 729	0
402	Microbial dysbiosis precedes signs of sea star wasting disease in wild populations of Pycnopodia helianthoides. 10,	0
401	The postbiotic of hawthorn-probiotic ameliorating constipation caused by loperamide in elderly mice by regulating intestinal microecology. 10,	0
400	Faecalibacterium prausnitzii prevents hepatic damage in a mouse model of NASH induced by a high-fructose high-fat diet. 14,	0
399	Influence of mental health medication on microbiota in the elderly population in the Valencian region. 14,	0
398	Bioinformatic and Statistical Analysis of Microbiome Data. **2023**, 183-229	0
397	Gut microbiome signatures of Yorkshire Terrier enteropathy during disease and remission. **2023**, 13,	0
396	Distribution characteristics of oral microbiota and its relationship with intestinal microbiota in patients with type 2 diabetes mellitus. 14,	0
395	Fungal diversity and surfactant-producing fungi in oil contaminated environments. **2023**, 134,	0
394	Comparative Gut Microbiome Differences between High and Low Aortic Arch Calcification Score in Patients with Chronic Diseases. **2023**, 24, 5673	0
393	Big data in genomic research for big questions with examples from covid-19 and other zoonoses. **2023**, 134,	0
392	Determinants of Total and Active Microbial Communities Associated with Cyanobacterial Aggregates in a Eutrophic Lake.	0

391	Community assembly and network structure of epiphytic and endophytic phyllosphere fungi in a subtropical mangrove ecosystem. 14,	0
390	Industrial and Ruminant Trans-Fatty Acids-Enriched Diets Differentially Modulate the Microbiome and Fecal Metabolites in C57BL/6 Mice. **2023**, 15, 1433	0
389	Vector mapping and bloodmeal metabarcoding demonstrate risk of urban Chagas disease transmission in Caracas, Venezuela. **2023**, 17, e0010613	0
388	From the Mountain to the Valley: Drivers of Groundwater Prokaryotic Communities along an Alpine River Corridor. **2023**, 11, 779	0
387	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. **2023**, 15,	0
386	Unveiling the interaction mechanisms of key functional microorganisms in the partial denitrification-anammox process induced by COD. **2023**, 17,	0
385	Chlorine Dioxide Reprograms Rhizosphere Microbial Communities to Enrich Interactions with Tobacco (Nicotiana tabacum). **2023**, 72, 47-60	0
384	Phylogeographic study using autonomous reef monitoring structures indicates fast range expansion of the invasive bryozoan Juxtacribrilina mutabilis.	0
383	Hippocampus guttulatus diet based on DNA metabarcoding. 10,	0
382	Garden soil bacteria transiently colonize gardeners’ skin after direct soil contact. **2023**, 8, 1-22	0
381	Seasonal variation in near-surface seasonally thawed active layer and permafrost soil microbial communities. **2023**, 18, 055001	0
380	Using simulated wildland fire to assess microbial survival at multiple depths from biocrust and bare soils. 14,	0
379	Artificial Cultivation Changes Foliar Endophytic Fungal Community of the Ornamental Plant Lirianthe delavayi. **2023**, 11, 775	0
378	Endorhizosphere of indigenous succulent halophytes: a valuable resource of plant growth promoting bacteria. **2023**, 18,	0
377	Clec12a tempers inflammation while restricting expansion of a colitogenic commensal.	0
376	Effects of Eimeria acervulina infection on the luminal and mucosal microbiota of the duodenum and jejunum in broiler chickens. 14,	0
375	Mucosa-Associated Oscillospira sp. Is Related to Intestinal Stricture and Post-Operative Disease Course in Crohn’s Disease. **2023**, 11, 794	0
374	Fungal Hyphosphere Microbiomes Are Distinct from Surrounding Substrates and Show Consistent Association Patterns. **2023**, 11,	0

373	Snow Microorganisms Colonise Arctic Soils Following Snow Melt.	0
372	Core species and interactions prominent in fish-associated microbiome dynamics. **2023**, 11,	0
371	Microbial response to warming and cellulose addition in a maritime Antarctic soil.	0
370	Bamboozle: A bioinformatic tool for identification and quantification of intraspecific barcodes.	0
369	Functional and Taxonomic Diversity of Anaerobes in Supraglacial Microbial Communities. **2023**, 11,	0
368	Lower respiratory tract microbiome composition and community interactions in smokers. **2023**, 5,	0
367	Microbial Drivers of Plant Performance during Drought Depend upon Community Composition and the Greater Soil Environment. **2023**, 11,	0
366	Comprehensive characterization of maternal, fetal, and neonatal microbiomes supports prenatal colonization of the gastrointestinal tract. **2023**, 13,	0
365	The Microbial Genetic Diversity and Succession Associated with Processing Waters at Different Broiler Processing Stages in an Abattoir in Australia. **2023**, 12, 488	0
364	Modulation of duodenal and jejunal microbiota by rifaximin in mice with CCl4-induced liver fibrosis. **2023**, 15,	0
363	Effects of Hanwoo (Korean cattle) manure as organic fertilizer on plant growth, feed quality, and soil bacterial community. 14,	0
362	HIV Tat Expression and Cocaine Exposure Lead to Sex- and Age-Specific Changes of the Microbiota Composition in the Gut. **2023**, 11, 799	0
361	Environments and host genetics influence the geographic distribution of plant microbiome structure.	0
360	Gut microbiota and host cytochrome P450 characteristics in the pseudo germ-free model: co-contributors to a diverse metabolic landscape. **2023**, 15,	0
359	Intestinal iron bio-accessibility changes by Lignin and the subsequent impact on cell metabolism and intestinal microbiome communities.	0
358	The gut microbiota of tropical marine fish is largely uncultured and distinct from surrounding water microbiota.	0
357	Impavido attenuates inflammation, reduces atherosclerosis, and alters gut microbiota in hyperlipidemic mice. **2023**, 26, 106453	0
356	Significant antimicrobial-producing vegetation uniquely shapes the stormwater biofilter microbiome with implications for enhanced faecal pathogen inactivation. **2023**, 2, e0000094	0

355	Differences in gut bacterial community composition between modern and slower-growing broiler breeder lines: Implications of growth selection on microbiome composition. 14,	0
354	Rumen biogeographical regions and their impact on microbial and metabolome variation. 4,	0
353	The Effect of a Diet Enriched with Jerusalem artichoke, Inulin, and Fluoxetine on Cognitive Functions, Neurogenesis, and the Composition of the Intestinal Microbiota in Mice. **2023**, 45, 2561-2579	0
352	Colonization order of bacterial isolates on treefrog embryos impacts microbiome structure in tadpoles. **2023**, 290,	0
351	Gut microbe-derived milnacipran enhances tolerance to gut ischemia/reperfusion injury. **2023**, 4, 100979	0
350	Next generation sequencing to examine associations between vaginal washing and vaginal microbiota: A cohort study. 095646242311608	0
349	Metabolic syndrome and the urinary microbiome of patients undergoing percutaneous nephrolithotomy. **2023**,	0
348	Combing fecal microbial community data to identify consistent obesity-specific microbial signatures and shared metabolic pathways. **2023**, 26, 106476	0
347	Whole-body Microbiota of Newborn Calves and Their Response to Prenatal Vitamin and Mineral Supplementation.	0
346	The Vaginal Microbiome of Transgender and Gender Nonbinary Individuals.	0
345	Increased Leaf Bacterial Network Complexity along the Native Plant Diversity Gradient Facilitates Plant Invasion?. **2023**, 12, 1406	0
344	Shorter sleep time relates to lower human defensin 5 secretion and compositional disturbance of the intestinal microbiota accompanied by decreased short-chain fatty acid production. **2023**, 15,	0
343	Oral Microbiome, Mental Health, and Sleep Outcomes During the COVID-19 Pandemic: An Observational Study in Chinese and Korean American Immigrants. **2023**, 27, 180-190	0
342	Host population effects on ectomycorrhizal fungi vary between low and high phosphorus soils of temperate rainforests.	0
341	Nanopore Is Preferable over Illumina for 16S Amplicon Sequencing of the Gut Microbiota When Species-Level Taxonomic Classification, Accurate Estimation of Richness, or Focus on Rare Taxa Is Required. **2023**, 11, 804	0
340	Effect of natural weed and Siratro cover crop on soil fungal diversity in a banana cropping system in southwestern China. 14,	0
339	Diversity and function of methyl-coenzyme M reductase-encoding archaea in Yellowstone hot springs revealed by metagenomics and mesocosm experiments. **2023**, 3,	0
338	Revisiting Microbial Diversity in Hypersaline Microbial Mats from Guerrero Negro for a Better Understanding of Methanogenic Archaeal Communities. **2023**, 11, 812	0

337	The persistence and stabilization of auxiliary genes in the human skin virome. **2023**, 20,	0
336	Co-occurrence network analysis unveils the actual differential impact on the olive root microbiota by two Verticillium wilt biocontrol rhizobacteria. **2023**, 18,	0
335	Uncovering plant microbiomes using long-read metagenomic sequencing.	0
334	First insights into nasal microbiome in wine tasters.	0
333	The Impact of Mineral and Energy Supplementation and Phytogenic Compounds on Rumen Microbial Diversity and Nitrogen Utilization in Grazing Beef Cattle. **2023**, 11, 810	0
332	Fine-scale mapping of physicochemical and microbial landscapes of the coral skeleton.	0
331	Heavy Metal Pollution Impacts Soil Bacterial Community Structure and Antimicrobial Resistance at the Birmingham 35th Avenue Superfund Site. **2023**, 11,	0
330	High-quality single amplicon sequencing method for illumina MiSeq platform using pool of N (0 10) spacer-linked target specific primers without PhiX spike-in. **2023**, 24,	0
329	Microbe-mineral interactions in the Plastisphere: Coastal biogeochemistry and consequences for degradation of plastics. 10,	0
328	Distribution of Antibiotic Resistance Genes and Their Associations with Bacterial Communities and Water Quality in Freshwater Lakes. **2023**, 234,	0
327	Functional Potential of Soil Microbial Communities and Their Subcommunities Varies with Tree Mycorrhizal Type and Tree Diversity. **2023**, 11,	0
326	Microbial and Biogeochemical Shifts in a Highly Anthropogenically Impacted Estuary (El Sauce Valparaíso). **2023**, 15, 1251	0
325	Microbiome typing in uveal melanoma is associated with plaque radiotherapy. **2023**, 100079	0
324	Estradiol-mediated protection against high-fat diet induced anxiety and obesity is associated with changes in the gut microbiota in female mice. **2023**, 13,	0
323	Changes in gut microbial community upon chronic kidney disease. **2023**, 18, e0283389	0
322	AmpSeqR: an R package for amplicon deep sequencing´data´analysis. 12, 327	0
321	Effects of recurrent summer droughts on arbuscular mycorrhizal and total fungal communities in experimental grasslands differing in plant diversity and community composition.	0
320	Wind and small mammals are complementary fungal dispersers.	0

319	Bidirectional effects of oral anticoagulants on gut microbiota in patients with atrial fibrillation. 13,	0
318	Longitudinal changes in subgingival biofilm composition following periodontal treatment.	0
317	Alterations of gut microbes and their correlation with clinical features in middle and end-stages chronic kidney disease. 13,	0
316	Evaluating the sampling effort for the metabarcoding-based detection of fish environmental DNA in the open ocean. **2023**, 13,	0
315	Metabarcoding and Metabolomics Reveal the Effect of the Invasive Alien Tree Miconia calvescens DC. on Soil Diversity on the Tropical Island of Moʻorea (French Polynesia). **2023**, 11, 832	0
314	Nasal microbiota profiles in shelter dogs with dermatological conditions carrying methicillin-resistant and methicillin-sensitive Staphylococcus species. **2023**, 13,	0
313	Long-term simulated microgravity alters gut microbiota and metabolome in mice. 14,	0
312	Interindividual differences contribute to variation in microbiota composition more than hormonal status: A prospective study. 14,	0
311	Contributions of carbon source, crop cultivation, and chemical property on microbial community assemblage in soil subjected to reductive disinfestation. 14,	0
310	Impact of High Salt-Intake on a Natural Gut Ecosystem in Wildling Mice. **2023**, 15, 1565	0
309	Skin and Blood Microbial Signatures of Sedentary and Migratory Trout (Salmo trutta) of the Kerguelen Islands. **2023**, 8, 174	0
308	Suspension of oral hygiene practices highlights key bacterial shifts in saliva, tongue, and tooth plaque during gingival inflammation and resolution. **2023**, 3,	0
307	No evidence for associations between brood size, gut microbiome diversity and survival in great tit (Parus major) nestlings. **2023**, 5,	0
306	Microbial composition of tumorous and adjacent gastric tissue is associated with prognosis of gastric cancer. **2023**, 13,	0
305	Bacillus subtilis KM0 Impacts gut Microbiota Profile and Transcription of Genes Related to Transcellular Transport in Zebrafish (Danio rerio). **2023**, 80,	0
304	Prospective, longitudinal analysis of the gut microbiome in patients with locally advanced rectal cancer predicts response to neoadjuvant concurrent chemoradiotherapy. **2023**, 21,	0
303	Potato root-associated microbiomes adapt to combined water and nutrient limitation and have a plant genotype-specific role for plant stress mitigation. **2023**, 18,	0
302	Core Microbiomes. **2023**, 240-271	0

301	Antibiotics promote intestinal growth of carbapenem-resistantEnterobacteriaceaeby enriching nutrients and depleting microbial metabolites.	0
300	Fungal communities on alpine cheese rinds in Southern Switzerland. **2023**, 64,	0
299	Soil pH and dissolved organic carbon shape microbial communities in wetlands with two different vegetation types in Changdu area, Tibet. **2023**, 20, 750-764	0
298	The microbiome of the marine flatworm Macrostomum lignano provides fitness advantages and exhibits circadian rhythmicity. **2023**, 6,	0
297	Effects of Phosphorus Limitation on the Bioavailability of DOM Released by Marine Heterotrophic Prokaryotes.	0
296	Through the e DNA looking glass: Responses of fjord benthic foraminiferal communities to contrasting environmental conditions.	0
295	Sulfur disproportionating microbial communities in a dynamic, microoxic-sulfidic karst system.	0
294	Parasitization of Aphis gossypii Glover by Binodoxys communis Gahan Causes Shifts in the Ovarian Bacterial Microbiota. **2023**, 14, 314	0
293	Emerging investigator series: differential effects of carbon nanotubes and graphene on the tomato rhizosphere microbiome.	0
292	Effects of Lumacaftor-Ivacaftor on Airway Microbiota-Mycobiota and Inflammation in Patients with Cystic Fibrosis Appear To Be Linked to Pseudomonas aeruginosa Chronic Colonization. **2023**, 11,	0
291	Comparison of the respiratory bacterial microbiome in cats with feline asthma and chronic bronchitis. 10,	0
290	Soil nutrients and vegetation along a karst slope gradient affect arbuscular mycorrhizal fungi colonization of roots rather than bulk soil AMF diversity.	0
289	Current levels of microplastic pollution impact wild seabird gut microbiomes.	0
288	Impact of testosterone use on the vaginal microbiota of transgender men, including susceptibility to bacterial vaginosis: study protocol for a prospective, observational study. **2023**, 13, e073068	0
287	Effect of Rice Straw and Stubble Burning on Soil Physicochemical Properties and Bacterial Communities in Central Thailand. **2023**, 12, 501	0
286	A Single Intranasal Dose of Bacterial Therapeutics to Calves Confers Longitudinal Modulation of the Nasopharyngeal Microbiota: a Pilot Study.	0
285	Mind the blind spot: lessons from fungal community sequencing in a plant‐soil feedback experiment. **2023**, 4,	0
284	Vaginal Microbiome Metagenome Inference Accuracy: Differential Measurement Error according to Community Composition.	0

283	The Succession of the Cellulolytic Microbial Community from the Soil during Oat Straw Decomposition. **2023**, 24, 6342	0
282	Amplicon sequencing allows differential quantification of closely related parasite species: an example from rodent coccidia (Eimeria).	0
281	Intestinal microbiota of Nearctic-Neotropical migratory birds vary more over seasons and years than between host species.	0
280	High throughput screening of fungal phytopathogens caught in Australian forestry insect surveillance traps. 6,	0
279	Lung Mycobiota Diversity Is Linked to Severity in Critically Ill Patients with Acute Exacerbation of Chronic Obstructive Pulmonary Disease. **2023**, 11,	0
278	Seasonal variations of soil bacterial and fungal communities in a subtropical Eucalyptus plantation and their responses to throughfall reduction. 14,	0
277	Biological Methanation in an Anaerobic Biofilm Reactor Trace Element and Mineral Requirements for Stable Operation. **2023**, 11, 1013	0
276	Glyphosate has a negligible impact on bacterial diversity and dynamics during composting.	0
275	Inhibition of Methylmercury and Methane Formation by Nitrous Oxide in Arctic Tundra Soil Microcosms. **2023**, 57, 5655-5665	0
274	Systemic Analysis of the Spatiotemporal Changes in Multi-Species Electroactive Biofilms to Clarify the Gradual Decline of Current Generation in Microbial Anodes.	0
273	External DNA contamination and efficiency of bleach decontamination for arthropod diet analysis.	0
272	Regulation of Gut Microbiota through Breast Milk Feeding Benefits Language and Cognitive Development of Preterm Toddlers. **2023**, 11, 866	0
271	From the Surface Ocean to the Seafloor: Linking Modern and Paleo-Genetics at the Sabrina Coast, East Antarctica (IN2017_V01). **2023**, 128,	0
270	Legacy Effects of Phytoremediation on Plant-Associated Prokaryotic Communities in Remediated Subarctic Soil Historically Contaminated with Petroleum Hydrocarbons. **2023**, 11,	0
269	Gut Microbiota Accelerate the Insecticidal Activity of Plastid-Expressed Bacillus thuringiensis Cry3Bb to a Leaf Beetle, Plagiodera versicolora. **2023**, 11,	0
268	Metal-Driven Anaerobic Oxidation of Methane as an Important Methane Sink in Methanic Cold Seep Sediments. **2023**, 11,	0
267	Sequence-Based Characterization of Microalgal Microbiomes: Impact of DNA Extraction Protocol on Yield and Community Composition. **2023**, 11,	0
266	Evaluation of Physicochemical and Microbial Properties of Extracts from Wine Lees Waste of Matelica Verdicchio and Their Applications in Novel Cosmetic Products. **2023**, 12, 816	0

265	Trait-based assembly of arbuscular mycorrhizal fungal communities determines soil carbon formation and retention.	0
264	Pathobionts from chemically disrupted gut microbiota induce insulin-dependent diabetes in mice. **2023**, 11,	0
263	Gut bacteria influence Blastocystis sp. phenotypes and may trigger pathogenicity. **2023**, 17, e0011170	0
262	Impact of the bacterial nasopharyngeal microbiota on the severity of genus enterovirus lower respiratory tract infection in children: A case□ontrol study.	0
261	Alteration of Community Metabolism by Prebiotics and Medicinal Herbs. **2023**, 11, 868	0
260	Alternative stable states, nonlinear behavior, and predictability of microbiome dynamics. **2023**, 11,	0
259	Assessing Efficacy of Plastic-free Alternative Ties For Coral Propagation in Reef Restoration.	0
258	Characterization of the oral and gut microbiome in children with obesity aged 3 to 5 years. 13,	0
257	Leaf Litter Breakdown and Soil Microbes in Catalpa bungei Plantations in Response to Various Fertilization Regimes. **2023**, 14, 699	0
256	Environmental DNA metabarcoding from flowers reveals arthropod pollinators, plant pests, parasites, and potential predator□rey interactions while revealing more arthropod diversity than camera traps.	0
255	Gut microbial features and dietary fiber intake predict gut microbiota response to resistant starch supplementation.	0
254	Eelgrass (Zostera spp.) associated phytomyxids are host-specific congeneric parasites and predominant eukaryotes in the eelgrass rhizosphere on a global scale.	0
253	Arresting microbiome development limits immune system maturation and resistance to infection in mice. **2023**, 31, 554-570.e7	0
252	Microbial interaction between human skin and Nukadoko, a fermented rice bran bed for pickling vegetables.	0
251	Microbiome differences in sugarcane and metabolically engineered oilcane accessions and their implications for bioenergy production. **2023**, 16,	0
250	Anaerobic Microbial Degradation of Polypropylene and Polyvinyl Chloride Samples. **2023**, 92, 83-93	0
249	Infection strategies of different chytrids in a diatom spring bloom.	0
248	A unique case in which Kimoto-style fermentation was completed with Leuconostoc as the dominant genus without transitioning to Lactobacillus. **2023**,	0

247	Oxidation state of bioavailable dissolved organic matter influences bacterioplankton respiration and growth efficiency.	0
246	The link between increased Desulfovibrio and disease severity in Parkinson’s disease. **2023**, 107, 3033-3045	0
245	Associations of HIV and iron status with gut microbiota composition, gut inflammation and gut integrity in South African school-age children: a two-way factorial case–control study.	0
244	Organic fertilization drives shifts in microbiome complexity and keystone taxa increase the resistance of microbial mediated functions to biodiversity loss. **2023**, 59, 441-458	0
243	Short Term Impact of Recycling-Derived Fertilizers on Their P Supply for Perennial Ryegrass (Lolium perenne).	0
242	The microbiota in feces of domestic pigeons in Seoul, Korea. **2023**, 9, e14997	0
241	Actinobacteria from Arctic and Atlantic deep-sea sediments—Biodiversity and bioactive potential. 14,	0
240	Taxonomical and functional responses of microbial communities from forest soils of differing tree species diversity to drying-rewetting cycles. **2023**, 150875	0
239	Dominant bacterial taxa drive microbiome differences of juvenile Pacific oysters of the same age and variable sizes. 2,	0
238	Differences in phyllosphere microbiomes among different Populus spp. in the same habitat. 14,	0
237	Reducing bias in microbiome research: Comparing methods from sample collection to sequencing. 14,	0
236	The Bacterial Microbiome of the Coral Skeleton Algal Symbiont Ostreobium Shows Preferential Associations and Signatures of Phylosymbiosis.	0
235	Development of a biomarker signature using grating-coupled fluorescence plasmonic microarray for diagnosis of MIS-C. 11,	0
234	High resolution functional analysis and community structure of photogranules.	0
233	Impacts of pre-existing diabetes mellitus on colorectal cancer in a mice model.	0
232	Neotropical Frog Foam Nests’ Microbiomes. **2023**, 11, 900	0
231	Oral microbiome changes associated with the menstrual cycle in healthy young adult females. 13,	0
230	Oral microbiome correlates with selected clinical biomarkers in individuals with no significant systemic disease. 13,	0

229	Interrogating the Diversity of Vaginal, Endometrial, and Fecal Microbiomes in Healthy and Metritis Dairy Cattle. **2023**, 13, 1221	0
228	Analysis of microbiota-host communication mediated by butyrate in Atlantic Salmon. **2023**,	0
227	Bacterial detoxification of plant defence secondary metabolites mediates the interaction between a shrub and frugivorous birds. **2023**, 14,	0
226	Engineered Escherichia coli for the in situ secretion of therapeutic nanobodies in the gut. **2023**, 31, 634-649.e8	0
225	Uniform selective pressures within redox zones drive gradual changes in microbial community composition in hadal sediments.	0
224	Bacterial distribution in long-term dioxin-contaminated soil in Vietnam and novel dioxin degrading bacteria isolated from Phu Cat airbase. 1-16	0
223	Climate Warming Does Not Override Eutrophication, but Facilitates Nutrient Release from Sediment and Motivates Eutrophic Process. **2023**, 11, 910	0
222	The Nonbacterial Microbiome: Fungal and Viral Contributions to the Preterm Infant Gut in Health and Disease. **2023**, 11, 909	0
221	Climate drivers alter nitrogen availability in surface peat and decouple N 2 fixation from CH 4 oxidation in the Sphagnum moss microbiome.	0
220	Characterization of the Root-Associated Microbiome Provides Insights into Endemism ofThymusSpecies Growing in the Kazdagi National Park.	0
219	Antibacterial plant combinations prevent postweaning diarrhea in organically raised piglets challenged with enterotoxigenic Escherichia coli F18. 10,	0
218	Enzymatic arabinose depletion of wheat arabinoxylan regulates in vitro fermentation profiles and potential microbial degraders. **2023**, 142, 108743	0
217	Deciphering the rhizosphere bacteriome associated with biological control of tobacco black shank disease. 14,	0
216	A Novel E3 Probiotics Formula Restored Gut Dysbiosis and Remodelled Gut Microbial Network and Microbiome Dysbiosis Index (MDI) in Southern Chinese Adult Psoriasis Patients. **2023**, 24, 6571	0
215	Iron oxide nanozymes stabilize stannous fluoride for targeted biofilm killing and synergistic oral disease prevention.	0
214	Short-term responses of plant growth-promoting bacterial community to the herbicides imazethapyr and flumioxazin. **2023**, 328, 138581	0
213	Viruses of a key coral symbiont exhibit temperature-driven productivity across a reefscape. **2023**, 3,	0
212	Successional dynamics of the cultivated kelp microbiome.	0

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211	Effects of intestinal microbes on obesity: A bibliometric analysis from 2013-2022.	0
210	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. 14,	0
209	Subclinical doses of dietary fumonisins and deoxynivalenol cause cecal microbiota dysbiosis in broiler chickens challenged with Clostridium perfringens. 14,	0
208	Bridging gut microbiota composition with extended-spectrum beta-lactamase Enterobacteriales faecal carriage in critically ill patients (microbe cohort study). **2023**, 13,	0
207	Soil Suppressiveness Against Pythium ultimum and Rhizoctonia solani in Two Land Management Systems and Eleven Soil Health Treatments.	0
206	Microbial and Biochemical Profile of Different Types of Greek Table Olives. **2023**, 12, 1527	0
205	Novel bacterial proteolytic and metabolic activity associated with dental erosion-induced oral dysbiosis. **2023**, 11,	0
204	The Impact of MOSE (Experimental Electromechanical Module) Flood Barriers on Microphytobenthic Community of the Venice Lagoon. **2023**, 11, 936	0
203	Date Palm Waste Compost Application Increases Soil Microbial Community Diversity in a Cropping Barley (Hordeum vulgare L.) Field. **2023**, 12, 546	0
202	Transcriptomic insights into archaeal nitrification in the Amundsen Sea Polynya, Antarctica.	0
201	Bacterial microbiome in tropical lichens and the effect of the isolation method on culturable lichen-derived actinobacteria. **2023**, 13,	0
200	Gluconic acid improves performance of newly weaned piglets associated with alterations in gut microbiome and fermentation. **2023**, 9,	0
199	Deterministic and stochastic processes generating alternative states of microbiomes.	0
198	Multiscale adaptive differential abundance analysis in microbial compositional data. **2023**, 39,	0
197	Bee breweries: The unusually fermentative, lactobacilli-dominated brood cell microbiomes of cellophane bees. 14,	0
196	Ecological divergence of a mesocosm in an eastern boundary upwelling system assessed with multi-marker environmental DNA metabarcoding. **2023**, 20, 1277-1298	0
195	Unveiling the role of emerging metagenomics for the examination of hypersaline environments. 1-39	0
194	A cryopreservation method to recover laboratory- and field-derived bacterial communities from mosquito larval habitats. **2023**, 17, e0011234	0

193	Reconnaissance of Oxygenic Denitrifiers in Agriculturally Impacted Soils.	0
192	Impacts of Nutrients on Alkene Biodegradation Rates and Microbial Community Composition in Enriched Consortia from Natural Inocula.	0
191	Evolving approaches to profiling the microbiome in skin disease. 14,	0
190	Extensive MHC class IIdiversity across multiple loci in the small-spotted catshark (Scyliorhinus canicula). **2023**, 13,	0
189	Sulfate reduction and homoacetogenesis at various hypersaline conditions: Implications for H2 underground gas storage. 11,	0
188	Information Scale Correction for Varying Length Amplicons Improves Eukaryotic Microbiome Data Integration. **2023**, 11, 949	0
187	Quantification of diversity sampling bias resulting from rice root bacterial isolation on popular and nitrogen-free culture media using 16S amplicon barcoding. **2023**, 18, e0279049	0
186	Exploring the microbiome of oral epithelial dysplasia as a predictor of malignant progression. **2023**, 23,	0
185	Microscale pollen release and dispersal patterns in flowering grass populations. **2023**, 880, 163345	0
184	Pelvic spine reduction affects diet but not gill raker morphology in two polymorphic brook stickleback (Culaea inconstans) populations.	0
183	Selecting 16S rRNA Primers for Microbiome Analysis in a HostMicrobe System: The Case of the Jellyfish Rhopilema nomadica. **2023**, 11, 955	0
182	Agroecosystem edge effects on vegetation, soil properties, and the soil microbial community in the Canadian prairie. **2023**, 18, e0283832	0
181	Gut Microbiota Contribution to Weight-Independent Glycemic Improvements after Gastric Bypass Surgery.	0
180	Wildlife gut microbiomes of sympatric generalist species respond differently to anthropogenic landscape disturbances. **2023**, 5,	0
179	Different approaches to processing environmental DNA samples in turbid waters have distinct effects for fish, bacterial and archaea communities. 3,	0
178	Bacillus- and Lactobacillus-Based Dietary Synbiotics Are Associated with Shifts in the Oropharyngeal, Proximal Colonic, and Vaginal Microbiomes of Korean Native Black Pigs. **2023**, 9, 359	0
177	Gut Bacterial Communities in HIV-Infected Individuals with Metabolic Syndrome: Effects of the Therapy with Integrase Strand Transfer Inhibitor-Based and Protease Inhibitor-Based Regimens. **2023**, 11, 951	0
176	Problematic Cannabis Use Is Associated with Reduced Rectal Microbial Species Richness and Diversity Among a Pilot Sample of Young Sexual and Gender Minorities.	0

175	Optimization of cacao beans fermentation by native species and electromagnetic fields. **2023**, 9, e15065	0
174	Methane emission, nutrient digestibility, and rumen microbiota in Holstein heifers fed 14 different grass or clover silages as the sole feed. **2023**,	0
173	Longevity of centenarians is reflected by the gut microbiome with youth-associated signatures. **2023**, 3, 436-449	0
172	Potential roles of the rectum keystone microbiota in modulating the microbial community and growth performance in goat model. **2023**, 14,	0
171	THAPBI PICT - a fast, cautious, and accurate metabarcoding analysis pipeline.	0
170	Fecal levels of SCFA and BCFA during capecitabine in patients with metastatic or unresectable colorectal cancer.	0
169	A pilot study: intraoperative 16S rRNA sequencing versus culture in predicting colorectal incisional surgical site infection.	0
168	Association between gut microbiota and anxiety symptoms: A large population-based study examining sex differences. **2023**, 333, 21-29	0
167	Characteristics and intrasubject variation in the respiratory microbiome in interstitial lung disease. **2023**, 102, e33402	0
166	Fungal Diversity Associated with Armadillidium Isopods: A Case Study in Central Park of Gwacheon, South Korea. **2023**, 15, 533	0
165	Mesophilic and thermophilic viruses are associated with nutrient cycling during hyperthermophilic composting.	0
164	Water temperature and disease alters bacterial diversity and cultivability from American lobster (Homarus americanus) shells. **2023**, 26, 106606	0
163	Experimental Factors Influence Diversity Metrics of the Gut Microbiome in Laboratory Mice.	0
162	Influence of carbon-based cathodes on biofilm composition and electrochemical performance in soil microbial fuel cells. **2023**, 100276	0
161	Shifts in the coral microbiome in response toin situexperimental deoxygenation.	0
160	A metabarcoding analysis of the wrackbed microbiome indicates a phylogeographic break along the North SeaBaltic Sea transition zone.	0
159	Comparative analysis of bacterial diversity in two hot springs in Hefei, China. **2023**, 13,	0
158	Dupilumab but not cyclosporine treatment shifts the microbiome toward a healthy skin flora in patients with moderate-to-severe atopic dermatitis.	0

157	Integrated Microbiota and Metabolite Changes following Rice Bran Intake during Murine Inflammatory Colitis-Associated Colon Cancer and in Colorectal Cancer Survivors. **2023**, 15, 2231	0
156	Towards a free wild-caught fishmeal, fish oil and soy protein in European sea bass diet using by-products from fishery and aquaculture. **2023**, 573, 739571	0
155	Wheat varietal diversity affects arbuscular mycorrhizal symbiosis and soil enzymatic activities in the root zone.	0
154	The regulatory effects of Lonicera japonica flos on fecal microbiota from humans with type 2 diabetes in a SHIME model. **2023**, 100654	0
153	O2 partitioning of sulfur oxidizing bacteria drives acidity and thiosulfate distributions in mining waters. **2023**, 14,	0
152	The mature phyllosphere microbiome of grapevine is associated with resistance against Plasmopara viticola. 14,	0
151	Ecology of food waste chain-elongating microbiome. 11,	0
150	Changes in soil fertility and microbial communities following cultivation of native grassland in Horqin Sandy Land, China: a 60-year chronosequence. **2023**, 12,	0
149	PhyloMed: a phylogeny-based test of mediation effect in microbiome. **2023**, 24,	0
148	Nitrogen transformation processes catalyzed by manure microbiomes in earthen pit and concrete storages on commercial dairy farms. **2023**, 18,	0
147	Profiles of oral microbiome associated with nasogastric tube feeding. **2023**, 15,	0
146	The Local Tumor Microbiome Is Associated with Survival in Late-Stage Colorectal Cancer Patients.	0
145	High methane flux in a tropical peatland post-fire is linked to homogenous selection of diverse methanogenic archaea.	0
144	The mycobiome of a successful crayfish invader and its changes along the environmental gradient. **2023**, 5,	0
143	In sickness and in health: the dynamics of the fruit bat gut microbiota under a bacterial antigen challenge and its association with the immune response. 14,	0
142	Effects of the probiotic Lactiplantibacillus plantarum IMC 510 on body composition, biochemical parameters, gut microbiota composition and function, and clinical symptoms of overweight/obese subjects. 10,	0
141	Comparison of two molecular barcodes for the study of equine strongylid communities with amplicon sequencing. 11, e15124	0
140	Unraveling multifunction of low-temperature Daqu in simultaneous saccharification and fermentation of Chinese light aroma type liquor. **2023**, 397, 110202	0

139	Legacy effects of precipitation and land use impact maize growth and microbiome assembly under drought stress.	0
138	Mycorrhiza Better Predict Soil Fungal Community Composition and Function than Aboveground Traits in Temperate Forest Ecosystems.	0
137	Tryptophan metabolites alleviates Intestinal Candida albicans Infection by reduction of IL-22 releasing from colonic lamina propria group 3 innate lymphoid cells and gut microbiome modification.	0
136	Application of Mendelian randomization to explore the causal role of the human gut microbiome in colorectal cancer. **2023**, 13,	0
135	Nitrogen dynamics and fixation control cyanobacterial abundance, diversity, and toxicity in Lake of the Woods (USA, Canada).	0
134	The impact of urine collection method on canine urinary microbiota detection: a cross-sectional study. **2023**, 23,	0
133	Dynamic Development of Viral and Bacterial Diversity during Grass Silage Preservation. **2023**, 15, 951	0
132	Differences in Gut Microbiome Profile between Healthy Children and Children with Inflammatory Bowel Disease and/or Autoimmune Liver Disease: A Case-Control Study. **2023**, 12, 585	0
131	Subgingival microbial diversity and respiratory decline: A cross-sectional study.	0
130	Direct and culture-enriched 16S rRNA sequencing of cecal content of healthy horses and horses with typhlocolitis. **2023**, 18, e0284193	0
129	Previously uncharacterized rectangular bacterial structures in the dolphin mouth. **2023**, 14,	0
128	The microbiomes of two Singaporean corals show site-specific differentiation and variability that correlates with the seasonal monsoons.	0
127	Niche modelling predicts that soil fungi occupy a precarious climate in boreal forests.	0
126	Combination of Lactobacillus plantarum HAC03 and Garcinia cambogia Has a Significant Anti-Obesity Effect in Diet-Induced Obesity Mice. **2023**, 15, 1859	0
125	Graphene oxide exposure alters gut microbial community composition and metabolism in an in vitro human model. **2023**, 100463	0
124	Association between the skin microbiome and MHC class II diversity in an amphibian.	0
123	Bringing Antarctica to the lab: a polar desert environmental chamber to study the response of Antarctic microbial communities to climate change.	0
122	Using Inflammatory Biological Age To Evaluate the Preventing Aging Effect of a Polyphenol-Probiotic-Enhanced Dietary Pattern in Adults Aged 50 Years and Older.	0

121	The nasal microbiome in patients suffering from non-steroidal anti-inflammatory drugs-exacerbated respiratory disease in absence of corticosteroids. 14,	0
120	Role of Dietary Fiber and Energy Intake on Gut Microbiome in Vegans, Vegetarians, and Flexitarians in Comparison to OmnivoresInsights from the Nutritional Evaluation (NuEva) Study. **2023**, 15, 1914	0
119	Characterization of the lung microbiome and inflammatory cytokine levels in women exposed to environmental risk factors: A pilot study. **2023**, 11,	0
118	A westernized diet changed the colonic bacterial composition and metabolite concentration in a dextran sulfate sodium pig model for ulcerative colitis. 14,	0
117	The challenge of implementing eDNA metabarcoding to detect elasmobranchs in a resource-limited MPA.	0
116	Dietary and Sexual Correlates of Gut Microbiota in the Japanese Gecko, Gekko japonicus (Schlegel, 1836). **2023**, 13, 1365	0
115	Halophilic nematodes live in America's Dead Sea.	0
114	Evaluation of DNA extraction methods and direct PCR in metabarcoding of mock and marine bacterial communities. 14,	0
113	Abundance of Oligoflexales bacteria is associated with algal symbiont density independent of thermal stress in Aiptasia anemones.	0
112	Groundwater environmental DNA metabarcoding reveals hidden diversity and reflects land-use and geology.	0
111	Gut Microbiome in Post-COVID-19 Patients Is Linked to Immune and Cardiovascular Health Status but Not COVID-19 Severity. **2023**, 11, 1036	0
110	The gut microbiota contributes to the pathogenesis of anorexia nervosa in humans and mice.	0
109	Rumen microbial community and milk quality in Holstein lactating cows fed olive oil pomace as part in a sustainable feeding strategy. **2023**, 100815	0
108	Alterations in vaginal microbiota in uterine fibroids patients with ultrasound-guided high-intensity focused ultrasound ablation. 14,	0
107	Elevated temperature alters microbial communities, but not decomposition rates, during three years of in-situ peat decomposition.	0
106	Primer design for the amplification of the ammonium transporter genes from the uncultured haptophyte algal species symbiotic with the marine nitrogen-fixing cyanobacterium UCYN-A1. 14,	0
105	The Major Histocompatibility Complex modulatesBatrachochytrium dendrobatidisandRanavirusinfections in three amphibian species.	0
104	Human milk-associated bacterial communities associate with the infant gut microbiome over the first year of life. 14,	0

103	Serratia marcescens Colonization in a Neonatal Intensive Care Unit Has Multiple Sources, with Sink Drains as a Major Reservoir.	0
102	Relationship between pepper (Capsicum annuum L.) root morphology, inter-root soil bacterial community structure and diversity under water□ir intercropping conditions. **2023**, 257,	0
101	Investigating the use of pollen DNA metabarcoding to quantify bee foraging and effects of threshold selection. **2023**, 18, e0282715	0
100	The Intestinal Microbiome in Dogs with Chronic Enteropathies and Cobalamin Deficiency or Normocobalaminemia□A Comparative Study. **2023**, 13, 1378	0
99	Screening the maize rhizobiome for consortia that improve Azospirillum brasilense root colonization and plant growth outcomes. 7,	0
98	Differences in the luminal and mucosal gut microbiomes and metabolomes of oriental rat snake (Ptyas mucosus).	0
97	Relationship of Distress and Quality of Life with Gut Microbiome composition in Newly Diagnosed Breast Cancer Patients: a prospective, observational study.	0
96	Sympatric rodents in a desert shrubland differ in arthropod consumption. **2023**, 214, 104999	0
95	Humic substances mitigate adverse effects of elevated temperature with potentially critical repercussions for coral reef resilience.	0
94	Seasonal variations in gut microbiota and disease course in patients with inflammatory bowel disease. **2023**, 18, e0283880	0
93	The microbiome of the endosymbiotic Symbiodiniaceae in corals exposed to thermal stress.	0
92	Environmental Impacts on Skin Microbiomes of Sympatric High Arctic Salmonids. **2023**, 8, 214	0
91	Rapid differentiation of soil and root microbiomes in response to plant composition and biodiversity in the field. **2023**, 3,	0
90	State-of-the-art of data analyses in environmental DNA approaches towards its applicability to sustainable fisheries management. 10,	0
89	Phage combination alleviates bacterial leaf blight of rice (Oryza sativa L.). 14,	0
88	Multi-factorial examination of amplicon sequencing workflows from sample preparation to bioinformatic analysis. **2023**, 23,	0
87	Bacterial community responses to planktonic and terrestrial substrates in coastal northern Baltic Sea. 10,	0
86	Maternal Bacterial Engraftment in Multiple Body Sites of Cesarean Section Born Neonates after Vaginal Seeding□ Randomized Controlled Trial.	0

85	Genetic determinants of switchgrass-root-associated microbiota in field sites spanning its natural range. **2023**,	0
84	Serum Metabolomics Combined With 16S rRNA Gene Sequencing to Analyze the Changes of Intestinal Flora in Rats With MI and the Intervention Effect of Fuling-Guizhi. **2023**, 18, 1934578X2311560	0
83	Contrasting geochemical and fungal controls on decomposition of lignin and soil carbon at continental scale. **2023**, 14,	0
82	Unraveling the Dysbiosis of Vaginal Microbiome to Understand Cervical Cancer Disease Etiology□An Explainable AI Approach. **2023**, 14, 936	0
81	Integrating Multi-Omics Data to Construct Reliable Interconnected Models of Signaling, Gene Regulatory, and Metabolic Pathways. **2023**, 139-151	0
80	Specific host metabolite and gut microbiome alterations are associated with bone loss during spaceflight. **2023**, 112299	0
79	Anti-diarrheal drug loperamide induces dysbiosis in zebrafish microbiota via bacterial inhibition.	0
78	Vibrio cholerae Invasion Dynamics of the Chironomid Host Are Strongly Influenced by Aquatic Cell Density and Can Vary by Strain.	0
77	Effects of inorganic and compost tea fertilizers application on the taxonomic and functional microbial diversity of the purslane rhizosphere. 14,	0
76	DNA extraction protocol impacts ocular surface microbiome profile. 14,	0
75	Comparative genomic insights into habitat adaptation of coral-associated Prosthecochloris. 14,	0
74	Oral and fecal microbiota perturbance in cocaine users: Can rTMS-induced cocaine abstinence support eubiosis restoration?. **2023**, 106627	0
73	Natural grassland conversion to cultivated pastures increases soil microbial niche specialization with consequences for ecological processes. **2023**, 188, 104913	0
72	Osmium-grafted Magnetic Nanobeads Improve Microbial Current Generation via Culture-free and Quick Enrichment of Electrogenic Bacteria. **2023**, 142936	0
71	SituSeq: an offline protocol for rapid and remote Nanopore 16S rRNA amplicon sequence analysis. **2023**, 3,	0
70	Dual use of solar power plants as biocrust nurseries for large-scale arid soil restoration.	0
69	Highly efficient nitrobenzene removal by coupling electrochemical filtration with a microbial electrolysis cell. **2023**, 109978	0
68	The effect of hypoxia on Daphnia magna performance and its associated microbial and bacterioplankton community: A scope for phenotypic plasticity and microbiome community interactions upon environmental stress?. 11,	0

67	Effects of indoor and outdoor rearing system on geese biochemical parameters and cecal microbial composition. **2023**, 102731	0
66	Interactions between rootstocks and compost influence the active rhizosphere bacterial communities in citrus. **2023**, 11,	0
65	Assessment of Multidimensional Healthcare Parameters Among Adult Men and Women in Japan for Developing a Virtual Human Generative Model: Protocol for a Cross-Sectional Study (Preprint).	0
64	Fungal Diversity and Dynamics during Long-Term Immersion of Conventional and Biodegradable Plastics in the Marine Environment. **2023**, 15, 579	0
63	Mucin-microbiome signatures shape the tumor microenvironment in gastric cancer. **2023**, 11,	0
62	Methane Cycle in a Littoral Site of a Temperate Freshwater Lake. **2023**, 92, 153-170	0
61	Microbial community and soil enzyme activities driving microbial metabolic efficiency patterns in riparian soils of the Three Gorges Reservoir. 14,	0
60	Investigating aerial diversity of non-fungal eukaryotes across a 40° latitudinal transect using DNA metabarcoding.	0
59	A new small-celled naviculoid diatom species, Mayamaea pannonica sp. nov. (Bacillariophyceae) from soda pans in Serbia. 1-9	0
58	Megamonas funiformis, Plasma Zonulin, and Sodium Intake Affect C3 Complement Levels in Inactive Systemic Lupus Erythematosus. **2023**, 15, 1999	0
57	Multi-omics signatures in new-onset diabetes predict metabolic response to dietary inulin: findings from an observational study followed by an interventional trial. **2023**, 13,	0
56	Field scale biodegradation of total petroleum hydrocarbons and soil restoration by Ecopiles: microbiological analysis of the process. 14,	0
55	Lung-gut axis of microbiome alterations following co-exposure to ultrafine carbon black and ozone. **2023**, 20,	0
54	Dynamics of Microbial Communities in Nitrite-Free and Nutritionally Improved Dry Fermented Sausages. **2023**, 9, 403	0
53	Disentangling temporal associations in marine microbial networks. **2023**, 11,	0
52	Intravenous antibiotics in preterm infants have a negative effect upon microbiome development throughout preterm life. **2023**, 15,	0
51	Semi-wet methanogen cathode composed of oak white charcoal for developing sustainable microbial fuel cells. **2023**,	0
50	Effects of recurrent summer droughts on arbuscular mycorrhizal and total fungal communities in experimental grasslands differing in plant diversity and community composition. 3,	0

49	Performance and mechanism of simultaneous nitrification and denitrification in zeolite spheres internal loop airlift reactor. **2023**, 129073	0
48	18S-NemaBase: Curated 18S rRNA Database of Nematode Sequences. **2023**, 55,	0
47	The hindgut microbiome contributes to host oxidative stress in postpartum dairy cows by affecting glutathione synthesis process. **2023**, 11,	0
46	IN SITU GROWTH OF MODERN ONCOIDS FROM SALADO RIVER, SALAR DE LA LAGUNA VERDE COMPLEX, ARGENTINA. **2023**, 106396	0
45	Early-life obesogenic environment integrates immunometabolic and epigenetic signatures governing neuroinflammation.	0
44	Genomic and 16S metabarcoding data of Holothuria tubulosa Gmelin, 1791. **2023**, 109171	0
43	Egg-laying by female Aedes aegypti shapes the bacterial communities of breeding sites. **2023**, 21,	0
42	Microbiome Diversity and Cellulose Decomposition Processes by Microorganisms on the Ancient Wooden Seawall of Qiantang River of Hangzhou, China.	0
41	Selective enrichment of the raw milk microbiota in cheese production: Concept of a natural adjunct milk culture. 14,	0
40	Effect of Nano Cerium Dioxide on Intestinal Microflora in Rats by Oral Subchronic Exposure.	0
39	Effects of partially hydrolyzed guar gums of different molecular weights on a human intestinal in´vitro fermentation model. **2023**,	0
38	Integrated Omic Analysis of Human Plasma Metabolites and Microbiota in a Hypertension Cohort. **2023**, 15, 2074	0
37	Inulin diet uncovers complex diet-microbiota-immune cell interactions remodeling the gut epithelium. **2023**, 11,	0
36	Diet of a threatened rattlesnake (eastern massasauga) revealed by DNA metabarcoding. **2023**, 13,	0
35	Successional changes in fungal communities occur a few weeks following wildfire in a mixed Douglas-fir-ponderosa pine forest. **2023**, 63, 101246	0
34	Cecal Microbiota Development and Physiological Responses of Broilers Following Early Life Microbial Inoculation Using Different Delivery Methods and Microbial Sources.	0
33	Sorbed environmental contaminants increase the harmful effects of microplastics in adult zebrafish, Danio rerio. **2023**, 259, 106544	0
32	Investigating the cecal microbiota of broilers raised in extensive and intensive production systems.	0

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31	Enhanced removal of triclosan from contaminated water by indigenous isolate Burkholderia sp. L303. **2023**, 1171, 012056	0
30	Longitudinal Analysis of the Impacts of Urogenital Schistosomiasis on the Gut microbiota of Adolescents in Nigeria.	0
29	Characterization of the Bacterial Communities Inhabiting Tropical Propolis of Puerto Rico. **2023**, 11, 1130	0
28	Bioaugmented Daqu-induced variation in community succession rate strengthens the interaction and metabolic function of microbiota during strong-flavor Baijiu fermentation. **2023**, 182, 114806	0
27	Structure of the river sediment microbiomes impacted by anthropogenic land uses, environmental and spatial variations. **2023**, 287, 108348	0
26	Bact-to-Batch: A Microbiota-Based Tool to Determine Optimal Animal Allocation in Experimental Designs. **2023**, 24, 7912	0
25	COMPOSITION OF BACTERIAL COMMUNITIES IN OIL-CONTAMINATED BOTTOM SEDIMENTS OF THE KAMENKA RIVER. **2023**, 78, 17-24	0
24	Assessing without harvesting: Pros and cons of environmental DNA sampling and image analysis for marine biodiversity evaluation. **2023**, 188, 106004	0
23	Prokaryotic Responses to Estuarine Coalescence Contribute to Planktonic Community Assembly in a Mediterranean Nutrient-Rich Estuary. **2023**, 11, 933	0
22	Ichthyoplankton metabarcoding: An efficient tool for early detection of invasive species establishment.	0
21	Metabarcoding of ichthyoplankton communities associated with a highly dynamic shelf region of the southwest Indian Ocean. **2023**, 18, e0284961	0
20	Software Tools for Microbiome Data Analysis. **2023**, 612-621	0
19	Rhizosphere-induced shift in the composition of bacterial community favors mineralization of crop residue nitrogen.	0
18	Unraveling microbial community by next-generation sequencing in living membrane bioreactors for wastewater treatment. **2023**, 886, 163965	0
17	Plastisphere and microorganisms involved in polyurethane biodegradation. **2023**, 886, 163932	0
16	A Metagenomic and Amplicon Sequencing Combined Approach Reveals the Best Primers to Study Marine Aerobic Anoxygenic Phototrophs.	0
15	Moso bamboo expansion decreased soil heterotrophic respiration but increased arbuscular mycorrhizal mycelial respiration in a subtropical broadleaved forest. **2023**, 10, 100116	0
14	Boosting resilience of microbial electrolysis cell-assisted anaerobic digestion of blackwater with granular activated carbon amendment. **2023**, 381, 129136	0

13	Peat loss collocates with a threshold in plant□mycorrhizal associations in drained peatlands encroached by trees.	0
12	Childhood lower respiratory tract infections linked to residential airborne bacterial and fungal microbiota. **2023**, 231, 116063	0
11	Metataxonomic characterization of the microbial community involved in the production of biogas with microcrystalline cellulose in pilot and laboratory scale. **2023**, 39,	0
10	Spatial scale impacts microbial community composition and distribution within and across stream ecosystems in North and Central America.	0
9	Positive associations matter: Microbial relationships drive tick microbiome composition.	0
8	Deep sea treasures - insights from museum archives shed light on coral microbial diversity and functioning within deepest ocean ecosystems.	0
7	Alkalihalobacillus clausii (formerly Bacillus clausii) spores lessen antibiotic-induced intestinal injury and reshape gut microbiota composition in mice. **2023**, 163, 114860	0
6	Permanent cover crop as a strategy to promote soil health and vineyard performance.	0
5	Microbiota and pathogens in an invasive bee: Megachile sculpturalis from native and invaded regions.	0
4	Safety, Tolerability, and Pharmacokinetics of □Cryptoxanthin Supplementation in Healthy Women: A Double-Blind, Randomized, Placebo-Controlled Clinical Trial. **2023**, 15, 2325	0
3	Distinct spatiotemporal succession of bacterial generalists and specialists in the lacustrine plastisphere.	0
2	N/S element transformation modulating lithospheric microbial communities by single-species manipulation. **2023**, 11,	0
1	Long-term deposition of fly ash regulates bacterial communities in different disturbance zones: Evidence from diversity, network complexity and predictive metabolic function. **2023**, 164244	0