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Normalization and microbial differential abundance strategies depend upon data characteristics

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1233	MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. <b>2017</b> , 45, W180-W188		706
1232	Stress and stability: applying the Anna Karenina principle to animal microbiomes. <b>2017</b> , 2, 17121		326
1231	A single early-in-life macrolide course has lasting effects on murine microbial network topology and immunity. <b>2017</b> , 8, 518		69
1230	Fungal endophyte communities in the temperate fern <i>Polystichum munitum</i> show early colonization and extensive temporal turnover. <b>2017</b> , 104, 1188-1194		10
1229	Genetic influences on the human oral microbiome. <b>2017</b> , 18, 659		44
1228	Enrichment of beneficial bacteria in the skin microbiota of bats persisting with white-nose syndrome. <i>Microbiome</i> , <b>2017</b> , 5, 115	16.6	51
1227	Root Hair Mutations Displace the Barley Rhizosphere Microbiota. <b>2017</b> , 8, 1094		45
1226	Vaginal and Uterine Bacterial Communities in Postpartum Lactating Cows. <b>2017</b> , 8, 1047		30
1225	Microbiome Datasets Are Compositional: And This Is Not Optional. <b>2017</b> , 8, 2224		815
1224	Composition of Micro-eukaryotes on the Skin of the Cascades Frog ( <i>Rana muscosa</i> ) and Patterns of Correlation between Skin Microbes and. <b>2017</b> , 8, 2350		9
1223	Enhancing the Resolution of Rumen Microbial Classification from Metatranscriptomic Data Using Kraken and Mothur. <b>2017</b> , 8, 2445		29
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1221	Emerging Statistical Methodologies in the Field of Microbiome Studies. <b>2017</b> , 37-52		
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1219	Morphological and genetic factors shape the microbiome of a seabird species ( <i>Oceanodroma leucorhoa</i> ) more than environmental and social factors. <i>Microbiome</i> , <b>2017</b> , 5, 146	16.6	40
1218	The Human Gut Microbiome: From Association to Modulation. <b>2018</b> , 172, 1198-1215		344
1217	A member of the Roseobacter clade, <i>Octadecabacter</i> sp., is the dominant symbiont in the brittle star <i>Amphipholis squamata</i> . <b>2018</b> , 94,		10

1216	Variations in the relative abundance of <i>Wolbachia</i> in the gut of <i>Nasutitermes arborum</i> across life stages and castes. <b>2018</b> , 365,	10
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1212	Meta-analysis of the lung microbiota in pulmonary tuberculosis. <b>2018</b> , 109, 102-108	33
1211	Shrub range expansion alters diversity and distribution of soil fungal communities across an alpine elevation gradient. <b>2018</b> , 27, 2461-2476	25
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1208	Performance of amplicon and shotgun sequencing for accurate biomass estimation in invertebrate community samples. <b>2018</b> , 18, 1020	70
1207	Citric acid as a functional supplement in diets for juvenile turbot, <i>Scophthalmus maximus</i> L.: Effects on phosphorus discharge, growth performance, and intestinal health. <b>2018</b> , 495, 643-653	13
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1197	MetaLonDA: a flexible R package for identifying time intervals of differentially abundant features in metagenomic longitudinal studies. <i>Microbiome</i> , <b>2018</b> , 6, 32	16.6	25
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1192	Gut microbiota composition is associated with environmental landscape in honey bees. <b>2018</b> , 8, 441-451		59
1191	Evidence from the gut microbiota of swarming alates of a vertical transmission of the bacterial symbionts in <i>Nasutitermes arborum</i> (Termitidae, Nasutitermitinae). <b>2018</b> , 111, 573-587		7
1190	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. <b>2018</b> , 9, 38-54		41
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1182	A comparative study of the gut microbiota in immune-mediated inflammatory diseases-does a common dysbiosis exist?. <i>Microbiome</i> , <b>2018</b> , 6, 221	16.6	114
1181	Performance Evaluation of Normalization Approaches for Metagenomic Compositional Data on Differential Abundance Analysis. <b>2018</b> , 329-344		3

1180	DNA Template Dilution Impacts Amplicon Sequencing-Based Estimates of Soil Fungal Diversity. <b>2018</b> , 2, 100-107		11
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1177	Distribution of Extracellular Flavins in a Coastal Marine Basin and Their Relationship to Redox Gradients and Microbial Community Members. <b>2018</b> , 52, 12265-12274		15
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1043	Emerging from the ice-fungal communities are diverse and dynamic in earliest soil developmental stages of a receding glacier. <b>2019</b> , 21, 1864-1880	20
1042	Microbe and host interaction in gastrointestinal homeostasis. <b>2019</b> , 236, 1623-1640	10
1041	Mycobiome Sequencing and Analysis Applied to Fungal Community Profiling of the Lower Respiratory Tract During Fungal Pathogenesis. <b>2019</b> , 10, 512	22
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1039	Foliar-feeding insects acquire microbiomes from the soil rather than the host plant. <b>2019</b> , 10, 1254	61
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1037	Divergent national-scale trends of microbial and animal biodiversity revealed across diverse temperate soil ecosystems. <b>2019</b> , 10, 1107	51

1036	A unified framework for unconstrained and constrained ordination of microbiome read count data. <b>2019</b> , 14, e0205474	7
1035	Rarity of microbial species: In search of reliable associations. <b>2019</b> , 14, e0200458	8
1034	Perinatal factors affect the gut microbiota up to four years after birth. <b>2019</b> , 10, 1517	114
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1030	Nitrification inhibitors effectively target N <sub>2</sub> O-producing <i>Nitrosospora</i> spp. in tropical soil. <b>2019</b> , 21, 1241-1254	17
1029	The Microbiome in Lung Cancer Tissue and Recurrence-Free Survival. <b>2019</b> , 28, 731-740	51
1028	Bioaerosol biomonitoring: Sampling optimization for molecular microbial ecology. <b>2019</b> , 19, 672-690	28
1027	The microbiome and lung cancer. <b>2019</b> , 11, 280-291	34
1026	The bacterial community associated with adult vine weevil ( <i>Otiorhynchus sulcatus</i> ) in UK populations growing on strawberry is dominated by <i>Candidatus Nardonella</i> . <b>2019</b> , 167, 186-196	5
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1023	The tea leaf microbiome shows specific responses to chemical pesticides and biocontrol applications. <b>2019</b> , 667, 33-40	26
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1017	Bayesian hierarchical negative binomial models for multivariable analyses with applications to human microbiome count data. <b>2019</b> , 14, e0220961	2
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1015	A Bayesian zero-inflated negative binomial regression model for the integrative analysis of microbiome data. <b>2021</b> , 22, 522-540	9
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1001	The Microbiome Stress Project: Toward a Global Meta-Analysis of Environmental Stressors and Their Effects on Microbial Communities. <b>2018</b> , 9, 3272	66

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983	Leaf resistance traits influence endophytic fungi colonization and community composition in a South American temperate rainforest. <b>2020</b> , 108, 1019-1029	13

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975	Co-cropping with three phytoremediation crops influences rhizosphere microbiome community in contaminated soil. <b>2020</b> , 711, 135067	18
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952	Irrigation of radish ( <i>Raphanus sativus</i> L.) with microcystin-enriched water holds low risk for plants and their associated rhizospheric and epiphytic microbiome. <b>2020</b> , 266, 115208	4
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944	Opioid agonist and antagonist use and the gut microbiota: associations among people in addiction treatment. <b>2020</b> , 10, 19471	6
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934	Parental Care Alters the Egg Microbiome of Maritime Earwigs. <b>2020</b> , 80, 920-934	5
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916	Applying the Anna Karenina principle for wild animal gut microbiota: Temporal stability of the bank vole gut microbiota in a disturbed environment. <b>2020</b> , 89, 2617-2630	8
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914	Investigating Both Mucosal Immunity and Microbiota in Response to Gut Enteritis in Yellowtail Kingfish. <b>2020</b> , 8,	7
913	Columbia spotted frogs ( <i>Rana luteiventris</i> ) have characteristic skin microbiota that may be shaped by cutaneous skin peptides and the environment. <b>2020</b> , 96,	6
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909	Metrics for Evaluating Inundation Impacts on the Decomposer Communities in a Southern California Coastal Salt Marsh. <b>2020</b> , 40, 2443-2459	2
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907	Editorial: Statistical and Computational Methods for Microbiome Multi-Omics Data. <b>2020</b> , 11, 927	0
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905	Reducing the arbitrary: fuzzy detection of microbial ecotones and ecosystems - focus on the pelagic environment. <b>2020</b> , 15, 16	3
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900	Mechanisms governing avian phylosymbiosis: Genetic dissimilarity based on neutral and MHC regions exhibits little relationship with gut microbiome distributions of Galapagos mockingbirds. <b>2020</b> , 10, 13345-13354	2
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886	Elucidating the influence of resident seed and soil microbiota on the developing creeping bentgrass microbiome. <b>2020</b> , 3, e20038		1
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882	Experimental metatranscriptomics reveals the costs and benefits of dissolved organic matter photo-alteration for freshwater microbes. <b>2020</b> , 22, 3505-3521		10
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879	Characterizing the microbiome of ectoparasitic louse flies feeding on migratory raptors. <b>2020</b> , 15, e0234050		1
878	Assessment of bacterial community composition within and among <i>Acropora loripes</i> colonies in the wild and in captivity. <b>2020</b> , 39, 1245-1255		5
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867	Fungal Dysbiosis and Intestinal Inflammation in Children With Beta-Cell Autoimmunity. <b>2020</b> , 11, 468	15
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862	The rodent vaginal microbiome across the estrous cycle and the effect of genital nerve electrical stimulation. <b>2020</b> , 15, e0230170	4
861	Effects of enrofloxacin treatment on the bacterial microbiota of milk from goats with persistent mastitis. <b>2020</b> , 10, 4421	3
860	Movement ecology and sex are linked to barn owl microbial community composition. <b>2020</b> , 29, 1358-1371	17
859	An empirically derived method for measuring human gut microbiome alpha diversity: Demonstrated utility in predicting health-related outcomes among a human clinical sample. <b>2020</b> , 15, e0229204	24
858	Standardization of Plant Microbiome Studies: Which Proportion of the Microbiota is Really Harvested?. <b>2020</b> , 8,	10
857	Soil textural heterogeneity impacts bacterial but not fungal diversity. <b>2020</b> , 144, 107766	36

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854	Effects of captivity, diet, and relocation on the gut bacterial communities of white-footed mice. <b>2020</b> , 10, 4677-4690	10
853	History of breastfeeding but not mode of delivery shapes the gut microbiome in childhood. <b>2020</b> , 15, e0235223	6
852	Insights in the Global Genetics and Gut Microbiome of Black Soldier Fly, : Implications for Animal Feed Safety Control. <b>2020</b> , 11, 1538	21
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848	The duodenal microbiome is altered in small intestinal bacterial overgrowth. <b>2020</b> , 15, e0234906	23
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846	Duckweed hosts a taxonomically similar bacterial assemblage as the terrestrial leaf microbiome. <b>2020</b> , 15, e0228560	15
845	Comparing Analytical Methods for the Gut Microbiome and Aging: Gut Microbial Communities and Body Weight in the Osteoporotic Fractures in Men (MrOS) Study. <b>2020</b> , 75, 1267-1275	3
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843	Think global, act local: The small-scale environment mainly influences microbial community development and function in lake sediment. <b>2020</b> , 65, S88	5
842	Agricultural land-use history and restoration impact soil microbial biodiversity. <b>2020</b> , 57, 852-863	21
841	Emerging Priorities for Microbiome Research. <b>2020</b> , 11, 136	50
840	Temporal changes in gut microbiota profile in children with acute lymphoblastic leukemia prior to commencement-, during-, and post-cessation of chemotherapy. <b>2020</b> , 20, 151	16
839	Machine learning methods for microbiome studies. <b>2020</b> , 58, 206-216	28

838	The Role of the Gut Microbiome in Cattle Production and Health: Driver or Passenger?. <b>2020</b> , 8, 199-220	39
837	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. <b>2020</b> , 15, e0229001	20
836	Microbial adaptation to high ammonia concentrations during anaerobic digestion of manure-based feedstock: biomethanation and 16S rRNA gene sequencing. <b>2020</b> , 95, 1970-1979	11
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834	Cloacal bacterial communities of tree swallows ( <i>Tachycineta bicolor</i> ): Similarity within a population, but not between pair-bonded social partners. <b>2020</b> , 15, e0228982	5
833	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. <b>2020</b> , 15, 799-821	346
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829	Ecotype differences in aggression, neural activity and behaviorally relevant gene expression in cichlid fish. <b>2020</b> , 19, e12657	13
828	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <b>2020</b> , 70, e100	63
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826	A Primer for Microbiome Time-Series Analysis. <b>2020</b> , 11, 310	13
825	Methodological Insight Into Mosquito Microbiome Studies. <b>2020</b> , 10, 86	8
824	Platforms for elucidating antibiotic resistance in single genomes and complex metagenomes. <b>2020</b> , 138, 105667	26
823	Impacts of directed evolution and soil management legacy on the maize rhizobiome. <b>2020</b> , 145, 107794	8
822	Soil bacterial diversity correlates with precipitation and soil pH in long-term maize cropping systems. <b>2020</b> , 10, 6012	14
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819	Soil fungal communities differ between shaded and sun-intensive coffee plantations in El Salvador. <b>2020</b> , 15, e0231875	4
818	Impact of Dietary Cellobiose on the Fecal Microbiota of Horses. <b>2020</b> , 91, 103106	6
817	Revegetation of urban green space rewilds soil microbiotas with implications for human health and urban design. <b>2020</b> , 28, S322	23
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815	House dust microbiota in relation to adult asthma and atopy in a US farming population. <b>2021</b> , 147, 910-920	4
814	Comparison of microbiome samples: methods and computational challenges. <b>2021</b> , 22, 88-95	9
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812	Adapting the algal microbiome for growth on domestic landfill leachate. <b>2021</b> , 319, 124246	6
811	Low root functional dispersion enhances functionality of plant growth by influencing bacterial activities in European forest soils. <b>2021</b> , 23, 1889-1906	8
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809	Quantitative profiling of built environment bacterial and fungal communities reveals dynamic material dependent growth patterns and microbial interactions. <b>2021</b> , 31, 188-205	4
808	Low-dose and long-term azithromycin significantly decreases <i>Staphylococcus aureus</i> in the microbiome of refractory CRS patients. <b>2021</b> , 11, 93-105	2
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805	Freshwater zooplankton metapopulations and metacommunities respond differently to environmental and spatial variation. <b>2021</b> , 102, e03224	1
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803	Site preparation impacts on soil biotic and abiotic properties, weed control, and native grass establishment. <b>2021</b> , 29, e13297	2

802	Metalimnetic chlorophyll maxima in Lake Kinneret - Chlorobium revisited. <b>2021</b> , 66, 468-480	0
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800	Predicting microbiomes through a deep latent space. <b>2021</b> , 37, 1444-1451	3
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798	Optimizing the quality of clinical studies on oral microbiome: A practical guide for planning, performing, and reporting. <b>2021</b> , 85, 210-236	22
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796	IFAA: Robust Association Identification and Inference for Absolute Abundance in Microbiome Analyses.. <b>2021</b> , 116, 1595-1608	2
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794	Joint Microbial and Metabolomic Network Estimation with the Censored Gaussian Graphical Model. <b>2021</b> , 13, 351-372	
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792	The quest for absolute abundance: The use of internal standards for DNA-based community ecology. <b>2021</b> , 21, 30-43	12
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788	Intraspecific Variability in Root Traits and Edaphic Conditions Influence Soil Microbiomes Across 12 Switchgrass Cultivars. <b>2021</b> , 5, 108-120	6
787	Resolving broad patterns of prokaryotic community structure in New Zealand pasture soils. <b>2021</b> , 64, 143-161	0
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776	CAMAMED: a pipeline for composition-aware mapping-based analysis of metagenomic data. <b>2021</b> , 3, lqaa107		2
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773	Reanalysis of the Mars500 experiment reveals common gut microbiome alterations in astronauts induced by long-duration confinement. <b>2021</b> , 19, 2223-2235		3
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769	Microbiome Analysis Using 16S Amplicon Sequencing: From Samples to ASVs. <b>2021</b> , 2243, 123-141		
768	Students in a Course-Based Undergraduate Research Experience Course Discovered Dramatic Changes in the Bacterial Community Composition Between Summer and Winter Lake Samples. <b>2021</b> , 12, 579325		1
767	Direct Conversion of Food Waste Extract into Caproate: Metagenomics Assessment of Chain Elongation Process. <b>2021</b> , 9,		8

766	Distinctive Microbial Signatures and Gut-Brain Crosstalk in Pediatric Patients with Coeliac Disease and Type 1 Diabetes Mellitus. <b>2021</b> , 22,	1
765	Data Analysis Strategies for Microbiome Studies in Human Populations-a Systematic Review of Current Practice. <b>2021</b> , 6,	4
764	Distinct Changes Occur in the Human Breast Milk Microbiome Between Early and Established Lactation in Breastfeeding Guatemalan Mothers. <b>2021</b> , 12, 557180	7
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761	Effects of Proton Pump Inhibitors on the Small Bowel and Stool Microbiomes. <b>2021</b> , 1	10
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758	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <b>2021</b> , 12, 635781	18
757	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. <b>2021</b> , 12, 634511	41
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754	Hierarchical non-negative matrix factorization using clinical information for microbial communities. <b>2021</b> , 22, 104	1
753	A bacteriophage cocktail significantly reduces <i>Listeria monocytogenes</i> without deleterious impact on the commensal gut microbiota under simulated gastro-intestinal conditions.	
752	Comparison study of sixteen differential abundance testing methods using two large Parkinson disease gut microbiome datasets.	0
751	Metabarcoding reveals hidden species and improves identification of marine zooplankton communities in the North Sea.	2
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749	Swine growth promotion with antibiotics or alternatives can increase antibiotic resistance gene mobility potential. <b>2021</b> , 11, 5485	5

748	Quantification of the covariation of lake microbiomes and environmental variables using a machine learning-based framework. <b>2021</b> , 30, 2131-2144	5
747	The Role of Crystalline Iron Oxides in Methane Mitigation through Anaerobic Oxidation of Methane. <b>2021</b> , 1, 1153-1160	2
746	Longitudinal metabarcoding analysis of karst bacterioplankton microbiomes provide evidence of epikarst to cave transport and community succession. <b>2021</b> , 9, e10757	3
745	Model-Based Microbiome Data Ordination: A Variational Approximation Approach. 1-13	4
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743	Overabundance of <i>Asaia</i> and <i>Serratia</i> bacteria is associated with deltamethrin insecticide susceptibility in <i>Anopheles coluzzii</i> from Agboville, Côte d'Ivoire.	0
742	DCMD: Distance-based classification using mixture distributions on microbiome data. <b>2021</b> , 17, e1008799	1
741	A novel stepwise integrative analysis pipeline reveals distinct microbiota-host interactions and link to symptoms in irritable bowel syndrome. <b>2021</b> , 11, 5521	2
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739	Gut microbiota diversity but not composition is related to saliva cortisol stress response at the age of 2.5 months. <b>2021</b> , 24, 551-560	3
738	Plant Microbiota Beyond Farming Practices: A Review. <b>2021</b> , 5,	1
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736	Soil Bacterial Community Diversity and Composition as Affected by Tillage Intensity Treatments in Corn-Soybean Production Systems. <b>2021</b> , 12, 157-172	2
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734	Comparison of zero replacement strategies for compositional data with large numbers of zeros. <b>2021</b> , 210, 104248	8
733	The pulmonary metatranscriptome prior to pediatric HCT identifies post-HCT lung injury. <b>2021</b> , 137, 1679-16896	
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731	Merged Affinity Network Association Clustering: Joint multi-omic/clinical clustering to identify disease endotypes. <b>2021</b> , 35, 108975	3

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729	A rarefaction-without-resampling extension of PERMANOVA for testing presence-absence associations in the microbiome.	4
728	Hyperlocal Variation in Soil Iron and the Rhizosphere Bacterial Community Determines Dollar Spot Development in Amenity Turfgrass. <b>2021</b> , 87,	1
727	Effects of Fermented Oat Straw as a Lovastatin Carrier on in vitro Methane Production and Rumen Microbiota. <b>2021</b> , 9,	2
726	Bacterial diversity assessment of world's largest sewage-fed fish farms with special reference to water quality: a Ramsar site. <b>2021</b> , 28, 42372-42386	4
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721	Parasites, niche modification and the host microbiome: A field survey of multiple parasites. <b>2021</b> , 30, 2404-2416	3
720	Salmon gut microbiota correlates with disease infection status: potential for monitoring health in farmed animals. <b>2021</b> , 3, 30	14
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717	Next generation sequencing approaches to evaluate water and wastewater quality. <b>2021</b> , 194, 116907	15
716	Effect of tectonic processes on biosphere-geosphere feedbacks across a convergent margin. <b>2021</b> , 14, 301-306	6
715	Hide B seq: Direct versus indirect metabarcoding of coral reef cryptic communities.	3
714	Characterization of gut microbiome and metabolome in Helicobacter pylori patients in an underprivileged community in the United States.	1
713	Microbiome Analysis Reveals Diversity and Function of Associated with the Eastern Oyster,. <b>2021</b> , 6,	4

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704	Plant-microbe interactions in response to grassland herbivory and nitrogen eutrophication. <b>2021</b> , 156, 108208	2
703	Benchmark of data processing methods and machine learning models for gut microbiome-based diagnosis of inflammatory bowel disease.	0
702	Global Diversity and Biogeography of the Mycobiome. <b>2021</b> , 87, e0279520	6
701	Amino Acid-Based Diet Prevents Lethal Infectious Diarrhea by Maintaining Body Water Balance in a Murine Infection Model. <b>2021</b> , 13,	2
700	Characterization of the microbiome and immune response in corals with chronic Montipora white syndrome. <b>2021</b> , 30, 2591-2606	1
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695	Comparable response of wild rodent gut microbiome to anthropogenic habitat contamination. <b>2021</b> , 30, 3485-3499	3

694	Microbiome differential abundance methods produce disturbingly different results across 38 datasets.	7
693	Comparison study of differential abundance testing methods using two large Parkinson disease gut microbiome datasets derived from 16S amplicon sequencing. <b>2021</b> , 22, 265	7
692	Association of aerobic anoxygenic phototrophs and zebra mussels, <i>Dreissena polymorpha</i> , within the littoral zone of Lake Winnipeg. <b>2021</b> , 47, 567-582	3
691	Experimental evidence pointing to rain as a reservoir of tomato phyllosphere microbiota.	1
690	Host-specific epibiomes of distinct <i>Acropora cervicornis</i> genotypes persist after field transplantation.	1
689	Impact of Cellulose-Rich Organic Soil Amendments on Growth Dynamics and Pathogenicity of. <b>2021</b> , 9,	3
688	Estimating the Time Since Deposition of Saliva Stains With a Targeted Bacterial DNA Approach: A Proof-of-Principle Study. <b>2021</b> , 12, 647933	3
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685	Plant Age Influences Microbiome Communities More Than Plant Compartment in Greenhouse Grown Creeping Bentgrass.	0
684	The Effect of Inoculation of a Diazotrophic Bacterial Consortium on the Indigenous Bacterial Community Structure of Sugarcane Apoplast Fluid. <b>2021</b> , 78, 3079-3091	0
683	Differential Response of the Microbiome of <i>Pocillopora acuta</i> to Reciprocal Transplantation Within Singapore. <b>2021</b> , 1	3
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679	Assessing the Diversity and Biomedical Potential of Microbes Associated With the Neptune's Cup Sponge. <b>2021</b> , 12, 631445	0
678	Microbial Community Heterogeneity Within Colorectal Neoplasia and its Correlation With Colorectal Carcinogenesis. <b>2021</b> , 160, 2395-2408	15
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675	A global metagenomic map of urban microbiomes and antimicrobial resistance. <b>2021</b> , 184, 3376-3393.e17	42
674	Gut microbiota signature in treatment-naïve attention-deficit/hyperactivity disorder. <b>2021</b> , 11, 382	5
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671	Changes in the diversity and predicted functional composition of the bulk and rhizosphere soil bacterial microbiomes of tomato and common bean after inorganic N-fertilization. <b>2021</b> , 18, 100362	4
670	mbImpute: an accurate and robust imputation method for microbiome data. <b>2021</b> , 22, 192	6
669	The presence of <i>Pseudogymnoascus destructans</i> , a fungal pathogen of bats, correlates with changes in microbial metacommunity structure. <b>2021</b> , 11, 11685	0
668	Comparative analysis of ocular surface tissue microbiome in human, mouse, rabbit, and guinea pig. <b>2021</b> , 207, 108609	3
667	HumGut: a comprehensive human gut prokaryotic genomes collection filtered by metagenome data. <i>Microbiome</i> , <b>2021</b> , 9, 165	16.6 4
666	Time outweighs the effect of host developmental stage on microbial community composition. <b>2021</b> , 97,	2
665	Fecal sample collection methods and time of day impact microbiome composition and short chain fatty acid concentrations. <b>2021</b> , 11, 13964	0
664	Weight shapes the intestinal microbiome in preterm infants: results of a prospective observational study. <b>2021</b> , 21, 219	3
663	Shifts in the Abundances of Saprotrophic and Ectomycorrhizal Fungi With Altered Leaf Litter Inputs. <b>2021</b> , 12, 682142	3
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661	Microbiome divergence of marine gastropod species separated by the Isthmus of Panama.	1
660	Shifts on archaeal community structure in pure and mixed <i>Eucalyptus grandis</i> and <i>Acacia mangium</i> plantations. <b>2021</b> , 492, 119218	3
659	A Metabolic Model of Intestinal Secretions: The Link between Human Microbiota and Colorectal Cancer Progression. <b>2021</b> , 11,	2

658	Rodent Virus Diversity and Differentiation across Post-Katrina New Orleans. <b>2021</b> , 13, 8034	0
657	Distribution-based comprehensive evaluation of methods for differential expression analysis in metatranscriptomics.	1
656	Oral infection with a periodontal pathogen alters oral and gut microbiomes. <b>2021</b> , 71, 102399	3
655	The microbial metabolite p-Cresol induces autistic-like behaviors in mice by remodeling the gut microbiota. <i>Microbiome</i> , <b>2021</b> , 9, 157	16.6 21
654	Transformation and differential abundance analysis of microbiome data incorporating phylogeny. <b>2021</b> ,	2
653	On the robustness of inference of association with the gut microbiota in stool, rectal swab and mucosal tissue samples. <b>2021</b> , 11, 14828	2
652	Microplastics accumulate fungal pathogens in terrestrial ecosystems. <b>2021</b> , 11, 13214	22
651	Feature selection and causal analysis for microbiome studies in the presence of confounding using standardization. <b>2021</b> , 22, 362	1
650	Using zooplankton metabarcoding to assess the efficacy of different techniques to clean-up an oil-spill in a boreal lake. <b>2021</b> , 236, 105847	1
649	Comparative analysis of the bronchoalveolar microbiome in Portuguese patients with different chronic lung disorders. <b>2021</b> , 11, 15042	0
648	Interactions between <i>Teladorsagia circumcincta</i> Infections and Microbial Composition of Sheep with or without Successful Monepantel Treatment: A Preliminary Study. <b>2021</b> , 1, 31-45	0
647	Gut microbiome and amyotrophic lateral sclerosis: A systematic review of current evidence. <b>2021</b> , 290, 758-788	4
646	Distinct Changes in Gut Microbiota Are Associated with Estradiol-Mediated Protection from Diet-Induced Obesity in Female Mice. <b>2021</b> , 11,	3
645	Microbiome assembly predictably shapes diversity across a range of disturbance frequencies.	1
644	Current Applications of Absolute Bacterial Quantification in Microbiome Studies and Decision-Making Regarding Different Biological Questions. <b>2021</b> , 9,	2
643	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <b>2021</b> , 16, e0237556	1
642	Drivers of change and stability in the gut microbiota of an omnivorous avian migrant exposed to artificial food supplementation. <b>2021</b> , 30, 4723-4739	2
641	Novel screening assay to preselect farm specific pre- and probiotics in pigs. <b>2021</b> , 12, 567-581	0

640	Gut microbiota in psychiatric disorders: Better understanding or more complexity to be resolved? <b>2021</b> , 110, 110302	
639	Resistance, resilience, and functional redundancy of freshwater bacterioplankton communities facing a gradient of agricultural stressors in a mesocosm experiment. <b>2021</b> , 30, 4771-4788	4
638	Exploring prevalence of potential pathogens and fecal indicators in geographically distinct river systems through comparative metagenomics. <b>2021</b> , 282, 117003	0
637	Nutrient pollution alters the gut microbiome of a territorial reef fish. <b>2021</b> , 169, 112522	4
636	Seaweed Dietary Fiber Sodium Alginate Suppresses the Migration of Colonic Inflammatory Monocytes and Diet-Induced Metabolic Syndrome via the Gut Microbiota. <b>2021</b> , 13,	1
635	Impact of Plant-Based Meat Alternatives on the Gut Microbiota of Consumers: A Real-World Study. <b>2021</b> , 10,	7
634	Opportunities and limits of combining microbiome and genome data for complex trait prediction. <b>2021</b> , 53, 65	3
633	Non-mycorrhizal root associated fungi of a tropical montane forest are relatively robust to the long-term addition of moderate rates of nitrogen and phosphorus.	
632	Impact of nisin on <i>Clostridioides difficile</i> and microbiota composition in a faecal fermentation model of the human colon. <b>2021</b> ,	1
631	Statistical analysis of microbiome data: The challenge of sparsity. <b>2021</b> , 19, 35-40	2
630	Do host-associated microbes show a contrarian latitudinal diversity gradient? Insights from <i>Mytilus californianus</i> , an intertidal foundation host. <b>2021</b> , 48, 2839	1
629	Soil microbial community coalescence and fertilization interact to drive the functioning of the legume-rhizobium symbiosis.	0
628	The impact of the host intestinal microbiome on carcinogenesis and the response to chemotherapy. <b>2021</b> , 17, 4371-4387	1
627	Dietary and Pharmacologic Manipulations of Host Lipids and Their Interaction With the Gut Microbiome in Non-human Primates. <b>2021</b> , 8, 646710	0
626	Comprehensive Wet-Bench and Bioinformatics Workflow for Complex Microbiota Using Oxford Nanopore Technologies. <b>2021</b> , 6, e0075021	5
625	The impacts of a logging road on the soil microbial communities, and carbon and nitrogen components in a Northern Zone Costa Rican forest. <b>2021</b> , 164, 103937	1
624	The Effect of Common Viral Inactivation Techniques on 16S rRNA Amplicon-Based Analysis of the Gut Microbiota. <b>2021</b> , 9,	
623	The complexities of inferring symbiont function: <i>Paraburkholderia</i> symbiont dynamics in social amoeba populations and its impact on the amoeba microbiome.	

622	Endophytic microbiome variation among single plant seeds.		1
621	Characterization of gut microbiome and metabolome in patients in an underprivileged community in the United States. <b>2021</b> , 27, 5575-5594		5
620	The spleen bacteriome of wild rodents and shrews from Marigat, Baringo County, Kenya. <b>2021</b> , 9, e12067		
619	Host genomic influence on bacterial composition in the switchgrass rhizosphere.		0
618	Geography-dependent symbiont communities in two oligophagous aphid species. <b>2021</b> , 97,		1
617	Biodiversity of coral reef cryptobiota shuffles but does not decline under the combined stressors of ocean warming and acidification. <b>2021</b> , 118,		4
616	Microbiome of a Reef-Building Coral Displays Signs of Acclimation to a Stressful Shallow Hydrothermal Vent Habitat. <b>2021</b> , 8,		
615	Deciphering microbial mechanisms underlying soil organic carbon storage in a wheat-maize rotation system. <b>2021</b> , 788, 147798		3
614	Spatial distribution of sediment archaeal and bacterial communities relates to the source of organic matter and hypoxia - a biogeographical study on Lake Remoray (France). <b>2021</b> , 97,		0
613	Longitudinal patterns in the skin microbiome of wild, individually marked frogs from the Sierra Nevada, California. <b>2021</b> , 1,		1
612	Powerful and robust non-parametric association testing for microbiome data via a zero-inflated quantile approach (ZINQ). <i>Microbiome</i> , <b>2021</b> , 9, 181	16.6	1
611	Large-scale differences in diversity and functional adaptations of prokaryotic communities from conserved and anthropogenically impacted mangrove sediments in a tropical estuary. <b>2021</b> , 9, e12229		1
610	Persistence of plant-mediated microbial soil legacy effects in soil and inside roots. <b>2021</b> , 12, 5686		13
609	Assessing the ecological risk of pesticides should not ignore the impact of their transformation byproducts - The case of chlorantraniliprole. <b>2021</b> , 418, 126270		4
608	Comparative Evaluation of Sucrosomal Iron and Iron Oxide Nanoparticles as Oral Supplements in Iron Deficiency Anemia in Piglets. <b>2021</b> , 22,		0
607	A critical perspective on interpreting amplicon sequencing data in soil ecological research. <b>2021</b> , 160, 108357		10
606	Characterization of oral and cloacal microbial communities of wild and rehabilitated loggerhead sea turtles ( <i>Caretta caretta</i> ). <b>2021</b> , 3, 59		2
605	Hydrodynamic disturbance controls microbial community assembly and biogeochemical processes in coastal sediments. <b>2021</b> ,		4

604	Microbial ecology to support integrative efficacy improvement of biocontrol agents for postharvest diseases management. <b>2021</b> , 179, 111572	8
603	Bacterial microbiome of dusky kob <i>Argyrosomus japonicus</i> eggs and rearing water and the bacteriostatic effect of selected disinfectants. <b>2021</b> , 542, 736882	0
602	The Clinical Relevance of the Microbiome in Hidradenitis Suppurativa: A Systematic Review. <b>2021</b> , 9,	1
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600	Insights into the gut bacterial communities of spider from wild with no evidence of phyllosymbiosis. <b>2021</b> , 28, 5913-5924	0
599	Restriction of soil bacteria promoting high yield of super hybrid rice in the Huaihe Valley in central China by conventional ploughing intensity. <b>2021</b> , 214, 105169	0
598	Changes in rumen fermentation and bacterial community in lactating dairy cows with subacute rumen acidosis following rumen content transplantation. <b>2021</b> , 104, 10780-10795	2
597	A gastrointestinal nematode in pregnant and lactating mice alters maternal and neonatal microbiomes. <b>2021</b> , 51, 945-957	
596	Early life stress causes persistent impacts on the microbiome of Atlantic salmon. <b>2021</b> , 40, 100888	1
595	Livestock microbial landscape patterns: Retail poultry microbiomes significantly vary by region and season. <b>2022</b> , 101, 103878	1
594	Composition and potential functional roles of soil fungal communities on arid farms in Arequipa (Southern Peru) characterized using SMRT sequencing. <b>2022</b> , 169, 104228	0
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592	A rarefaction-based extension of the LDM for testing presence-absence associations in the microbiome. <b>2021</b> ,	6
591	Effects of dietary cellobiose on the intestinal microbiota and excretion of nitrogen metabolites in healthy adult dogs. <b>2021</b> , 105, 569-578	4
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584	Multivariable Association Discovery in Population-scale Meta-omics Studies.	71
583	Metagenomic Data Mining in Oil Spill Studies. <b>2019</b> , 211-223	1
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579	Wheat dwarfing influences selection of the rhizosphere microbiome. <b>2020</b> , 10, 1452	28
578	Estimating diversity in networked ecological communities. <b>2020</b> ,	24
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574	Characterizing dysbiosis of gut microbiome in PD: Evidence for overabundance of opportunistic pathogens.	3
573	Assessment of statistical methods from single cell, bulk RNA-seq and metagenomics applied to microbiome data.	1
572	Early life stress causes persistent impacts on the microbiome of Atlantic salmon.	3
571	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota.	1
570	A footprint of plant eco-geographic adaptation on the composition of the barley rhizosphere bacterial microbiota.	1
569	A Quantitative Sequencing Framework for Absolute Abundance Measurements of Mucosal and Luminal Microbial Communities.	1

568	mbImpute: an accurate and robust imputation method for microbiome data.	4
567	HumGut: A comprehensive Human Gut prokaryotic genomes collection filtered by metagenome data.	1
566	Predicting microbiomes through a deep latent space.	0
565	Specific and conserved patterns of microbiota-structuring by maize benzoxazinoids in the field.	0
564	Differential Response of Digesta- and Mucosa-Associated Intestinal Microbiota to Dietary Black Soldier Fly ( <i>Hermetia illucens</i> ) Larvae Meal in Seawater Phase Atlantic Salmon ( <i>Salmo salar</i> ).	4
563	The microbial metabolite p-Cresol induces autistic-like behaviors in mice by remodeling the gut microbiota.	3
562	Patterns of microbiome variation among infrapopulations of permanent bloodsucking parasites.	1
561	Abiotic treatment to common bean plants results in an altered seed microbiome.	1
560	Seasonal shifts in the gut microbiome indicate plastic responses to diet in wild geladas.	1
559	Meta-analysis of the gut microbiome of Parkinson's disease patients suggests alterations linked to intestinal inflammation.	3
558	Hyperlocal Variation in Soil Iron and Rhizosphere Microbiome Determines Disease Development in Amenity Turfgrass.	1
557	Balances: a new perspective for microbiome analysis.	3
556	Differential expression analysis of log-ratio transformed counts: benchmarking methods for RNA-Seq data.	1
555	Rarefaction, alpha diversity, and statistics.	6
554	DATest: a framework for choosing differential abundance or expression method.	17
553	DivNet: Estimating diversity in networked communities.	17
552	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples.	2
551	Shrinkage improves estimation of microbial associations under different normalization methods.	6

550	Initial Sequencing and Characterization of Gastrointestinal and Oral Microbiota in Urban Pakistani Adults Reveals Abnormally High Levels of Potentially Starch Metabolizing Bacteria in the General Population.	2
549	Analysis of the gut and gill microbiome of resistant and susceptible lines of rainbow trout ( <i>Oncorhynchus mykiss</i> ).	1
548	Statistical Considerations in the Design and Analysis of Longitudinal Microbiome Studies.	5
547	Naught all zeros in sequence count data are the same.	20
546	PUMA: A tool for processing 16S rRNA taxonomy data for analysis and visualization.	4
545	A probabilistic model to identify the core microbial community.	1
544	Fungal Communities in Soybean Cyst Nematode-Infested Soil under Long Term Corn and Soybean Monoculture and Crop Rotation.	1
543	MAGMA: inference of sparse microbial association networks.	7
542	Environmental plasticity and colonisation history in the Atlantic salmon microbiome: a translocation experiment.	4
541	Watered-down biodiversity? A comparison of metabarcoding results from DNA extracted from matched water and bulk tissue biomonitoring samples.	5
540	End-to-end assessment of fecal bacteriome analysis: from sample processing to DNA sequencing and bioinformatics results.	3
539	Biomarker discovery in inflammatory bowel diseases using network-based feature selection.	1
538	Dirichlet-multinomial modelling outperforms alternatives for analysis of microbiome and other ecological count data.	1
537	High-resolution QTL mapping with Diversity Outbred mice identifies genetic variants that impact gut microbiome composition.	1
536	Global Genetic Cartography of Urban Metagenomes and Anti-Microbial Resistance.	16
535	Compositional knockoff filter for high-dimensional regression analysis of microbiome data.	2
534	Discrete False-Discovery Rate Improves Identification of Differentially Abundant Microbes. <b>2017</b> , 2,	48
533	Zero-Inflated gaussian mixed models for analyzing longitudinal microbiome data. <b>2020</b> , 15, e0242073	4



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531	Targeting the Infant Gut Microbiota Through a Perinatal Educational Dietary Intervention: Protocol for a Randomized Controlled Trial. <b>2019</b> , 8, e14771	9
530	Microbiome dynamics of two differentially resilient corals. <b>2018</b> , 131, 213-226	4
529	Systematic Comparisons for Composition Profiles, Taxonomic Levels, and Machine Learning Methods for Microbiome-Based Disease Prediction. <b>2020</b> , 7, 610845	6
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525	Viromes of one year old infants reveal the impact of birth mode on microbiome diversity. <b>2018</b> , 6, e4694	68
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523	Phytobiomes are compositionally nested from the ground up. <b>2019</b> , 7, e6609	19
522	Shared mycorrhizae but distinct communities of other root-associated microbes on co-occurring native and invasive maples. <b>2019</b> , 7, e7295	5
521	Diets with and without edible cricket support a similar level of diversity in the gut microbiome of dogs. <b>2019</b> , 7, e7661	13
520	Microbial and chemical dynamics of a toxic dinoflagellate bloom. <b>2020</b> , 8, e9493	4
519	Improved normalization of species count data in ecology by scaling with ranked subsampling (SRS): application to microbial communities. <b>2020</b> , 8, e9593	27
518	Towards bacterioplankton composition as indicator of environmental status: proof of principle using indicator value analysis of estuarine communities.	0
517	Overabundance of and Bacteria Is Associated with Deltamethrin Insecticide Susceptibility in from Agboville, CÔte d'Ivoire. <b>2021</b> , 9, e0015721	2
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515	Milking system and premilking routines have strong effect on the microbial community in bulk tank milk. <b>2021</b> ,	1

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513	A Novel Method for Performance Measurement of Public Educational Institutions Using Machine Learning Models. <b>2021</b> , 11, 9296	10
512	Prospective study of oral microbiome and gastric cancer risk among Asian, African American and European American populations. <b>2021</b> ,	2
511	The invasive cactus <i>Opuntia stricta</i> creates fertility islands in African savannas and benefits from those created by native trees. <b>2021</b> , 11, 20748	2
510	Bacterial community dynamics during embryonic development of the little skate ( <i>Leucoraja erinacea</i> ). <b>2021</b> , 3, 72	1
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504	Microbiomes of North American Triatominae: the grounds for Chagas disease epidemiology.	
503	Detection of Multidimensional Co-Exclusion Patterns in Microbial Communities.	
502	Rarity of microbial species: In search of reliable associations.	
501	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.	1
500	Mian: Interactive Web-Based 16S rRNA Operational Taxonomic Unit Table Data Visualization and Discovery Platform.	1
499	Variable Selection for High Dimensional Metagenomic Data. <b>2019</b> , 19-32	
498	Fecal microbiota dysbiosis in macaques and humans within a shared environment.	0
497	Mouse vendor influence on the bacterial and viral gut composition exceeds the effect of diet.	1

496	COI metabarcoding primer choice affects richness and recovery of indicator taxa in freshwater systems.	1
495	Nitrogen availability modulates the host control of the barley rhizosphere microbiota.	1
494	The rodent vaginal microbiome across the estrous cycle and the effect of genital nerve electrical stimulation.	
493	Meta-taxonomic Analysis of Prokaryotic and Eukaryotic Gut Flora in Stool Samples from Visceral Leishmaniasis Cases and Endemic Controls in Bihar State India.	1
492	Symbiont frequency predicts microbiome composition in a model bryozoan-bacterial symbiosis. <b>2019</b> , 83, 1-13	1
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490	Differential Activity of Coexisting Prochlorococcus Ecotypes. <b>2019</b> , 6,	1
489	A Rarefaction-Based Extension of the LDM for Testing Presence-Absence Associations in the Microbiome.	
488	Mucin-derived O-glycans supplemented to diet mitigate diverse microbiota perturbations.	
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484	Artificial classification of cervical squamous lesions in ThinPrep cytologic tests using a deep convolutional neural network. <b>2020</b> , 20, 113	0
483	ResistoXplorer: a web-based tool for visual, statistical and exploratory data analysis of resistome data.	
482	Salivary microbiome profiling reveals a dysbiotic schizophrenia-associated microbiota. <b>2021</b> , 7, 51	4
481	Phenology-dependent root bacteria enhance yield of Brassica napus. <b>2021</b> , 166, 108468	0
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- 465 Natural bacterial assemblages in *Arabidopsis thaliana* tissues become more distinguishable and diverse during host development. 1
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459	Multi-scale Adaptive Differential Abundance Analysis in Microbial Compositional Data.	0
458	Opportunities and limits of combining microbiome and genome data for complex trait prediction.	
457	Persistence of plant-mediated microbial soil legacy effects in soil and inside roots.	
456	A network approach to investigating the key microbes and stability of gut microbial communities in a mouse neuropathic pain model. <b>2020</b> , 20, 295	3
455	Joint Microbial and Metabolomic Network Estimation with the Censored Gaussian Graphical Model.	1
454	The gut microbiome stability of a butterflyfish is disrupted on severely degraded Caribbean coral reefs.	1
453	A zero inflated log-normal model for inference of sparse microbial association networks.	1
452	Identifying the Specific Root Microbiome of the Hyperaccumulator Growing in Non-metalliferous Soils. <b>2021</b> , 12, 639997	
451	Metagenomic approaches to study the culture-independent bacterial diversity of a polluted environment— case study on north-eastern coast of Bay of Bengal, India. <b>2022</b> , 81-107	0
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448	The relationship between land cover and microbial community composition in European lakes.	
447	Power Play of Commensal Bacteria in the Buccal Cavity of Female Nile Tilapia. <b>2021</b> , 12, 773351	0
446	Enhancing diversity analysis by repeatedly rarefying next generation sequencing data describing microbial communities. <b>2021</b> , 11, 22302	11
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444	Improved quantitative microbiome profiling for environmental antibiotic resistance surveillance. <b>2021</b> , 16, 21	0
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439	Effects of Milkfat on the Gut Microbiome of Patients After Bariatric Surgery, a Pilot Study. <b>2021</b> , 1	1
438	Analysing microbiome intervention design studies: Comparison of alternative multivariate statistical methods. <b>2021</b> , 16, e0259973	1
437	Autism-related dietary preferences mediate autism-gut microbiome associations. <b>2021</b> , 184, 5916-5931.e17	30
436	Multivariable association discovery in population-scale meta-omics studies. <b>2021</b> , 17, e1009442	72
435	Applications of the indole-alkaloid gramine modulate the assembly of individual members of the barley rhizosphere microbiota.. <b>2021</b> , 9, e12498	1
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432	Defining and quantifying the core microbiome: Challenges and prospects. <b>2021</b> , 118,	21
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427	Saccharomyces boulardii CNCM I-745 supplementation modifies the fecal resistome during Helicobacter pylori eradication therapy.. <b>2022</b> , e12870	1
426	The Rest Is Noise: Finding Signals in Lung Microbiome Data Analysis. <b>2022</b> , 35-57	
425	Divergent belowground carbon allocation patterns of winter wheat shape rhizosphere microbial communities and nitrogen cycling activities. <b>2022</b> , 165, 108518	1

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