

Quality-filtering vastly improves diversity estimates from

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Citation Report

#	ARTICLE	IF	CITATIONS
1	UPARSE: highly accurate OTU sequences from microbial amplicon reads. <i>Nature Methods</i> , 2013, 10, 996-998.	9.0	13,193
2	Development of a Dual-Index Sequencing Strategy and Curation Pipeline for Analyzing Amplicon Sequence Data on the MiSeq Illumina Sequencing Platform. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5112-5120.	1.4	5,923
3	Computational Methods for High-Throughput Comparative Analyses of Natural Microbial Communities. <i>Methods in Enzymology</i> , 2013, 531, 353-370.	0.4	38
4	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
5	Improved Selection of Internal Transcribed Spacer-Specific Primers Enables Quantitative, Ultra-High-Throughput Profiling of Fungal Communities. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2519-2526.	1.4	442
6	Surface Microbes in the Neonatal Intensive Care Unit: Changes with Routine Cleaning and over Time. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2617-2624.	1.8	73
7	Facility-Specific "House" Microbiome Drives Microbial Landscapes of Artisan Cheesemaking Plants. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5214-5223.	1.4	232
8	Distribution-Based Clustering: Using Ecology To Refine the Operational Taxonomic Unit. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6593-6603.	1.4	140
9	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. <i>ELife</i> , 2013, 2, e01104.	2.8	270
10	Monitoring Seasonal Changes in Winery-Resident Microbiota. <i>PLoS ONE</i> , 2013, 8, e66437.	1.1	167
11	Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms. <i>Biogeosciences</i> , 2013, 10, 555-566.	1.3	60
12	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e93827.	1.1	508
13	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. <i>PLoS ONE</i> , 2014, 9, e114804.	1.1	110
14	Variations in brain DNA. <i>Frontiers in Aging Neuroscience</i> , 2014, 6, 323.	1.7	6
15	Evaluation of Automated Ribosomal Intergenic Spacer Analysis for Bacterial Fingerprinting of Rumen Microbiome Compared to Pyrosequencing Technology. <i>Pathogens</i> , 2014, 3, 109-120.	1.2	31
16	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. <i>ISME Journal</i> , 2014, 8, 1904-1919.	4.4	150
17	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. <i>Frontiers in Microbiology</i> , 2014, 5, 298.	1.5	130
18	Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for <i>Clostridium difficile</i> susceptibility. <i>Microbiome</i> , 2014, 2, 42.	4.9	128

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19	Temporal changes and the effect of subtherapeutic concentrations of antibiotics in the gut microbiota of swine. <i>FEMS Microbiology Ecology</i> , 2014, 90, 599-608.	1.3	75
20	Deodorization of pig slurry and characterization of bacterial diversity using 16S rDNA sequence analysis. <i>Journal of Microbiology</i> , 2014, 52, 918-929.	1.3	8
21	Individuals' diet diversity influences gut microbial diversity in two freshwater fish (threespine stickleback and fathead minnow). <i>Journal of Applied Microbiology</i> , 2014, 116, 1066-1074.	3.0	288
22	Analysis of plant-microbe interactions in the era of next generation sequencing technologies. <i>Frontiers in Plant Science</i> , 2014, 5, 216.	1.7	194
23	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014, 15, 531.	3.8	355
24	Analysis, Optimization and Verification of Illumina-Generated 16S rRNA Gene Amplicon Surveys. <i>PLoS ONE</i> , 2014, 9, e94249.	1.1	287
25	Cyanobacteria in New Zealand indigenous grasslands. <i>New Zealand Journal of Botany</i> , 2014, 52, 100-115.	0.8	5
26	DRISEE overestimates errors in metagenomic sequencing data. <i>Briefings in Bioinformatics</i> , 2014, 15, 783-787.	3.2	5
27	The amphibian skin-associated microbiome across species, space and life history stages. <i>Molecular Ecology</i> , 2014, 23, 1238-1250.	2.0	360
28	Meta-QC-Chain: Comprehensive and Fast Quality Control Method for Metagenomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 52-56.	3.0	17
29	Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. <i>Environmental Microbiology</i> , 2014, 16, 2659-2671.	1.8	291
30	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317.	2.0	311
31	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders (<i>Plethodon cinereus</i>). <i>ISME Journal</i> , 2014, 8, 830-840.	4.4	316
32	Comparing the anterior nares bacterial community of two discrete human populations using Illumina amplicon sequencing. <i>Environmental Microbiology</i> , 2014, 16, 2939-2952.	1.8	177
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35	Patchiness of deep-sea benthic Foraminifera across the Southern Ocean: Insights from high-throughput DNA sequencing. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2014, 108, 17-26.	0.6	59
36	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E139-48.	3.3	791

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38	Temperature response of denitrification and anaerobic ammonium oxidation rates and microbial community structure in Arctic fjord sediments. <i>Environmental Microbiology</i> , 2014, 16, 3331-3344.	1.8	84
39	Cultivation-based multiplex phenotyping of human gut microbiota allows targeted recovery of previously uncultured bacteria. <i>Nature Communications</i> , 2014, 5, 4714.	5.8	123
40	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	13.5	625
41	Getting Started with Microbiome Analysis: Sample Acquisition to Bioinformatics. <i>Current Protocols in Human Genetics</i> , 2014, 82, 18.8.1-29.	3.5	111
42	Data analysis for 16S microbial profiling from different benchtop sequencing platforms. <i>Journal of Microbiological Methods</i> , 2014, 107, 30-37.	0.7	221
43	Beyond genome sequencing: Lineage tracking with barcodes to study the dynamics of evolution, infection, and cancer. <i>Genomics</i> , 2014, 104, 417-430.	1.3	81
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46	Amphibian skin may select for rare environmental microbes. <i>ISME Journal</i> , 2014, 8, 2207-2217.	4.4	255
47	Indigenous Bacteria and Fungi Drive Traditional Kimoto Sake Fermentations. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5522-5529.	1.4	86
48	Analysis of Multiple Tsetse Fly Populations in Uganda Reveals Limited Diversity and Species-Specific Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4301-4312.	1.4	95
49	<i>Bifidobacterium longum</i> subsp. <i>infantis</i> in experimental necrotizing enterocolitis: alterations in inflammation, innate immune response, and the microbiota. <i>Pediatric Research</i> , 2014, 76, 326-333.	1.1	95
50	Persistent gut microbiota immaturity in malnourished Bangladeshi children. <i>Nature</i> , 2014, 510, 417-421.	13.7	1,019
51	Comparison of the vaginal microbial communities in women with recurrent genital HSV receiving acyclovir intravaginal rings. <i>Antiviral Research</i> , 2014, 102, 87-94.	1.9	19
52	Interplay of host microbiota, genetic perturbations, and inflammation promotes local development of intestinal neoplasms in mice. <i>Journal of Experimental Medicine</i> , 2014, 211, 457-472.	4.2	71
53	Association between Group 2 Innate Lymphoid Cells enrichment, nasal polyps and allergy in Chronic Rhinosinusitis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2014, 69, 1154-1161.	2.7	151
54	Next-Generation Environmental Diversity Surveys of Foraminifera: Preparing the Future. <i>Biological Bulletin</i> , 2014, 227, 93-106.	0.7	68

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61	The Role of Curcumin in Modulating Colonic Microbiota During Colitis and Colon Cancer Prevention. Inflammatory Bowel Diseases, 2015, 21, 2483-2494.	0.9	166
62	Bacterial biogeography in the coastal waters of northern <sc>Z</sc>hejiang, <sc>E</sc>ast <sc>C</sc>hina <sc>S</sc>ea is highly controlled by spatially structured environmental gradients. Environmental Microbiology, 2015, 17, 3898-3913.	1.8	93
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73	Microbial biogeography of the transnational fermented milk matsoni. Food Microbiology, 2015, 50, 12-19.	2.1	47

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85	Prepartum and Postpartum Rumen Fluid Microbiomes: Characterization and Correlation with Production Traits in Dairy Cows. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1327-1337.	1.4	145
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88	Transmission of Atherosclerosis Susceptibility with Gut Microbial Transplantation. <i>Journal of Biological Chemistry</i> , 2015, 290, 5647-5660.	1.6	400
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97	Dietary input of microbes and host genetic variation shape among-population differences in stickleback gut microbiota. <i>ISME Journal</i> , 2015, 9, 2515-2526.	4.4	291
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122	Tracking Strains in the Microbiome: Insights from Metagenomics and Models. Frontiers in Microbiology, 2016, 7, 712.	1.5	44
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132	Structural Change in Microbiota by a Probiotic Cocktail Enhances the Gut Barrier and Reduces Cancer via TLR2 Signaling in a Rat Model of Colon Cancer. <i>Digestive Diseases and Sciences</i> , 2016, 61, 2908-2920.	1.1	121
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148	Advances in DNA metabarcoding for food and wildlife forensic species identification. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 4615-4630.	1.9	180
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150	Oceanic fronts: transition zones for bacterioplankton community composition. <i>Environmental Microbiology Reports</i> , 2016, 8, 132-138.	1.0	65
151	Amplicon-based metabarcoding reveals temporal response of soil microbial community to fumigation-derived products. <i>Applied Soil Ecology</i> , 2016, 103, 83-92.	2.1	28
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889	Supplementation with compound polysaccharides contributes to the development and metabolic activity of young rat intestinal microbiota. <i>Food and Function</i> , 2019, 10, 2658-2675.	2.1	28
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893	Long-term N fertilization altered ¹³ C-labeled fungal community composition but not diversity in wheat rhizosphere of Chinese black soil. <i>Soil Biology and Biochemistry</i> , 2019, 135, 117-126.	4.2	21
895	Cultivated rice rhizomicrobiome is more sensitive to environmental shifts than that of wild rice in natural environments. <i>Applied Soil Ecology</i> , 2019, 140, 68-77.	2.1	17
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1323	Differences in Microbiota Between Two Multilocus Lineages of the Sugarcane Aphid (<i>Melanaphis</i>) Tj ETQq1 1 0.784314 rgBT /Over 113, 257-265.	1.3	13
1324	Analysis of by high-throughput sequencing: <i>Helicobacter pylori</i> infection and salivary microbiome. <i>BMC Oral Health</i> , 2020, 20, 84.	0.8	24
1325	Quality Evaluation and Characterization of Specific Spoilage Organisms of Spanish Mackerel by High-Throughput Sequencing during 0 °C Cold Chain Logistics. <i>Foods</i> , 2020, 9, 312.	1.9	20
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1327	Deep Insights into Gut Microbiota in Four Carnivorous Coral Reef Fishes from the South China Sea. <i>Microorganisms</i> , 2020, 8, 426.	1.6	22
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1331	Gut microbiota shifts in the giant tiger shrimp, <i>Penaeus monodon</i> , during the postlarvae, juvenile, and adult stages. <i>Aquaculture International</i> , 2020, 28, 1421-1433.	1.1	22
1332	Fungal communities differentially respond to warming and drought in tropical grassland soil. <i>Molecular Ecology</i> , 2020, 29, 1550-1559.	2.0	41
1333	The international sinonasal microbiome study: A multicentre, multinational characterization of sinonasal bacterial ecology. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2037-2049.	2.7	55
1334	Effects of a Diet Supplemented with Exogenous Catalase from <i>Penicillium notatum</i> on Intestinal Development and Microbiota in Weaned Piglets. <i>Microorganisms</i> , 2020, 8, 391.	1.6	14
1335	Association between the sinus microbiota with eosinophilic inflammation and prognosis in chronic rhinosinusitis with nasal polyps. <i>Experimental and Molecular Medicine</i> , 2020, 52, 978-987.	3.2	14
1336	Effects of stocking density on the growth performance, physiological response and intestinal microbiota of juvenile <i>Echiura</i> worms (<i>Urechis unicinctus</i>). <i>Aquaculture Research</i> , 2020, 51, 3983-3992.	0.9	8
1337	The circadian disruption of night work alters gut microbiota consistent with elevated risk for future metabolic and gastrointestinal pathology. <i>Chronobiology International</i> , 2020, 37, 1067-1081.	0.9	32
1338	Seasonal effects of river flow on microbial community coalescence and diversity in a riverine network. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	33
1339	Effects of Drinking Water Temperature and Flow Rate during Cold Season on Growth Performance, Nutrient Digestibility and Cecum Microflora of Weaned Piglets. <i>Animals</i> , 2020, 10, 1048.	1.0	6

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1341	Impacts of Anthropogenic Pollutants on Benthic Prokaryotic Communities in Mediterranean Touristic Ports. <i>Frontiers in Microbiology</i> , 2020, 11, 1234.	1.5	15
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1343	The use of Unmanned Aerial Vehicles (UAVs) to sample the blow microbiome of small cetaceans. <i>PLoS ONE</i> , 2020, 15, e0235537.	1.1	27
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1346	Dynamic distribution of gut microbiota during embryonic development in chicken. <i>Poultry Science</i> , 2020, 99, 5079-5090.	1.5	28
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1353	Diagnosis of cytomegalovirus infection from clinical whole genome sequencing. <i>Scientific Reports</i> , 2020, 10, 11020.	1.6	6
1354	Microbial communities of container aquatic habitats shift in response to <i>Culex restuans</i> larvae. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	6
1355	Fine-scale succession patterns and assembly mechanisms of bacterial community of <i>Litopenaeus vannamei</i> larvae across the developmental cycle. <i>Microbiome</i> , 2020, 8, 106.	4.9	52
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1362	Are migratory waterfowl vectors of seagrass pathogens?. <i>Ecology and Evolution</i> , 2020, 10, 2062-2073.	0.8	7
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1368	Colorectal cancer diagnostic model utilizing metagenomic and metabolomic data of stool microbial extracellular vesicles. <i>Scientific Reports</i> , 2020, 10, 2860.	1.6	57
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1374	Next-Generation Sequencing: The Enabler and the Way Ahead. , 2020, , 175-200.		2
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1384	Comparison of serum microbiome composition in bipolar and major depressive disorders. <i>Journal of Psychiatric Research</i> , 2020, 123, 31-38.	1.5	23
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1393	Bacterial community profile after the lethal infection of <i>Steinernema</i> â€“ <i>Xenorhabdus</i> pairs into soil-reared <i>Tenebrio molitor</i> larvae. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	13

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1397	Murine Genetic Background Overcomes Gut Microbiota Changes to Explain Metabolic Response to High-Fat Diet. <i>Nutrients</i> , 2020, 12, 287.	1.7	25
1398	Response of the <i>Litopenaeus vananmei</i> intestinal bacteria and antioxidant system to rearing density and exposure to <i>Vibrio parahaemolyticus</i> E1. <i>Journal of Invertebrate Pathology</i> , 2020, 170, 107326.	1.5	7
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1400	Insight into the assembly of root-associated microbiome in the medicinal plant <i>Polygonum cuspidatum</i> . <i>Industrial Crops and Products</i> , 2020, 145, 112163.	2.5	38
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1407	&p>Characteristics of Gastric Microbiota in GK Rats with Spontaneous Diabetes: A Comparative Study<p>. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2020, Volume 13, 1435-1447.	1.1	12
1408	Methodological Insight Into Mosquito Microbiome Studies. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 86.	1.8	15
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1413	Application of Viral Metagenomics for Study of Emerging and Reemerging Tick-Borne Viruses. <i>Vector-Borne and Zoonotic Diseases</i> , 2020, 20, 557-565.	0.6	8
1414	Reintroducing mothur: 10 Years Later. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	160
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1416	Microbiotyping the Sinonasal Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 137.	1.8	21
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1446	AmpliCI: a high-resolution model-based approach for denoising Illumina amplicon data. <i>Bioinformatics</i> , 2021, 36, 5151-5158.	1.8	15
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1449	Dietary supplementation with <i>Bacillus</i> mixture modifies the intestinal ecosystem of weaned piglets in an overall beneficial way. <i>Journal of Applied Microbiology</i> , 2021, 130, 233-246.	1.4	20
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1456	Community diversity and abundance of ammonia-oxidizing archaea and bacteria in shrimp pond sediment at different culture stages. <i>Journal of Applied Microbiology</i> , 2021, 130, 1442-1455.	1.4	18
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1574	Spatiotemporal variation of bacterial communities in three cascade reservoirs in a southern city of China. <i>Water Science and Technology: Water Supply</i> , 2021, 21, 2532-2542.	1.0	1
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1593	Gut dysbiosis and clinical phases of pancolitis in patients with ulcerative colitis. <i>MicrobiologyOpen</i> , 2021, 10, e1181.	1.2	13
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1599	Microbiota-associated risk factors for asymptomatic gut colonisation with multi-drug-resistant organisms in a Dutch nursing home. <i>Genome Medicine</i> , 2021, 13, 54.	3.6	19
1600	Metabarcoding of environmental samples suggest wide distribution of eelgrass (<i>Zostera marina</i>) pathogens in the north Pacific. <i>Metabarcoding and Metagenomics</i> , 0, 5, .	0.0	5
1601	Collection of a Bacterial Community Reconstructed from Marine Metagenomes Derived from Jinhae Bay, South Korea. <i>Data</i> , 2021, 6, 44.	1.2	0
1602	Genetic Diversity in Marine Planktonic Ciliates (Alveolata, Ciliophora) Suggests Distinct Geographical Patterns – Data From Chinese and European Coastal Waters. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	8
1603	Dietary Fiber Ameliorates Lipopolysaccharide-Induced Intestinal Barrier Function Damage in Piglets by Modulation of Intestinal Microbiome. <i>MSystems</i> , 2021, 6, .	1.7	26
1604	Evaluation of microbial species inactivation and purification of pond sewage by a custom-built air surface discharge plasma. <i>Plasma Processes and Polymers</i> , 2021, 18, 2100004.	1.6	8
1605	Bioinformatic pipelines combining denoising and clustering tools allow for more comprehensive prokaryotic and eukaryotic metabarcoding. <i>Molecular Ecology Resources</i> , 2021, 21, 1904-1921.	2.2	43
1606	Hide –n seq: Direct versus indirect metabarcoding of coral reef cryptic communities. <i>Environmental DNA</i> , 2022, 4, 93-107.	3.1	14
1608	Ciliates (Alveolata, Ciliophora) as bioindicators of environmental pressure: A karstic river case. <i>Ecological Indicators</i> , 2021, 124, 107430.	2.6	20
1609	Diversity of Endophytes in <i>Fagopyrum esculentum</i> Moench. Seeds from Different Locations in China. <i>Russian Journal of Plant Physiology</i> , 2021, 68, 413-420.	0.5	2
1610	Influence of genetic background and dietary oleic acid on gut microbiota composition in Duroc and Iberian pigs. <i>PLoS ONE</i> , 2021, 16, e0251804.	1.1	4
1611	Variations in Soil Enzyme Activities and Microbial Communities along an Altitudinal Gradient on the Eastern Qinghai –Tibetan Plateau. <i>Forests</i> , 2021, 12, 681.	0.9	8
1612	Metagenomic analysis of pathogen mastitis in cow –milk from Cicurug, Sukabumi, West Java, Indonesia. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 762, 012064.	0.2	2
1613	Treatment of petroleum hydrocarbon-polluted groundwater with innovative in situ sulfate-releasing biobarrier. <i>Journal of Cleaner Production</i> , 2021, 295, 126424.	4.6	14

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1615	Effect of an intramammary lipopolysaccharide challenge on the hindgut microbial composition and fermentation of dairy cattle experiencing intermittent subacute ruminal acidosis. <i>Journal of Dairy Science</i> , 2021, 104, 5417-5431.	1.4	12
1616	Effect of metaphylactic administration of tildipirosin on the incidence of pneumonia and otitis and on the upper respiratory tract and fecal microbiome of preweaning Holstein calves. <i>Journal of Dairy Science</i> , 2021, 104, 6020-6038.	1.4	7
1617	Diet, habitat environment and lifestyle conversion affect the gut microbiomes of giant pandas. <i>Science of the Total Environment</i> , 2021, 770, 145316.	3.9	27
1618	Distinct microhabitats affect the relative balance of ecological processes shaping the spatial distribution of bacterial communities in lakeshore habitats. <i>Freshwater Biology</i> , 2021, 66, 1475-1489.	1.2	4
1619	Temporal Bacterial Community Diversity in the <i>Nicotiana tabacum</i> Rhizosphere Over Years of Continuous Monocropping. <i>Frontiers in Microbiology</i> , 2021, 12, 641643.	1.5	14
1620	Dynamic Observation of the Effect of Maternal Caries on the Oral Microbiota of Infants Aged 12â€“24 Months. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 637394.	1.8	3
1621	Coexistence of Three Dominant Bacterial Symbionts in a Social Aphid and Implications for Ecological Adaptation. <i>Insects</i> , 2021, 12, 416.	1.0	7
1622	Spatial and seasonal variations in biofilm formation on microplastics in coastal waters. <i>Science of the Total Environment</i> , 2021, 770, 145303.	3.9	71
1623	Fungal diversity driven by bark features affects phorophyte preference in epiphytic orchids from southern China. <i>Scientific Reports</i> , 2021, 11, 11287.	1.6	13
1624	Detoxification of Oral Exposure to Benzo(a)pyrene by <i>Lactobacillus plantarum</i> CICC 23121 in Mice. <i>Molecular Nutrition and Food Research</i> , 2021, 65, 2001149.	1.5	2
1625	Phylogeny- and Abundance-Based Metrics Allow for the Consistent Comparison of Core Gut Microbiome Diversity Indices Across Host Species. <i>Frontiers in Microbiology</i> , 2021, 12, 659918.	1.5	14
1626	Effects of Flurochloridone Application on Rhizosphere Soil Fungal Community and Composition in Potato Growing Areas of the Qinghai-Tibet Plateau. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 420.	1.5	2
1627	Illumina MiSeq sequencing reveals microbial community succession in salted peppers with different salinity during preservation. <i>Food Research International</i> , 2021, 143, 110234.	2.9	16
1628	Land use intensification destabilizes stream microbial biodiversity and decreases metabolic efficiency. <i>Science of the Total Environment</i> , 2021, 767, 145440.	3.9	6
1629	Bacterial Diversity and Community Structure in the Rhizosphere of Four Halophytes. <i>Current Microbiology</i> , 2021, 78, 2720-2732.	1.0	8
1630	Tobacco Smoking and the Fecal Microbiome in a Large, Multi-ethnic Cohort. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1328-1335.	1.1	17
1631	<i>Bacillus Subtilis</i> 29784 as a Feed Additive for Broilers Shifts the Intestinal Microbial Composition and Supports the Production of Hypoxanthine and Nicotinic Acid. <i>Animals</i> , 2021, 11, 1335.	1.0	11

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1633	Gut microbiota are associated with sex and age of host: Evidence from semi-provisioned rhesus macaques in southwest Guangxi, China. <i>Ecology and Evolution</i> , 2021, 11, 8096-8122.	0.8	14
1634	Mixing of biochar, vinegar and mushroom residues regulates soil microbial community and increases cucumber yield under continuous cropping regime. <i>Applied Soil Ecology</i> , 2021, 161, 103883.	2.1	27
1635	Association of aerobic anoxygenic phototrophs and zebra mussels, <i>Dreissena polymorpha</i> , within the littoral zone of Lake Winnipeg. <i>Journal of Great Lakes Research</i> , 2021, 47, 567-582.	0.8	8
1636	Gut Microbiota Signature Among Asian Post-gestational Diabetes Women Linked to Macronutrient Intakes and Metabolic Phenotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 680622.	1.5	13
1637	Managing Contamination and Diverse Bacterial Loads in 16S rRNA Deep Sequencing of Clinical Samples: Implications of the Law of Small Numbers. <i>MBio</i> , 2021, 12, e0059821.	1.8	8
1638	Correlations Between Intestinal Microbial Community and Hematological Profile in Native Tibetans and Han Immigrants. <i>Frontiers in Microbiology</i> , 2021, 12, 615416.	1.5	8
1639	Effect of co-application of <i>Trichoderma</i> spp. with organic composts on plant growth enhancement, soil enzymes and fungal community in soil. <i>Archives of Microbiology</i> , 2021, 203, 4281-4291.	1.0	21
1640	Weaning-associated feed deprivation stress causes microbiota disruptions in a novel mucin-containing in vitro model of the piglet colon (MPigut-IVM). <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 75.	2.1	7
1641	Geography, Host Genetics, and Cross-Domain Microbial Networks Structure the Skin Microbiota of Fragmented Brazilian Atlantic Forest Frog Populations. <i>Ecology and Evolution</i> , 2021, 11, 9293-9307.	0.8	11
1643	Effects of silver nanoparticles on performance of anaerobic digestion of sewage sludge and associated microbial communities. <i>Renewable Energy</i> , 2021, 171, 1014-1025.	4.3	28
1644	Effects of the Denitrification Inhibitor <i>Procyanidin</i> on the Diversity, Interactions, and Potential Functions of Rhizosphere-Associated Microbiome. <i>Microorganisms</i> , 2021, 9, 1406.	1.6	4
1645	<i>In situ</i> microcosms deployed at the coast of British Columbia (Canada) to study dilbit weathering and associated microbial communities under marine conditions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
1646	Structural and Functional Impacts of Microbiota on <i>Pyropia yezoensis</i> and Surrounding Seawater in Cultivation Farms along Coastal Areas of the Yellow Sea. <i>Microorganisms</i> , 2021, 9, 1291.	1.6	9
1648	Anorexia and fat aversion induced by vertical sleeve gastrectomy is attenuated in neurotensin receptor 1 deficient mice. <i>Endocrinology</i> , 2021, 162, .	1.4	5
1649	Characterization of the microbiome of the invasive Asian toad in Madagascar across the expansion range and comparison with a native co-occurring species. <i>PeerJ</i> , 2021, 9, e11532.	0.9	7
1650	Microbial community responses to land-use types and its ecological roles in mining area. <i>Science of the Total Environment</i> , 2021, 775, 145753.	3.9	20
1651	Long-term phytoremediation using the symbiotic <i>Pongamia pinnata</i> reshaped soil micro-ecological environment. <i>Science of the Total Environment</i> , 2021, 774, 145112.	3.9	9

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1653	Optimized bacterial DNA isolation method for microbiome analysis of human tissues. <i>MicrobiologyOpen</i> , 2021, 10, e1191.	1.2	21
1654	Comparative Analysis of Fecal Microbiota of Grazing Mongolian Cattle from Different Regions in Inner Mongolia, China. <i>Animals</i> , 2021, 11, 1938.	1.0	10
1655	Larval Diet Abundance Influences Size and Composition of the Midgut Microbiota of <i>Aedes aegypti</i> Mosquitoes. <i>Frontiers in Microbiology</i> , 2021, 12, 645362.	1.5	19
1656	Particle size rather than concentration of silver nanoparticles mainly affects soil N ₂ -fixing bacterial communities. <i>International Journal of Environmental Science and Technology</i> , 2022, 19, 5611-5622.	1.8	3
1657	Validity and safety of ID-JPL934 in lower gastrointestinal symptom improvement. <i>Scientific Reports</i> , 2021, 11, 13046.	1.6	6
1658	Use of High-Throughput Sequencing to Identify Fungal Communities on the Surface of Citri Reticulatae Pericarpium During the 3-Year Aging Process. <i>Current Microbiology</i> , 2021, 78, 3142-3151.	1.0	12
1659	Tree species composition and nutrient availability affect soil microbial diversity and composition across forest types in subtropical China. <i>Catena</i> , 2021, 201, 105224.	2.2	14
1660	Identification of Microbiological Activities in Wet Flue Gas Desulfurization Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 675628.	1.5	1
1661	The impact of caries status on supragingival plaque and salivary microbiome in children with mixed dentition: a cross-sectional survey. <i>BMC Oral Health</i> , 2021, 21, 319.	0.8	19
1662	Changes in Digestive Microbiota, Rumen Fermentations and Oxidative Stress around Parturition Are Alleviated by Live Yeast Feed Supplementation to Gestating Ewes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 447.	1.5	8
1663	Synergistic Application of Molecular Markers and Community-Based Microbial Source Tracking Methods for Identification of Fecal Pollution in River Water During Dry and Wet Seasons. <i>Frontiers in Microbiology</i> , 2021, 12, 660368.	1.5	9
1664	Comparison of fungal community composition within different intestinal segments of tilapia and bighead carp. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1961-1971.	0.6	7
1665	Functional differentiation related to decomposing complex carbohydrates of intestinal microbes between two wild zokor species based on 16SrRNA sequences. <i>BMC Veterinary Research</i> , 2021, 17, 216.	0.7	14
1666	Soil Buffering Capacity Can Be Used To Optimize Biostimulation of Psychrotrophic Hydrocarbon Remediation. <i>Environmental Science & Technology</i> , 2021, 55, 9864-9875.	4.6	4
1667	Oral Ferric Maltol Does Not Adversely Affect the Intestinal Microbiome of Patients or Mice, but Ferrous Sulphate Does. <i>Nutrients</i> , 2021, 13, 2269.	1.7	10
1668	Untapped Potential of Moving Bed Biofilm Reactors with Different Biocarrier Types for Bilge Water Treatment: A Laboratory-Scale Study. <i>Water (Switzerland)</i> , 2021, 13, 1810.	1.2	11
1669	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. <i>ISME Communications</i> , 2021, 1, .	1.7	60

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1670	Anaerobic degradation of high-concentration polycyclic aromatic hydrocarbons (PAHs) in seawater sediments. <i>Marine Pollution Bulletin</i> , 2021, 167, 112294.	2.3	13
1671	Two <i>Apriona</i> Species Sharing a Host Niche Have Different Gut Microbiome Diversity. <i>Microbial Ecology</i> , 2022, 83, 1059-1072.	1.4	10
1673	Resistance to permethrin alters the gut microbiota of <i>Aedes aegypti</i> . <i>Scientific Reports</i> , 2021, 11, 14406.	1.6	14
1674	Analysis of Microbiota and Mycobiota in Fungal Ball Rhinosinusitis: Specific Interaction between <i>Aspergillus fumigatus</i> and <i>Haemophilus influenzae</i> ?. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 550.	1.5	9
1675	The Development of the Gut Microbiota and Short-Chain Fatty Acids of Layer Chickens in Different Growth Periods. <i>Frontiers in Veterinary Science</i> , 2021, 8, 666535.	0.9	28
1676	Responses of CH ₄ flux and microbial diversity to changes in rainfall amount and frequencies in a wet meadow in the Tibetan Plateau. <i>Catena</i> , 2021, 202, 105253.	2.2	23
1677	The association between serum microbial DNA composition and symptoms of depression and anxiety in mood disorders. <i>Scientific Reports</i> , 2021, 11, 13987.	1.6	16
1678	Roux-en-Y Gastric Bypass Improved Insulin Resistance via Alteration of the Human Gut Microbiome and Alleviation of Endotoxemia. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	5
1679	Exploring the Microdiversity Within Marine Bacterial Taxa: Toward an Integrated Biogeography in the Southern Ocean. <i>Frontiers in Microbiology</i> , 2021, 12, 703792.	1.5	9
1680	Looking in the medicine cabinet: methods for using real-world data to assess the impact of measles, mumps and rubella (MMR) and recombinant adjuvanted varicella-zoster vaccines on coronavirus disease 2019 (COVID-19) prevention and case fatality. <i>Gates Open Research</i> , 0, 5, 115.	2.0	0
1681	Assessment of total bacterial diversity in whiteleg shrimps and its aquaculture environment in Pangkajene and Banyuwangi, Indonesia. <i>Asia-Pacific Journal of Molecular Biology and Biotechnology</i> , 0, , 26-37.	0.2	0
1682	Changes in microbial communities and their predictive functionalities during fermentation of toddy, an alcoholic beverage of India. <i>Microbiological Research</i> , 2021, 248, 126769.	2.5	24
1683	From the bellies of babes: a larval-based approach to ant molecular gut content analysis. <i>Insectes Sociaux</i> , 2021, 68, 245-253.	0.7	3
1684	Compositional analysis of ruminal bacteria from ewes selected for somatic cell score and milk persistency. <i>PLoS ONE</i> , 2021, 16, e0254874.	1.1	17
1685	Characterization of fungal microbial diversity in healthy and diarrheal Tibetan piglets. <i>BMC Microbiology</i> , 2021, 21, 204.	1.3	8
1686	Decomposition of Microbial Necromass Is Divergent at the Individual Taxonomic Level in Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 679793.	1.5	6
1687	Bacterial Community Characteristics in the Gastrointestinal Tract of Yak (<i>Bos grunniens</i>) Fully Grazed on Pasture of the Qinghai-Tibetan Plateau of China. <i>Animals</i> , 2021, 11, 2243.	1.0	5
1688	Links between fecal microbiota and the response to vaccination against influenza A virus in pigs. <i>Npj Vaccines</i> , 2021, 6, 92.	2.9	13

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1690	Potential effects of <i>Rhodococcus qingshengii</i> strain djl-6 on the bioremediation of carbendazim-contaminated soil and the assembly of its microbiome. <i>Journal of Hazardous Materials</i> , 2021, 414, 125496.	6.5	30
1691	Study on Microbial Community Succession and Protein Hydrolysis of Donkey Meat during Refrigerated Storage Based on Illumina NOVA Sequencing Technology. <i>Food Science of Animal Resources</i> , 2021, 41, 701-714.	1.7	4
1692	Description of Microbial Communities of Phosphate Mine Wastes in Morocco, a Semi-Arid Climate, Using High-Throughput Sequencing and Functional Prediction. <i>Frontiers in Microbiology</i> , 2021, 12, 666936.	1.5	7
1693	Impact of anthropogenic activities on changes of ichthyofauna in the middle and lower Xiang River. <i>Aquaculture and Fisheries</i> , 2022, 7, 693-702.	1.2	10
1695	Coupling Between the Responses of Plants, Soil, and Microorganisms Following Grazing Exclusion in an Overgrazed Grassland. <i>Frontiers in Plant Science</i> , 2021, 12, 640789.	1.7	16
1696	Pathogen Challenge and Dietary Shift Alter Microbiota Composition and Activity in a Mucin-Associated <i>in vitro</i> Model of the Piglet Colon (MPigut-IVM) Simulating Weaning Transition. <i>Frontiers in Microbiology</i> , 2021, 12, 703421.	1.5	8
1697	Exploring the plant environmental DNA diversity in soil from two sites on Deception Island (Antarctica, South Shetland Islands) using metabarcoding. <i>Antarctic Science</i> , 2021, 33, 469-478.	0.5	8
1698	Assessing age, breeding stage, and mating activity as drivers of variation in the reproductive microbiome of female tree swallows. <i>Ecology and Evolution</i> , 2021, 11, 11398-11413.	0.8	9
1699	Oceanographic structure and seasonal variation contribute to high heterogeneity in mesozooplankton over small spatial scales. <i>ICES Journal of Marine Science</i> , 2021, 78, 3288-3302.	1.2	5
1700	Effects of Dietary Supplementation with Protected Sodium Butyrate on Gut Microbiota in Growing-Finishing Pigs. <i>Animals</i> , 2021, 11, 2137.	1.0	15
1701	On-site chlorination responsible for effective disinfection of wastewater from hospital. <i>Science of the Total Environment</i> , 2021, 776, 145951.	3.9	27
1702	Dynamic Alterations of the Distal Intestinal Microbiota, Transcriptome, and Metabolome of Hybrid Grouper by \hat{I}^2 -Conglycinin With Reconciliations by Sodium Butyrate in Feed. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
1703	An Exploratory Study for the Association of Gut Microbiome with Efficacy of Immune Checkpoint Inhibitor in Patients with Hepatocellular Carcinoma. <i>Journal of Hepatocellular Carcinoma</i> , 2021, Volume 8, 809-822.	1.8	17
1704	Dynamics of soil fertility and microbial community response to stocking density in rice-turtle co-culture. <i>Aquaculture Reports</i> , 2021, 20, 100765.	0.7	10
1705	DiTing: A Pipeline to Infer and Compare Biogeochemical Pathways From Metagenomic and Metatranscriptomic Data. <i>Frontiers in Microbiology</i> , 2021, 12, 698286.	1.5	21
1706	The Novel Interplay between Commensal Gut Bacteria and Metabolites in Diet-Induced Hyperlipidemic Rats Treated with Simvastatin. <i>Journal of Proteome Research</i> , 2021, , .	1.8	5
1707	The microbial population structure and function of peanut peanut and their effects on aflatoxin contamination. <i>LWT - Food Science and Technology</i> , 2021, 148, 111285.	2.5	4

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1708	Associations between the gut microbiome and metabolome in early life. <i>BMC Microbiology</i> , 2021, 21, 238.	1.3	23
1709	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <i>PLoS ONE</i> , 2021, 16, e0237556.	1.1	4
1710	Intercropping improves heavy metal phytoremediation efficiency through changing properties of rhizosphere soil in bamboo plantation. <i>Journal of Hazardous Materials</i> , 2021, 416, 125898.	6.5	60
1711	Supplementing Chitosan Oligosaccharide Positively Affects Hybrid Grouper (<i>Epinephelus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Concentrate: Effects on Growth, Gut Microbiota, Antioxidant Function and Immune Response. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
1712	Changes in Gut Microbiota Induced by Doxycycline Influence in Vascular Function and Development of Hypertension in DOCA-Salt Rats. <i>Nutrients</i> , 2021, 13, 2971.	1.7	11
1713	GATA6 Deficiency Leads to Epithelial Barrier Dysfunction and Enhances Susceptibility to Gut Inflammation. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 301-311.	0.6	15
1714	Succession of Fungal Communities at Different Developmental Stages of Cabernet Sauvignon Grapes From an Organic Vineyard in Xinjiang. <i>Frontiers in Microbiology</i> , 2021, 12, 718261.	1.5	18
1715	Assessment of Carbon Substrate Catabolism Pattern and Functional Metabolic Pathway for Microbiota of Limestone Caves. <i>Microorganisms</i> , 2021, 9, 1789.	1.6	18
1716	Rumen Fermentation, Digestive Enzyme Activity, and Bacteria Composition between Pre-Weaning and Post-Weaning Dairy Calves. <i>Animals</i> , 2021, 11, 2527.	1.0	14
1717	Nitrogen isotopes in the soil-to-tree continuum â€” Tree rings express the soil biogeochemistry of boreal forests exposed to moderate airborne emissions. <i>Science of the Total Environment</i> , 2021, 780, 146581.	3.9	8
1718	Groundwater bacterial communities evolve over time in response to recharge. <i>Water Research</i> , 2021, 201, 117290.	5.3	35
1719	High-Throughput Metabarcoding Characterizes Fungal Endophyte Diversity in the Phyllosphere of a Barley Crop. <i>Phytobiomes Journal</i> , 2021, 5, 316-325.	1.4	11
1720	Gut Microbial Diversity in Female Patients With Invasive Mole and Choriocarcinoma and Its Differences Versus Healthy Controls. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 704100.	1.8	4
1721	Impact of onboard chitosan treatment of whole cod (<i>Gadus morhua</i>) on the shelf life and spoilage bacteria of loins stored superchilled under different atmospheres. <i>Food Microbiology</i> , 2021, 97, 103723.	2.1	13
1722	Effects of Age, Diet CP, NDF, EE, and Starch on the Rumen Bacteria Community and Function in Dairy Cattle. <i>Microorganisms</i> , 2021, 9, 1788.	1.6	9
1723	Influence of different phytoremediation on soil microbial diversity and community composition in saline-alkaline land. <i>International Journal of Phytoremediation</i> , 2022, 24, 507-517.	1.7	9
1724	Mining the Factors Driving the Evolution of the Pit Mud Microbiome under the Impact of Long-Term Production of Strong-Flavor Baijiu. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0088521.	1.4	36
1725	Evaluation of the Dietary Black Soldier Fly Larvae Meal (<i>Hermetia illucens</i>) on Growth Performance, Intestinal Health, and Disease Resistance to <i>Vibrio parahaemolyticus</i> of the Pacific White Shrimp (<i>Litopenaeus vannamei</i>). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11

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1726	Phylosymbiotic Structures of the Microbiota in <i>Mollitrichosiphum tenuicorpus</i> (Hemiptera: Aphididae: TJ ETQq0 0 Q r BT /Ovgrlock 10 T	1.4	3
1727	A qPCR-based method for rapid quantification of six intestinal homeostasis-relevant bacterial genera in feces. <i>Future Microbiology</i> , 2021, 16, 895-906.	1.0	1
1728	Dietary nanoparticles alter the composition and function of the gut microbiota in mice at dose levels relevant for human exposure. <i>Food and Chemical Toxicology</i> , 2021, 154, 112352.	1.8	16
1729	Matrix Effects on the Delivery Efficacy of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 on Fecal Microbiota, Gut Transit Time, and Short-Chain Fatty Acids in Healthy Young Adults. <i>MSphere</i> , 2021, 6, e0008421.	1.3	11
1730	Association of obstructive sleep apnea severity with the composition of the upper airway microbiome. <i>Journal of Clinical Sleep Medicine</i> , 2021, , .	1.4	3
1731	Effects of dietary exposure to the engineered nanomaterials CeO ₂ , SiO ₂ , Ag, and TiO ₂ on the murine gut microbiome. <i>Nanotoxicology</i> , 2021, 15, 1-17.	1.6	6
1732	Bio-activation of soil with beneficial microbes after soil fumigation reduces soil-borne pathogens and increases tomato yield. <i>Environmental Pollution</i> , 2021, 283, 117160.	3.7	40
1733	Plant beneficial rhizobacteria community structure changes through developmental stages of peanut and maize. <i>Rhizosphere</i> , 2021, 19, 100407.	1.4	15
1734	Effects of mulberry leaf silage on antioxidant and immunomodulatory activity and rumen bacterial community of lambs. <i>BMC Microbiology</i> , 2021, 21, 250.	1.3	15
1735	Composition of the microbial communities at different body sites in women with preterm birth and their newborns. <i>Medicine in Microecology</i> , 2021, 9, 100046.	0.7	3
1736	Biogeography rather than substrate type determines bacterial colonization dynamics of marine plastics. <i>PeerJ</i> , 2021, 9, e12135.	0.9	15
1737	Sediment microbiota in polyculture of shrimp and fish pattern is distinctive from those in monoculture intensive shrimp or fish ponds. <i>Science of the Total Environment</i> , 2021, 787, 147594.	3.9	16
1738	Geography-dependent symbiont communities in two oligophagous aphid species. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
1739	Accumulation of beneficial bacteria in the rhizosphere of maize (<i>Zea mays</i> L.) grown in a saline soil in responding to a consortium of plant growth promoting rhizobacteria. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	20
1740	Biodiversity of coral reef cryptobiota shuffles but does not decline under the combined stressors of ocean warming and acidification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
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1760	<i>Saccharomyces Cerevisiae</i> Var <i>Boulardii</i> CNCM 1079 Reduces Expression of Genes Involved in Inflammatory Response in Porcine Cells Challenged by Enterotoxigenic <i>E. Coli</i> and Influences Bacterial Communities in an In Vitro Model of the Weaning Piglet Colon. <i>Antibiotics</i> , 2021, 10, 1101.	1.5	0
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2100	Methanogenesis pathways of methanogens and their responses to substrates and temperature in sediments from the South Yellow Sea. <i>Science of the Total Environment</i> , 2022, 815, 152645.	3.9	11
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2120	The Role of Diversity in Mediating Microbiota Structural and Functional Differences in Two Sympatric Species of Abalone Under Stressed Withering Syndrome Conditions. <i>Microbial Ecology</i> , 2022, , 1.	1.4	0
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2142	Impact of nutrient removal on microbial community in bioretention facilities with different underlying types/built times at field scale. <i>Ecological Engineering</i> , 2022, 176, 106542.	1.6	9

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2183	Microbiome structure and response to watering in rhizosphere of <i>Nitrosalsola vermiculata</i> and surrounding bulk soil. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2022, 50, 12567.	0.5	1
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2188	Morel Production Associated with Soil Nitrogen-Fixing and Nitrifying Microorganisms. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 299.	1.5	24
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2202	Comparative study of gut microbiota from decomposer fauna in household composter using metataxonomic approach. <i>Archives of Microbiology</i> , 2022, 204, 210.	1.0	6
2203	Sex differences associate with late microbiome alterations after murine surgical sepsis. <i>Journal of Trauma and Acute Care Surgery</i> , 2022, 93, 137-146.	1.1	8
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2246	Capture and Ex-Situ Analysis of Environmental Biofilms in Livestock Buildings. <i>Microorganisms</i> , 2022, 10, 2.	1.6	7
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2266	Maternal Dietary Betaine Prevents High-Fat Diet-Induced Metabolic Disorders and Gut Microbiota Alterations in Mouse Dams and Offspring From Young to Adult. <i>Frontiers in Microbiology</i> , 2022, 13, 809642.	1.5	6
2267	Ecological impacts of sea-crossing bridge construction on local sediment microbiome in East China. <i>Regional Studies in Marine Science</i> , 2022, , 102363.	0.4	1
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2647	Polystyrene microplastics induce gut microbiome and metabolome changes in Javanese medaka fish (<i>Oryzias javanicus</i> Bleeker, 1854). <i>Toxicology Reports</i> , 2022, 9, 1369-1379.	1.6	10
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2656	Synergy of Dietary Quercetin and Vitamin E Improves Cecal Microbiota and Its Metabolite Profile in Aged Breeder Hens. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
2657	Contextâ€dependent role of abiotic and biotic factors structuring nematode communities along two environmental gradients. <i>Molecular Ecology</i> , 2022, 31, 3903-3916.	2.0	5
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2685	Diurnal and eating-associated microbial patterns revealed via high-frequency saliva sampling. <i>Genome Research</i> , 2022, 32, 1112-1123.	2.4	3
2686	Glyphosate-based herbicide exposure: effects on gill microbiota of rainbow trout (<i>Oncorhynchus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5	1.3	6
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2693	<i>Lactococcus lactis</i> NCDO2118 exerts visceral antinociceptive properties in rat via GABA production in the gastro-intestinal tract. <i>ELife</i> , 0, 11, .	2.8	12
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2697	Diversity and network structure of epiphytic bacterial communities on different submerged macrophytes. <i>Hupo Kexue/Journal of Lake Sciences</i> , 2022, 34, 1234-1249.	0.3	2
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2711	Characterization and manipulation of the bacterial community in the midgut of <i>Ixodes ricinus</i> . <i>Parasites and Vectors</i> , 2022, 15, .	1.0	8
2712	Effect of Doxycycline Use in the Early Broiler Production Cycle on the Microbiome. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
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2722	Effect of Bergamot and Laoxianghuang Polysaccharides on Gut Microbiota Derived from Patients with Hyperlipidemia: An Integrative Analysis of Microbiome and Metabolome during In Vitro Fermentation. <i>Foods</i> , 2022, 11, 2039.	1.9	3
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2724	Healthy Gut Microbiome Composition Enhances Disease Resistance and Fat Deposition in Tibetan Pigs. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
2725	Polyvinyl chloride microplastics induced gut barrier dysfunction, microbiota dysbiosis and metabolism disorder in adult mice. <i>Ecotoxicology and Environmental Safety</i> , 2022, 241, 113809.	2.9	25
2726	Application of potential probiotic strain <i>Streptomyces</i> sp. SH5 on anti- <i>Aeromonas</i> infection in zebrafish larvae. <i>Fish and Shellfish Immunology</i> , 2022, 127, 375-385.	1.6	8

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2728	Integrated 16S rDNA, metabolomics, and TNF- α /NF- κ B signaling pathway analyses to explain the modulatory effect of <i>Poria cocos</i> aqueous extract on anxiety-like behavior. <i>Phytomedicine</i> , 2022, 104, 154300.	2.3	5
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2734	Rhizosphere bacterial communities and soil nutrient conditions reveal sexual dimorphism of <i>Populus deltoides</i> . <i>Journal of Forestry Research</i> , 2023, 34, 761-771.	1.7	6
2735	The impact of symbiotic population crash (or reduction) on microbiome structure and composition. <i>International Journal of Pest Management</i> , 0, , 1-12.	0.9	0
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2740	Environmental filtering drives the establishment of the distinctive rhizosphere, bulk, and root nodule bacterial communities of <i>Sophora davidii</i> in hilly and gully regions of the Loess Plateau of China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
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2743	Rhizosphere Microbial Communities and Geochemical Constraining Mechanism of Antimony Mine Waste-Adapted Plants in Southwestern China. <i>Microorganisms</i> , 2022, 10, 1507.	1.6	4
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2749	Effect of a diet rich in galactose or fructose, with or without fructooligosaccharides, on gut microbiota composition in rats. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	1
2750	Seasonal Dynamics of Lake Winnipeg's Microbial Communities Reveal Aerobic Anoxygenic Phototrophic Populations Coincide with Sunlight Availability. <i>Microorganisms</i> , 2022, 10, 1690.	1.6	2
2751	Relationship between rumen microbial differences and traits among Hu sheep, Tan sheep, and Dorper sheep. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	11
2752	Effects of scale worm parasitism on interactions between the symbiotic gill microbiome and gene regulation in deep sea mussel hosts. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
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3042	Palmitoleic Acid on Top of HFD Ameliorates Insulin Resistance Independent of Diacylglycerols and Alters Gut Microbiota in C57BL/6J Mice. , 2023, , 1-24.		0
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