

FLASH: fast length adjustment of short reads to improv

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Citation Report

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7	The role of memory for past test in the underconfidence with practice effect.. Journal of Experimental Psychology: Learning Memory and Cognition, 2007, 33, 238-244.	0.9	128
8	COPE: an accurate <i>k</i> -mer-based pair-end reads connection tool to facilitate genome assembly. Bioinformatics, 2012, 28, 2870-2874.	4.1	145
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15	Ultra-deep mutant spectrum profiling: improving sequencing accuracy using overlapping read pairs. BMC Genomics, 2013, 14, 96.	2.8	40
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23	De novo transcriptomic analyses for non-model organisms: an evaluation of methods across a multi-species data set. Molecular Ecology Resources, 2013, 13, 403-416.	4.8	71
24	Horizontal Gene Transfer from Diverse Bacteria to an Insect Genome Enables a Tripartite Nested Mealybug Symbiosis. Cell, 2013, 153, 1567-1578.	28.9	373

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26	In-depth analysis of interrelation between quality scores and real errors in illumina reads. , 2013, 2013, 635-8.		15
27	The Genome of the Anaerobic Fungus Orpinomyces sp. Strain C1A Reveals the Unique Evolutionary History of a Remarkable Plant Biomass Degradar. Applied and Environmental Microbiology, 2013, 79, 4620-4634.	3.1	224
28	The Draft Genome Sequence of Sphingomonas paucimobilis Strain HER1398 (<i>Proteobacteria</i>), Host to the Giant PAU Phage, Indicates That It Is a Member of the Genus <i>Sphingobacterium</i> () Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	1
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940	Lingual microbiota profiles of patients with geographic tongue. <i>Journal of Oral Microbiology</i> , 2017, 9, 1355206.	2.7	16
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1051	Metagenomic Analysis of Hot Springs in Central India Reveals Hydrocarbon Degrading Thermophiles and Pathways Essential for Survival in Extreme Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 2123.	3.5	96
1052	Compositions and Abundances of Sulfate-Reducing and Sulfur-Oxidizing Microorganisms in Water-Flooded Petroleum Reservoirs with Different Temperatures in China. <i>Frontiers in Microbiology</i> , 2017, 08, 143.	3.5	84

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1053	Assessment of Ruminal Bacterial and Archaeal Community Structure in Yak (<i>Bos grunniens</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 179.	3.5	68
1054	Variable Colonization after Reciprocal Fecal Microbiota Transfer between Mice with Low and High Richness Microbiota. <i>Frontiers in Microbiology</i> , 2017, 8, 196.	3.5	64
1055	Anti-obesity Effect of Capsaicin in Mice Fed with High-Fat Diet Is Associated with an Increase in Population of the Gut Bacterium <i>Akkermansia muciniphila</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 272.	3.5	118
1056	Differences in Ureolytic Bacterial Composition between the Rumen Digesta and Rumen Wall Based on ureC Gene Classification. <i>Frontiers in Microbiology</i> , 2017, 8, 385.	3.5	65
1057	Untangling Genomes of Novel Planctomycetal and Verrucomicrobial Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning. <i>Frontiers in Microbiology</i> , 2017, 8, 472.	3.5	70
1058	Inferring Microbial Interactions in the Gut of the Hong Kong Whipping Frog (<i>Polypedates</i>) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	3.5	37
1059	Exploring the Ecological Coherence between the Spatial and Temporal Patterns of Bacterioplankton in Boreal Lakes. <i>Frontiers in Microbiology</i> , 2017, 8, 636.	3.5	13
1060	A Critical Assessment of the Microorganisms Proposed to be Important to Enhanced Biological Phosphorus Removal in Full-Scale Wastewater Treatment Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 718.	3.5	212
1061	Alterations in the Rumen Liquid-, Particle- and Epithelium-Associated Microbiota of Dairy Cows during the Transition from a Silage- and Concentrate-Based Ration to Pasture in Spring. <i>Frontiers in Microbiology</i> , 2017, 8, 744.	3.5	78
1062	Differing Complex Microbiota Alter Disease Severity of the IL-10 ^{-/-} Mouse Model of Inflammatory Bowel Disease. <i>Frontiers in Microbiology</i> , 2017, 8, 792.	3.5	56
1063	A Metagenomic Approach to Cyanobacterial Genomics. <i>Frontiers in Microbiology</i> , 2017, 8, 809.	3.5	98
1064	The Bacteriophage EF-P29 Efficiently Protects against Lethal Vancomycin-Resistant <i>Enterococcus faecalis</i> and Alleviates Gut Microbiota Imbalance in a Murine Bacteremia Model. <i>Frontiers in Microbiology</i> , 2017, 8, 837.	3.5	78
1065	Impact of Ferrous Iron on Microbial Community of the Biofilm in Microbial Fuel Cells. <i>Frontiers in Microbiology</i> , 2017, 8, 920.	3.5	19
1066	Cable Bacteria and the Bioelectrochemical Snorkel: The Natural and Engineered Facets Playing a Role in Hydrocarbons Degradation in Marine Sediments. <i>Frontiers in Microbiology</i> , 2017, 8, 952.	3.5	48
1067	Different Types of Dietary Fibers Trigger Specific Alterations in Composition and Predicted Functions of Colonic Bacterial Communities in BALB/c Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 966.	3.5	47
1068	Zinc Oxide Nanoparticles Influence Microflora in Ileal Digesta and Correlate Well with Blood Metabolites. <i>Frontiers in Microbiology</i> , 2017, 8, 992.	3.5	44
1069	Diversity and Composition of Sulfate-Reducing Microbial Communities Based on Genomic DNA and RNA Transcription in Production Water of High Temperature and Corrosive Oil Reservoir. <i>Frontiers in Microbiology</i> , 2017, 8, 1011.	3.5	63
1070	Non-pylori <i>Helicobacters</i> (NHPHs) Induce Shifts in Gastric Microbiota in <i>Helicobacter pylori</i> -Infected Patients. <i>Frontiers in Microbiology</i> , 2017, 8, 1038.	3.5	16

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1072	The Arbuscular Mycorrhizal Fungus <i>Funneliformis mosseae</i> Alters Bacterial Communities in Subtropical Forest Soils during Litter Decomposition. <i>Frontiers in Microbiology</i> , 2017, 8, 1120.	3.5	36
1073	Microbial Eukaryote Diversity and Activity in the Water Column of the South China Sea Based on DNA and RNA High Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 1121.	3.5	63
1074	Preparing the Gut with Antibiotics Enhances Gut Microbiota Reprogramming Efficiency by Promoting Xenomicrobiota Colonization. <i>Frontiers in Microbiology</i> , 2017, 8, 1208.	3.5	75
1075	The Gut Microbiota of Healthy Chilean Subjects Reveals a High Abundance of the Phylum Verrucomicrobia. <i>Frontiers in Microbiology</i> , 2017, 8, 1221.	3.5	225
1076	Oral Probiotics Alter Healthy Feline Respiratory Microbiota. <i>Frontiers in Microbiology</i> , 2017, 8, 1287.	3.5	25
1077	The Cyanobacteria-Dominated Sponge <i>Dactylospongia elegans</i> in the South China Sea: Prokaryotic Community and Metagenomic Insights. <i>Frontiers in Microbiology</i> , 2017, 8, 1387.	3.5	15
1078	Watershed Urbanization Linked to Differences in Stream Bacterial Community Composition. <i>Frontiers in Microbiology</i> , 2017, 8, 1452.	3.5	94
1079	Intestinal Bacterial Communities of Trypanosome-Infected and Uninfected <i>Glossina palpalis palpalis</i> from Three Human African Trypanomiasis Foci in Cameroon. <i>Frontiers in Microbiology</i> , 2017, 8, 1464.	3.5	13
1080	Long-term Fertilization Structures Bacterial and Archaeal Communities along Soil Depth Gradient in a Paddy Soil. <i>Frontiers in Microbiology</i> , 2017, 8, 1516.	3.5	72
1081	High Spatial and Temporal Variations of Microbial Community along the Southern Catfish Gastrointestinal Tract: Insights into Dynamic Food Digestion. <i>Frontiers in Microbiology</i> , 2017, 8, 1531.	3.5	29
1082	Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. <i>Frontiers in Microbiology</i> , 2017, 8, 1561.	3.5	265
1083	High-Resolution Microbiome Profiling for Detection and Tracking of <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1587.	3.5	31
1084	Identification of Fungal Communities Associated with the Biodeterioration of Waterlogged Archeological Wood in a Han Dynasty Tomb in China. <i>Frontiers in Microbiology</i> , 2017, 8, 1633.	3.5	27
1085	Modulation of Gut Microbiome Composition and Function in Experimental Colitis Treated with Sulfasalazine. <i>Frontiers in Microbiology</i> , 2017, 8, 1703.	3.5	89
1086	Isolation and Characterization of <i>Pseudomonas</i> spp. Strains That Efficiently Decompose Sodium Dodecyl Sulfate. <i>Frontiers in Microbiology</i> , 2017, 8, 1872.	3.5	28
1087	Patterns and Processes in Marine Microeukaryotic Community Biogeography from Xiamen Coastal Waters and Intertidal Sediments, Southeast China. <i>Frontiers in Microbiology</i> , 2017, 8, 1912.	3.5	108
1088	<i>Myriophyllum aquaticum</i> Constructed Wetland Effectively Removes Nitrogen in Swine Wastewater. <i>Frontiers in Microbiology</i> , 2017, 8, 1932.	3.5	44

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1089	Diversity and Structure of Diazotrophic Communities in Mangrove Rhizosphere, Revealed by High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2032.	3.5	49
1090	Microbial Diversity and Community Structure of Sulfate-Reducing and Sulfur-Oxidizing Bacteria in Sediment Cores from the East China Sea. <i>Frontiers in Microbiology</i> , 2017, 8, 2133.	3.5	53
1091	Stratified Bacterial and Archaeal Community in Mangrove and Intertidal Wetland Mudflats Revealed by High Throughput 16S rRNA Gene Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2148.	3.5	91
1092	An Integrated Insight into the Relationship between Soil Microbial Community and Tobacco Bacterial Wilt Disease. <i>Frontiers in Microbiology</i> , 2017, 8, 2179.	3.5	108
1093	Low-Molecular-Weight Chitosan Supplementation Increases the Population of <i>Prevotella</i> in the Cecal Contents of Weanling Pigs. <i>Frontiers in Microbiology</i> , 2017, 8, 2182.	3.5	31
1094	Illumina-Based Analysis of Endophytic and Rhizosphere Bacterial Diversity of the Coastal Halophyte <i>Messerschmidia sibirica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2288.	3.5	84
1095	The Gut Entomotype of Red Palm Weevil <i>Rhynchophorus ferrugineus</i> Olivier (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td 2291.	3.5	96
1096	Resource Legacies of Organic and Conventional Management Differentiate Soil Microbial Carbon Use. <i>Frontiers in Microbiology</i> , 2017, 8, 2293.	3.5	38
1097	Environmental Factors Shape Water Microbial Community Structure and Function in Shrimp Cultural Enclosure Ecosystems. <i>Frontiers in Microbiology</i> , 2017, 8, 2359.	3.5	137
1098	Balanced Fertilization Decreases Environmental Filtering on Soil Bacterial Community Assemblage in North China. <i>Frontiers in Microbiology</i> , 2017, 8, 2376.	3.5	44
1099	Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. <i>Frontiers in Microbiology</i> , 2017, 8, 2384.	3.5	60
1100	EPSP of <i>L. casei</i> BL23 Protected against the Infection Caused by <i>Aeromonas veronii</i> via Enhancement of Immune Response in Zebrafish. <i>Frontiers in Microbiology</i> , 2017, 8, 2406.	3.5	28
1101	Glyphosate Shapes a Dinoflagellate-Associated Bacterial Community While Supporting Algal Growth as Sole Phosphorus Source. <i>Frontiers in Microbiology</i> , 2017, 8, 2530.	3.5	42
1102	Patterns and Drivers of Vertical Distribution of the Ciliate Community from the Surface to the Abyssopelagic Zone in the Western Pacific Ocean. <i>Frontiers in Microbiology</i> , 2017, 8, 2559.	3.5	37
1103	<i>Bacillus amyloliquefaciens</i> L-S60 Reforms the Rhizosphere Bacterial Community and Improves Growth Conditions in Cucumber Plug Seedling. <i>Frontiers in Microbiology</i> , 2017, 8, 2620.	3.5	39
1104	Uncovering the Potential of Termite Gut Microbiome for Lignocellulose Bioconversion in Anaerobic Batch Bioreactors. <i>Frontiers in Microbiology</i> , 2017, 8, 2623.	3.5	64
1105	L-Glutamine Supplementation Alleviates Constipation during Late Gestation of Mini Sows by Modifying the Microbiota Composition in Feces. <i>BioMed Research International</i> , 2017, 2017, 1-9.	1.9	28
1106	Metagenome of the Siberian Underground Water Reservoir. <i>Genome Announcements</i> , 2017, 5, .	0.8	9

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1107	Draft Genome Sequence of <i>Terrimicrobium saccharophilum</i> NM-5 ^T , a Facultative Anaerobic Soil Bacterium of the Class <i>Spartobacteria</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1108	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	2.8	51
1109	Rapid evolutionary divergence of diploid and allotetraploid <i>Gossypium</i> mitochondrial genomes. <i>BMC Genomics</i> , 2017, 18, 876.	2.8	23
1110	Effects of dietary nutrient levels on microbial community composition and diversity in the ileal contents of pregnant Huanjiang mini-pigs. <i>PLoS ONE</i> , 2017, 12, e0172086.	2.5	28
1111	An in vivo system for directed experimental evolution of rabbit haemorrhagic disease virus. <i>PLoS ONE</i> , 2017, 12, e0173727.	2.5	10
1112	<i>Tuber indicum</i> shapes the microbial communities of ectomycorrhizosphere soil and ectomycorrhizae of an indigenous tree (<i>Pinus armandii</i>). <i>PLoS ONE</i> , 2017, 12, e0175720.	2.5	25
1113	New gSSR and EST-SSR markers reveal high genetic diversity in the invasive plant <i>Ambrosia artemisiifolia</i> L. and can be transferred to other invasive <i>Ambrosia</i> species. <i>PLoS ONE</i> , 2017, 12, e0176197.	2.5	23
1114	Bacterial community and arsenic functional genes diversity in arsenic contaminated soils from different geographic locations. <i>PLoS ONE</i> , 2017, 12, e0176696.	2.5	40
1115	Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716.	2.5	107
1116	The Agassizâ€™s desert tortoise genome provides a resource for the conservation of a threatened species. <i>PLoS ONE</i> , 2017, 12, e0177708.	2.5	33
1117	Phylogenetic analysis of emergent <i>Streptococcus pneumoniae</i> serotype 22F causing invasive pneumococcal disease using whole genome sequencing. <i>PLoS ONE</i> , 2017, 12, e0178040.	2.5	21
1118	Decreased emergence of HIV-1 drug resistance mutations in a cohort of Ugandan women initiating option B+ for PMTCT. <i>PLoS ONE</i> , 2017, 12, e0178297.	2.5	11
1119	Bacterial communities found in placental tissues are associated with severe chorioamnionitis and adverse birth outcomes. <i>PLoS ONE</i> , 2017, 12, e0180167.	2.5	97
1120	<i>Methanobrevibacter</i> attenuation via probiotic intervention reduces flatulence in adult human: A non-randomised paired-design clinical trial of efficacy. <i>PLoS ONE</i> , 2017, 12, e0184547.	2.5	20
1121	<i>Lactobacillus paracasei</i> feeding improves immune control of influenza infection in mice. <i>PLoS ONE</i> , 2017, 12, e0184976.	2.5	76
1122	BBMerge â€“ Accurate paired shotgun read merging via overlap. <i>PLoS ONE</i> , 2017, 12, e0185056.	2.5	897
1123	Intestinal microbiota profiles associated with low and high residual feed intake in chickens across two geographical locations. <i>PLoS ONE</i> , 2017, 12, e0187766.	2.5	73
1124	Diversity and characterization of bacteria associated with the deep-sea hydrothermal vent crab <i>Austinograea</i> sp. comparing with those of two shallow-water crabs by 16S ribosomal DNA analysis. <i>PLoS ONE</i> , 2017, 12, e0187842.	2.5	22

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1126	Endosphere microbiome comparison between symptomatic and asymptomatic roots of <i>Brassica napus</i> infected with <i>Plasmodiophora brassicae</i> . PLoS ONE, 2017, 12, e0185907.	2.5	53
1127	Impact of Glyphosate on the Rhizosphere Microbial Communities of An EPSPS-Transgenic Soybean Line ZUTS31 by Metagenome Sequencing. Current Genomics, 2017, 19, 36-49.	1.6	10
1128	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters!. PLoS ONE, 2017, 12, e0169662.	2.5	186
1129	Characterization of the urinary microbiome in healthy dogs. PLoS ONE, 2017, 12, e0177783.	2.5	43
1130	Diversity of <i>Ktedonobacteria</i> with Actinomycetes-Like Morphology in Terrestrial Environments. Microbes and Environments, 2017, 32, 61-70.	1.6	83
1131	16S rRNA gene-based association study identified microbial taxa associated with pork intramuscular fat content in feces and cecum lumen. BMC Microbiology, 2017, 17, 162.	3.3	77
1132	Highly efficient methane generation from untreated microalgae biomass. Biotechnology for Biofuels, 2017, 10, 186.	6.2	63
1133	Coexistence and competition of sulfate-reducing and methanogenic populations in an anaerobic hexadecane-degrading culture. Biotechnology for Biofuels, 2017, 10, 207.	6.2	36
1134	A quantitative and qualitative comparison of illumina MiSeq and 454 amplicon sequencing for genotyping the highly polymorphic major histocompatibility complex (MHC) in a non-model species. BMC Research Notes, 2017, 10, 346.	1.4	12
1135	Gene and transcript abundances of bacterial type III secretion systems from the rumen microbiome are correlated with methane yield in sheep. BMC Research Notes, 2017, 10, 367.	1.4	8
1136	Doxycycline induces dysbiosis in female C57BL/6NCrl mice. BMC Research Notes, 2017, 10, 644.	1.4	29
1137	Metagenomic analysis reveals potential interactions in an artificial coculture. AMB Express, 2017, 7, 193.	3.0	17
1138	A novel ultra high-throughput 16S rRNA gene amplicon sequencing library preparation method for the Illumina HiSeq platform. Microbiome, 2017, 5, 68.	11.1	93
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1140	Season, but not symbiont state, drives microbiome structure in the temperate coral <i>Astrangia poculata</i> . Microbiome, 2017, 5, 120.	11.1	105
1141	Associations among dietary non-fiber carbohydrate, ruminal microbiota and epithelium G-protein-coupled receptor, and histone deacetylase regulations in goats. Microbiome, 2017, 5, 123.	11.1	74
1142	Indoor microbiota in severely moisture damaged homes and the impact of interventions. Microbiome, 2017, 5, 138.	11.1	40

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1144	A multiplex marker set for microsatellite typing and sexing of sooty terns <i>Onychoprion fuscatus</i> . <i>BMC Research Notes</i> , 2017, 10, 756.	1.4	3
1145	The gut microbiota in larvae of the housefly <i>Musca domestica</i> and their horizontal transfer through feeding. <i>AMB Express</i> , 2017, 7, 147.	3.0	49
1146	Endolysin LysEF-P10 shows potential as an alternative treatment strategy for multidrug-resistant <i>Enterococcus faecalis</i> infections. <i>Scientific Reports</i> , 2017, 7, 10164.	3.3	38
1147	The contribution of Late Pleistocene megafauna finds to submerged archaeology and the interpretation of ancient coastal landscapes. <i>Journal of Archaeological Science: Reports</i> , 2017, 15, 290-298.	0.5	2
1148	Effect of <i>Ageratina adenophora</i> invasion on the composition and diversity of soil microbiome. <i>Journal of General and Applied Microbiology</i> , 2017, 63, 114-121.	0.7	14
1149	Draft Genome Sequence of <i>Paludibacter jiangxiensis</i> NM7 ^T , a Propionate-Producing Fermentative Bacterium. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1150	Gut microbial diversity analysis using Illumina sequencing for functional dyspepsia with liver depression-spleen deficiency syndrome and the interventional Xiaoyaosan in a rat model. <i>World Journal of Gastroenterology</i> , 2017, 23, 810.	3.3	38
1151	Exploring the Impacts of Anthropogenic Disturbance on Seawater and Sediment Microbial Communities in Korean Coastal Waters Using Metagenomics Analysis. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 130.	2.6	38
1152	Clonal Clusters and Virulence Factors of Group C and G <i>Streptococcus</i> Causing Severe Infections, Manitoba, Canada, 2012–2014. <i>Emerging Infectious Diseases</i> , 2017, 23, 1079-1088.	4.3	20
1153	Effect of Sewage and Industrial Effluents on Bacterial and Archaeal Communities of Creek Sediments in the Taihu Basin. <i>Water (Switzerland)</i> , 2017, 9, 373.	2.7	17
1154	Contrasting dynamics and environmental controls of dispersed bacteria along a hydrologic gradient. <i>Advances in Oceanography and Limnology</i> , 2017, 8, .	0.6	13
1155	Understory Dwarf Bamboo Affects Microbial Community Structures and Soil Properties in a <i>Betula ermanii</i> Forest in Northern Japan. <i>Microbes and Environments</i> , 2017, 32, 103-111.	1.6	5
1156	Vertical profiles of sediment methanogenic potential and communities in two plateau freshwater lakes. <i>Biogeosciences</i> , 2017, 14, 341-351.	3.3	28
1157	Patterns of host gene expression associated with harboring a foregut microbial community. <i>BMC Genomics</i> , 2017, 18, 697.	2.8	4
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1159	Collaborative environmental DNA sampling from petal surfaces of flowering cherry <i>Cerasus yedoensis</i> ‘Somei-yoshino’ across the Japanese archipelago. <i>Journal of Plant Research</i> , 2018, 131, 709-717.	2.0	1
1160	The Variation of Microbial Communities in a Depth Profile of Peat in the Gahai Lake Wetland Natural Conservation Area. <i>Geomicrobiology Journal</i> , 2018, 35, 484-490.	2.0	8

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1162	Planktonic bivalve larvae identification and quantification in Gomso Bay, South Korea, using next-generation sequencing analysis and microscopic observations. <i>Aquaculture</i> , 2018, 490, 297-302.	3.5	4
1163	Phenol removal performance and microbial community shift during pH shock in a moving bed biofilm reactor (MBBR). <i>Journal of Hazardous Materials</i> , 2018, 351, 71-79.	12.4	38
1164	Insights into protein structure, stability and function from saturation mutagenesis. <i>Current Opinion in Structural Biology</i> , 2018, 50, 117-125.	5.7	26
1165	Drought consistently alters the composition of soil fungal and bacterial communities in grasslands from two continents. <i>Global Change Biology</i> , 2018, 24, 2818-2827.	9.5	221
1166	The influence of caging, bedding, and diet on the composition of the microbiota in different regions of the mouse gut. <i>Scientific Reports</i> , 2018, 8, 4065.	3.3	137
1167	Alterations in the gut microbiota of patients with acquired immune deficiency syndrome. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2263-2271.	3.6	63
1168	Market Integration Predicts Human Gut Microbiome Attributes across a Gradient of Economic Development. <i>MSystems</i> , 2018, 3, .	3.8	31
1169	Intestinal bacterial signatures of white feces syndrome in shrimp. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3701-3709.	3.6	118
1170	Integrating molecular and ecological approaches to identify potential polymicrobial pathogens over a shrimp disease progression. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3755-3764.	3.6	44
1171	Conservation genomics of desert dwelling California voles (<i>Microtus californicus</i>) and implications for management of endangered Amargosa voles (<i>Microtus californicus scirpensis</i>). <i>Conservation Genetics</i> , 2018, 19, 383-395.	1.5	12
1172	Biochars change the sorption and degradation of thiacloprid in soil: Insights into chemical and biological mechanisms. <i>Environmental Pollution</i> , 2018, 236, 158-167.	7.5	128
1173	Multilocus phylogenetic analysis of the first molecular data from the rare and monotypic Amarsipidae places the family within the Pelagia and highlights limitations of existing data sets in resolving pelagian interrelationships. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 172-180.	2.7	7
1174	Fuzhuan Brick Tea Polysaccharides Attenuate Metabolic Syndrome in High-Fat Diet Induced Mice in Association with Modulation in the Gut Microbiota. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 2783-2795.	5.2	166
1175	Dietary lipid levels could improve growth and intestinal microbiota of juvenile swimming crab, <i>Portunus trituberculatus</i> . <i>Aquaculture</i> , 2018, 490, 208-216.	3.5	65
1176	Neuroprotective effects of fecal microbiota transplantation on MPTP-induced Parkinson's disease mice: Gut microbiota, glial reaction and TLR4/TNF- α signaling pathway. <i>Brain, Behavior, and Immunity</i> , 2018, 70, 48-60.	4.1	448
1177	Land-use type strongly shapes community composition, but not always diversity of soil microbes in tropical China. <i>Catena</i> , 2018, 165, 369-380.	5.0	56
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1181	The Gills of Reef Fish Support a Distinct Microbiome Influenced by Host-Specific Factors. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	96
1182	Thermal regime and host clade, rather than geography, drive Symbiodinium and bacterial assemblages in the scleractinian coral <i>Pocillopora damicornis</i> sensu lato. <i>Microbiome</i> , 2018, 6, 39.	11.1	100
1183	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	12.8	36
1184	Shrub encroachment is associated with changes in soil bacterial community composition in a temperate grassland ecosystem. <i>Plant and Soil</i> , 2018, 425, 539-551.	3.7	30
1185	The influence of microbial communities for triadimefon enantiomerization in soils with different pH values. <i>Chirality</i> , 2018, 30, 293-301.	2.6	12
1186	The effect of probiotics and polysaccharides on the gut microbiota composition and function of weaned rats. <i>Food and Function</i> , 2018, 9, 1864-1877.	4.6	25
1187	Draft Genome Assemblies of Xylose-Utilizing <i>Candida tropicalis</i> and <i>Candida boidinii</i> with Potential Application in Biochemical and Biofuel Production. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
1188	Featured article: Structure moderation of gut microbiota in liraglutide-treated diabetic male rats. <i>Experimental Biology and Medicine</i> , 2018, 243, 34-44.	2.4	56
1189	The divergence between fungal and bacterial communities in seasonal and spatial variations of wastewater treatment plants. <i>Science of the Total Environment</i> , 2018, 628-629, 969-978.	8.0	79
1190	Polyadenylation and degradation of structurally abnormal mitochondrial tRNAs in human cells. <i>Nucleic Acids Research</i> , 2018, 46, 5209-5226.	14.5	14
1191	Community composition, diversity, and metabolism of intestinal microbiota in cultivated European eel (<i>Anguilla anguilla</i>). <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4143-4157.	3.6	22
1192	Functional groups of soil fungi decline under grazing. <i>Plant and Soil</i> , 2018, 426, 51-60.	3.7	33
1193	Arbuscular mycorrhizal fungal communities associated with two dominant species differ in their responses to long-term nitrogen addition in temperate grasslands. <i>Functional Ecology</i> , 2018, 32, 1575-1588.	3.6	39
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1195	Changes in community structure of active protistan assemblages from the lower Pearl River to coastal Waters of the South China Sea. <i>European Journal of Protistology</i> , 2018, 63, 72-82.	1.5	34
1196	One-time phosphate fertilizer application to grassland columns modifies the soil microbiota and limits its role in ecosystem services. <i>Science of the Total Environment</i> , 2018, 630, 849-858.	8.0	87
1197	Light-dependent processes on the cathode enhance the electrical outputs of sediment microbial fuel cells. <i>Bioelectrochemistry</i> , 2018, 122, 1-10.	4.6	14

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1199	Dense infraspecific sampling reveals rapid and independent trajectories of plastome degradation in a heterotrophic orchid complex. <i>New Phytologist</i> , 2018, 218, 1192-1204.	7.3	56
1200	Effects of Baicalein on Cortical Proinflammatory Cytokines and the Intestinal Microbiome in Senescence Accelerated Mouse Prone 8. <i>ACS Chemical Neuroscience</i> , 2018, 9, 1714-1724.	3.5	47
1201	Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex1. <i>Journal of Animal Science</i> , 2018, 96, 1405-1418.	0.5	50
1202	Decline of genetic diversity in ancient domestic stallions in Europe. <i>Science Advances</i> , 2018, 4, eaap9691.	10.3	29
1203	A combination of <i>Lactobacillus mali</i> APS1 and dieting improved the efficacy of obesity treatment via manipulating gut microbiome in mice. <i>Scientific Reports</i> , 2018, 8, 6153.	3.3	31
1204	Application of high-throughput sequencing for microbial diversity detection in feces of specific-pathogen-free ducks. <i>Poultry Science</i> , 2018, 97, 2278-2286.	3.4	10
1205	Symbiotic N2-Fixer Community Composition, but Not Diversity, Shifts in Nodules of a Single Host Legume Across a 2-Million-Year Dune Chronosequence. <i>Microbial Ecology</i> , 2018, 76, 1009-1020.	2.8	9
1206	Diversity of herbaceous plants and bacterial communities regulates soil resistome across forest biomes. <i>Environmental Microbiology</i> , 2018, 20, 3186-3200.	3.8	55
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1208	Revealing the microbiota of marketed edible insects through PCR-DGGE, metagenomic sequencing and real-time PCR. <i>International Journal of Food Microbiology</i> , 2018, 276, 54-62.	4.7	34
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1210	MitoFish and MiFish Pipeline: A Mitochondrial Genome Database of Fish with an Analysis Pipeline for Environmental DNA Metabarcoding. <i>Molecular Biology and Evolution</i> , 2018, 35, 1553-1555.	8.9	169
1211	Changes in intestinal microbiota across an altitudinal gradient in the lizard <i>Phrynocephalus vlangalii</i>. <i>Ecology and Evolution</i> , 2018, 8, 4695-4703.	1.9	51
1212	High-throughput sequencing for algal systematics. <i>European Journal of Phycology</i> , 2018, 53, 256-272.	2.0	33
1213	Highly efficient removal of nitrogen and phosphorus in an electrolysis-integrated horizontal subsurface-flow constructed wetland amended with biochar. <i>Water Research</i> , 2018, 139, 301-310.	11.3	80
1214	Connection Between BMI-Related Plasma Metabolite Profile and Gut Microbiota. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 1491-1501.	3.6	163
1215	Effect of daidzein on fermentation parameters and bacterial community of finishing Xianan cattle. <i>Italian Journal of Animal Science</i> , 2018, 17, 950-958.	1.9	7

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1220	Gut-dependent microbial translocation induces inflammation and cardiovascular events after ST-elevation myocardial infarction. <i>Microbiome</i> , 2018, 6, 66.	11.1	185
1221	Conversion of sulfur compounds and microbial community in anaerobic treatment of fish and pork waste. <i>Waste Management</i> , 2018, 76, 383-393.	7.4	35
1222	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	7.3	30
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1224	Effect of <i>Lactobacillus rhamnosus</i> GG Supplementation on Intestinal Inflammation Assessed by PET/MRI Scans and Gut Microbiota Composition in HIV-Infected Individuals. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2018, 78, 450-457.	2.1	26
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1236	Long-term fertilisation form, level and duration affect the diversity, structure and functioning of soil microbial communities in the field. Soil Biology and Biochemistry, 2018, 122, 91-103.	8.8	134
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1268	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. <i>ISME Journal</i> , 2018, 12, 1344-1359.	9.8	84
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1341	Microbial community dynamics analysis by high-throughput sequencing in chilled beef longissimus steaks packaged under modified atmospheres. Meat Science, 2018, 141, 94-102.	5.5	65

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1343	Moss habitats distinctly affect their associated bacterial community structures as revealed by the high-throughput sequencing method. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 58.	3.6	13
1344	Response of the microbial community structure of biofilms to ferric iron in microbial fuel cells. <i>Science of the Total Environment</i> , 2018, 631-632, 695-701.	8.0	43
1345	Structure and dynamics of microbiomes associated with the marine sponge <i>Tedania</i> sp. during its life cycle. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	18
1346	A High-Throughput Mutational Scan of an Intrinsically Disordered Acidic Transcriptional Activation Domain. <i>Cell Systems</i> , 2018, 6, 444-455.e6.	6.2	135
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1348	Designer epigenome modifiers enable robust and sustained gene silencing in clinically relevant human cells. <i>Nucleic Acids Research</i> , 2018, 46, 4456-4468.	14.5	63
1349	Nutrient enrichment during shrimp cultivation alters bacterioplankton assemblies and destroys community stability. <i>Ecotoxicology and Environmental Safety</i> , 2018, 156, 366-374.	6.0	30
1350	Transformation, CO ₂ formation and uptake of four organic micropollutants by carrier-attached microorganisms. <i>Water Research</i> , 2018, 141, 405-416.	11.3	27
1351	Earthworm-induced shifts in microbial diversity in soils with rare versus established invasive earthworm populations. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	19
1352	Biodiversity of fungi on <i>Vitis vinifera</i> L. revealed by traditional and high-resolution culture-independent approaches. <i>Fungal Diversity</i> , 2018, 90, 1-84.	12.3	101
1353	<i>Solidago canadensis</i> invasion affects soil N-fixing bacterial communities in heterogeneous landscapes in urban ecosystems in East China. <i>Science of the Total Environment</i> , 2018, 631-632, 702-713.	8.0	64
1354	Phylum-Level Archaeal Distributions in the Sediments of Chinese Lakes With a Large Range of Salinity. <i>Geomicrobiology Journal</i> , 2018, 35, 404-410.	2.0	14
1355	SeekDeep: single-base resolution de novo clustering for amplicon deep sequencing. <i>Nucleic Acids Research</i> , 2018, 46, e21-e21.	14.5	134
1356	Shifts of Sediment Microbial Community Structure along a Salinized and Degraded River Continuum. <i>Journal of Coastal Research</i> , 2018, 342, 443-450.	0.3	5
1357	Gut Microbial Dysbiosis in Indian Children with Autism Spectrum Disorders. <i>Microbial Ecology</i> , 2018, 76, 1102-1114.	2.8	130
1358	Community Structure Analysis and Biodegradation Potential of Aniline-Degrading Bacteria in Biofilters. <i>Current Microbiology</i> , 2018, 75, 918-924.	2.2	33
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1361	Functional evaluation of pollutant transformation in sediment from combined sewer system. <i>Environmental Pollution</i> , 2018, 238, 85-93.	7.5	35
1362	Expansions, diversification, and interindividual copy number variations of AID/APOBEC family cytidine deaminase genes in lampreys. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3211-E3220.	7.1	23
1363	Vanillic acid changed cucumber (<i>Cucumis sativus</i> L.) seedling rhizosphere total bacterial, <i>Pseudomonas</i> and <i>Bacillus</i> spp. communities. <i>Scientific Reports</i> , 2018, 8, 4929.	3.3	31
1364	Gut microbiota analysis of juvenile genetically improved farmed tilapia (<i>Oreochromis niloticus</i>) by dietary supplementation of different resveratrol concentrations. <i>Fish and Shellfish Immunology</i> , 2018, 77, 200-207.	3.6	37
1365	Plant sterols and human gut microbiota relationship: An in vitro colonic fermentation study. <i>Journal of Functional Foods</i> , 2018, 44, 322-329.	3.4	27
1366	Salinity shifts in marine sediment: Importance of number of fluctuation rather than their intensities on bacterial denitrifying community. <i>Marine Pollution Bulletin</i> , 2018, 130, 76-83.	5.0	13
1367	Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, .	3.6	31
1368	Lower dietary concentrate level increases bacterial diversity in the rumen of <i>Cervus elaphus</i> <i>yarkandensis</i> . <i>Canadian Journal of Microbiology</i> , 2018, 64, 501-509.	1.7	10
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1370	A global comparison of the microbiome compositions of three gut locations in commercial pigs with extreme feed conversion ratios. <i>Scientific Reports</i> , 2018, 8, 4536.	3.3	121
1371	Soil pH is equally important as salinity in shaping bacterial communities in saline soils under halophytic vegetation. <i>Scientific Reports</i> , 2018, 8, 4550.	3.3	68
1372	Dynamics of the human gut phageome during antibiotic treatment. <i>Computational Biology and Chemistry</i> , 2018, 74, 420-427.	2.3	15
1373	Microbial dynamics and metabolite changes in Chinese Rice Wine fermentation from sorghum with different tannin content. <i>Scientific Reports</i> , 2018, 8, 4639.	3.3	45
1374	Independent of Birth Mode or Gestational Age, Very-Low-Birth-Weight Infants Fed Their Mothers' Milk Rapidly Develop Personalized Microbiotas Low in <i>Bifidobacterium</i> . <i>Journal of Nutrition</i> , 2018, 148, 326-335.	2.9	22
1375	Changes in the soil bacterial community structure and enzyme activities after intercrop mulch with cover crop for eight years in an orchard. <i>European Journal of Soil Biology</i> , 2018, 86, 34-41.	3.2	81
1376	Imbalance of gut microbiome and intestinal epithelial barrier dysfunction in patients with high blood pressure. <i>Clinical Science</i> , 2018, 132, 701-718.	4.3	328
1377	Opportunistic pathogens are abundant in the gut of cultured giant spiny frog (<i>Paa spinosa</i>). <i>Aquaculture Research</i> , 2018, 49, 2033-2041.	1.8	51

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1382	A comparative study of gut microbiota profiles of earthworms fed in three different substrates. <i>Symbiosis</i> , 2018, 74, 21-29.	2.3	51
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1387	Responses of the soil fungal communities to the co-invasion of two invasive species with different cover classes. <i>Plant Biology</i> , 2018, 20, 151-159.	3.8	43
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1394	Fate of antibiotic resistance genes and metal resistance genes during thermophilic aerobic digestion of sewage sludge. <i>Bioresource Technology</i> , 2018, 249, 635-643.	9.6	48
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1398	Use of a filtering process to remove solid waste and antibiotic resistance genes from effluent of a flow-through fish farm. <i>Science of the Total Environment</i> , 2018, 615, 289-296.	8.0	26
1399	Influence of resistance breeding in common bean on rhizosphere microbiome composition and function. <i>ISME Journal</i> , 2018, 12, 212-224.	9.8	296
1400	Prevalence of antibiotic resistance genes from effluent of coastal aquaculture, South Korea. <i>Environmental Pollution</i> , 2018, 233, 1049-1057.	7.5	127
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1408	Obesity increases the risk of small intestinal bacterial overgrowth (<sc>SIBO</sc>). <i>Neurogastroenterology and Motility</i> , 2018, 30, e13199.	3.0	35
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1415	Bacterial community structures in air conditioners installed in Japanese residential buildings. Antonie Van Leeuwenhoek, 2018, 111, 45-53.	1.7	6
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1417	Distribution of apple and blackcurrant microbiota in Lithuania and the Czech Republic. Microbiological Research, 2018, 206, 1-8.	5.3	44
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1454	Targeted DNA enrichment and whole genome sequencing of <i>Neisseria meningitidis</i> directly from clinical specimens. <i>International Journal of Medical Microbiology</i> , 2018, 308, 256-262.	3.6	36
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1488	Comparison of differences in microbial compositions between negative controls and subject samples with varying analysis configurations. <i>Allergy Asthma & Respiratory Disease</i> , 2018, 6, 255.	0.2	0
1489	A Pipeline for Variant Calling in Tumor Panels Using Amplicon Sequencing Data. , 2018, , .		0
1490	The first complete genomic structure of <i>Butyrivibrio fibrisolvens</i> and its chromid. <i>Microbial Genomics</i> , 2018, 4, .	2.0	9
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1645	Isolation and characterization of microsatellite loci from <i>Oxytropis diversifolia</i> (Fabaceae). <i>Applications in Plant Sciences</i> , 2018, 6, e01168.	2.1	3
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1648	The response of dominant and rare taxa for fungal diversity within different root environments to the cultivation of Bt and conventional cotton varieties. <i>Microbiome</i> , 2018, 6, 184.	11.1	29
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1651	Effects of endogenous inhibitors on the evolution of antibiotic resistance genes during high solid anaerobic digestion of swine manure. <i>Bioresource Technology</i> , 2018, 270, 328-336.	9.6	30
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1654	Isolation by Miniaturized Culture Chip of an Antarctic bacterium <i>Aequorivita</i> sp. with antimicrobial and anthelmintic activity. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2018, 20, e00281.	4.4	11
1655	Cucumber (<i>Cucumis sativus</i> L.) Seedling Rhizosphere <i>Trichoderma</i> and <i>Fusarium</i> spp. Communities Altered by Vanillic Acid. <i>Frontiers in Microbiology</i> , 2018, 9, 2195.	3.5	36
1656	Insight Into the Pico- and Nano-Phytoplankton Communities in the Deepest Biosphere, the Mariana Trench. <i>Frontiers in Microbiology</i> , 2018, 9, 2289.	3.5	30
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1658	Soil fungal taxonomic and functional community composition as affected by biochar properties. <i>Soil Biology and Biochemistry</i> , 2018, 126, 159-167.	8.8	57
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1660	The Genetic Basis of Adaptation following Plastic Changes in Coloration in a Novel Environment. <i>Current Biology</i> , 2018, 28, 2970-2977.e7.	3.9	83
1661	Comparisons of gut microbiota profiles in wild-type and gelatinase B/matrix metalloproteinase-9-deficient mice in acute DSS-induced colitis. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 18.	6.4	10
1662	Venom gland transcriptomics and microRNA profiling of juvenile and adult yellow-bellied sea snake, <i>Hydrophis platurus</i> , from Playa del Coco (Guanacaste, Costa Rica). <i>Toxicon</i> , 2018, 153, 96-105.	1.6	14
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1666	Benthic deep-sea fungi in submarine canyons of the Mediterranean Sea. <i>Progress in Oceanography</i> , 2018, 168, 57-64.	3.2	39
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1669	Direct-fed microbial supplementation influences the bacteria community composition of the gastrointestinal tract of pre- and post-weaned calves. <i>Scientific Reports</i> , 2018, 8, 14147.	3.3	50
1670	Short-term impacts of anthropogenic stressors on <i>Aedes albopictus</i> mosquito vector microbiota. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	22
1671	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. <i>Scientific Reports</i> , 2018, 8, 13314.	3.3	54
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1673	Effects of extruded aquafeed on growth performance and gut microbiome of juvenile <i>Totoaba macdonaldi</i> . <i>Animal Feed Science and Technology</i> , 2018, 245, 91-103.	2.2	34
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1682	From Short Reads to Chromosome-Scale Genome Assemblies. <i>Methods in Molecular Biology</i> , 2018, 1848, 151-197.	0.9	7
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1685	Comparative Genomic Analysis of <i>Vibrio diabolus</i> and Six Taxonomic Synonyms: A First Look at the Distribution and Diversity of the Expanded Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1893.	3.5	24

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1702	Bloom of a denitrifying methanotroph, <i>Candidatus</i> <i>Methyloirabilis limnetica</i> ™, in a deep stratified lake. <i>Environmental Microbiology</i> , 2018, 20, 2598-2614.	3.8	87
1703	Ecology of sleeping: the microbial and arthropod associates of chimpanzee beds. <i>Royal Society Open Science</i> , 2018, 5, 180382.	2.4	7

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1713	Metagenomic study of bacterial microbiota in persistent endodontic infections using Next-generation sequencing. <i>International Endodontic Journal</i> , 2018, 51, 1336-1348.	5.0	51
1714	Effects of permafrost thaw-subsidence on soil bacterial communities in the southern Qinghai-Tibetan Plateau. <i>Applied Soil Ecology</i> , 2018, 128, 81-88.	4.3	33
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1716	Comparative analysis of the bacterial community compositions of the shrimp intestine, surrounding water and sediment. <i>Journal of Applied Microbiology</i> , 2018, 125, 792-799.	3.1	72
1717	The gut microbiome is associated with behavioural task in honey bees. <i>Insectes Sociaux</i> , 2018, 65, 419-429.	1.2	90
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1720	Multiple effects of secondary metabolites on amino acid cycling in white clover rhizosphere. <i>Soil Biology and Biochemistry</i> , 2018, 123, 54-63.	8.8	30
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1743	Characteristics of fecal microbiota in non-alcoholic fatty liver disease patients. <i>Science China Life Sciences</i> , 2018, 61, 770-778.	4.9	46
1744	The High-Quality Genome Sequence of the Oceanic Island Endemic Species <i>Drosophila guanche</i> Reveals Signals of Adaptive Evolution in Genes Related to Flight and Genome Stability. <i>Genome Biology and Evolution</i> , 2018, 10, 1956-1969.	2.5	14
1745	Characterization of Microbial Communities in Pilot-Scale Constructed Wetlands with <i>Salicornia</i> for Treatment of Marine Aquaculture Effluents. <i>Archaea</i> , 2018, 2018, 1-12.	2.3	17
1746	Temporal and spatial distribution of ammonia-oxidizing organisms of two types of wetlands in Northeast China. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7195-7205.	3.6	19
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1749	Predators and nutrient availability favor protozoa-resisting bacteria in aquatic systems. <i>Scientific Reports</i> , 2018, 8, 8415.	3.3	20
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1751	Biofilm and planktonic bacterial communities in a drinking water distribution system supplied with untreated groundwater. <i>Archives of Microbiology</i> , 2018, 200, 1323-1331.	2.2	2
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1754	Complete Genome Sequences of Three Related Avian Avulavirus 1 Isolates from Poultry Farmers in Pakistan. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
1755	Pea-protein alginate encapsulation adversely affects development of clinical signs of <i>Citrobacter rodentium</i> -induced colitis in mice treated with probiotics. <i>Canadian Journal of Microbiology</i> , 2018, 64, 744-760.	1.7	5
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1766	Bioinformatics for Biomonitoring: Species Detection and Diversity Estimates Across Next-Generation Sequencing Platforms. Advances in Ecological Research, 2018, , 1-32.	2.7	3
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1778	Application of Sodium Silicate Enhances Cucumber Resistance to Fusarium Wilt and Alters Soil Microbial Communities. <i>Frontiers in Plant Science</i> , 2018, 9, 624.	3.6	30
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1784	Dynamics and Biodiversity of Bacterial and Yeast Communities during Fermentation of Cocoa Beans. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	66
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1786	Novel Insights into Selection for Antibiotic Resistance in Complex Microbial Communities. <i>MBio</i> , 2018, 9, .	4.1	110
1787	Microbiota assemblages of water, sediment, and intestine and their associations with environmental factors and shrimp physiological health. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8585-8598.	3.6	101
1788	Coreopsis Tinctoria Modulates Lipid Metabolism by Decreasing Low-Density Lipoprotein and Improving Gut Microbiota. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 1060-1074.	1.6	9
1789	A novel locus on mouse chromosome 7 that influences survival after infection with tick-borne encephalitis virus. <i>BMC Neuroscience</i> , 2018, 19, 39.	1.9	14
1790	Effects of straw return on bacterial communities in a wheat-maize rotation system in the North China Plain. <i>PLoS ONE</i> , 2018, 13, e0198087.	2.5	28
1791	Comparison of Microbiota in Patients Treated by Surgery or Chemotherapy by 16S rRNA Sequencing Reveals Potential Biomarkers for Colorectal Cancer Therapy. <i>Frontiers in Microbiology</i> , 2018, 9, 1607.	3.5	103
1792	Profiling white wine seed vinegar bacterial diversity through viable counting, metagenomic sequencing and PCR-DGGE. <i>International Journal of Food Microbiology</i> , 2018, 286, 66-74.	4.7	16
1793	Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. <i>Scientific Reports</i> , 2018, 8, 11159.	3.3	60

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1794	Fucoidan alleviates dyslipidemia and modulates gut microbiota in high-fat diet-induced mice. <i>Journal of Functional Foods</i> , 2018, 48, 220-227.	3.4	55
1795	Beneficial changes of gut microbiota and metabolism in weaned rats with <i>Lactobacillus acidophilus</i> NCFM and <i>Bifidobacterium lactis</i> Bi-07 supplementation. <i>Journal of Functional Foods</i> , 2018, 48, 252-265.	3.4	28
1796	Succession of bacterioplankton community in intensive shrimp (<i>Litopenaeus vannamei</i>) aquaculture systems. <i>Aquaculture</i> , 2018, 497, 200-213.	3.5	35
1797	Response of host's bacterial colonization in shrimp to developmental stage, environment and disease. <i>Molecular Ecology</i> , 2018, 27, 3686-3699.	3.9	82
1798	Contrasting Soil Bacterial Community, Diversity, and Function in Two Forests in China. <i>Frontiers in Microbiology</i> , 2018, 9, 1693.	3.5	72
1799	Chronic Rhinosinusitis: Potential Role of Microbial Dysbiosis and Recommendations for Sampling Sites. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 57.	3.9	75
1800	Ecological Restoration of Antibiotic-Disturbed Gastrointestinal Microbiota in Foregut and Hindgut of Cows. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 79.	3.9	31
1801	The Subgingival Microbiome of Periodontal Pockets With Different Probing Depths in Chronic and Aggressive Periodontitis: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 124.	3.9	73
1802	Association Between Gut Microbiota and <i>Helicobacter pylori</i> -Related Gastric Lesions in a High-Risk Population of Gastric Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 202.	3.9	106
1803	Distinct Nitrogen Provisioning From Organic Amendments in Soil as Influenced by Farming System and Water Regime. <i>Frontiers in Environmental Science</i> , 2018, 6, .	3.3	17
1804	Diversity of Immunoglobulin Light Chain Genes in Non-Teleost Ray-Finned Fish Uncovers IgL Subdivision into Five Ancient Isotypes. <i>Frontiers in Immunology</i> , 2018, 9, 1079.	4.8	5
1805	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018, 9, 31.	3.5	45
1806	Metagenomic Study Suggests That the Gut Microbiota of the Giant Panda (<i>Ailuropoda melanoleuca</i>) May Not Be Specialized for Fiber Fermentation. <i>Frontiers in Microbiology</i> , 2018, 9, 229.	3.5	70
1807	Indigenous <i>Pseudomonas</i> spp. Strains from the Olive (<i>Olea europaea</i> L.) Rhizosphere as Effective Biocontrol Agents against <i>Verticillium dahliae</i> : From the Host Roots to the Bacterial Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 277.	3.5	79
1808	Physiological and Metagenomic Characterizations of the Synergistic Relationships between Ammonia- and Nitrite-Oxidizing Bacteria in Freshwater Nitrification. <i>Frontiers in Microbiology</i> , 2018, 9, 280.	3.5	15
1809	Response of Nitrifier and Denitrifier Abundance and Microbial Community Structure to Experimental Warming in an Agricultural Ecosystem. <i>Frontiers in Microbiology</i> , 2018, 9, 474.	3.5	35
1810	Exploring Biogeochemistry and Microbial Diversity of Extant Microbialites in Mexico and Cuba. <i>Frontiers in Microbiology</i> , 2018, 9, 510.	3.5	29
1811	Gut Microbiome Associates With Lipid-Lowering Effect of Rosuvastatin in Vivo. <i>Frontiers in Microbiology</i> , 2018, 9, 530.	3.5	86

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1813	Stair-Step Pattern of Soil Bacterial Diversity Mainly Driven by pH and Vegetation Types Along the Elevational Gradients of Gongga Mountain, China. <i>Frontiers in Microbiology</i> , 2018, 9, 569.	3.5	90
1814	Alfalfa Intervention Alters Rumen Microbial Community Development in Hu Lambs During Early Life. <i>Frontiers in Microbiology</i> , 2018, 9, 574.	3.5	65
1815	Benthic Algal Community Structures and Their Response to Geographic Distance and Environmental Variables in the Qinghai-Tibetan Lakes With Different Salinity. <i>Frontiers in Microbiology</i> , 2018, 9, 578.	3.5	23
1816	Spatiotemporal Distribution and Assemblages of Planktonic Fungi in the Coastal Waters of the Bohai Sea. <i>Frontiers in Microbiology</i> , 2018, 9, 584.	3.5	37
1817	Depth-Resolved Distribution of Particle-Attached and Free-Living Bacterial Communities in the Water Column of the New Britain Trench. <i>Frontiers in Microbiology</i> , 2018, 9, 625.	3.5	52
1818	Partitioning of Fungal Endophyte Assemblages in Root-Parasitic Plant <i>Cynomorium songaricum</i> and Its Host <i>Nitraria tangutorum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 666.	3.5	28
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1823	Agricultural Freshwater Pond Supports Diverse and Dynamic Bacterial and Viral Populations. <i>Frontiers in Microbiology</i> , 2018, 9, 792.	3.5	27
1824	Key Role of Alphaproteobacteria and Cyanobacteria in the Formation of Stromatolites of Lake Dziani Dzaha (Mayotte, Western Indian Ocean). <i>Frontiers in Microbiology</i> , 2018, 9, 796.	3.5	33
1825	Microbial Community Analyses of the Deteriorated Storeroom Objects in the Tianjin Museum Using Culture-Independent and Culture-Dependent Approaches. <i>Frontiers in Microbiology</i> , 2018, 9, 802.	3.5	32
1826	Dietary Deoxynivalenol Contamination and Oral Lipopolysaccharide Challenge Alters the Cecal Microbiota of Broiler Chickens. <i>Frontiers in Microbiology</i> , 2018, 9, 804.	3.5	49
1827	Trichoderma Biofertilizer Links to Altered Soil Chemistry, Altered Microbial Communities, and Improved Grassland Biomass. <i>Frontiers in Microbiology</i> , 2018, 9, 848.	3.5	89
1828	Oral Microbiota Community Dynamics Associated With Oral Squamous Cell Carcinoma Staging. <i>Frontiers in Microbiology</i> , 2018, 9, 862.	3.5	211
1829	Taxon-Function Decoupling as an Adaptive Signature of Lake Microbial Metacommunities Under a Chronic Polymetallic Pollution Gradient. <i>Frontiers in Microbiology</i> , 2018, 9, 869.	3.5	19

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1831	Alpha-Ketoglutarate in Low-Protein Diets for Growing Pigs: Effects on Cecal Microbial Communities and Parameters of Microbial Metabolism. <i>Frontiers in Microbiology</i> , 2018, 9, 1057.	3.5	40
1832	Acclimation and Institutionalization of the Mouse Microbiota Following Transportation. <i>Frontiers in Microbiology</i> , 2018, 9, 1085.	3.5	55
1833	Sediment Depth-Dependent Spatial Variations of Bacterial Communities in Mud Deposits of the Eastern China Marginal Seas. <i>Frontiers in Microbiology</i> , 2018, 9, 1128.	3.5	32
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1835	Microbial Interactions With Dissolved Organic Matter Drive Carbon Dynamics and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 1234.	3.5	107
1836	5-Aminosalicylic Acid Alters the Gut Bacterial Microbiota in Patients With Ulcerative Colitis. <i>Frontiers in Microbiology</i> , 2018, 9, 1274.	3.5	113
1837	Diversity of Fungal Communities in Heshang Cave of Central China Revealed by Mycobiome-Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 1400.	3.5	23
1838	Nitrospira Cluster 8a Plays a Predominant Role in the Nitrification Process of a Subtropical Ultisol under Long-Term Inorganic and Organic Fertilization. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	42
1839	Vex-seq: high-throughput identification of the impact of genetic variation on pre-mRNA splicing efficiency. <i>Genome Biology</i> , 2018, 19, 71.	8.8	66
1840	<scp>eDNA</scp> metabarcoding as a new surveillance approach for coastal Arctic biodiversity. <i>Ecology and Evolution</i> , 2018, 8, 7763-7777.	1.9	154
1841	Microbial Community Dynamics and Assembly Follow Trajectories of an Early-Spring Diatom Bloom in a Semienclosed Bay. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	41
1842	Quantitative PCR Analysis of Gut Disease-Discriminatory Phyla for Determining Shrimp Disease Incidence. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	10
1843	Bacillales Members from the Olive Rhizosphere Are Effective Biological Control Agents against the Defoliating Pathotype of <i>Verticillium dahliae</i> . <i>Agriculture (Switzerland)</i> , 2018, 8, 90.	3.1	39
1844	Exposure to Formaldehyde Perturbs the Mouse Gut Microbiome. <i>Genes</i> , 2018, 9, 192.	2.4	11
1845	Ancient DNA from Giant Panda (<i>Ailuropoda melanoleuca</i>) of South-Western China Reveals Genetic Diversity Loss during the Holocene. <i>Genes</i> , 2018, 9, 198.	2.4	14
1846	Probiotic <i>Lactobacillus Paracasei</i> Expressing a Nucleic Acid-Hydrolyzing Minibody (3D8 Scfv) Enhances Probiotic Activities in Mice Intestine as Revealed by Metagenomic Analyses. <i>Genes</i> , 2018, 9, 276.	2.4	10
1847	Disentangling the drivers of functional complexity at the metagenomic level in Shark Bay microbial mat microbiomes. <i>ISME Journal</i> , 2018, 12, 2619-2639.	9.8	94

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1849	Spatial distribution of microbial community composition along a steep slope plot of the Loess Plateau. <i>Applied Soil Ecology</i> , 2018, 130, 226-236.	4.3	22
1850	Soil aggregate size mediates the responses of microbial communities to crop rotation. <i>European Journal of Soil Biology</i> , 2018, 88, 48-56.	3.2	25
1851	Responses of fungal and bacterial community and network to organic inputs vary among different spatial habitats in soil. <i>Soil Biology and Biochemistry</i> , 2018, 125, 54-63.	8.8	142
1852	Development of outbred CD1 mouse colonies with distinct standardized gut microbiota profiles for use in complex microbiota targeted studies. <i>Scientific Reports</i> , 2018, 8, 10107.	3.3	30
1853	Optimized knock-in of point mutations in zebrafish using CRISPR/Cas9. <i>Nucleic Acids Research</i> , 2018, 46, e102-e102.	14.5	50
1854	Targeted resequencing of coding <scp>DNA</scp> sequences for <scp>SNP</scp> discovery in nonmodel species. <i>Molecular Ecology Resources</i> , 2018, 18, 1356-1373.	4.8	19
1855	toaSTR: A web application for forensic STR genotyping by massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2018, 37, 21-28.	3.1	19
1856	Seasonal changes in the diversity and composition of the litter fauna in native forests and rubber plantations. <i>Scientific Reports</i> , 2018, 8, 10232.	3.3	7
1857	Siglec-6 on Chronic Lymphocytic Leukemia Cells Is a Target for Post-Allogeneic Hematopoietic Stem Cell Transplantation Antibodies. <i>Cancer Immunology Research</i> , 2018, 6, 1008-1013.	3.4	10
1858	Effects of cover crop in an apple orchard on microbial community composition, networks, and potential genes involved with degradation of crop residues in soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 743-759.	4.3	85
1859	Bioturbation by the razor clam (<i>Sinonovacula constricta</i>) on the microbial community and enzymatic activities in the sediment of an ecological aquaculture wastewater treatment system. <i>Science of the Total Environment</i> , 2018, 643, 1098-1107.	8.0	57
1860	Disentangling the complexity of permafrost soil by using high resolution profiling of microbial community composition, key functions and respiration rates. <i>Environmental Microbiology</i> , 2018, 20, 4328-4342.	3.8	37
1861	Dietary Supplementation with a Magnesium-Rich Marine Mineral Blend Enhances the Diversity of Gastrointestinal Microbiota. <i>Marine Drugs</i> , 2018, 16, 216.	4.6	41
1862	Monitoring of the Apple Fruit Moth: Detection of Genetic Variation and Structure Applying a Novel Multiplex Set of 19 STR Markers. <i>Molecules</i> , 2018, 23, 850.	3.8	3
1863	High-Glucose or -Fructose Diet Cause Changes of the Gut Microbiota and Metabolic Disorders in Mice without Body Weight Change. <i>Nutrients</i> , 2018, 10, 761.	4.1	310
1864	Combined Use of <i>C. butyricum</i> Sx-01 and <i>L. salivarius</i> C-1-3 Improves Intestinal Health and Reduces the Amount of Lipids in Serum via Modulation of Gut Microbiota in Mice. <i>Nutrients</i> , 2018, 10, 810.	4.1	32
1865	Root exudate metabolites drive plant-soil feedbacks on growth and defense by shaping the rhizosphere microbiota. <i>Nature Communications</i> , 2018, 9, 2738.	12.8	861

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1867	Hydrothermal chimneys host habitat-specific microbial communities: analogues for studying the possible impact of mining seafloor massive sulfide deposits. Scientific Reports, 2018, 8, 10386.	3.3	30
1868	Bio-cord plays a similar role as submerged macrophytes in harboring bacterial assemblages in an eco-ditch. Environmental Science and Pollution Research, 2018, 25, 26550-26561.	5.3	10
1869	Metabolic Biosynthesis Pathways Identified from Fecal Microbiome Associated with Prostate Cancer. European Urology, 2018, 74, 575-582.	1.9	117
1870	Response of antibiotic and heavy metal resistance genes to two different temperature sequences in anaerobic digestion of waste activated sludge. Bioresource Technology, 2018, 267, 303-310.	9.6	45
1871	Anti-CRISPR Phages Cooperate to Overcome CRISPR-Cas Immunity. Cell, 2018, 174, 908-916.e12.	28.9	179
1872	Dietary values of macroalgae <i>Porphyra haitanensis</i> in <i>Litopenaeus vannamei</i> under normal rearing and WSSV challenge conditions: Effect on growth, immune response and intestinal microbiota. Fish and Shellfish Immunology, 2018, 81, 135-149.	3.6	35
1873	Microbial community response to growing season and plant nutrient optimisation in a boreal Norway spruce forest. Soil Biology and Biochemistry, 2018, 125, 197-209.	8.8	64
1874	Exon-Capture-Based Phylogeny and Diversification of the Venomous Gastropods (Neogastropoda,) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	8.9	46
1875	Thermal processing of food reduces gut microbiota diversity of the host and triggers adaptation of the microbiota: evidence from two vertebrates. Microbiome, 2018, 6, 99.	11.1	42
1876	Huddling remodels gut microbiota to reduce energy requirements in a small mammal species during cold exposure. Microbiome, 2018, 6, 103.	11.1	90
1877	Prevalence and Epidemiologic Profile of Oral Infection with Alpha, Beta, and Gamma Papillomaviruses in an Asian Chinese Population. Journal of Infectious Diseases, 2018, 218, 388-397.	4.0	43
1878	Saturated long-chain fatty acid-producing bacteria contribute to enhanced colonic motility in rats. Microbiome, 2018, 6, 107.	11.1	92
1879	Genomic analysis of MHC-based mate choice in the monogamous California mouse. Behavioral Ecology, 2018, 29, 1167-1180.	2.2	9
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1881	Resource Availability Drives Responses of Soil Microbial Communities to Short-term Precipitation and Nitrogen Addition in a Desert Shrubland. Frontiers in Microbiology, 2018, 9, 186.	3.5	82
1882	The nasopharyngeal microbiota in patients with viral respiratory tract infections is enriched in bacterial pathogens. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 1725-1733.	2.9	78
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1885	Microbiota dynamics and volatilome profile during stink bean fermentation (Sataw-Dong) with <i>Lactobacillus plantarum</i> KJ03 as a starter culture. <i>Food Microbiology</i> , 2018, 76, 91-102.	4.2	28
1886	Analysis of microbial abundance and community composition in esophagus and intestinal tract of wild veined rapa whelk (<i>Rapana venosa</i>) by 16S rRNA gene sequencing. <i>Journal of General and Applied Microbiology</i> , 2018, 64, 158-166.	0.7	18
1887	<i>Plasmodium falciparum</i> genetic variation of var2csa in the Democratic Republic of the Congo. <i>Malaria Journal</i> , 2018, 17, 46.	2.3	13
1888	Host contributes to longitudinal diversity of fecal microbiota in swine selected for lean growth. <i>Microbiome</i> , 2018, 6, 4.	11.1	90
1889	Crawling-induced floor dust resuspension affects the microbiota of the infant breathing zone. <i>Microbiome</i> , 2018, 6, 25.	11.1	40
1890	Filter forensics: microbiota recovery from residential HVAC filters. <i>Microbiome</i> , 2018, 6, 22.	11.1	35
1891	A reservoir of “historical” antibiotic resistance genes in remote pristine Antarctic soils. <i>Microbiome</i> , 2018, 6, 40.	11.1	244
1892	DNA-SIP Reveals the Diversity of Chemolithoautotrophic Bacteria Inhabiting Three Different Soil Types in Typical Karst Rocky Desertification Ecosystems in Southwest China. <i>Microbial Ecology</i> , 2018, 76, 976-990.	2.8	16
1893	Disruption of bacterial balance in the gut of <i>Portunus trituberculatus</i> induced by <i>Vibrio alginolyticus</i> infection. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1891-1898.	1.3	8
1894	Exploring abundance, diversity and variation of a widespread antibiotic resistance gene in wastewater treatment plants. <i>Environment International</i> , 2018, 117, 186-195.	10.0	40
1895	Analyses of microbial community of naturally homemade soybean pastes in Liaoning Province of China by Illumina Miseq Sequencing. <i>Food Research International</i> , 2018, 111, 50-57.	6.2	45
1896	Different rearing conditions alter gut microbiota composition and host physiology in Shaoxing ducks. <i>Scientific Reports</i> , 2018, 8, 7387.	3.3	38
1897	Enhanced and Complete Removal of Phenylurea Herbicides by Combinational Transgenic Plant-Microbe Remediation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	22
1898	Unrevealing variation of microbial communities and correlation with environmental variables in a full culture-cycle of <i>Undaria pinnatifida</i> . <i>Marine Environmental Research</i> , 2018, 139, 46-56.	2.5	26
1899	Predatory flying squids are detritivores during their early planktonic life. <i>Scientific Reports</i> , 2018, 8, 3440.	3.3	26
1900	Mapping distribution of cysts of recent dinoflagellate and <i>Cochlodinium polykrikoides</i> using next-generation sequencing and morphological approaches in South Sea, Korea. <i>Scientific Reports</i> , 2018, 8, 7011.	3.3	17
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1903	Multilevel social structure and diet shape the gut microbiota of the gelada monkey, the only grazing primate. <i>Microbiome</i> , 2018, 6, 84.	11.1	56
1904	Intestinal microbiota in growing pigs: effects of stocking density. <i>Food and Agricultural Immunology</i> , 2018, 29, 524-535.	1.4	2
1905	Progressive biogeochemical transformation of placer gold particles drives compositional changes in associated biofilm communities. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	18
1906	Gut microbiota profiling in Han Chinese with type 1 diabetes. <i>Diabetes Research and Clinical Practice</i> , 2018, 141, 256-263.	2.8	68
1907	Changes in the gut microbiota composition during pregnancy in patients with gestational diabetes mellitus (GDM). <i>Scientific Reports</i> , 2018, 8, 12216.	3.3	162
1908	The Microbial Composition of Bacteroidetes Species in Ulcerative Colitis Is Effectively Improved by Combination Therapy With Fecal Microbiota Transplantation and Antibiotics. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 2590-2598.	1.9	27
1909	Bacterial biogeography of adult airways in atopic asthma. <i>Microbiome</i> , 2018, 6, 104.	11.1	93
1910	Gut Microbiota in Tibetan Herdsmen Reflects the Degree of Urbanization. <i>Frontiers in Microbiology</i> , 2018, 9, 1745.	3.5	33
1911	2,3,5,4'â€tetrahydroxyâ€stilbeneâ€2â€Oâ€Î²â€Dâ€glucoside attenuates methionine and cholineâ€deficient dietâ€induced nonâ€alcoholic fatty liver disease. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1087-1094.	1.8	9
1912	Dietary l-arginine Supplementation Alleviates the Intestinal Injury and Modulates the Gut Microbiota in Broiler Chickens Challenged by <i>Clostridium perfringens</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1716.	3.5	64
1913	Responses of soil N-fixing bacterial communities to redroot pigweed (<i>Amaranthus retroflexus</i> L.) invasion under Cu and Cd heavy metal soil pollution. <i>Agriculture, Ecosystems and Environment</i> , 2018, 267, 15-22.	5.3	25
1914	Concentration and Community of Airborne Bacteria in Response to Cyclical Haze Events During the Fall and Midwinter in Beijing, China. <i>Frontiers in Microbiology</i> , 2018, 9, 1741.	3.5	35
1915	Effect of Sugarcane Straw and Goat Manure on Soil Nutrient Transformation and Bacterial Communities. <i>Sustainability</i> , 2018, 10, 2361.	3.2	35
1916	Diversity of Bacterial Communities in the Intestinal Tracts of Two Geographically Distant Populations of <i>Bactrocera dorsalis</i> (Diptera: Tephritidae). <i>Journal of Economic Entomology</i> , 2018, 111, 2861-2868.	1.8	20
1917	Gut microbiota alterations in moderate to severe acne vulgaris patients. <i>Journal of Dermatology</i> , 2018, 45, 1166-1171.	1.2	59
1918	Broad Phylogenetic Diversity Associated with Nitrogen Loss through Sulfur Oxidation in a Large Public Marine Aquarium. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	7
1919	Sanger and Next Generation Sequencing Approaches to Evaluate HIV-1 Virus in Blood Compartments. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 1697.	2.6	35

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1921	Gut microbiota composition and butyrate production in children affected by non-IgE-mediated cow's milk allergy. <i>Scientific Reports</i> , 2018, 8, 12500.	3.3	80
1922	Study of Microbiomes in Aseptically Collected Samples of Human Breast Tissue Using Needle Biopsy and the Potential Role of in situ Tissue Microbiomes for Promoting Malignancy. <i>Frontiers in Oncology</i> , 2018, 8, 318.	2.8	102
1923	Gene expression profiling reveals deep-sea coral response to the Deepwater Horizon oil spill. <i>Molecular Ecology</i> , 2018, 27, 4066-4077.	3.9	24
1924	Sulfated polysaccharide from sea cucumber modulates the gut microbiota and its metabolites in normal mice. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 502-512.	7.5	57
1925	Biogenic amines analysis and microbial contribution in traditional fermented food of Douchi. <i>Scientific Reports</i> , 2018, 8, 12567.	3.3	29
1926	Dynamics of compost microbiota during the cultivation of <i>Agaricus bisporus</i> in the presence of <i>Bacillus velezensis</i> QST713 as biocontrol agent against <i>Trichoderma aggressivum</i> . <i>Biological Control</i> , 2018, 127, 39-54.	3.0	18
1927	Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818.	18.8	208
1928	Oceanographic boundaries constrain microbial diversity gradients in the South Pacific Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8266-E8275.	7.1	96
1929	Cecal microbiome profile altered by <i>Salmonella enterica</i> , serovar Enteritidis inoculation in chicken. <i>Gut Pathogens</i> , 2018, 10, 34.	3.4	56
1930	Impacts of n-alkane concentration on soil bacterial community structure and alkane monooxygenase genes abundance during bioremediation processes. <i>Frontiers of Environmental Science and Engineering</i> , 2018, 12, 1.	6.0	18
1931	Protective effects of <i>Paederia scandens</i> extract on rheumatoid arthritis mouse model by modulating gut microbiota. <i>Journal of Ethnopharmacology</i> , 2018, 226, 97-104.	4.1	35
1932	Influence of Temperature on the Bacterial Community in Substrate and Extracellular Enzyme Activity of <i>Auricularia cornea</i> . <i>Mycobiology</i> , 2018, 46, 224-235.	1.7	7
1933	Plant host habitat and root exudates shape fungal diversity. <i>Mycorrhiza</i> , 2018, 28, 451-463.	2.8	63
1934	Yellow Canopy Syndrome in sugarcane is associated with shifts in the rhizosphere soil metagenome but not with overall soil microbial function. <i>Soil Biology and Biochemistry</i> , 2018, 125, 275-285.	8.8	9
1935	Analysis of sequencing strategies and tools for taxonomic annotation: Defining standards for progressive metagenomics. <i>Scientific Reports</i> , 2018, 8, 12034.	3.3	93
1936	Snake fungal disease alters skin bacterial and fungal diversity in an endangered rattlesnake. <i>Scientific Reports</i> , 2018, 8, 12147.	3.3	35
1937	Comparison of Fecal Collection Methods for Microbiome and Metabolomics Studies. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 301.	3.9	114

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1938	Microbial Biogeography Along the Gastrointestinal Tract of a Red Panda. <i>Frontiers in Microbiology</i> , 2018, 9, 1411.	3.5	26
1939	Rhizosphere Bacterial Communities Differ According to Fertilizer Regimes and Cabbage (Brassica) Tj ETQq1 1 0.784314 rgBT /Overload 1620.	3.5	38
1940	Linking microbial co-occurrences to soil ecological processes across a woodland-grassland ecotone. <i>Ecology and Evolution</i> , 2018, 8, 8217-8230.	1.9	38
1941	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1635.	3.5	51
1942	Profiling of the TCR β repertoire in non-model species using high-throughput sequencing. <i>Scientific Reports</i> , 2018, 8, 11613.	3.3	13
1943	Bacterial diversity among the fruit bodies of ectomycorrhizal and saprophytic fungi and their corresponding hyphosphere soils. <i>Scientific Reports</i> , 2018, 8, 11672.	3.3	27
1944	Manure amendment reduced plant uptake and enhanced rhizodegradation of 2,4,4'-tetrabrominated diphenyl ether in soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 807-817.	4.3	15
1945	Volatile Oil of <i>Amomum villosum</i> Inhibits Nonalcoholic Fatty Liver Disease via the Gut-Liver Axis. <i>BioMed Research International</i> , 2018, 2018, 1-16.	1.9	27
1946	Comparison between complete genomes of an isolate of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> from Japan and a New Zealand isolate of the pandemic lineage. <i>Scientific Reports</i> , 2018, 8, 10915.	3.3	23
1947	Improved sgRNA design in bacteria via genome-wide activity profiling. <i>Nucleic Acids Research</i> , 2018, 46, 7052-7069.	14.5	73
1948	The effect of several activated biochars on Cd immobilization and microbial community composition during in-situ remediation of heavy metal contaminated sediment. <i>Chemosphere</i> , 2018, 208, 655-664.	8.2	113
1949	Functional Relevance of Improbable Antibody Mutations for HIV Broadly Neutralizing Antibody Development. <i>Cell Host and Microbe</i> , 2018, 23, 759-765.e6.	11.0	98
1950	Intermittent Fasting Confers Protection in CNS Autoimmunity by Altering the Gut Microbiota. <i>Cell Metabolism</i> , 2018, 27, 1222-1235.e6.	16.2	352
1951	Analysis of gut microbiota revealed <i>Lactococcus garviae</i> could be an indicative of skin ulceration syndrome in farmed sea cucumber <i>Apostichopus japonicus</i> . <i>Fish and Shellfish Immunology</i> , 2018, 80, 148-154.	3.6	33
1952	Temporal dynamics of microbiota before and after host death. <i>ISME Journal</i> , 2018, 12, 2076-2085.	9.8	21
1953	Seasonal dynamics of the bacterioplankton community in a large, shallow, highly dynamic freshwater lake. <i>Canadian Journal of Microbiology</i> , 2018, 64, 786-797.	1.7	10
1954	<i>Eimeria tenella</i> infection perturbs the chicken gut microbiota from the onset of oocyst shedding. <i>Veterinary Parasitology</i> , 2018, 258, 30-37.	1.8	45
1955	Insights into the bacterial symbiont diversity in spiders. <i>Ecology and Evolution</i> , 2018, 8, 4899-4906.	1.9	46

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1956	Season, age, and sex affect the fecal mycobiota of free-ranging Tibetan macaques (<i>Macaca</i>) Tj ETQq0 0 0 rgBT, /Overlock, 10 Tf 50 7	1.7	24
1957	Analyzing High-Throughput Microbial Amplicon Sequence Data Using Multiple Markers. , 2018, , 121-138.		2
1958	Integrated interrogation of causes of membrane fouling in a pilot-scale anoxic-oxic membrane bioreactor treating oil refinery wastewater. Science of the Total Environment, 2018, 642, 77-89.	8.0	21
1959	Effects of a homogeneous polysaccharide from Sijunzi decoction on human intestinal microbes and short chain fatty acids in vitro. Journal of Ethnopharmacology, 2018, 224, 465-473.	4.1	69
1960	Removal of benzene, toluene, xylene and styrene by biotrickling filters and identification of their interactions. PLoS ONE, 2018, 13, e0189927.	2.5	30
1961	Does the biological treatment or membrane separation reduce the antibiotic resistance genes from swine wastewater through a sequencing-batch membrane bioreactor treatment process. Environment International, 2018, 118, 274-281.	10.0	39
1962	<i>Marteilia refringens</i> and <i>Marteilia pararefringens</i> sp. nov. are distinct parasites of bivalves and have different European distributions. Parasitology, 2018, 145, 1483-1492.	1.5	16
1963	16S rRNA analysis of diversity of manure microbial community in dairy farm environment. PLoS ONE, 2018, 13, e0190126.	2.5	47
1964	The biogeochemical vertical structure renders a meromictic volcanic lake a trap for geogenic CO ₂ (Lake Averno, Italy). PLoS ONE, 2018, 13, e0193914.	2.5	16
1965	Microbial community analysis in biologically active filters exhibiting efficient removal of emerging contaminants and impact of operational conditions. Science of the Total Environment, 2018, 640-641, 1455-1464.	8.0	23
1966	Biogeographic patterns of abundant and rare bacterioplankton in three subtropical bays resulting from selective and neutral processes. ISME Journal, 2018, 12, 2198-2210.	9.8	269
1967	Microbial communities and natural fermentation of corn silages prepared with farm bunker-silo in Southwest China. Bioresource Technology, 2018, 265, 282-290.	9.6	180
1968	Individuality and convergence of the infant gut microbiota during the first year of life. Nature Communications, 2018, 9, 2233.	12.8	85
1969	Effect of different types of olive oil pomace dietary supplementation on the rumen microbial community profile in Comisana ewes. Scientific Reports, 2018, 8, 8455.	3.3	46
1970	Putative Role of Flavobacterium, Dokdonella and Methylophilus Strains in Paracetamol Biodegradation. Water, Air, and Soil Pollution, 2018, 229, 1.	2.4	39
1971	HIV-1 Protease Evolvability Is Affected by Synonymous Nucleotide Recoding. Journal of Virology, 2018, 92, .	3.4	9
1972	Microbiome and butyrate production are altered in the gut of rats fed a glycated fish protein diet. Journal of Functional Foods, 2018, 47, 423-433.	3.4	56
1973	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. Science, 2018, 360, 1355-1358.	12.6	234

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1975	Distinct patterns and processes of abundant and rare eukaryotic plankton communities following a reservoir cyanobacterial bloom. ISME Journal, 2018, 12, 2263-2277.	9.8	412
1976	How does marker choice affect your diet analysis: comparing genetic markers and digestion levels for diet metabarcoding of tropical-reef piscivores. Marine and Freshwater Research, 2019, 70, 8.	1.3	27
1977	Modulation of intestinal microbiota and immunometabolic parameters by caloric restriction and lactic acid bacteria. Food Research International, 2019, 124, 188-199.	6.2	16
1978	Rhizosphere microbiota assemblage associated with wild and cultivated soybeans grown in three types of soil suspensions. Archives of Agronomy and Soil Science, 2019, 65, 74-87.	2.6	28
1979	Harnessing microfluidic streak plate technique to investigate the gut microbiome of Reticulitermes chinensis. MicrobiologyOpen, 2019, 8, e00654.	3.0	16
1980	Temporal and long-term gut microbiota variation in allergic disease: A prospective study from infancy to school age. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 176-185.	5.7	67
1981	Insights into Endophytic Bacterial Community Structures of Seeds Among Various Oryza sativa L. Rice Genotypes. Journal of Plant Growth Regulation, 2019, 38, 93-102.	5.1	44
1982	High-throughput characterization of antibiotic resistome in soil amended with commercial organic fertilizers. Journal of Soils and Sediments, 2019, 19, 641-651.	3.0	11
1983	The Impact of Anthropogenic Disturbance on Bacterioplankton Communities During the Construction of Donghu Tunnel (Wuhan, China). Microbial Ecology, 2019, 77, 277-287.	2.8	17
1984	Magnesium lithospermate B improves the gut microbiome and bile acid metabolic profiles in a mouse model of diabetic nephropathy. Acta Pharmacologica Sinica, 2019, 40, 507-513.	6.1	33
1985	A diet rich in C 3 plants reveals the sensitivity of an alpine mammal to climate change. Molecular Ecology, 2019, 28, 250-265.	3.9	31
1986	Anaerobic ammonium oxidation coupled to iron reduction in constructed wetland mesocosms. Science of the Total Environment, 2019, 648, 984-992.	8.0	66
1987	Characterization of the bacterial community of braised chicken, a specialty poultry product in China. Poultry Science, 2019, 98, 1055-1063.	3.4	13
1988	Simulated Marine Heat Wave Alters Abundance and Structure of Vibrio Populations Associated with the Pacific Oyster Resulting in a Mass Mortality Event. Microbial Ecology, 2019, 77, 736-747.	2.8	116
1989	Profiling the Gut Microbiome: Practice and Potential. , 2019, , 200-217.		0
1990	The oral microbiome in oral lichen planus during a 1-year randomized clinical trial. Oral Diseases, 2019, 25, 327-338.	3.0	15
1991	Bacterial community and quality characteristics of the fermented potherb mustard (Brassica juncea) Tj ETQq1 1 0.784314 rgBT /Over	6.2	15

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1993	High Doses of Copper and Mercury Changed Cecal Microbiota in Female Mice. <i>Biological Trace Element Research</i> , 2019, 189, 134-144.	3.5	47
1994	Increasing aridity affects soil archaeal communities by mediating soil niches in semi-arid regions. <i>Science of the Total Environment</i> , 2019, 647, 699-707.	8.0	29
1995	Bacterial communities in natural versus pesticide-treated <i>Aphis gossypii</i> populations in North China. <i>MicrobiologyOpen</i> , 2019, 8, e00652.	3.0	17
1996	Gravel mulching effects on soil physicochemical properties and microbial community composition in the Loess Plateau, northwestern China. <i>European Journal of Soil Biology</i> , 2019, 94, 103115.	3.2	13
1997	Compositional shifts in the fungal diversity of garlic scapes during postharvest transportation and cold storage. <i>LWT - Food Science and Technology</i> , 2019, 115, 108453.	5.2	12
1998	Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019, 3, 1298-1308.	7.8	34
1999	Gut microbiota alterations associated with reduced bone mineral density in older adults. <i>Rheumatology</i> , 2019, 58, 2295-2304.	1.9	106
2000	Environmental filtering increases with elevation for the assembly of gut microbiota in wild pikas. <i>Microbial Biotechnology</i> , 2019, 12, 976-992.	4.2	55
2001	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal <i>Salmonella enterica</i> Serovars by Using Machine Learning. <i>MSystems</i> , 2019, 4, .	3.8	21
2002	Supplemental Plant Extracts From <i>Flos Ionicerae</i> in Combination With Baikal skullcap Attenuate Intestinal Disruption and Modulate Gut Microbiota in Laying Hens Challenged by <i>Salmonella pullorum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1681.	3.5	50
2003	Effect of dietary xylan on immune response, tight junction protein expression and bacterial community in the intestine of juvenile turbot (<i>Scophthalmus maximus</i> L.). <i>Aquaculture</i> , 2019, 512, 734361.	3.5	24
2004	Bovine mastitis is a polymicrobial disease requiring a polydiagnostic approach. <i>International Dairy Journal</i> , 2019, 99, 104539.	3.0	11
2005	Mechanistic Understanding of Predatory Bacteria-Induced Biolysis for Waste Sludge Dewaterability Improvement. <i>Water, Air, and Soil Pollution</i> , 2019, 230, 1.	2.4	10
2006	Reduced genetic potential for butyrate fermentation in the gut microbiome of infants who develop allergic sensitization. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1638-1647.e3.	2.9	95
2007	Application of organic fertilizer improves microbial community diversity and alters microbial network structure in tea (<i>Camellia sinensis</i>) plantation soils. <i>Soil and Tillage Research</i> , 2019, 195, 104356.	5.6	117
2008	Microbiota of newborn calves and their mothers reveals possible transfer routes for newborn calves' gastrointestinal microbiota. <i>PLoS ONE</i> , 2019, 14, e0220554.	2.5	61
2009	Impacts of uORF codon identity and position on translation regulation. <i>Nucleic Acids Research</i> , 2019, 47, 9358-9367.	14.5	46

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2011	Changes of porcine gut microbiota in response to dietary chlorogenic acid supplementation. Applied Microbiology and Biotechnology, 2019, 103, 8157-8168.	3.6	47
2012	Dominant plant species influence nematode richness by moderating understory diversity and microbial assemblages. Soil Biology and Biochemistry, 2019, 137, 107566.	8.8	30
2013	Dynamics of Vaginal and Rectal Microbiota Over Several Menstrual Cycles in Female Cynomolgus Macaques. Frontiers in Cellular and Infection Microbiology, 2019, 9, 188.	3.9	24
2014	Feedback of airborne bacterial consortia to haze pollution with different PM2.5 levels in typical mountainous terrain of Jinan, China. Science of the Total Environment, 2019, 695, 133912.	8.0	17
2015	Development of omics-based protocols for the microbiological characterization of multi-strain formulations marketed as probiotics: the case of VSL#3. Microbial Biotechnology, 2019, 12, 1371-1386.	4.2	30
2016	Arbuscular mycorrhizal fungi shape the adaptive strategy of plants by mediating nutrient acquisition in a shrub-dominated community in the Mu Us Desert. Plant and Soil, 2019, 443, 549-564.	3.7	15
2017	Response of gut microbiota in type 2 diabetes to hypoglycemic agents. Endocrine, 2019, 66, 485-493.	2.3	59
2018	<i>Lactobacillus acidophilus</i> alleviates type 2 diabetes by regulating hepatic glucose, lipid metabolism and gut microbiota in mice. Food and Function, 2019, 10, 5804-5815.	4.6	139
2019	Evidence of Spatial Homogeneity in an Electromethanogenic Cathodic Microbial Community. Frontiers in Microbiology, 2019, 10, 1747.	3.5	19
2020	Biochar application on paddy and purple soils in southern China: soil carbon and biotic activity. Royal Society Open Science, 2019, 6, 181499.	2.4	21
2021	Diluted conventional media improve the microbial cultivability from aquarium seawater. Journal of Microbiology, 2019, 57, 759-768.	2.8	7
2022	Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes. Cell, 2019, 178, 795-806.e12.	28.9	830
2023	Comparative analysis of the gut microbial communities between two dominant amphipods from the Challenger Deep, Mariana Trench. Deep-Sea Research Part I: Oceanographic Research Papers, 2019, 151, 103081.	1.4	16
2024	Phylogenetic reconciliation reveals the natural history of glycopeptide antibiotic biosynthesis and resistance. Nature Microbiology, 2019, 4, 1862-1871.	13.3	67
2025	Comparative Analyses of Fecal Microbiota in European Mouflon (<i>Ovis orientalis musimon</i>) and Blue Sheep (<i>Pseudois nayaur</i>) Living at Low or High Altitudes. Frontiers in Microbiology, 2019, 10, 1735.	3.5	27
2026	Biogeographical patterns in soil bacterial communities across the Arctic region. FEMS Microbiology Ecology, 2019, 95, .	2.7	53
2027	Contemporary Demographic Reconstruction Methods Are Robust to Genome Assembly Quality: A Case Study in Tasmanian Devils. Molecular Biology and Evolution, 2019, 36, 2906-2921.	8.9	84

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2028	Bacterial community and composition in Jiang-shui and Suan-cai revealed by high-throughput sequencing of 16S rRNA. <i>International Journal of Food Microbiology</i> , 2019, 306, 108271.	4.7	61
2029	Large dataset enables prediction of repair after CRISPR-Cas9 editing in primary T cells. <i>Nature Biotechnology</i> , 2019, 37, 1034-1037.	17.5	87
2030	Following legume establishment, microbial and chemical associations facilitate improved productivity in degraded grasslands. <i>Plant and Soil</i> , 2019, 443, 273-292.	3.7	14
2031	Functional Differences in the Blooming Phytoplankton <i>Heterosigma akashiwo</i> and <i>Prorocentrum donghaiense</i> Revealed by Comparative Metaproteomics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	19
2032	Natural Farming Improves Soil Quality and Alters Microbial Diversity in a Cabbage Field in Japan. <i>Sustainability</i> , 2019, 11, 3131.	3.2	26
2033	Taking insight into the gut microbiota of three spider species: No characteristic symbiont was found corresponding to the special feeding style of spiders. <i>Ecology and Evolution</i> , 2019, 9, 8146-8156.	1.9	19
2034	Genetic Characterization and Enhanced Surveillance of Ceftriaxone-Resistant <i>Neisseria gonorrhoeae</i> Strain, Alberta, Canada, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 1660-1667.	4.3	24
2035	Long-Term Monoculture Negatively Regulates Fungal Community Composition and Abundance of Tea Orchards. <i>Agronomy</i> , 2019, 9, 466.	3.0	43
2036	Phylogeny of <i>Paullinia</i> L. (Paullinieae: Sapindaceae), a diverse genus of lianas with dynamic fruit evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106577.	2.7	15
2037	Impact of Antibiotic Gut Exposure on the Temporal Changes in Microbiome Diversity. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	35
2038	Altered diversity and composition of the gut microbiome in patients with cervical cancer. <i>AMB Express</i> , 2019, 9, 40.	3.0	55
2039	Changes in cecal microbiota community of suckling piglets infected with porcine epidemic diarrhea virus. <i>PLoS ONE</i> , 2019, 14, e0219868.	2.5	26
2040	Molecular characterization of alterations in the intestinal microbiota of patients with grade 3 hypertension. <i>International Journal of Molecular Medicine</i> , 2019, 44, 513-522.	4.0	30
2041	Effects of different concentrations and types of Cu and Pb on soil N-fixing bacterial communities in the wheat rhizosphere. <i>Applied Soil Ecology</i> , 2019, 144, 51-59.	4.3	29
2042	Stick or leave - Pushing methanogens to biofilm formation for ex situ biomethanation. <i>Bioresource Technology</i> , 2019, 291, 121784.	9.6	33
2043	Cyanobacterial bloom mitigation by sanguinarine and its effects on aquatic microbial community structure. <i>Environmental Pollution</i> , 2019, 253, 497-506.	7.5	13
2044	More than the eye can see: Genomic insights into the drivers of genetic differentiation in Royal/Macaroni penguins across the Southern Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106563.	2.7	21
2045	Crypt- and Mucosa-Associated Core Microbiotas in Humans and Their Alteration in Colon Cancer Patients. <i>MBio</i> , 2019, 10, .	4.1	94

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2047	Novel production of natural bacteriocin via internalization of dextran nanoparticles into probiotics. <i>Biomaterials</i> , 2019, 218, 119360.	11.4	23
2048	Zooming in on Butyrate-Producing Clostridial Consortia in the Fermented Grains of Baijiu via Gene Sequence-Guided Microbial Isolation. <i>Frontiers in Microbiology</i> , 2019, 10, 1397.	3.5	37
2049	Effects of dietary multi-strain probiotics supplementation in a low fishmeal diet on growth performance, nutrient utilization, proximate composition, immune parameters, and gut microbiota of juvenile olive flounder (<i>Paralichthys olivaceus</i>). <i>Fish and Shellfish Immunology</i> , 2019, 93, 258-268.	3.6	58
2050	Dysbiosis of the gut microbiome is associated with CKD5 and correlated with clinical indices of the disease: a caseâ€“controlled study. <i>Journal of Translational Medicine</i> , 2019, 17, 228.	4.4	29
2051	Glutamic acid supplementation reduces body fat weight in finishing pigs when provided solely or in combination with arginine and it is associated with colonic propionate and butyrate concentrations. <i>Food and Function</i> , 2019, 10, 4693-4704.	4.6	28
2052	Detection of low-density <i>Plasmodium falciparum</i> infections using amplicon deep sequencing. <i>Malaria Journal</i> , 2019, 18, 219.	2.3	40
2053	Analysis of the Relationship Between the Degree of Dysbiosis in Gut Microbiota and Prognosis at Different Stages of Primary Hepatocellular Carcinoma. <i>Frontiers in Microbiology</i> , 2019, 10, 1458.	3.5	78
2054	Multiple Maize Reference Genomes Impact the Identification of Variants by Genomeâ€“Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	2.8	37
2055	Nitrogen application increases soil respiration but decreases temperature sensitivity: Combined effects of crop and soil properties in a semiarid agroecosystem. <i>Geoderma</i> , 2019, 353, 320-330.	5.1	19
2056	Acidobacteria Subgroups and Their Metabolic Potential for Carbon Degradation in Sugarcane Soil Amended With Vinasse and Nitrogen Fertilizers. <i>Frontiers in Microbiology</i> , 2019, 10, 1680.	3.5	61
2057	Comparing the Microbial Community in Four Stomach of Dairy Cattle, Yellow Cattle and Three Yak Herds in Qinghai-Tibetan Plateau. <i>Frontiers in Microbiology</i> , 2019, 10, 1547.	3.5	67
2058	In vivo evaluation of the effect of arsenite on the intestinal epithelium and associated microbiota in mice. <i>Archives of Toxicology</i> , 2019, 93, 2127-2139.	4.2	21
2059	Metagenomics and transcriptomics data from human colorectal cancer. <i>Scientific Data</i> , 2019, 6, 116.	5.3	7
2060	Petunia- and Arabidopsis-Specific Root Microbiota Responses to Phosphate Supplementation. <i>Phytobiomes Journal</i> , 2019, 3, 112-124.	2.7	37
2061	Contrasting Winter Versus Summer Microbial Communities and Metabolic Functions in a Permafrost Thaw Lake. <i>Frontiers in Microbiology</i> , 2019, 10, 1656.	3.5	65
2062	Variation in rhizosphere microbiota correlates with edaphic factor in an abandoned antimony tailing dump. <i>Environmental Pollution</i> , 2019, 253, 141-151.	7.5	56
2063	Bacterial community composition in aquatic and sediment samples with spatiotemporal dynamics in large, shallow, eutrophic Lake Chaohu, China. <i>Journal of Freshwater Ecology</i> , 2019, 34, 575-589.	1.2	32

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2065	Association between the cervicovaginal microbiome, BRCA1 mutation status, and risk of ovarian cancer: a case-control study. <i>Lancet Oncology</i> , The, 2019, 20, 1171-1182.	10.7	108
2066	Bacterial Communities and Virulence Associated with Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> from Different <i>Pinus</i> spp.. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3342.	4.1	17
2067	Polyhydroxyalkanoates production from methane emissions in <i>Sphagnum</i> mosses: Assessing the effect of temperature and phosphorus limitation. <i>Science of the Total Environment</i> , 2019, 688, 684-690.	8.0	15
2068	Cultivation of a versatile manganese-oxidizing aerobic granular sludge for removal of organic micropollutants from wastewater. <i>Science of the Total Environment</i> , 2019, 690, 417-425.	8.0	16
2069	Spatial heterogeneity of the planktonic protistan community in a semi-closed eutrophic bay, China. <i>Journal of Plankton Research</i> , 2019, 41, 223-239.	1.8	7
2070	Effects of mixing <i>Neolamarckia cadamba</i> leaves on fermentation quality, microbial community of high moisture alfalfa and stylo silage. <i>Microbial Biotechnology</i> , 2019, 12, 869-878.	4.2	35
2071	Biological treatment of DMSO-containing wastewater from semiconductor industry under aerobic and methanogenic conditions. <i>Chemosphere</i> , 2019, 236, 124291.	8.2	13
2072	Gut Microbiota Differs Between Parkinson's Disease Patients and Healthy Controls in Northeast China. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 171.	2.9	100
2073	Gut microbiome and serum metabolome analyses identify molecular biomarkers and altered glutamate metabolism in fibromyalgia. <i>EBioMedicine</i> , 2019, 46, 499-511.	6.1	128
2074	Response of fungal communities in different soils to biochar and chemical fertilizers under simulated rainfall conditions. <i>Science of the Total Environment</i> , 2019, 691, 654-663.	8.0	32
2075	Sulfonate-based networks between eukaryotic phytoplankton and heterotrophic bacteria in the surface ocean. <i>Nature Microbiology</i> , 2019, 4, 1706-1715.	13.3	120
2076	Development and evolution of age-dependent defenses in ant-acacias. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15596-15601.	7.1	34
2077	Cyanobacterial diversity in mat sample obtained from hypersaline desert, Rann of Kachchh. <i>3 Biotech</i> , 2019, 9, 304.	2.2	8
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2079	Photovoltaic electrolysis improves nitrogen and phosphorus removals of biochar-amended constructed wetlands. <i>Ecological Engineering</i> , 2019, 138, 71-78.	3.6	20
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2370	Microbial biofilm formation and community structure on low-density polyethylene microparticles in lake water microcosms. <i>Environmental Pollution</i> , 2019, 252, 94-102.	7.5	126

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2372	A systematic approach re-analyzing the effects of temperature disturbance on the microbial community of mesophilic anaerobic digestion. <i>Scientific Reports</i> , 2019, 9, 6560.	3.3	13
2373	Concurrent and long-term associations between the endometrial microbiota and endometrial transcriptome in postpartum dairy cows. <i>BMC Genomics</i> , 2019, 20, 405.	2.8	13
2374	Age-based dynamic changes of phylogenetic composition and interaction networks of health pig gut microbiome feeding in a uniformed condition. <i>BMC Veterinary Research</i> , 2019, 15, 172.	1.9	74
2375	Effect of intestinal tapeworms on the gut microbiota of the common carp, <i>Cyprinus carpio</i> . <i>Parasites and Vectors</i> , 2019, 12, 252.	2.5	22
2376	Tracing the history of LINE and SINE extinction in sigmodontine rodents. <i>Mobile DNA</i> , 2019, 10, 22.	3.6	17
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2378	Comparison of Bacterial Populations in the Ceca of Swine at Two Different Stages and Their Functional Annotations. <i>Genes</i> , 2019, 10, 382.	2.4	13
2379	Changes in the Soil Bacterial Community in a Chronosequence of Temperate Walnut-Based Intercropping Systems. <i>Forests</i> , 2019, 10, 299.	2.1	22
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2381	Soil microbiome mediates positive plant diversity-productivity relationships in late successional grassland species. <i>Ecology Letters</i> , 2019, 22, 1221-1232.	6.4	54
2382	Sediment pH, not the bacterial diversity, determines <i>Escherichia coli</i> O157:H7 survival in estuarine sediments. <i>Environmental Pollution</i> , 2019, 252, 1078-1086.	7.5	15
2383	Compositional and Functional Analysis of the Microbiome in Tissue and Saliva of Oral Squamous Cell Carcinoma. <i>Frontiers in Microbiology</i> , 2019, 10, 1439.	3.5	50
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2385	Sludge bio-drying followed by land application could control the spread of antibiotic resistance genes. <i>Environment International</i> , 2019, 130, 104906.	10.0	26
2386	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019, 4, 1826-1831.	13.3	149
2387	Farm-like indoor microbiota in non-farm homes protects children from asthma development. <i>Nature Medicine</i> , 2019, 25, 1089-1095.	30.7	219
2388	Salivary Microbial Dysbiosis is Associated with Systemic Inflammatory Markers and Predicted Oral Metabolites in Non-Small Cell Lung Cancer Patients. <i>Journal of Cancer</i> , 2019, 10, 1651-1662.	2.5	57

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2392	Modulation of Growth Performance and Intestinal Microbiota in Chickens Fed Plant Extracts or Virginiamycin. Frontiers in Microbiology, 2019, 10, 1333.	3.5	47
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2408	Nonferrous metal (loid)s mediate bacterial diversity in an abandoned mine tailing impoundment. <i>Environmental Science and Pollution Research</i> , 2019, 26, 24806-24818.	5.3	7
2409	Changes in endophytic bacterial communities during different growth stages of cucumber (<i>Cucumis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.6	12
2410	High-Quality Library Preparation for NGS-Based Immunoglobulin Germline Gene Inference and Repertoire Expression Analysis. <i>Frontiers in Immunology</i> , 2019, 10, 660.	4.8	55
2411	Marine microplastic-associated bacterial community succession in response to geography, exposure time, and plastic type in China's coastal seawaters. <i>Marine Pollution Bulletin</i> , 2019, 145, 278-286.	5.0	100
2412	The influence of chlorination timing and concentration on microbial communities in labyrinth channels: implications for biofilm removal. <i>Biofouling</i> , 2019, 35, 401-415.	2.2	12
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2414	Parthenogenesis in a captive Asian water dragon (<i>Physignathus cocincinus</i>) identified with novel microsatellites. <i>PLoS ONE</i> , 2019, 14, e0217489.	2.5	11
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2419	Behavior and gut bacteria of <i>Partamona helleri</i> under sublethal exposure to a bioinsecticide and a leaf fertilizer. <i>Chemosphere</i> , 2019, 234, 187-195.	8.2	26
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2426	Probiotic <i>Lactobacillus casei</i> : Effective for Managing Childhood Diarrhea by Altering Gut Microbiota and Attenuating Fecal Inflammatory Markers. <i>Nutrients</i> , 2019, 11, 1150.	4.1	80
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2429	Key extracellular enzymes triggered high-efficiency composting associated with bacterial community succession. <i>Bioresource Technology</i> , 2019, 288, 121576.	9.6	62
2430	Biogeochemical gold cycling selects metal-resistant bacteria that promote gold particle transformation. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	14
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2432	Response of Fish Gut Microbiota to Toxin-Containing Cyanobacterial Extracts: A Microcosm Study on the Medaka (<i>Oryzias latipes</i>). <i>Environmental Science and Technology Letters</i> , 2019, 6, 341-347.	8.7	31
2433	Dietary probiotics have different effects on the composition of fecal microbiota in farmed raccoon dog (<i>Nyctereutes procyonoides</i>) and silver fox (<i>Vulpes vulpes fulva</i>). <i>BMC Microbiology</i> , 2019, 19, 109.	3.3	14
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2435	Metataxonomic analysis of the bacterial diversity in table olive dressing components. <i>Food Control</i> , 2019, 105, 190-197.	5.5	9
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2437	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019, 11, 484.	3.3	27
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2447	Spatial differences in bacterial communities preserved in soils archived for a decade. <i>Applied Soil Ecology</i> , 2019, 142, 64-71.	4.3	3
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2454	Mucosa-Associated Microbiota in Gastric Cancer Tissues Compared With Non-cancer Tissues. <i>Frontiers in Microbiology</i> , 2019, 10, 1261.	3.5	80
2455	Effects of rumen-protected glucose on ileal microbiota and genes involved in ileal epithelial metabolism and immune homeostasis in transition dairy cows. <i>Animal Feed Science and Technology</i> , 2019, 254, 114199.	2.2	14
2456	Oral microbial dysbiosis linked to worsened periodontal condition in rheumatoid arthritis patients. <i>Scientific Reports</i> , 2019, 9, 8379.	3.3	94
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2460	Dynamic Alterations in the Gut Microbiota of Collagen-Induced Arthritis Rats Following the Prolonged Administration of Total Glucosides of <i>Paeyony</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 204.	3.9	44

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2465	Gut dysbiosis and lack of short chain fatty acids in a Chinese cohort of patients with multiple sclerosis. <i>Neurochemistry International</i> , 2019, 129, 104468.	3.8	96
2466	Analysis of marine microbial communities colonizing various metallic materials and rust layers. <i>Biofouling</i> , 2019, 35, 429-442.	2.2	39
2467	Substrate and spatial variables are major determinants of fungal community in karst caves in Southwest China. <i>Journal of Biogeography</i> , 2019, 46, 1504-1518.	3.0	21
2468	IgA-Targeted <i>Lactobacillus jensenii</i> Modulated Gut Barrier and Microbiota in High-Fat Diet-Fed Mice. <i>Frontiers in Microbiology</i> , 2019, 10, 1179.	3.5	22
2469	Isolation of phytase-producing yeasts from rice seedlings for prospective probiotic applications. <i>3 Biotech</i> , 2019, 9, 216.	2.2	8
2470	Effect of different forage-to-concentrate ratios on ruminal bacterial structure and real-time methane production in sheep. <i>PLoS ONE</i> , 2019, 14, e0214777.	2.5	24
2471	Biogeochemistry, microbial activity, and diversity in surface and subsurface deep-sea sediments of South China Sea. <i>Limnology and Oceanography</i> , 2019, 64, 2252-2270.	3.1	33
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2473	The roles of morphological traits, resource variation and resource partitioning associated with the dietary niche expansion in the fish-eating bat <i>Myotis pilosus</i> . <i>Molecular Ecology</i> , 2019, 28, 2944-2954.	3.9	22
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2480	Analysis of the Rumen Microbiota of Beef Calves Supplemented During the Suckling Phase. <i>Frontiers in Microbiology</i> , 2019, 10, 1131.	3.5	15
2481	Genome-wide reconstitution of chromatin transactions reveals that RSC preferentially disrupts H2AZ-containing nucleosomes. <i>Genome Research</i> , 2019, 29, 988-998.	5.5	21
2482	The Variation of Nasal Microbiota Caused by Low Levels of Gaseous Ammonia Exposure in Growing Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 1083.	3.5	19
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2484	Bioturbation of blood clam <i>Tegillarca granosa</i> on benthic nutrient fluxes and microbial community in an aquaculture wastewater treatment system. <i>International Biodeterioration and Biodegradation</i> , 2019, 142, 73-82.	3.9	27
2485	Microbial production and consumption of dissolved organic matter in glacial ecosystems on the Tibetan Plateau. <i>Water Research</i> , 2019, 160, 18-28.	11.3	78
2486	Prediction of pathogenicity genes involved in adaptation to a lupin host in the fungal pathogens <i>Botrytis cinerea</i> and <i>Sclerotinia sclerotiorum</i> via comparative genomics. <i>BMC Genomics</i> , 2019, 20, 385.	2.8	11
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2488	Haem iron reshapes colonic luminal environment: impact on mucosal homeostasis and microbiome through aldehyde formation. <i>Microbiome</i> , 2019, 7, 72.	11.1	38
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2491	Predicting Growth and Carcass Traits in Swine Using Microbiome Data and Machine Learning Algorithms. <i>Scientific Reports</i> , 2019, 9, 6574.	3.3	38
2492	Characterization of 15 nuclear microsatellite markers for <i>Azvelia africana</i> (Fabaceae) and related species. <i>Applications in Plant Sciences</i> , 2019, 7, e01249.	2.1	2
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2494	How do zinc oxide and zero valent iron nanoparticles impact the occurrence of antibiotic resistance genes in landfill leachate?. <i>Environmental Science: Nano</i> , 2019, 6, 2141-2151.	4.3	23
2495	Gut Microbiota Changes in Patients with Bipolar Depression. <i>Advanced Science</i> , 2019, 6, 1900752.	11.2	98
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2498	Longitudinal Analysis of the Human B Cell Response to Ebola Virus Infection. <i>Cell</i> , 2019, 177, 1566-1582.e17.	28.9	153
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2500	Characteristics of the intestinal flora of specific pathogen free chickens with age. <i>Microbial Pathogenesis</i> , 2019, 132, 325-334.	2.9	44
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2503	Microbial assemblages reflect environmental heterogeneity in alpine streams. <i>Global Change Biology</i> , 2019, 25, 2576-2590.	9.5	42
2504	Growth, health, rumen fermentation, and bacterial community of Holstein calves fed <i>Lactobacillus rhamnosus</i> GG during the preweaning stage1. <i>Journal of Animal Science</i> , 2019, 97, 2598-2608.	0.5	30
2505	Gut microbiota of newborn piglets with intrauterine growth restriction have lower diversity and different taxonomic abundances. <i>Journal of Applied Microbiology</i> , 2019, 127, 354-369.	3.1	68
2506	Biogas upgrading with hydrogenotrophic methanogenic biofilms. <i>Bioresource Technology</i> , 2019, 287, 121422.	9.6	33
2507	The effect of temperature during culture enrichment on methanotrophic polyhydroxyalkanoate production. <i>International Biodeterioration and Biodegradation</i> , 2019, 140, 144-151.	3.9	23
2508	Characterization and source-tracking of antibiotic resistomes in the sediments of a peri-urban river. <i>Science of the Total Environment</i> , 2019, 679, 88-96.	8.0	41
2509	Survival of Extremotolerant Bacteria from the Mukundpura Meteorite Impact Crater. <i>Astrobiology</i> , 2019, 19, 785-796.	3.0	6
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2511	Impact of DNA extraction methods on the observed microbial communities from the intestinal flora of the penaeid shrimp <i>Litopenaeus vannamei</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	4
2512	Engineering banana endosphere microbiome to improve <i>Fusarium</i> wilt resistance in banana. <i>Microbiome</i> , 2019, 7, 74.	11.1	70
2513	The diet of red-throated divers (<i>Gavia stellata</i>) overwintering in the German Bight (North Sea) analysed using molecular diagnostics. <i>Marine Biology</i> , 2019, 166, 1.	1.5	17
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2515	Gut microbial diversity increases with social rank in the African cichlid fish, <i>Astatotilapia burtoni</i> . <i>Animal Behaviour</i> , 2019, 152, 79-91.	1.9	7
2516	Linking microbial community structure to carbon substrate chemistry in soils following aboveground and belowground litter additions. <i>Applied Soil Ecology</i> , 2019, 141, 18-25.	4.3	21
2517	Iron Corrosion via Direct Metal-Microbe Electron Transfer. <i>MBio</i> , 2019, 10, .	4.1	107
2518	Whole-Genome Sequence of <i>Acinetobacter baumannii</i> HUMV-3743, Isolated from a Human Wound Exudate. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
2519	Pakchoi Antioxidant Improvement and Differential Rhizobacterial Community Composition under Organic Fertilization. <i>Sustainability</i> , 2019, 11, 2424.	3.2	4
2520	Green manures of Indian mustard and wild rocket enhance cucumber resistance to <i>Fusarium</i> wilt through modulating rhizosphere bacterial community composition. <i>Plant and Soil</i> , 2019, 441, 283-300.	3.7	26
2521	Kappa chain maturation helps drive rapid development of an infant HIV-1 broadly neutralizing antibody lineage. <i>Nature Communications</i> , 2019, 10, 2190.	12.8	31
2522	Assessment of rumen bacteria in dairy cows with varied milk protein yield. <i>Journal of Dairy Science</i> , 2019, 102, 5031-5041.	3.4	59
2523	Characterizing Relationship of Microbial Diversity and Metabolite in Sichuan Xiaoqu. <i>Frontiers in Microbiology</i> , 2019, 10, 696.	3.5	57
2524	Inulin Can Alleviate Metabolism Disorders in <i>ob/ob</i> Mice by Partially Restoring Leptin-related Pathways Mediated by Gut Microbiota. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 64-75.	6.9	134
2525	Gut microbiome-derived phenyl sulfate contributes to albuminuria in diabetic kidney disease. <i>Nature Communications</i> , 2019, 10, 1835.	12.8	173
2526	Characterizing pre-transplant and post-transplant kidney rejection risk by B cell immune repertoire sequencing. <i>Nature Communications</i> , 2019, 10, 1906.	12.8	38
2527	Antibesity Effects of <i>Lactobacillus plantarum</i> LMT1-48 Accompanied by Inhibition of <i>Enterobacter cloacae</i> in the Intestine of Diet-Induced Obese Mice. <i>Journal of Medicinal Food</i> , 2019, 22, 560-566.	1.5	27
2528	Complete Genome Sequence of an <i>Ehrlichia minasensis</i> Strain Isolated from Cattle. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	11
2529	Plant Stage, Not Drought Stress, Determines the Effect of Cultivars on Bacterial Community Diversity in the Rhizosphere of Broomcorn Millet (<i>Panicum miliaceum</i> L.). <i>Frontiers in Microbiology</i> , 2019, 10, 828.	3.5	31
2530	Regional and Microenvironmental Scale Characterization of the <i>Zostera muelleri</i> Seagrass Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 1011.	3.5	53
2531	Supplementation with compound polysaccharides contributes to the development and metabolic activity of young rat intestinal microbiota. <i>Food and Function</i> , 2019, 10, 2658-2675.	4.6	28
2532	Why the cFos/cJun complex is extremely conserved: An in vitro evolution exploration by combining cDNA display and proximity ligation. <i>FEBS Letters</i> , 2019, 593, 1040-1049.	2.8	0

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2534	The combined effect of ozone treatment and polyethylene packaging on postharvest quality and biodiversity of <i>Toona sinensis</i> (A.Juss.) M.Roem. Postharvest Biology and Technology, 2019, 154, 1-10.	6.0	30
2535	Long-term N fertilization altered ¹³ C-labeled fungal community composition but not diversity in wheat rhizosphere of Chinese black soil. Soil Biology and Biochemistry, 2019, 135, 117-126.	8.8	21
2536	Thermal disruption of soil bacterial assemblages decreases diversity and assemblage similarity. Ecosphere, 2019, 10, e02598.	2.2	2
2537	Do different livestock dwellings on single grassland share similar faecal microbial communities?. Applied Microbiology and Biotechnology, 2019, 103, 5023-5037.	3.6	4
2538	Cultivated rice rhizomicrobiome is more sensitive to environmental shifts than that of wild rice in natural environments. Applied Soil Ecology, 2019, 140, 68-77.	4.3	17
2539	Data on microbial community composition of sludge from high altitude wastewater treatment plants determined by 16S rRNA gene sequencing. Data in Brief, 2019, 23, 103739.	1.0	10
2540	Estimate of the diversity of viral and bacterial assemblage in the coastal water of Lake Baikal. FEMS Microbiology Letters, 2019, 366, .	1.8	13
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2542	Diversity and Succession of Microbiota during Fermentation of the Traditional Indian Food Idli. Applied and Environmental Microbiology, 2019, 85, .	3.1	25
2543	MHC structuring and divergent allele advantage in a urodele amphibian: a hierarchical multi-scale approach. Heredity, 2019, 123, 593-607.	2.6	7
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2545	Decolorization and detoxification of Direct Blue 2B by indigenous bacterial consortium. Journal of Environmental Management, 2019, 242, 229-237.	7.8	57
2546	Alteration of microbial community for improving flavor character of Daqu by inoculation with <i>Bacillus velezensis</i> and <i>Bacillus subtilis</i> . LWT - Food Science and Technology, 2019, 111, 1-8.	5.2	83
2547	The invasive tree staghorn sumac affects soil N ² fixing bacterial communities in north China. Plant Biology, 2019, 21, 951-960.	3.8	13
2548	Berberine Influences Blood Glucose via Modulating the Gut Microbiome in Grass Carp. Frontiers in Microbiology, 2019, 10, 1066.	3.5	49
2549	Endophytic Mycobiota of Jingbai Pear Trees in North China. Forests, 2019, 10, 260.	2.1	9
2550	Epiphytic bacterial community composition on the surface of the submerged macrophyte <i>Myriophyllum spicatum</i> in a low-salinity sea area of Hangzhou Bay. Oceanological and Hydrobiological Studies, 2019, 48, 43-55.	0.7	5

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2553	Heterotrophic Bacteria Dominate the Diazotrophic Community in the Eastern Indian Ocean (EIO) during Pre-Southwest Monsoon. Microbial Ecology, 2019, 78, 804-819.	2.8	41
2554	Reshaping the rhizosphere microbiome by bio-organic amendment to enhance crop yield in a maize-cabbage rotation system. Applied Soil Ecology, 2019, 142, 136-146.	4.3	76
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2563	Diagnosing and tracing the pathogens of infantile infectious diarrhea by amplicon sequencing. Gut Pathogens, 2019, 11, 12.	3.4	7
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2567	Different gut microbiome composition in obese Guizhou minipigs between female and castrated male. Folia Microbiologica, 2019, 64, 889-898.	2.3	4
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2570	Correlation of Gut Microbiome Between ASD Children and Mothers and Potential Biomarkers for Risk Assessment. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 26-38.	6.9	72
2571	Shedding Light on a Secretive Tertiary Urodelean Relict: Hynobiid Salamanders (<i>Paradactylodon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 Genes, 2019, 10, 306.	2.4	4
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2573	The Association Between the Developing Nasal Microbiota of Hospitalized Neonates and <i>Staphylococcus aureus</i> Colonization. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz062.	0.9	12
2574	Bacterial composition of biofilms formed on dairy-processing equipment. <i>Preparative Biochemistry and Biotechnology</i> , 2019, 49, 477-484.	1.9	10
2575	Characterization of gut microbiota composition and functions in patients with chronic alcohol overconsumption. <i>Gut Microbes</i> , 2019, 10, 663-675.	9.8	118
2576	Rare Plankton Subcommunities Are Far More Affected by DNA Extraction Kits Than Abundant Plankton. <i>Frontiers in Microbiology</i> , 2019, 10, 454.	3.5	24
2577	Growth of <i>Salmonella enterica</i> Serovars Typhimurium and Enteritidis in Iron-Poor Media and in Meat: Role of Catecholate and Hydroxamate Siderophore Transporters. <i>Journal of Food Protection</i> , 2019, 82, 548-560.	1.7	8
2578	An Allosteric Network for Spliceosome Activation Revealed by High-Throughput Suppressor Analysis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 212, 111-124.	2.9	3
2579	Restoration of Long-Term Monoculture Degraded Tea Orchard by Green and Goat Manures Applications System. <i>Sustainability</i> , 2019, 11, 1011.	3.2	16
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2582	Extensive allopolyploidy in the neotropical genus <i>Lachemilla</i> (Rosaceae) revealed by <i>PCR</i> -based target enrichment of the nuclear ribosomal <i>DNA</i> cistron and plastid phylogenomics. <i>American Journal of Botany</i> , 2019, 106, 415-437.	1.7	14
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2584	Vaginal Glycogen, Not Estradiol, Is Associated With Vaginal Bacterial Community Composition in Black Adolescent Women. <i>Journal of Adolescent Health</i> , 2019, 65, 130-138.	2.5	16
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2593	Conjunctival microbiome changes associated with fungal keratitis: metagenomic analysis. International Journal of Ophthalmology, 2019, 12, 194-200.	1.1	38
2594	Title is missing!. Turkish Journal of Fisheries and Aquatic Sciences, 2019, 19, .	0.9	9
2595	Bacterial and eukaryote microbiomes of mosquito habitats in dengue-endemic southern Taiwan. Journal of Asia-Pacific Entomology, 2019, 22, 471-480.	0.9	9
2596	<i>In vitro</i> and <i>in vivo</i> evaluation of an exopolysaccharide produced by <i>Lactobacillus helveticus</i> KLD51.8701 for the alleviative effect on oxidative stress. Food and Function, 2019, 10, 1707-1717.	4.6	34
2597	Modulation of the intestinal microbiota of dogs by kefir as a functional dairy product. Journal of Dairy Science, 2019, 102, 3903-3911.	3.4	31
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2606	Application of next generation sequencing for species identification in meat and poultry products: A DNA metabarcoding approach. <i>Food Control</i> , 2019, 101, 173-179.	5.5	46
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2613	Study of gut bacterial diversity of <i>Bombyx mandarina</i> and <i>Bombyx mori</i> through 16S rRNA gene sequencing. <i>Journal of Asia-Pacific Entomology</i> , 2019, 22, 522-530.	0.9	10
2614	Profiling the Clostridia with butyrate-producing potential in the mud of Chinese liquor fermentation cellar. <i>International Journal of Food Microbiology</i> , 2019, 297, 41-50.	4.7	79
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2616	Tick Genomes' organ engagement in lipid metabolism revealed by a combined transcriptomic and proteomic approach. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 787-797.	2.7	12
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2618	Characterization of the gut microbiota of invasive <i>Agrilus mali</i> Matsumara (Coleoptera: Buprestidae) using high-throughput sequencing: uncovering plant cell-wall degrading bacteria. <i>Scientific Reports</i> , 2019, 9, 4923.	3.3	29
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2622	The Perturbation of Infant Gut Microbiota Caused by Cesarean Delivery Is Partially Restored by Exclusive Breastfeeding. <i>Frontiers in Microbiology</i> , 2019, 10, 598.	3.5	65

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2624	Microbial groups and their functions control the decomposition of coniferous litter: A comparison with broadleaved tree litters. <i>Soil Biology and Biochemistry</i> , 2019, 133, 196-207.	8.8	55
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2626	Effect of green tea and mulberry leaf powders on the gut microbiota of chicken. <i>BMC Veterinary Research</i> , 2019, 15, 77.	1.9	29
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2628	Fe(III) reduction and vivianite formation in activated sludge. <i>Separation and Purification Technology</i> , 2019, 220, 126-135.	7.9	47
2629	Microbial Engraftment and Efficacy of Fecal Microbiota Transplant for <i>Clostridium Difficile</i> in Patients With and Without Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 969-979.	1.9	38
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2631	Microbial composition changes on the surface of strawberries from the field and market by 16SrDNA sequencing. <i>Journal of Food Safety</i> , 2019, 39, e12630.	2.3	4
2632	Bioremediation of dibutyl phthalate in a simulated agricultural ecosystem by <i>Gordonia</i> sp. strain QH-11 and the microbial ecological effects in soil. <i>Science of the Total Environment</i> , 2019, 667, 691-700.	8.0	54
2633	Anaerobic Process for Bioenergy Recovery From Dairy Waste: Meta-Analysis and Enumeration of Microbial Community Related to Intermediates Production. <i>Frontiers in Microbiology</i> , 2018, 9, 3229.	3.5	42
2634	Functional Genes and Bacterial Communities During Organohalide Respiration of Chloroethenes in Microcosms of Multi-Contaminated Groundwater. <i>Frontiers in Microbiology</i> , 2019, 10, 89.	3.5	21
2635	A cascade of a denitrification bioreactor and an aerobic biofilm reactor for heavy oil refinery wastewater treatment. <i>RSC Advances</i> , 2019, 9, 7495-7504.	3.6	11
2636	Evolution of the HIV-1 Rev Response Element during Natural Infection Reveals Nucleotide Changes That Correlate with Altered Structure and Increased Activity over Time. <i>Journal of Virology</i> , 2019, 93, .	3.4	14
2637	Whole-Genome Sequencing of <i>Legionella jordanis</i> Strains NML 060502 and NML 130005, Recovered from a Lower Respiratory Tract Infection and Water, Respectively. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
2638	A census-based estimate of Earth's bacterial and archaeal diversity. <i>PLoS Biology</i> , 2019, 17, e3000106.	5.6	139
2639	Nitrogen- and phosphorus-starved <i>Triticum aestivum</i> show distinct belowground microbiome profiles. <i>PLoS ONE</i> , 2019, 14, e0210538.	2.5	26
2640	The nasal and oropharyngeal microbiomes of healthy livestock workers. <i>PLoS ONE</i> , 2019, 14, e0212949.	2.5	18

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2641	Succession of Composition and Function of Soil Bacterial Communities During Key Rice Growth Stages. <i>Frontiers in Microbiology</i> , 2019, 10, 421.	3.5	36
2642	Rotations with Indian Mustard and Wild Rocket Suppressed Cucumber Fusarium Wilt Disease and Changed Rhizosphere Bacterial Communities. <i>Microorganisms</i> , 2019, 7, 57.	3.6	22
2643	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. <i>MSphere</i> , 2019, 4, .	2.9	14
2645	Disordered intestinal microbes are associated with the activity of Systemic Lupus Erythematosus. <i>Clinical Science</i> , 2019, 133, 821-838.	4.3	119
2646	Solid-state fermented Chinese alcoholic beverage (baijiu) and ethanol resulted in distinct metabolic and microbiome responses. <i>FASEB Journal</i> , 2019, 33, 7274-7288.	0.5	20
2647	Bacterial community in cold and alkaline environments of Hoh Xil basin in Qinghaiâ€‘Tibet Plateau and isolation of potential sources of microbiota. <i>Annals of Microbiology</i> , 2019, 69, 567-576.	2.6	8
2648	Analysis of rhizosphere bacterial and fungal communities associated with rusty root disease of <i>Panax ginseng</i> . <i>Applied Soil Ecology</i> , 2019, 138, 245-252.	4.3	31
2649	Spatial Heterogeneity of <i>Vibrio</i> spp. in Sediments of Chinese Marginal Seas. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	18
2650	Microbiome diversity in carriers of fluoroquinolone resistant <i>Escherichia coli</i> . <i>Investigative and Clinical Urology</i> , 2019, 60, 75.	2.0	3
2651	Authentication and Assessment of Contamination in Ancient DNA. <i>Methods in Molecular Biology</i> , 2019, 1963, 163-194.	0.9	23
2652	Divergent responses of bacterial activity, structure, and co-occurrence patterns to long-term unbalanced fertilization without nitrogen, phosphorus, or potassium in a cultivated vertisol. <i>Environmental Science and Pollution Research</i> , 2019, 26, 12741-12754.	5.3	19
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2654	Temperate airborne grass pollen defined by spatio-temporal shifts in community composition. <i>Nature Ecology and Evolution</i> , 2019, 3, 750-754.	7.8	75
2655	Mass coral bleaching of <i>P. versipora</i> in Sydney Harbour driven by the 2015â€‘2016 heatwave. <i>Coral Reefs</i> , 2019, 38, 815-830.	2.2	20
2656	Rhizosphere microbiota compositional changes reflect potato blackleg disease. <i>Applied Soil Ecology</i> , 2019, 140, 11-17.	4.3	9
2657	Unveiling hÃ¡karl: A study of the microbiota of the traditional Icelandic fermented fish. <i>Food Microbiology</i> , 2019, 82, 560-572.	4.2	41
2658	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , 2019, 364, .	12.6	576
2659	Alteration of vaginal microbiota in patients with unexplained recurrent miscarriage. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 3307-3316.	1.8	25

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2660	Environmental factors promote pathogen-induced skin ulceration syndrome outbreak by readjusting the hindgut microbiome of <i>Apostichopus japonicus</i> . <i>Aquaculture</i> , 2019, 507, 155-163.	3.5	28
2661	<i>ε</i> -APOE genotype influences the gut microbiome structure and function in humans and mice: relevance for Alzheimer's disease pathophysiology. <i>FASEB Journal</i> , 2019, 33, 8221-8231.	0.5	124
2662	Effects of a gut microbiota transfer on emotional reactivity in Japanese quails (<i>Coturnix</i>). <i>Journal of Applied Microbiology</i> , 2019, 127, 1506-1515.	1.7	15
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2803	Metagenomic insights into the structure and function of intestinal microbiota of the farmed Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2019, 499, 109-118.	3.5	69

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2804	Plant growth promoting bacteria increases biomass, effective constituent, and modifies rhizosphere bacterial communities of <i>Panax ginseng</i> . <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 2019, 69, 135-146.	0.6	4
2805	Submicron magnetite-enhanced tribromophenol removal and methanogenesis under microaerobic condition. <i>Journal of Chemical Technology and Biotechnology</i> , 2019, 94, 730-738.	3.2	7
2806	Evaluation of the bacterial diversity of Spanish-type chorizo during the ripening process using high-throughput sequencing and physicochemical characterization. <i>Meat Science</i> , 2019, 150, 7-13.	5.5	46
2807	Turning pig manure into biochar can effectively mitigate antibiotic resistance genes as organic fertilizer. <i>Science of the Total Environment</i> , 2019, 649, 902-908.	8.0	83
2808	Seed mucilage interacts with soil microbial community and physiochemical processes to affect seedling emergence on desert sand dunes. <i>Plant, Cell and Environment</i> , 2019, 42, 591-605.	5.7	18
2809	Karst rocky desertification progress: Soil calcium as a possible driving force. <i>Science of the Total Environment</i> , 2019, 649, 1250-1259.	8.0	72
2810	Impacts of Mo application on biological nitrogen fixation and diazotrophic communities in a flooded rice-soil system. <i>Science of the Total Environment</i> , 2019, 649, 686-694.	8.0	49
2811	Tree Diversity Determines the Diversity of the Taxonomic and Functional Structure of the Fungal Community in Forest Litter in Southern China. <i>Forest Science</i> , 2019, 65, 40-47.	1.0	2
2812	Characterization of the vaginal microbiome during cytolytic vaginosis using high-throughput sequencing. <i>Journal of Clinical Laboratory Analysis</i> , 2019, 33, e22653.	2.1	17
2813	Genomic insights into <i>Candidatus Amarolinea aalborgensis</i> gen. nov., sp. nov., associated with settleability problems in wastewater treatment plants. <i>Systematic and Applied Microbiology</i> , 2019, 42, 77-84.	2.8	58
2814	Effects of dietary lysozyme levels on growth performance, intestinal morphology, immunity response and microbiota community of growing pigs. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 1643-1650.	3.5	34
2815	Changes of microbial community and metabolite in kimchi inoculated with different microbial community starters. <i>Food Chemistry</i> , 2019, 274, 558-565.	8.2	58
2816	Dysbiosis of the gut microbiome is associated with thyroid cancer and thyroid nodules and correlated with clinical index of thyroid function. <i>Endocrine</i> , 2019, 64, 564-574.	2.3	78
2817	<i>Thiothrix eikelboomii</i> interferes oxygen transfer in activated sludge. <i>Water Research</i> , 2019, 151, 134-143.	11.3	63
2818	Effects of <i>Saccharomyces Cerevisiae</i> Fermentation Products on the Microbial Community throughout the Gastrointestinal Tract of Calves. <i>Animals</i> , 2019, 9, 4.	2.3	9
2819	Comparison of the gut microbiota of obese individuals from different geographic origins. <i>New Microbes and New Infections</i> , 2019, 27, 40-47.	1.6	12
2820	Multiple forms of selection shape reproductive isolation in a primate hybrid zone. <i>Molecular Ecology</i> , 2019, 28, 1056-1069.	3.9	24
2821	Addition of algicidal bacterium CZBC1 and molasses to inhibit cyanobacteria and improve microbial communities, water quality and shrimp performance in culture systems. <i>Aquaculture</i> , 2019, 502, 303-311.	3.5	24

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2823	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. Nucleic Acids Research, 2019, 47, D637-D648.	14.5	70
2824	The Influence of Bt Maize Cultivation on Communities of Arbuscular Mycorrhizal Fungi Revealed by MiSeq Sequencing. Frontiers in Microbiology, 2018, 9, 3275.	3.5	15
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2826	Large-scale mapping of microbial diversity in artisanal Brazilian cheeses. Food Microbiology, 2019, 80, 40-49.	4.2	83
2827	Spruce and beech as local determinants of forest fungal community structure in litter, humus and mineral soil. FEMS Microbiology Ecology, 2019, 95, .	2.7	24
2828	Microbial communities in swine lungs and their association with lung lesions. Microbial Biotechnology, 2019, 12, 289-304.	4.2	24
2829	Diet composition and gut microbiome of 0-group European plaice <i>Pleuronectes platessa</i> L. - Strong homogeneity and subtle spatial and temporal differences. Journal of Sea Research, 2019, 144, 67-77.	1.6	4
2830	Rhizosphere fungal community structure succession of Xinjiang continuously cropped cotton. Fungal Biology, 2019, 123, 42-50.	2.5	7
2831	Biodiversity and dynamics of cyanobacterial communities during blooms in temperate lake (Harsha) Tj ETQq1 1 0.784314 rgBT /Overl	4.8	15
2832	Microtopographic differences in soil properties and microbial community composition at the field scale. Soil Biology and Biochemistry, 2019, 131, 71-80.	8.8	32
2833	Biofilter scaling procedures for organics removal: A potential alternative to piloting. Water Research, 2019, 151, 87-97.	11.3	13
2834	Biodiversity of the microbiota in <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae). Journal of Applied Microbiology, 2019, 126, 1199-1208.	3.1	35
2835	Compound polysaccharides ameliorate experimental colitis by modulating gut microbiota composition and function. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 1554-1562.	2.8	46
2836	Research on the hydrolysis of human urine using biological activated carbon and its application in bioregenerative life support system. Acta Astronautica, 2019, 155, 191-199.	3.2	4
2837	Effect of in situ sediment remediation combining oyster shells and bottom microporous aeration on nitrogen removal and microbiota. Aquaculture Research, 2019, 50, 331-341.	1.8	7
2838	Fertilisation practice changes rhizosphere microbial community structure in the agroecosystem. Annals of Applied Biology, 2019, 174, 123-132.	2.5	16
2839	Competition among Nasal Bacteria Suggests a Role for Siderophore-Mediated Interactions in Shaping the Human Nasal Microbiota. Applied and Environmental Microbiology, 2019, 85, .	3.1	57

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2841	Lateral variations and vertical structure of the microbial methane cycle in the sediment of Lake Onego (Russia). <i>Inland Waters</i> , 2019, 9, 205-226.	2.2	8
2842	Geochemistry Shapes Bacterial Communities and their Metabolic Potentials in Tertiary Coalbed. <i>Geomicrobiology Journal</i> , 2019, 36, 179-187.	2.0	14
2843	Genomic insights into the metabolism of <i>Candidatus</i> <i>Defluviicoccus seivourii</i> ™, a member of <i>Defluviicoccus</i> cluster III abundant in industrial activated sludge. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	17
2844	Diazotrophic microbial community and abundance in acidic subtropical natural and re-vegetated forest soils revealed by high-throughput sequencing of nifH gene. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 995-1005.	3.6	35
2845	Additional reduction of antibiotic resistance genes and human bacterial pathogens via thermophilic aerobic digestion of anaerobically digested sludge. <i>Bioresource Technology</i> , 2019, 273, 259-268.	9.6	33
2846	<i>Spartina alterniflora</i> invasion alters soil bacterial communities and enhances soil N ₂ O emissions by stimulating soil denitrification in mangrove wetland. <i>Science of the Total Environment</i> , 2019, 653, 231-240.	8.0	126
2847	Environmental and spatial variables determine the taxonomic but not functional structure patterns of microbial communities in alpine grasslands. <i>Science of the Total Environment</i> , 2019, 654, 960-968.	8.0	11
2848	Chikungunya Virus Fidelity Variants Exhibit Differential Attenuation and Population Diversity in Cell Culture and Adult Mice. <i>Journal of Virology</i> , 2019, 93, .	3.4	22
2849	Cooperation of lactic acid bacteria regulated by the AI-2/LuxS system involve in the biopreservation of refrigerated shrimp. <i>Food Research International</i> , 2019, 120, 679-687.	6.2	36
2850	Response of freshwater sediment archaeal community to metal spill. <i>Chemosphere</i> , 2019, 217, 584-590.	8.2	26
2851	Revegetated shrub species recruit different soil fungal assemblages in a desert ecosystem. <i>Plant and Soil</i> , 2019, 435, 81-93.	3.7	7
2852	Effects of the biological nitrification inhibitor 1,9-decanediol on nitrification and ammonia oxidizers in three agricultural soils. <i>Soil Biology and Biochemistry</i> , 2019, 129, 48-59.	8.8	61
2853	Experimental Evaluation of Coevolution in a Self-Assembling Particle. <i>Biochemistry</i> , 2019, 58, 1527-1538.	2.5	19
2854	Construction and next-generation sequencing analysis of a large phage-displayed VNAR single-domain antibody library from six naïve nurse sharks. <i>Antibody Therapeutics</i> , 2019, 2, 1-11.	1.9	53
2855	An Improved Genome Assembly for <i>Drosophila navojoa</i> , the Basal Species in the <i>mojavensis</i> Cluster. <i>Journal of Heredity</i> , 2019, 110, 118-123.	2.4	7
2856	Elevational patterns and hierarchical determinants of biodiversity across microbial taxonomic scales. <i>Molecular Ecology</i> , 2019, 28, 86-99.	3.9	34
2857	Selective colonization ability of human fecal microbes in different mouse gut environments. <i>ISME Journal</i> , 2019, 13, 805-823.	9.8	39

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2859	Mixotrophic acidophiles increase cadmium soluble fraction and phytoextraction efficiency from cadmium contaminated soils. <i>Science of the Total Environment</i> , 2019, 655, 347-355.	8.0	30
2860	Gut and Whole-Body Microbiota of the Honey Bee Separate Thriving and Non-thriving Hives. <i>Microbial Ecology</i> , 2019, 78, 195-205.	2.8	39
2861	Genes regulating gland development in the cotton plant. <i>Plant Biotechnology Journal</i> , 2019, 17, 1142-1153.	8.3	42
2862	Altered fecal microbiota composition in the Flinders sensitive line rat model of depression. <i>Psychopharmacology</i> , 2019, 236, 1445-1457.	3.1	44
2863	Comparison of chemical composition and airborne bacterial community structure in PM2.5 during haze and non-haze days in the winter in Guilin, China. <i>Science of the Total Environment</i> , 2019, 655, 202-210.	8.0	60
2864	Targeted panel sequencing in adult patients with left ventricular non-compaction reveals a large genetic heterogeneity. <i>Clinical Genetics</i> , 2019, 95, 356-367.	2.0	56
2865	Evidence for positive selection of hepatitis A virus antigenic variants in vaccinated men-having-sex-with men patients: Implications for immunization policies. <i>EBioMedicine</i> , 2019, 39, 348-357.	6.1	22
2866	SPG-56 from Sweet potato Zhongshu-1 delayed growth of tumor xenografts in nude mice by modulating gut microbiota. <i>Journal of Functional Foods</i> , 2019, 52, 291-301.	3.4	0
2867	Silage fermentation and bacterial community of bur clover, annual ryegrass and their mixtures prepared with microbial inoculant and chemical additive. <i>Animal Feed Science and Technology</i> , 2019, 247, 285-293.	2.2	91
2868	Shelf-life and microbial community dynamics of super-chilled beef imported from Australia to China. <i>Food Research International</i> , 2019, 120, 784-792.	6.2	50
2869	Bacterial communities in prepared foods available at supermarkets in Beijing, China. <i>Food Research International</i> , 2019, 120, 668-678.	6.2	15
2870	Influence of microbial communities on the chemical and sensory features of Falanghina sweet passito wines. <i>Food Research International</i> , 2019, 120, 740-747.	6.2	22
2871	Profiles of bacterial assemblages from microplastics of tropical coastal environments. <i>Science of the Total Environment</i> , 2019, 655, 313-320.	8.0	130
2872	Genotype-free estimation of allele frequencies reduces bias and improves demographic inference from RADSeq data. <i>Molecular Ecology Resources</i> , 2019, 19, 586-596.	4.8	33
2873	Study of bacterial and fungal community structures in traditional koumiss from Inner Mongolia. <i>Journal of Dairy Science</i> , 2019, 102, 1972-1984.	3.4	34
2874	Analysis of the community composition and bacterial diversity of the rhizosphere microbiome across different plant taxa. <i>MicrobiologyOpen</i> , 2019, 8, e00762.	3.0	41
2875	Strain-specific changes in the gut microbiota profiles of the white shrimp <i>Litopenaeus vannamei</i> in response to cold stress. <i>Aquaculture</i> , 2019, 503, 357-366.	3.5	48

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2877	Insight into the correlation between biochar amendment and shifts in bacterial community 4 years after a single incorporation in soybean- and maize-planted soils in northeastern China. <i>Canadian Journal of Microbiology</i> , 2019, 65, 353-364.	1.7	8
2878	Investigating responses of soil bacterial community composition to hardwood biochar amendment using high-throughput PCR sequencing. <i>Applied Soil Ecology</i> , 2019, 136, 80-85.	4.3	33
2879	Aqueous raw and ripe Pu-erh tea extracts alleviate obesity and alter cecal microbiota composition and function in diet-induced obese rats. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1823-1835.	3.6	31
2880	<i>Bacillus amyloliquefaciens</i> B1408 suppresses <i>Fusarium</i> wilt in cucumber by regulating the rhizosphere microbial community. <i>Applied Soil Ecology</i> , 2019, 136, 55-66.	4.3	76
2881	Linking Exoproteome Function and Structure to Anammox Biofilm Development. <i>Environmental Science & Technology</i> , 2019, 53, 1490-1500.	10.0	77
2882	Bacterial communities involved directly or indirectly in the anaerobic degradation of cellulose. <i>Biology and Fertility of Soils</i> , 2019, 55, 201-211.	4.3	52
2883	Bacterial community and metabolome shifts in the cecum and colon of captive sika deer (<i>Cervus</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	11
2884	High-throughput amplicon sequencing demonstrates extensive diversity of xylanase genes in the sediment of soda lake Dabusu. <i>Biotechnology Letters</i> , 2019, 41, 409-418.	2.2	2
2885	Impact of 36 years of nitrogen fertilization on microbial community composition and soil carbon cycling-related enzyme activities in rhizospheres and bulk soils in northeast China. <i>Applied Soil Ecology</i> , 2019, 136, 148-157.	4.3	74
2886	Alleviating effects of walnut green husk extract on disorders of lipid levels and gut bacteria flora in high fat diet-induced obesity rats. <i>Journal of Functional Foods</i> , 2019, 52, 576-586.	3.4	40
2887	Combination of ribosome display and next generation sequencing as a powerful method for identification of affibody binders against β -lactamase CTX-M15. <i>New Biotechnology</i> , 2019, 50, 60-69.	4.4	7
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2889	The Metabolic Response to a Low Amino Acid Diet is Independent of Diet-Induced Shifts in the Composition of the Gut Microbiome. <i>Scientific Reports</i> , 2019, 9, 67.	3.3	16
2890	Soil pH dominates elevational diversity pattern for bacteria in high elevation alkaline soils on the Tibetan Plateau. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	83
2891	Repeated Evolution Versus Common Ancestry: Sex Chromosome Evolution in the Haplochromine Cichlid <i>Pseudocrenilabrus philander</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 439-458.	2.5	26
2892	Plastome-Wide Rearrangements and Gene Losses in Carnivorous Droseraceae. <i>Genome Biology and Evolution</i> , 2019, 11, 472-485.	2.5	40
2893	The microbiomic and environmental analysis of sediments in the Indo-Pacific humpback dolphin (<i>Sousa</i>) Tj ETQq1 1 0.784314 rgBT /Ove 2019, 26, 6957-6970.	5.3	8

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2895	Plastid Genomes and Proteins Illuminate the Evolution of Eustigmatophyte Algae and Their Bacterial Endosymbionts. <i>Genome Biology and Evolution</i> , 2019, 11, 362-379.	2.5	29
2896	A roadmap for high-throughput sequencing studies of wild animal populations using noninvasive samples and hybridization capture. <i>Molecular Ecology Resources</i> , 2019, 19, 609-622.	4.8	24
2897	Modulation of fat metabolism and gut microbiota by resveratrol on high-fat diet-induced obese mice. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 97-107.	2.4	58
2898	Metataxonomic comparison between internal transcribed spacer and 26S ribosomal large subunit (LSU) rDNA gene. <i>International Journal of Food Microbiology</i> , 2019, 290, 132-140.	4.7	46
2899	Characteristics of atmospheric bacterial and fungal communities in PM2.5 following biomass burning disturbance in a rural area of North China Plain. <i>Science of the Total Environment</i> , 2019, 651, 2727-2739.	8.0	71
2900	Changes in the Microbial Community of <i>Pinus arizonica</i> Saplings After Being Colonized by the Bark Beetle <i>Dendroctonus rhizophagus</i> (Curculionidae: Scolytinae). <i>Microbial Ecology</i> , 2019, 78, 102-112.	2.8	12
2901	Phylogenetic imprint of woody plants on the soil mycobiome in natural mountain forests of eastern China. <i>ISME Journal</i> , 2019, 13, 686-697.	9.8	76
2902	The rhizomicrobiomes of wild and cultivated crops react differently to fungicides. <i>Archives of Microbiology</i> , 2019, 201, 477-486.	2.2	13
2903	Rhizosphere responses to environmental conditions in <i>Radix pseudostellariae</i> under continuous monoculture regimes. <i>Agriculture, Ecosystems and Environment</i> , 2019, 270-271, 19-31.	5.3	47
2904	Comparison of long-term ceramic membrane bioreactors without and with in-situ ozonation in wastewater treatment: Membrane fouling, effluent quality and microbial community. <i>Science of the Total Environment</i> , 2019, 652, 788-799.	8.0	47
2905	Dietary shifts influenced by livestock grazing shape the gut microbiota composition and co-occurrence networks in a local rodent species. <i>Journal of Animal Ecology</i> , 2019, 88, 302-314.	2.8	36
2906	Fate of microbial pollutants and evolution of antibiotic resistance in three types of soil amended with swine slurry. <i>Environmental Pollution</i> , 2019, 245, 353-362.	7.5	41
2907	Different responses of absorptive roots and arbuscular mycorrhizal fungi to fertilization provide diverse nutrient acquisition strategies in Chinese fir. <i>Forest Ecology and Management</i> , 2019, 433, 64-72.	3.2	45
2908	Fungi participate in driving home-field advantage of litter decomposition in a subtropical forest. <i>Plant and Soil</i> , 2019, 434, 467-480.	3.7	51
2909	Comparison between kinetics of autochthonous marine bacteria in activated sludge and granular sludge systems at different salinity and SRTs. <i>Water Research</i> , 2019, 148, 425-437.	11.3	76
2910	Effect of dietary L-tryptophan on the survival, immune response and gut microbiota of the Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 1007-1017.	3.6	32
2911	Cumulative effect of yeast extract and fructooligosaccharide supplementation on composition and metabolic activity of elderly colonic microbiota in vitro. <i>Journal of Functional Foods</i> , 2019, 52, 43-53.	3.4	12

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2913	Prokaryotic Diversity and Distribution in Different Habitats of an Alpine Rock Glacier-Pond System. <i>Microbial Ecology</i> , 2019, 78, 70-84.	2.8	12
2914	Transcriptome analysis of grass carp provides insights into disease-related genes and novel regulation pattern of bile acid feedback in response to lithocholic acid. <i>Aquaculture</i> , 2019, 500, 613-621.	3.5	21
2915	Bacterial community changes in a glacial-fed Tibetan lake are correlated with glacial melting. <i>Science of the Total Environment</i> , 2019, 651, 2059-2067.	8.0	21
2916	Altered host-gut microbes symbiosis in severely malnourished anorexia nervosa (AN) patients undergoing enteral nutrition: An explicative factor of functional intestinal disorders?. <i>Clinical Nutrition</i> , 2019, 38, 2304-2310.	5.0	62
2917	Injury, dysbiosis, and filaggrin deficiency drive skin inflammation through keratinocyte IL-1 β release. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1426-1443.e6.	2.9	56
2918	Composition and diversity of endophytic bacterial community in seeds of super hybrid rice "Shenliangyou 5814" (Oryza sativa L.) and its parental lines. <i>Plant Growth Regulation</i> , 2019, 87, 257-266.	3.4	26
2919	Tree species identity surpasses richness in affecting soil microbial richness and community composition in subtropical forests. <i>Soil Biology and Biochemistry</i> , 2019, 130, 113-121.	8.8	111
2920	Cyanate and urea are substrates for nitrification by Thaumarchaeota in the marine environment. <i>Nature Microbiology</i> , 2019, 4, 234-243.	13.3	103
2921	Characterization of Mauritian Cynomolgus Macaque Fc γ 3R Alleles Using Long-Read Sequencing. <i>Journal of Immunology</i> , 2019, 202, 151-159.	0.8	8
2922	Fall webworm genomes yield insights into rapid adaptation of invasive species. <i>Nature Ecology and Evolution</i> , 2019, 3, 105-115.	7.8	82
2923	Fate of antibiotic resistance genes during anaerobic digestion of sewage sludge: Role of solids retention times in different configurations. <i>Bioresource Technology</i> , 2019, 274, 488-495.	9.6	50
2924	Linkages between Epithelial Microbiota and Host Transcriptome in the Ileum during High-Grain Challenges: Implications for Gut Homeostasis in Goats. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 551-561.	5.2	17
2925	The genome of the jellyfish Aurelia and the evolution of animal complexity. <i>Nature Ecology and Evolution</i> , 2019, 3, 96-104.	7.8	86
2926	Soil ameliorants alter physicochemical properties and fungal communities in saline-sodic soils of Northeast China. <i>Archives of Agronomy and Soil Science</i> , 2019, 65, 1147-1159.	2.6	7
2927	Danshen can interact with intestinal bacteria from normal and chronic renal failure rats. <i>Biomedicine and Pharmacotherapy</i> , 2019, 109, 1758-1771.	5.6	22
2928	Resuscitation of anammox bacteria after >10,000 years of dormancy. <i>ISME Journal</i> , 2019, 13, 1098-1109.	9.8	51
2929	Faecal freezing preservation period influences colonization ability for faecal microbiota transplantation. <i>Journal of Applied Microbiology</i> , 2019, 126, 973-984.	3.1	19

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2931	Changes in gut bacterial communities in canaries infected by <i>Macrorhabdus ornithogaster</i> . <i>Avian Pathology</i> , 2019, 48, 111-120.	2.0	10
2932	Endophytic bacterial communities of Jingbai Pear trees in north China analyzed with Illumina sequencing of 16S rDNA. <i>Archives of Microbiology</i> , 2019, 201, 199-208.	2.2	22
2933	Soil aggregate-associated bacterial metabolic activity and community structure in different aged tea plantations. <i>Science of the Total Environment</i> , 2019, 654, 1023-1032.	8.0	76
2934	The correlation of methanogenic communities' dynamics and process performance of anaerobic digestion of thermal hydrolyzed sludge at short hydraulic retention times. <i>Bioresource Technology</i> , 2019, 272, 180-187.	9.6	41
2935	Dibutyl phthalate contamination remodeled the fungal community in agro-environmental system. <i>Chemosphere</i> , 2019, 215, 189-198.	8.2	27
2936	Evolution of intestinal microbiota and body compartments during spontaneous hyperphagia in the Greylag goose. <i>Poultry Science</i> , 2019, 98, 1390-1402.	3.4	6
2937	Structural and functional profiles of the gut microbial community in polycystic ovary syndrome with insulin resistance (IR-PCOS): a pilot study. <i>Research in Microbiology</i> , 2019, 170, 43-52.	2.1	103
2938	Bacterial community variations in paddy soils induced by application of veterinary antibiotics in plant-soil systems. <i>Ecotoxicology and Environmental Safety</i> , 2019, 167, 44-53.	6.0	50
2939	High-production dairy cattle exhibit different rumen and fecal bacterial community and rumen metabolite profile than low-production cattle. <i>MicrobiologyOpen</i> , 2019, 8, e00673.	3.0	38
2940	Long-term application of manure over plant residues mitigates acidification, builds soil organic carbon and shifts prokaryotic diversity in acidic Ultisols. <i>Applied Soil Ecology</i> , 2019, 133, 24-33.	4.3	76
2941	Protective effects of lentinan on lipopolysaccharide induced inflammatory response in intestine of juvenile taimen (<i>Hucho taimen</i> , Pallas). <i>International Journal of Biological Macromolecules</i> , 2019, 121, 317-325.	7.5	35
2942	<i>Vibrio alginolyticus</i> infection induces coupled changes of bacterial community and metabolic phenotype in the gut of swimming crab. <i>Aquaculture</i> , 2019, 499, 251-259.	3.5	42
2943	Genetic drift shaped MHC IIB diversity of an endangered anuran species within the Italian glacial refugium. <i>Journal of Zoology</i> , 2019, 307, 61-70.	1.7	12
2944	Roux-en-Y Gastric-Bypass and sleeve gastrectomy induces specific shifts of the gut microbiota without altering the metabolism of bile acids in the intestinal lumen. <i>International Journal of Obesity</i> , 2019, 43, 428-431.	3.4	19
2945	Detecting host-parasitoid interactions in an invasive Lepidopteran using nested tagging DNA metabarcoding. <i>Molecular Ecology</i> , 2019, 28, 471-483.	3.9	57
2946	Biases from different DNA extraction methods in intestine microbiome research based on 16S rDNA sequencing: a case in the koi carp, <i>Cyprinus carpio</i> var. <i>Koi</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00626.	3.0	13
2947	Effects of redox potential on soil cadmium solubility: Insight into microbial community. <i>Journal of Environmental Sciences</i> , 2019, 75, 224-232.	6.1	87

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2948	Effects of <i>Spartina alterniflora</i> invasion on <i>Kandelia candel</i> rhizospheric bacterial community as determined by high-throughput sequencing analysis. <i>Journal of Soils and Sediments</i> , 2019, 19, 332-344.	3.0	19
2949	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , 2019, 20, 1032-1056.	6.5	10
2950	Annual bacterial community cycle in a seasonally ice-covered river reflects environmental and climatic conditions. <i>Limnology and Oceanography</i> , 2020, 65, S21.	3.1	59
2951	Mucosa-Associated Microbiota in the Gastrointestinal Tract of Healthy Japanese Subjects. <i>Digestion</i> , 2020, 101, 107-120.	2.3	16
2952	Effects of a formula with a probiotic <i>Bifidobacterium lactis</i> Supplement on the gut microbiota of low birth weight infants. <i>European Journal of Nutrition</i> , 2020, 59, 1493-1503.	3.9	20
2953	Variation pattern of antibiotic resistance genes and microbial community succession during swine manure composting under different aeration strategies. <i>Journal of Chemical Technology and Biotechnology</i> , 2020, 95, 466-473.	3.2	26
2954	Biocontrol of Root Diseases and Growth Promotion of the Tuberous Plant <i>Aconitum carmichaelii</i> Induced by Actinomycetes Are Related to Shifts in the Rhizosphere Microbiota. <i>Microbial Ecology</i> , 2020, 79, 134-147.	2.8	30
2955	Prominence of ileal mucosa-associated microbiota to predict postoperative endoscopic recurrence in Crohn's disease. <i>Gut</i> , 2020, 69, 462-472.	12.1	76
2956	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota \pm -Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020, 70, 615-627.	5.8	65
2957	Antibiotic exposure perturbs the bacterial community in the small brown planthopper <i>Laodelphax striatellus</i> . <i>Insect Science</i> , 2020, 27, 895-907.	3.0	28
2958	Fungi participate in the dysbiosis of gut microbiota in patients with primary sclerosing cholangitis. <i>Gut</i> , 2020, 69, 92-102.	12.1	136
2959	Arabinoxylan oligosaccharides and polyunsaturated fatty acid effects on gut microbiota and metabolic markers in overweight individuals with signs of metabolic syndrome: A randomized cross-over trial. <i>Clinical Nutrition</i> , 2020, 39, 67-79.	5.0	68
2960	Effect of super absorbent polymer sodium polyacrylate on the bacterial community and associated chemistry of loessial soil. <i>Archives of Agronomy and Soil Science</i> , 2020, 66, 70-82.	2.6	5
2961	Multi-hydrolytic enzyme accumulation and microbial community structure of anaerobic co-digestion of food waste and waste-activated sludge. <i>Environmental Technology (United Kingdom)</i> , 2020, 41, 478-487.	2.2	10
2962	Microbial Diversity in High-Temperature Heavy Oil Reservoirs. <i>Geomicrobiology Journal</i> , 2020, 37, 59-66.	2.0	9
2963	Seed-Associated Fungal Diversity and the Molecular Identification of <i>Fusarium</i> with Potential Threat to Ginseng (<i>Panax ginseng</i>) in China. <i>Plant Disease</i> , 2020, 104, 330-339.	1.4	7
2964	The effects of artificial light at night on Eurasian tree sparrow (<i>Passer montanus</i>): Behavioral rhythm disruption, melatonin suppression and intestinal microbiota alterations. <i>Ecological Indicators</i> , 2020, 108, 105702.	6.3	28
2965	The diversity and biogeography of microeukaryotes in the euphotic zone of the northwestern Pacific Ocean. <i>Science of the Total Environment</i> , 2020, 698, 134289.	8.0	34

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2967	Isolation of virulent phages infecting dominant mesophilic aerobic bacteria in cucumber pickle fermentation. <i>Food Microbiology</i> , 2020, 86, 103330.	4.2	29
2968	Biostimulation of sewage sludge solubilization and methanization by hyper-thermophilic pre-hydrolysis stage and the shifts of microbial structure profiles. <i>Science of the Total Environment</i> , 2020, 699, 134373.	8.0	10
2969	Analysis of endophytic bacterial community diversity and metabolic correlation in <i>Cinnamomum camphora</i> . <i>Archives of Microbiology</i> , 2020, 202, 181-189.	2.2	13
2970	Carboxymethyl chitosan perturbs inflammation profile and colonic microbiota balance in mice. <i>Journal of Food and Drug Analysis</i> , 2020, 28, 175-182.	1.9	11
2971	Effects of multi-year biofumigation on soil bacterial and fungal communities and strawberry yield. <i>Environmental Pollution</i> , 2020, 256, 113415.	7.5	20
2972	Relationship of tongue coating microbiome on volatile sulfur compounds in healthy and halitosis adults. <i>Journal of Breath Research</i> , 2020, 14, 016005.	3.0	39
2973	Sandy soils amended with bentonite induced changes in soil microbiota and fungistasis in maize fields. <i>Applied Soil Ecology</i> , 2020, 146, 103378.	4.3	26
2974	Data, time and money: evaluating the best compromise for inferring molecular phylogenies of non-model animal taxa. <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106660.	2.7	13
2975	Factors Contributing to Interindividual Variation in Retronasal Odor Perception from Aroma Glycosides: The Role of Odorant Sensory Detection Threshold, Oral Microbiota, and Hydrolysis in Saliva. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 10299-10309.	5.2	25
2976	Fungal community demonstrates stronger dispersal limitation and less network connectivity than bacterial community in sediments along a large river. <i>Environmental Microbiology</i> , 2020, 22, 832-849.	3.8	115
2977	Fire affects the taxonomic and functional composition of soil microbial communities, with cascading effects on grassland ecosystem functioning. <i>Global Change Biology</i> , 2020, 26, 431-442.	9.5	45
2978	Ectopic osteogenesis by type I collagen loaded with a novel synthesized PTH-related peptide in vivo. <i>Journal of Biomedical Materials Research - Part A</i> , 2020, 108, 166-177.	4.0	12
2979	Sorgoleone release from sorghum roots shapes the composition of nitrifying populations, total bacteria, and archaea and determines the level of nitrification. <i>Biology and Fertility of Soils</i> , 2020, 56, 145-166.	4.3	57
2980	Fungicide azoxystrobin induced changes on the soil microbiome. <i>Applied Soil Ecology</i> , 2020, 145, 103343.	4.3	22
2981	The effect of inulin and resistant maltodextrin on weight loss during energy restriction: a randomised, placebo-controlled, double-blinded intervention. <i>European Journal of Nutrition</i> , 2020, 59, 2507-2524.	3.9	36
2982	Paenibacillus polymyxa improves the growth, immune and antioxidant activity, intestinal health, and disease resistance in Litopenaeus vannamei challenged with Vibrio parahaemolyticus. <i>Aquaculture</i> , 2020, 518, 734563.	3.5	36
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2985	Absorption of 1,3-dioleoyl-2-palmitoylglycerol and intestinal flora profiles changes in mice. <i>International Journal of Food Sciences and Nutrition</i> , 2020, 71, 296-306.	2.8	8
2986	Changes in Intestinal Microbiota of Type 2 Diabetes in Mice in Response to Dietary Supplementation With Instant Tea or Matcha. <i>Canadian Journal of Diabetes</i> , 2020, 44, 44-52.	0.8	51
2987	Impact of Sugarcane–Legume Intercropping on Diazotrophic Microbiome. <i>Sugar Tech</i> , 2020, 22, 52-64.	1.8	26
2988	A Metagenomic Study of Intestinal Microbial Diversity in Relation to Feeding Habits of Surface and Cave-Dwelling <i>Sinocyclocheilus</i> Species. <i>Microbial Ecology</i> , 2020, 79, 299-311.	2.8	22
2989	NirS-type N ₂ O-producers and nosZ II-type N ₂ O-reducers determine the N ₂ O emission potential in farmland rhizosphere soils. <i>Journal of Soils and Sediments</i> , 2020, 20, 461-471.	3.0	24
2990	Ecological Processes Shaping Bulk Soil and Rhizosphere Microbiome Assembly in a Long-Term Amazon Forest-to-Agriculture Conversion. <i>Microbial Ecology</i> , 2020, 79, 110-122.	2.8	41
2991	Dietary administration of resistant starch improved caecal barrier function by enhancing intestinal morphology and modulating microbiota composition in meat duck. <i>British Journal of Nutrition</i> , 2020, 123, 172-181.	2.3	24
2992	Source of hemolymph microbiota and their roles in the immune system of mud crab. <i>Developmental and Comparative Immunology</i> , 2020, 102, 103470.	2.3	26
2993	Severe Intestinal Dysbiosis in Rat Models of Short Bowel Syndrome with Ileocecal Resection. <i>Digestive Diseases and Sciences</i> , 2020, 65, 431-441.	2.3	12
2994	Effects of <i>Bacillus Subtilis</i> -Zinc on Rats with Congenital Zinc Deficiency. <i>Biological Trace Element Research</i> , 2020, 194, 482-492.	3.5	1
2995	Modification of Rhizosphere Bacterial Community Structure and Functional Potentials to Control <i>Pseudostellaria heterophylla</i> Replant Disease. <i>Plant Disease</i> , 2020, 104, 25-34.	1.4	20
2996	Composition of the arbuscular mycorrhizal fungal community and changes in diversity of the rhizosphere of <i>Clematis fruticosa</i> over three seasons across different elevations. <i>European Journal of Soil Science</i> , 2020, 71, 511-523.	3.9	7
2997	Dietary dl-methionyl-dl-methionine supplementation increased growth performance, antioxidant ability, the content of essential amino acids and improved the diversity of intestinal microbiota in Nile tilapia (<i>Oreochromis niloticus</i>). <i>British Journal of Nutrition</i> , 2020, 123, 72-83.	2.3	22
2998	Intake of <i>Ganoderma lucidum</i> polysaccharides reverses the disturbed gut microbiota and metabolism in type 2 diabetic rats. <i>International Journal of Biological Macromolecules</i> , 2020, 155, 890-902.	7.5	124
2999	Soil bacterial community differences along a coastal restoration chronosequence. <i>Plant Ecology</i> , 2020, 221, 795-811.	1.6	12
3000	Ambient temperature alters body size and gut microbiota of <i>Xenopus tropicalis</i> . <i>Science China Life Sciences</i> , 2020, 63, 915-925.	4.9	20
3001	Different milk replacers alter growth performance and rumen bacterial diversity of dairy bull calves. <i>Livestock Science</i> , 2020, 231, 103862.	1.6	5

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3003	Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications. <i>Water Research</i> , 2020, 169, 115250.	11.3	21
3004	The fungal community and its interaction with the concentration of short-chain fatty acids in the faeces of Chenghua, Yorkshire and Tibetan pigs. <i>Microbial Biotechnology</i> , 2020, 13, 509-521.	4.2	17
3005	Fungal community composition in sodic soils subjected to long-term rice cultivation. <i>Archives of Agronomy and Soil Science</i> , 2020, 66, 1410-1423.	2.6	8
3006	Exploring the accuracy of amplicon-based internal transcribed spacer markers for a fungal community. <i>Molecular Ecology Resources</i> , 2020, 20, 170-184.	4.8	49
3007	Microbial composition of Korean kefir and antimicrobial activity of <i>Acetobacter fabarum</i> DH1801. <i>Journal of Food Safety</i> , 2020, 40, e12728.	2.3	11
3008	Bacterial communities in the solid, liquid, dorsal, and ventral epithelium fractions of yak (<i>Bos</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5	3.0	43
3009	Distribution of Protists in the Deep South China Sea Revealed by High-Throughput Sequencing. <i>Journal of Ocean University of China</i> , 2020, 19, 161-170.	1.2	3
3010	Microbial taxonomic and functional attributes consistently predict soil CO ₂ emissions across contrasting croplands. <i>Science of the Total Environment</i> , 2020, 702, 134885.	8.0	13
3011	Long-term organic fertilization improves the productivity of kiwifruit (<i>Actinidia chinensis</i> Planch.) through increasing rhizosphere microbial diversity and network complexity. <i>Applied Soil Ecology</i> , 2020, 147, 103426.	4.3	56
3012	Bacterial succession and the dynamics of flavor compounds in the Huangjiu fermented from corn. <i>Archives of Microbiology</i> , 2020, 202, 299-308.	2.2	15
3013	Development of genomic microsatellite markers for <i>Aconitum gymnantrum</i> (Ranunculaceae) by next generation sequencing (NGS). <i>Molecular Biology Reports</i> , 2020, 47, 727-729.	2.3	4
3014	Short-term impact of fire-deposited charcoal on soil microbial community abundance and composition in a subtropical plantation in China. <i>Geoderma</i> , 2020, 359, 113992.	5.1	14
3015	Chloropicrin fumigation alters the soil phosphorus and the composition of the encoding alkaline phosphatase PhoD gene microbial community. <i>Science of the Total Environment</i> , 2020, 711, 135080.	8.0	29
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3018	Oral cancer-associated tertiary lymphoid structures: gene expression profile and prognostic value. <i>Clinical and Experimental Immunology</i> , 2020, 199, 172-181.	2.6	44
3019	Microbial diversity of sediments from an inactive hydrothermal vent field, Southwest Indian Ridge. <i>Marine Life Science and Technology</i> , 2020, 2, 73-86.	4.6	19

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3021	eDNA metabarcoding as a promising conservation tool for monitoring fish diversity in a coastal wetland of the Pearl River Estuary compared to bottom trawling. <i>Science of the Total Environment</i> , 2020, 702, 134704.	8.0	85
3022	Ecological processes underlying community assembly of aquatic bacteria and macroinvertebrates under contrasting climates on the Tibetan Plateau. <i>Science of the Total Environment</i> , 2020, 702, 134974.	8.0	15
3023	Geographical distribution and risk assessment of heavy metals: a case study of mine tailings pond. <i>Chemistry and Ecology</i> , 2020, 36, 1-15.	1.6	9
3024	Dietary resistant starch modifies the composition and function of caecal microbiota of broilers. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 1274-1284.	3.5	38
3025	Bacterial communities in digestive and excretory organs of cicadas. <i>Archives of Microbiology</i> , 2020, 202, 539-553.	2.2	11
3026	An Illumina approach to MHC typing of Atlantic salmon. <i>Immunogenetics</i> , 2020, 72, 89-100.	2.4	7
3027	Different toxic effects of ferulic and p-hydroxybenzoic acids on cucumber seedling growth were related to their different influences on rhizosphere microbial composition. <i>Biology and Fertility of Soils</i> , 2020, 56, 125-136.	4.3	39
3028	<i>Artemisia sphaerocephala</i> Krasch polysaccharide mediates lipid metabolism and metabolic endotoxaemia in associated with the modulation of gut microbiota in diet-induced obese mice. <i>International Journal of Biological Macromolecules</i> , 2020, 147, 1008-1017.	7.5	51
3029	Anti-obesity effect of <i>Lactobacillus rhamnosus</i> LS-8 and <i>Lactobacillus crustorum</i> MN047 on high-fat and high-fructose diet mice base on inflammatory response alleviation and gut microbiota regulation. <i>European Journal of Nutrition</i> , 2020, 59, 2709-2728.	3.9	69
3030	Bacteriome and Mycobiome in <i>Nicotiana tabacum</i> Fields Affected by Black Shank Disease. <i>Plant Disease</i> , 2020, 104, 315-319.	1.4	5
3031	Diversity and dynamics of microbial communities in brown planthopper at different developmental stages revealed by high-throughput amplicon sequencing. <i>Insect Science</i> , 2020, 27, 883-894.	3.0	28
3032	Wheat-associated microbiota and their correlation with stripe rust reaction. <i>Journal of Applied Microbiology</i> , 2020, 128, 544-555.	3.1	19
3033	Effects of dietary calcium pyruvate on gastrointestinal tract development, intestinal health and growth performance of newly weaned piglets fed low-protein diets. <i>Journal of Applied Microbiology</i> , 2020, 128, 355-365.	3.1	14
3034	Presence of diverse nitrate-dependent anaerobic methane oxidizing archaea in sewage sludge. <i>Journal of Applied Microbiology</i> , 2020, 128, 775-783.	3.1	9
3035	Porcine Epidemic Diarrhea Altered Colonic Microbiota Communities in Suckling Piglets. <i>Genes</i> , 2020, 11, 44.	2.4	7
3036	The Diversity of Associated Microorganisms in Different Organs and Rhizospheric Soil of <i>Arctium lappa</i> L.. <i>Current Microbiology</i> , 2020, 77, 746-754.	2.2	6
3037	Vertical changes in bacterial community composition down to a depth of 20 cm on the degraded Loess Plateau in China. <i>Land Degradation and Development</i> , 2020, 31, 1300-1313.	3.9	20

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3038	Dietary effect of low fish meal aquafeed on gut microbiota in olive flounder (<i>Paralichthys</i>) Tj ETQq0 0 0 rgBT /Overlock 10, Tf 50 742 T	3.0	24
3039	Altered Intestinal Microbiota Composition Associated with Enteritis in Yellow Seahorses <i>Hippocampus kuda</i> (Bleeker, 1852). <i>Current Microbiology</i> , 2020, 77, 730-737.	2.2	20
3040	A new sea surface temperature proxy based on bacterial 3-hydroxy fatty acids. <i>Organic Geochemistry</i> , 2020, 141, 103975.	1.8	13
3041	Evaluation of the Bacterial Diversity of Inner Mongolian Acidic Gruel Using Illumina MiSeq and PCR-DGGE. <i>Current Microbiology</i> , 2020, 77, 434-442.	2.2	13
3042	Exploitation of the Cooperative Behaviors of Anti-CRISPR Phages. <i>Cell Host and Microbe</i> , 2020, 27, 189-198.e6.	11.0	39
3043	Effect of time-restricted feeding on metabolic risk and circadian rhythm associated with gut microbiome in healthy males. <i>British Journal of Nutrition</i> , 2020, 123, 1216-1226.	2.3	98
3044	Microbes Associated With Black Soldier Fly (Diptera: Stratiomiidae) Degradation of Food Waste. <i>Environmental Entomology</i> , 2020, 49, 405-411.	1.4	38
3045	DNA sequencing reveals bacterial communities in midgut and other parts of the larvae of <i>Spodoptera exigua</i> Hubner (Lepidoptera: Noctuidae). <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	6
3046	Colon Cancer Prevention with Walnuts: A Longitudinal Study in Mice from the Perspective of a Gut Enterotype-like Cluster. <i>Cancer Prevention Research</i> , 2020, 13, 15-24.	1.5	3
3047	Biodegradation of skatole by <i>Burkholderia</i> sp. IDO3 and its successful bioaugmentation in activated sludge systems. <i>Environmental Research</i> , 2020, 182, 109123.	7.5	21
3048	Longitudinal analysis of the antibody repertoire of a Zika virus-infected patient revealed dynamic changes in antibody response. <i>Emerging Microbes and Infections</i> , 2020, 9, 111-123.	6.5	13
3049	Progressive Microbial Community Networks with Incremental Organic Loading Rates Underlie Higher Anaerobic Digestion Performance. <i>MSystems</i> , 2020, 5, .	3.8	15
3050	Salivary Microbiome and Cigarette Smoking: A First of Its Kind Investigation in Jordan. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 256.	2.6	41
3051	Probiotic Supplementation in a <i>Clostridium difficile</i> -Infected Gastrointestinal Model Is Associated with Restoring Metabolic Function of Microbiota. <i>Microorganisms</i> , 2020, 8, 60.	3.6	19
3052	Postnatal development of the microbiota and gut barrier function follows different paths in the small and large intestine in piglets. <i>FASEB Journal</i> , 2020, 34, 1430-1446.	0.5	26
3053	Insight into the microbiology of nitrogen cycle in the dairy manure composting process revealed by combining high-throughput sequencing and quantitative PCR. <i>Bioresource Technology</i> , 2020, 301, 122760.	9.6	76
3054	Chronic periodontitis induces microbiota-gut-brain axis disorders and cognitive impairment in mice. <i>Experimental Neurology</i> , 2020, 326, 113176.	4.1	34
3055	An interdependent relationship between microbial ecosystems and ferromanganese nodules from the Western Pacific Ocean. <i>Sedimentary Geology</i> , 2020, 398, 105588.	2.1	13

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3056	Characterization of the core microbiome in tobacco leaves during aging. MicrobiologyOpen, 2020, 9, e984.	3.0	38
3057	<i>Lactobacillus rhamnosus</i> from human breast milk shows therapeutic function against foodborne infection by multi-drug resistant <i>Escherichia coli</i> in mice. Food and Function, 2020, 11, 435-447.	4.6	24
3058	High-throughput single-cell cultivation reveals the underexplored rare biosphere in deep-sea sediments along the Southwest Indian Ridge. Lab on A Chip, 2020, 20, 363-372.	6.0	31
3059	Differential intestinal and oral microbiota features associated with gestational diabetes and maternal inflammation. American Journal of Physiology - Endocrinology and Metabolism, 2020, 319, E247-E253.	3.5	44
3060	Berberine ameliorates colonic damage accompanied with the modulation of dysfunctional bacteria and functions in ulcerative colitis rats. Applied Microbiology and Biotechnology, 2020, 104, 1737-1749.	3.6	39
3061	Organic amendment mitigates the negative impacts of mineral fertilization on bacterial communities in Shajiang black soil. Applied Soil Ecology, 2020, 150, 103457.	4.3	24
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3063	High rate anaerobic digestion of swine wastewater in an anaerobic membrane bioreactor. Energy, 2020, 193, 116783.	8.8	56
3064	Environmental antibiotics drives the genetic functions of resistome dynamics. Environment International, 2020, 135, 105398.	10.0	29
3065	Silver nanoparticles are lethal to the ciliate model Tetrahymena and safe to the pike silverside <i>Chirostoma estor</i> . Experimental Parasitology, 2020, 209, 107825.	1.2	9
3066	Bioturbation effect of fortified Daqu on microbial community and flavor metabolite in Chinese strong-flavor liquor brewing microecosystem. Food Research International, 2020, 129, 108851.	6.2	86
3067	Metagenomic analysis of viruses, bacteria and protozoa in irrigation water. International Journal of Hygiene and Environmental Health, 2020, 224, 113440.	4.3	29
3068	Aerobic composting as an effective cow manure management strategy for reducing the dissemination of antibiotic resistance genes: An integrated meta-omics study. Journal of Hazardous Materials, 2020, 386, 121895.	12.4	68
3069	Green tea polyphenols decrease weight gain, ameliorate alteration of gut microbiota, and mitigate intestinal inflammation in canines with high-fat-diet-induced obesity. Journal of Nutritional Biochemistry, 2020, 78, 108324.	4.2	82
3070	Microbial indicators are better predictors of wheat yield and quality than N fertilization. FEMS Microbiology Ecology, 2020, 96, .	2.7	31
3071	Disordered cutaneous microbiota in systemic lupus erythematosus. Journal of Autoimmunity, 2020, 108, 102391.	6.5	35
3072	Soil microbiotic homogenization occurred after long-term agricultural development in desert areas across northern China. Land Degradation and Development, 2020, 31, 1014-1025.	3.9	7
3073	Revealing the impact of global mass bleaching on coral microbiome through 16S rRNA gene-based metagenomic analysis. Microbiological Research, 2020, 233, 126408.	5.3	7

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3075	<i>Staphylococcus epidermidis</i> Contributes to Healthy Maturation of the Nasal Microbiome by Stimulating Antimicrobial Peptide Production. <i>Cell Host and Microbe</i> , 2020, 27, 68-78.e5.	11.0	99
3076	Tossed "good luck" coins as vectors for anthropogenic pollution into aquatic environment. <i>Environmental Pollution</i> , 2020, 259, 113800.	7.5	4
3077	Microbial community and geochemical analyses of trans-trench sediments for understanding the roles of hadal environments. <i>ISME Journal</i> , 2020, 14, 740-756.	9.8	99
3078	Insights into protist diversity and biogeography in intertidal sediments sampled across a range of spatial scales. <i>Limnology and Oceanography</i> , 2020, 65, 1103-1115.	3.1	28
3079	Direct and indirect effects of long-term ditch-buried straw return on soil bacterial community in a rice-wheat rotation system. <i>Land Degradation and Development</i> , 2020, 31, 851-867.	3.9	24
3080	Gut butyrate-producing organisms correlate to Placenta Specific 8 protein: Importance to colorectal cancer progression. <i>Journal of Advanced Research</i> , 2020, 22, 7-20.	9.5	22
3081	Manganese/iron-supported sulfate-dependent anaerobic oxidation of methane by archaea in lake sediments. <i>Limnology and Oceanography</i> , 2020, 65, 863-875.	3.1	54
3082	Deciphering microbiomes in anaerobic reactors with superior trichloroethylene dechlorination performance at low pH conditions. <i>Environmental Pollution</i> , 2020, 257, 113567.	7.5	14
3083	Restoration-mediated secondary contact leads to introgression of alewife ecotypes separated by a colonial-era dam. <i>Evolutionary Applications</i> , 2020, 13, 652-664.	3.1	10
3084	Black Soldier Fly (<i>Hermetia illucens</i>) reared on roasted coffee by-product and <i>Schizochytrium</i> sp. as a sustainable terrestrial ingredient for aquafeeds production. <i>Aquaculture</i> , 2020, 518, 734659.	3.5	60
3085	Long-term nitrogen application decreases the abundance and copy number of predatory myxobacteria and alters the myxobacterial community structure in the soil. <i>Science of the Total Environment</i> , 2020, 708, 135114.	8.0	28
3086	Genome analysis of sponge symbiont <i>Candidatus Halichondribacter symbioticus</i> shows genomic adaptation to a host-dependent lifestyle. <i>Environmental Microbiology</i> , 2020, 22, 483-498.	3.8	20
3087	Exploring microbial dynamics associated with flavours production during highland barley wine fermentation. <i>Food Research International</i> , 2020, 130, 108971.	6.2	32
3088	Effects of pesticide residues on bacterial community diversity and structure in typical greenhouse soils with increasing cultivation years in Northern China. <i>Science of the Total Environment</i> , 2020, 710, 136321.	8.0	32
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3731	Dynamic change of bacterial community during dairy manure composting process revealed by high-throughput sequencing and advanced bioinformatics tools. <i>Bioresource Technology</i> , 2020, 306, 123091.	9.6	93
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3747	Soil protist communities in burrowing and casting hotspots of different earthworm species. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107774.	8.8	13
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3770	Spatial Variation in Soil Fungal Communities across Paddy Fields in Subtropical China. <i>MSystems</i> , 2020, 5, .	3.8	56
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3791	Modulation of Gut Microbial Community and Metabolism by Dietary Glycyl-Glutamine Supplementation May Favor Weaning Transition in Piglets. <i>Frontiers in Microbiology</i> , 2019, 10, 3125.	3.5	20
3792	Agricultural Selection of Wheat Has Been Shaped by Plant-Microbe Interactions. <i>Frontiers in Microbiology</i> , 2020, 11, 132.	3.5	53
3793	Distinct Assembly Mechanisms Underlie Similar Biogeographic Patterns of Rare and Abundant Bacterioplankton in Cascade Reservoirs of a Large River. <i>Frontiers in Microbiology</i> , 2020, 11, 158.	3.5	37

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3795	Biochanin A Inhibits Ruminal Nitrogen-Metabolizing Bacteria and Alleviates the Decomposition of Amino Acids and Urea In Vitro. <i>Animals</i> , 2020, 10, 368.	2.3	9
3796	Diversity of Intestinal Bacterial Microbiota of Indigenous and Commercial Strains of Chickens Using 16S rDNA-Based Analysis. <i>Animals</i> , 2020, 10, 391.	2.3	6
3797	Slope Position Rather Than Thinning Intensity Affects Arbuscular Mycorrhizal Fungi (AMF) Community in Chinese Fir Plantations. <i>Forests</i> , 2020, 11, 273.	2.1	12
3798	Effects of Hydraulic Retention Time and Influent Nitrate-N Concentration on Nitrogen Removal and the Microbial Community of an Aerobic Denitrification Reactor Treating Recirculating Marine Aquaculture System Effluent. <i>Water (Switzerland)</i> , 2020, 12, 650.	2.7	7
3799	Effects of mineral substrate on ectomycorrhizal fungal colonization and bacterial community structure. <i>Science of the Total Environment</i> , 2020, 721, 137663.	8.0	15
3800	Mild changes in the mucosal microbiome during terminal ileum inflammation. <i>Microbial Pathogenesis</i> , 2020, 142, 104104.	2.9	8
3801	Consumption of salt leads to ameliorate symptoms of metabolic disorder and change of gut microbiota. <i>European Journal of Nutrition</i> , 2020, 59, 3779-3790.	3.9	6
3802	Effects of the long-term application of atrazine on soil enzyme activity and bacterial community structure in farmlands in China. <i>Environmental Pollution</i> , 2020, 262, 114264.	7.5	60
3803	A comprehensive non-redundant reference transcriptome for the Atlantic silverside <i>Menidia menidia</i> . <i>Marine Genomics</i> , 2020, 53, 100738.	1.1	6
3804	The invader <i>Carpobrotus edulis</i> promotes a specific rhizosphere microbiome across globally distributed coastal ecosystems. <i>Science of the Total Environment</i> , 2020, 719, 137347.	8.0	26
3805	Rhizodegradation of Petroleum Oily Sludge-contaminated Soil Using <i>Cajanus cajan</i> Increases the Diversity of Soil Microbial Community. <i>Scientific Reports</i> , 2020, 10, 4094.	3.3	49
3806	Characterization of the Esophageal Microbiota and Prediction of the Metabolic Pathways Involved in Esophageal Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 268.	3.9	35
3807	Horizontal gene transfer and silver nanoparticles production in a new <i>Marinomonas</i> strain isolated from the Antarctic psychrophilic ciliate <i>Euplotes focardii</i> . <i>Scientific Reports</i> , 2020, 10, 10218.	3.3	22
3808	The distinct microbial community in <i>Aurelia coerulea</i> polyps versus medusae and its dynamics after exposure to $^{60}\text{Co-}\beta$ radiation. <i>Environmental Research</i> , 2020, 188, 109843.	7.5	3
3809	Dietary quinoa (<i>Chenopodium quinoa</i> Willd.) polysaccharides ameliorate high-fat diet-induced hyperlipidemia and modulate gut microbiota. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 55-65.	7.5	61
3810	A Comprehensive Multi-Omic Approach Reveals a Relatively Simple Venom in a Diet Generalist, the Northern Short-Tailed Shrew, <i>Blarina brevicauda</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 1148-1166.	2.5	12
3811	Effects of stocking density on the growth performance, physiological response and intestinal microbiota of juvenile <i>Echiura</i> worms (<i>Urechis unicinctus</i>). <i>Aquaculture Research</i> , 2020, 51, 3983-3992.	1.8	8

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3812	Diversity and Function of Endo-Bacteria in <i>Bursaphelenchus xylophilus</i> from <i>Pinus massoniana</i> Lamb. in Different Regions. <i>Forests</i> , 2020, 11, 487.	2.1	10
3813	The circadian disruption of night work alters gut microbiota consistent with elevated risk for future metabolic and gastrointestinal pathology. <i>Chronobiology International</i> , 2020, 37, 1067-1081.	2.0	32
3814	Gut microbiota profiles of commercial laying hens infected with tumorigenic viruses. <i>BMC Veterinary Research</i> , 2020, 16, 218.	1.9	1
3815	Behçet's Disease Under Microbiotic Surveillance? A Combined Analysis of Two Cohorts of Behçet's Disease Patients. <i>Frontiers in Immunology</i> , 2020, 11, 1192.	4.8	28
3816	In silico and empirical evaluation of twelve metabarcoding primer sets for insectivorous diet analyses. <i>Ecology and Evolution</i> , 2020, 10, 6310-6332.	1.9	28
3817	Dried fruit pomace inclusion in poultry diet: growth performance, intestinal morphology and physiology. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 63.	5.3	16
3818	The Effect of Plant Geographical Location and Developmental Stage on Root-Associated Microbiomes of <i>Gymnadenia conopsea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1257.	3.5	30
3819	Variability of Gut Microbiota Across the Life Cycle of <i>Grapholita molesta</i> (Lepidoptera: Tortricidae). <i>Frontiers in Microbiology</i> , 2020, 11, 1366.	3.5	38
3820	Diazotroph Diversity Associated With Scleractinian Corals and Its Relationships With Environmental Variables in the South China Sea. <i>Frontiers in Physiology</i> , 2020, 11, 615.	2.8	8
3821	Recent infection by <i>Wolbachia</i> alters microbial communities in wild <i>Laodelphax striatellus</i> populations. <i>Microbiome</i> , 2020, 8, 104.	11.1	43
3822	Insights into aphid prey consumption by ladybirds: Optimising field sampling methods and primer design for high throughput sequencing. <i>PLoS ONE</i> , 2020, 15, e0235054.	2.5	7
3823	Increased organic fertilizer application and reduced chemical fertilizer application affect the soil properties and bacterial communities of grape rhizosphere soil. <i>Scientific Reports</i> , 2020, 10, 9568.	3.3	77
3824	Complete mitogenome of the noble volute <i>Cymbiola nobilis</i> from the Vietnamese Island of Phú Quốc. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1661-1662.	0.4	0
3825	Effects of bird aggregation on the soil properties and microbial community diversity of urban forest fragments. <i>Science of the Total Environment</i> , 2020, 737, 140250.	8.0	4
3826	Coupling 16S rDNA Sequencing and Untargeted Mass Spectrometry for Milk Microbial Composition and Metabolites from Dairy Cows with Clinical and Subclinical Mastitis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8496-8508.	5.2	22
3827	The Beta-Diversity of <i>Siganus fuscescens</i> -Associated Microbial Communities From Different Habitats Increases With Body Weight. <i>Frontiers in Microbiology</i> , 2020, 11, 1562.	3.5	9
3828	Differential Dynamics of the Ruminal Microbiome of Jersey Cows in a Heat Stress Environment. <i>Animals</i> , 2020, 10, 1127.	2.3	21
3829	Spatiotemporal dynamics of the total and active <i>Vibrio</i> spp. populations throughout the Changjiang estuary in China. <i>Environmental Microbiology</i> , 2020, 22, 4438-4455.	3.8	22

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3831	Dynamic distribution of gut microbiota during embryonic development in chicken. <i>Poultry Science</i> , 2020, 99, 5079-5090.	3.4	28
3832	The earliest domestic cat on the Silk Road. <i>Scientific Reports</i> , 2020, 10, 11241.	3.3	9
3833	Co-association of Two nir Denitrifiers Under the Influence of Emergent Macrophytes. <i>Microbial Ecology</i> , 2020, 80, 809-821.	2.8	13
3834	Trichoderma koningiopsis controls Fusarium oxysporum causing damping-off in Pinus massoniana seedlings by regulating active oxygen metabolism, osmotic potential, and the rhizosphere microbiome. <i>Biological Control</i> , 2020, 150, 104352.	3.0	18
3835	CuO Nanoparticles Alter the Rhizospheric Bacterial Community and Local Nitrogen Cycling for Wheat Grown in a Calcareous Soil. <i>Environmental Science & Technology</i> , 2020, 54, 8699-8709.	10.0	65
3836	Acyl homoserine lactone-mediated quorum sensing in the oral cavity: a paradigm revisited. <i>Scientific Reports</i> , 2020, 10, 9800.	3.3	34
3837	Heritability and genome-wide association of swine gut microbiome features with growth and fatness parameters. <i>Scientific Reports</i> , 2020, 10, 10134.	3.3	47
3838	Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. <i>Molecular Biology and Evolution</i> , 2020, 37, 3105-3117.	8.9	20
3839	Culturing Bacteria From Fermentation Pit Muds of Baijiu With Culturomics and Amplicon-Based Metagenomic Approaches. <i>Frontiers in Microbiology</i> , 2020, 11, 1223.	3.5	24
3840	Effects of Fermented Soybean Meal Supplementation on the Growth Performance and Cecal Microbiota Community of Broiler Chickens. <i>Animals</i> , 2020, 10, 1098.	2.3	42
3841	A novel quantitative real-time PCR diagnostic assay for fecal and nasal swab detection of an otariid lungworm, <i>Parafilaroides decorus</i> . <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 12, 85-92.	1.5	4
3842	Diversity hotspot and unique community structure of foraminifera in the world's deepest marine blue hole – Sansha Yongle Blue Hole. <i>Scientific Reports</i> , 2020, 10, 10257.	3.3	14
3843	Metagenomics analysis of fungal communities associated with postharvest diseases in pear fruits under the effect of management practices. <i>Archives of Microbiology</i> , 2020, 202, 2391-2400.	2.2	13
3844	Steel slag and biochar amendments decreased CO2 emissions by altering soil chemical properties and bacterial community structure over two-year in a subtropical paddy field. <i>Science of the Total Environment</i> , 2020, 740, 140403.	8.0	30
3845	Macrofaunal control of microbial community structure in continental margin sediments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15911-15922.	7.1	40
3846	Reservoirs of antimicrobial resistance genes in retail raw milk. <i>Microbiome</i> , 2020, 8, 99.	11.1	47
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3849	Microbial Community Composition and Function in Sediments from the Pearl River Mouth Basin. <i>Journal of Ocean University of China</i> , 2020, 19, 941-953.	1.2	12
3850	Dynamics of airborne bacterial community during biofiltration of gases from a swine house. <i>Science of the Total Environment</i> , 2020, 740, 139898.	8.0	8
3851	Preservation of the fecal samples at ambient temperature for microbiota analysis with a cost-effective and reliable stabilizer EfficGut. <i>Science of the Total Environment</i> , 2020, 741, 140423.	8.0	11
3852	Osmotic stress induces gut microbiota community shift in fish. <i>Environmental Microbiology</i> , 2020, 22, 3784-3802.	3.8	31
3853	Fine-scale succession patterns and assembly mechanisms of bacterial community of <i>Litopenaeus vannamei</i> larvae across the developmental cycle. <i>Microbiome</i> , 2020, 8, 106.	11.1	52
3854	A novel approach for the forensic diagnosis of drowning by microbiological analysis with next-generation sequencing and unweighted UniFrac-based PCoA. <i>International Journal of Legal Medicine</i> , 2020, 134, 2149-2159.	2.2	19
3855	Invasive <i>Nicotiana glauca</i> shifts the soil microbial community composition and functioning of harsh and disturbed semiarid Mediterranean environments. <i>Biological Invasions</i> , 2020, 22, 2923-2940.	2.4	8
3856	The environmental contribution to the dissemination of carbapenem and (fluoro)quinolone resistance genes by discharged and reused wastewater effluents: The role of cellular and extracellular DNA. <i>Water Research</i> , 2020, 182, 116011.	11.3	32
3857	The colonic mucosa-associated microbiome in SIV infection: shift towards Bacteroidetes coincides with mucosal CD4+ T cell depletion and enterocyte damage. <i>Scientific Reports</i> , 2020, 10, 10887.	3.3	9
3858	Effects of dietary <i>Hermetia illucens</i> meal inclusion on cecal microbiota and small intestinal mucin dynamics and infiltration with immune cells of weaned piglets. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 64.	5.3	20
3859	Application of biofertilizer containing <i>Bacillus subtilis</i> reduced the nitrogen loss in agricultural soil. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107911.	8.8	80
3860	Comparative evaluation of peptidome and microbiota in different types of saliva samples. <i>Annals of Translational Medicine</i> , 2020, 8, 686-686.	1.7	2
3861	Successive mineral nitrogen or phosphorus fertilization alone significantly altered bacterial community rather than bacterial biomass in plantation soil. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7213-7224.	3.6	12
3862	Integrated genome-wide investigations of the housefly, a global vector of diseases reveal unique dispersal patterns and bacterial communities across farms. <i>BMC Genomics</i> , 2020, 21, 66.	2.8	13
3863	Geographical Isolation, Buried Depth, and Physicochemical Traits Drive the Variation of Species Diversity and Prokaryotic Community in Three Typical Hypersaline Environments. <i>Microorganisms</i> , 2020, 8, 120.	3.6	17
3864	Identification and Quantification of Nonviable <i>Lactobacillus pentosus</i> Cells in a Health Food Product. <i>Journal of AOAC INTERNATIONAL</i> , 2020, 103, 223-226.	1.5	0
3865	Defining endogenous barcoding sites for CRISPR/Cas9-based cell lineage tracing in zebrafish. <i>Journal of Genetics and Genomics</i> , 2020, 47, 85-91.	3.9	8

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3867	Novel 28 microsatellite loci using high-throughput sequencing for an endangered species on <i>Metasequoia glyptostroboides</i> (Cupressaceae). <i>Molecular Biology Reports</i> , 2020, 47, 2991-2996.	2.3	0
3868	Response of bacterial communities and plant-mediated soil processes to nitrogen deposition and precipitation in a desert steppe. <i>Plant and Soil</i> , 2020, 448, 277-297.	3.7	23
3869	Immune and gut bacterial successions of large yellow croaker (<i>Larimichthys crocea</i>) during <i>Pseudomonas plecoglossicida</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 99, 176-183.	3.6	20
3870	Taxonomic classification and abundance estimation using 16S and WGS—A comparison using controlled reference samples. <i>Forensic Science International: Genetics</i> , 2020, 46, 102257.	3.1	31
3871	Altered gut microbiota by azithromycin attenuates airway inflammation in allergic asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1466-1469.e8.	2.9	20
3872	Ammonia oxidizers in river sediments of the Qinghai-Tibet Plateau and their adaptations to high-elevation conditions. <i>Water Research</i> , 2020, 173, 115589.	11.3	44
3873	Urbanization drives riverine bacterial antibiotic resistome more than taxonomic community at watershed scale. <i>Environment International</i> , 2020, 137, 105524.	10.0	76
3874	Salmon Gravlax Biopreservation With Lactic Acid Bacteria: A Polyphasic Approach to Assessing the Impact on Organoleptic Properties, Microbial Ecosystem and Volatilome Composition. <i>Frontiers in Microbiology</i> , 2019, 10, 3103.	3.5	35
3875	Rhizobium Inoculation Drives the Shifting of Rhizosphere Fungal Community in a Host Genotype Dependent Manner. <i>Frontiers in Microbiology</i> , 2019, 10, 3135.	3.5	23
3876	The effect of intramammary pirlimycin hydrochloride on the fecal microbiome of early-lactation heifers. <i>Journal of Dairy Science</i> , 2020, 103, 3459-3469.	3.4	0
3877	Interaction of Oral and Toothbrush Microbiota Affects Oral Cavity Health. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 17.	3.9	17
3878	The bacteria from large-sized bioflocs are more associated with the shrimp gut microbiota in culture system. <i>Aquaculture</i> , 2020, 523, 735159.	3.5	48
3879	Effects of a blend of <i>Saccharomyces cerevisiae</i> -based direct-fed microbial and fermentation products on plasma carbonyl-metabolome and fecal bacterial community of beef steers. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 14.	5.3	12
3880	Dietary encapsulated essential oils and organic acids mixture improves gut health in broiler chickens challenged with necrotic enteritis. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 18.	5.3	86
3881	Entomopathogenic nematode-associated microbiota: from monoxenic paradigm to pathobiome. <i>Microbiome</i> , 2020, 8, 25.	11.1	49
3882	Nanoliter-scale next-generation sequencing library-mediated high-throughput 16S rRNA microbial community profiling. <i>BioTechniques</i> , 2020, 68, 204-210.	1.8	1
3883	Pollution Gradients Altered the Bacterial Community Composition and Stochastic Process of Rural Polluted Ponds. <i>Microorganisms</i> , 2020, 8, 311.	3.6	16

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3884	Warming exerts a stronger effect than nitrogen addition on the soil arbuscular mycorrhizal fungal community in a young subtropical <i>Cunninghamia lanceolata</i> plantation. <i>Geoderma</i> , 2020, 367, 114273.	5.1	27
3885	16S rRNA gene sequencing reveals an altered composition of the gut microbiota in chickens infected with a nephropathogenic infectious bronchitis virus. <i>Scientific Reports</i> , 2020, 10, 3556.	3.3	10
3886	Structure, Function, Diversity, and Composition of Fungal Communities in Rhizospheric Soil of <i>Coptis chinensis</i> Franch under a Successive Cropping System. <i>Plants</i> , 2020, 9, 244.	3.5	34
3887	Generating and testing ecological hypotheses at the pondscape with environmental DNA metabarcoding: A case study on a threatened amphibian. <i>Environmental DNA</i> , 2020, 2, 184-199.	5.8	13
3888	Identification of an anaerobic bacterial consortium that degrades roxarsone. <i>MicrobiologyOpen</i> , 2020, 9, e1003.	3.0	5
3889	Bacterioplankton community variation in Bohai Bay (China) is explained by joint effects of environmental and spatial factors. <i>MicrobiologyOpen</i> , 2020, 9, e997.	3.0	12
3890	<i>Nicotiana tabacum</i> seed endophytic communities share a common core structure and genotype-specific signatures in diverging cultivars. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 287-295.	4.1	35
3891	Distinct mechanisms shape soil bacterial and fungal co-occurrence networks in a mountain ecosystem. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	62
3892	Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 8.	6.4	68
3893	Novel <i>Rickettsia</i> genotypes in ticks in French Guiana, South America. <i>Scientific Reports</i> , 2020, 10, 2537.	3.3	13
3894	Contrasting microbiomes of raw and ripened Pu-erh tea associated with distinct chemical profiles. <i>LWT - Food Science and Technology</i> , 2020, 124, 109147.	5.2	11
3895	Molecular diversity and spatial distribution of benthic foraminifera of the seamounts and adjacent abyssal plains in the tropical Western Pacific Ocean. <i>Marine Micropaleontology</i> , 2020, 156, 101850.	1.2	10
3896	Differentiation strategies of soil rare and abundant microbial taxa in response to changing climatic regimes. <i>Environmental Microbiology</i> , 2020, 22, 1327-1340.	3.8	164
3897	Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. <i>Gut</i> , 2020, 69, 1218-1228.	12.1	465
3898	Sowing Methods Influence Soil Bacterial Diversity and Community Composition in a Winter Wheat-Summer Maize Rotation System on the Loess Plateau. <i>Frontiers in Microbiology</i> , 2020, 11, 192.	3.5	10
3899	Effect of inclusion of HMBi in the ration of goats on feed intake, nutrient digestibility, rumen bacteria community and blood serum parameters. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2020, 104, 987-997.	2.2	11
3900	Nitrate Stabilizes the Rhizospheric Fungal Community to Suppress <i>Fusarium</i> Wilt Disease in Cucumber. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 590-599.	2.6	17
3901	Comparative study on archaeal diversity in the sediments of two urban landscape water bodies. <i>PLoS ONE</i> , 2020, 15, e0229097.	2.5	1

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3903	<i>Myzus persicae</i> (Hemiptera: Aphididae) infestation increases the risk of bacterial contamination and alters nutritional content in storage Chinese cabbage. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 3007-3012.	3.5	4
3904	Using high-throughput sequencing quantitatively to investigate soil nematode community composition in a steppe-forest ecotone. <i>Applied Soil Ecology</i> , 2020, 152, 103562.	4.3	38
3905	Rice waste biochars produced at different pyrolysis temperatures for arsenic and cadmium abatement and detoxification in sediment. <i>Chemosphere</i> , 2020, 250, 126268.	8.2	56
3906	Supplementation with nanobubble water alleviates obesity-associated markers through modulation of gut microbiota in high-fat diet fed mice. <i>Journal of Functional Foods</i> , 2020, 67, 103820.	3.4	10
3907	The effect of plant compartments on the <i>Broussonetia papyrifera</i> -associated fungal and bacterial communities. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 3627-3641.	3.6	16
3908	Dissipation of S-metolachlor and butachlor in agricultural soils and responses of bacterial communities: Insights from compound-specific isotope and biomolecular analyses. <i>Journal of Environmental Sciences</i> , 2020, 92, 163-175.	6.1	26
3909	Microbial Community and Its Association With Physicochemical Factors During Compost Bedding for Dairy Cows. <i>Frontiers in Microbiology</i> , 2020, 11, 254.	3.5	28
3910	Bioprospecting potential of microbial communities in solid waste landfills for novel enzymes through metagenomic approach. <i>World Journal of Microbiology and Biotechnology</i> , 2020, 36, 34.	3.6	25
3911	Industrial development as a key factor explaining variances in soil and grass phyllosphere microbiomes in urban green spaces. <i>Environmental Pollution</i> , 2020, 261, 114201.	7.5	19
3912	Characterization of the microbial communities and their correlations with chemical profiles in assorted vegetable Sichuan pickles. <i>Food Control</i> , 2020, 113, 107174.	5.5	55
3913	Role of microbial diversity for sustainable pyrite oxidation control in acid and metalliferous drainage prevention. <i>Journal of Hazardous Materials</i> , 2020, 393, 122338.	12.4	19
3914	Viable bacterial colonization is highly limited in the human intestine in utero. <i>Nature Medicine</i> , 2020, 26, 599-607.	30.7	180
3915	Fecal bacteria and metabolite responses to dietary lysozyme in a sow model from late gestation until lactation. <i>Scientific Reports</i> , 2020, 10, 3210.	3.3	13
3916	Bacterial community responses to tourism development in the Xixi National Wetland Park, China. <i>Science of the Total Environment</i> , 2020, 720, 137570.	8.0	40
3917	Roles of Organic Matter-Induced Heterotrophic Bacteria in Nitrification Reactors: Ammonium Removal and Bacterial Interactions. <i>ACS Sustainable Chemistry and Engineering</i> , 2020, 8, 3976-3985.	6.7	17
3918	<i>Ganoderma lucidum</i> cultivation affect microbial community structure of soil, wood segments and tree roots. <i>Scientific Reports</i> , 2020, 10, 3435.	3.3	16
3919	Draft Genome Sequences of <i>Leptospira interrogans</i> Serovar Copenhageni Strains Isolated from Patients with Weil's Disease in Brazil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0

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3921	The canine oral microbiome: variation in bacterial populations across different niches. BMC Microbiology, 2020, 20, 42.	3.3	41
3922	Pyrodextrin enhances intestinal function through changing the intestinal microbiota composition and metabolism in early weaned piglets. Applied Microbiology and Biotechnology, 2020, 104, 4141-4154.	3.6	18
3923	Cyanobacteria in an urban lake: hidden diversity revealed by metabarcoding. Aquatic Ecology, 2020, 54, 671-675.	1.5	3
3924	Assembly and shifts of the bacterial rhizobiome of field grown transgenic maize line carrying mcrY1Ab and mcrY2Ab genes at different developmental stages. Plant Growth Regulation, 2020, 91, 113-126.	3.4	8
3925	Distribution characteristics of fungal communities with depth in paddy fields of three soil types in China. Journal of Microbiology, 2020, 58, 279-287.	2.8	10
3926	Application of enhanced bioreduction for hexavalent chromium-polluted groundwater cleanup: Microcosm and microbial diversity studies. Environmental Research, 2020, 184, 109296.	7.5	18
3927	Amino acid and microbial community dynamics during the fermentation of Hong Qu glutinous rice wine. Food Microbiology, 2020, 90, 103467.	4.2	45
3928	Variations in the gut microbiota of sympatric François's langurs and rhesus macaques living in limestone forests in southwest Guangxi, China. Global Ecology and Conservation, 2020, 22, e00929.	2.1	14
3929	Effects of Eimeria tenella infection on the barrier damage and microbiota diversity of chicken cecum. Poultry Science, 2020, 99, 1297-1305.	3.4	34
3930	Long-term performance and microbial community characteristics of pilot-scale anaerobic reactors for thermal hydrolyzed sludge digestion under mesophilic and thermophilic conditions. Science of the Total Environment, 2020, 720, 137566.	8.0	27
3931	Decoupled diversity patterns in bacteria and fungi across continental forest ecosystems. Soil Biology and Biochemistry, 2020, 144, 107763.	8.8	78
3932	The Removal of Antibiotics in Relation to a Microbial Community in an Integrated Constructed Wetland for Tail Water Decontamination. Wetlands, 2020, 40, 993-1004.	1.5	14
3933	The first glimpse of the endometrial microbiota in early pregnancy. American Journal of Obstetrics and Gynecology, 2020, 222, 296-305.	1.3	40
3934	The Influence of Land Use Patterns on Soil Bacterial Community Structure in the Karst Graben Basin of Yunnan Province, China. Forests, 2020, 11, 51.	2.1	18
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4081	Probiotics and fructo-oligosaccharide intervention modulate the microbiota-gut brain axis to improve autism spectrum reducing also the hyper-serotonergic state and the dopamine metabolism disorder. <i>Pharmacological Research</i> , 2020, 157, 104784.	7.1	135

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4097	Dysbiosis of saliva microbiome in patients with oral lichen planus. <i>BMC Microbiology</i> , 2020, 20, 75.	3.3	30
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4220	Dietary vitamin A supplementation prevents early obesogenic diet-induced microbiota, neuronal and cognitive alterations. <i>International Journal of Obesity</i> , 2021, 45, 588-598.	3.4	18
4221	The impact of cropping system, tillage and season on shaping soil fungal community in a long-term field trial. <i>European Journal of Soil Biology</i> , 2021, 102, 103253.	3.2	12
4222	Variable characteristics of microbial communities on the surface of sweet cherries under different storage conditions. <i>Postharvest Biology and Technology</i> , 2021, 173, 111408.	6.0	22
4223	Monthly distribution of ammonia-oxidizing microbes in a tropical bay. <i>Journal of Microbiology</i> , 2021, 59, 10-19.	2.8	1
4224	Microbial Community Characterizing Vermiculatons from Karst Caves and Its Role in Their Formation. <i>Microbial Ecology</i> , 2021, 81, 884-896.	2.8	29
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4228	Manure application increases microbiome complexity in soil aggregate fractions: Results of an 18-year field experiment. <i>Agriculture, Ecosystems and Environment</i> , 2021, 307, 107249.	5.3	54
4229	On-farm soil resistome is modified after treating dairy calves with the antibiotic florfenicol. <i>Science of the Total Environment</i> , 2021, 750, 141694.	8.0	11
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4231	Protist taxonomic and functional diversity in soil, freshwater and marine ecosystems. <i>Environment International</i> , 2021, 146, 106262.	10.0	110
4232	Derived habitats of indoor microbes are associated with asthma symptoms in Chinese university dormitories. <i>Environmental Research</i> , 2021, 194, 110501.	7.5	18
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4234	Whole exome sequencing identifies the potential for genetic rescue in iconic and critically endangered Panamanian harlequin frogs. <i>Global Change Biology</i> , 2021, 27, 50-70.	9.5	15
4235	Metabolites of microbiota response to tryptophan and intestinal mucosal immunity: A therapeutic target to control intestinal inflammation. <i>Medicinal Research Reviews</i> , 2021, 41, 1061-1088.	10.5	68
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4240	Genome editing in human hematopoietic stem and progenitor cells via CRISPR-Cas9-mediated homology-independent targeted integration. <i>Molecular Therapy</i> , 2021, 29, 1611-1624.	8.2	17
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4242	Gut Microbiome Components Predict Response to Neoadjuvant Chemoradiotherapy in Patients with Locally Advanced Rectal Cancer: A Prospective, Longitudinal Study. <i>Clinical Cancer Research</i> , 2021, 27, 1329-1340.	7.0	82
4243	Metagenomic Approach to Bacterial Diversity and Lipolytic Enzymes™ Genes from a Steam Soil of Los Humeros Geothermal Field (Puebla, MÃ©xico). <i>Geomicrobiology Journal</i> , 2021, 38, 304-314.	2.0	0

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4245	Assessment of fungal diversity in soil rhizosphere associated with <i>Rhazya stricta</i> and some desert plants using metagenomics. <i>Archives of Microbiology</i> , 2021, 203, 1211-1219.	2.2	2
4246	Floral fungal-bacterial community structure and co-occurrence patterns in four sympatric island plant species. <i>Fungal Biology</i> , 2021, 125, 49-61.	2.5	14
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4248	Effect of Gender Bias on Equine Fecal Microbiota. <i>Journal of Equine Veterinary Science</i> , 2021, 97, 103355.	0.9	8
4249	Effects of dietary four different woody forages on gut microbiota of Nile tilapia (<i>Oreochromis</i> Tj ETQq1 1 0.784314 rgBT ₆ Overlook	1.8	1
4250	The structure of plant-herbivore interaction networks varies along elevational gradients in the European Alps. <i>Journal of Biogeography</i> , 2021, 48, 465-476.	3.0	15
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4253	Network-directed isolation of the cooperator <i>Pseudomonas aeruginosa</i> ZM03 enhanced the dibutyl phthalate degradation capacity of <i>Arthrobacter nicotianae</i> ZM05 under pH stress. <i>Journal of Hazardous Materials</i> , 2021, 410, 124667.	12.4	19
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4257	Large-scale evidence for microbial response and associated carbon release after permafrost thaw. <i>Global Change Biology</i> , 2021, 27, 3218-3229.	9.5	44
4258	Rapid microbial community evolution in initial <i>Carex</i> litter decomposition stages in Bayinbuluk alpine wetland during the freeze-thaw period. <i>Ecological Indicators</i> , 2021, 121, 107180.	6.3	25
4259	Microbial Metabolism of Theaflavin-3,3'-digallate and Its Gut Microbiota Composition Modulatory Effects. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 232-245.	5.2	40
4260	Soil prokaryotic community shows no response to 20 years of simulated nitrogen deposition in an arid ecosystem in northwestern China. <i>Environmental Microbiology</i> , 2021, 23, 1222-1237.	3.8	15
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4266	Applying machine learning to predict viral assembly for adeno-associated virus capsid libraries. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 20, 276-286.	4.1	25
4267	High-throughput sequencing-based analysis of the intestinal microbiota of broiler chickens fed with compound small peptides of Chinese medicine. <i>Poultry Science</i> , 2021, 100, 100897.	3.4	12
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4270	Evaluation of rhizoremediation and methane emission in diesel-contaminated soil cultivated with tall fescue (<i>Festuca arundinacea</i>). <i>Environmental Research</i> , 2021, 194, 110606.	7.5	25
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4283	Sediment resuspension drives protist metacommunity structure and assembly in grass carp (<i>Ctenopharyngodon idella</i>) aquaculture ponds. <i>Science of the Total Environment</i> , 2021, 764, 142840.	8.0	19
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4286	The impact of heavy rain event on groundwater microbial communities in Xikuangshan, Hunan Province, P.R. China. <i>Journal of Hydrology</i> , 2021, 595, 125674.	5.4	10
4287	Biofilm and microbiome response of attached growth nitrification systems across incremental decreases to low temperatures. <i>Journal of Water Process Engineering</i> , 2021, 39, 101730.	5.6	8
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4290	Stochasticity versus determinism: Microbial community assembly patterns under specific conditions in petrochemical activated sludge. <i>Journal of Hazardous Materials</i> , 2021, 407, 124372.	12.4	32
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4294	Microbiome variations in preschool children with halitosis. <i>Oral Diseases</i> , 2021, 27, 1059-1068.	3.0	9
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4302	Diversity of bacteria associated with Hormaphidinae aphids (Hemiptera: Aphididae). <i>Insect Science</i> , 2021, 28, 165-179.	3.0	20
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4306	Bacterial and Fungal Microbiome Profiling in Chilhuacle Negro Chili (<i>Capsicum annuum</i> L.) Associated With Fruit Rot Disease. <i>Plant Disease</i> , 2021, 105, 2618-2627.	1.4	3
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4318	Effect of <i>Senecio scandens</i> ethanol extract on gut microbiota composition in mice. <i>Archives of Microbiology</i> , 2021, 203, 1477-1488.	2.2	1
4320	Investigating the microbiota of fermented fish products (Pla-ra) from different communities of northeastern Thailand. <i>PLoS ONE</i> , 2021, 16, e0245227.	2.5	21
4321	Gut microbiota dynamics in carnivorous European seabass (<i>Dicentrarchus labrax</i>) fed plant-based diets. <i>Scientific Reports</i> , 2021, 11, 447.	3.3	34
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4323	A high-throughput ultrasonic spraying inoculation method promotes colony cultivation of rare microbial species. <i>Environmental Microbiology</i> , 2021, 23, 1275-1285.	3.8	3
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4333	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. <i>Eurosurveillance</i> , 2021, 26, .	7.0	9
4334	Effects of Mesobiliverdin IX α -Enriched Microalgae Feed on Gut Health and Microbiota of Broilers. <i>Frontiers in Veterinary Science</i> , 2020, 7, 586813.	2.2	7
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4357	Investigation of bacterial diversity in <i>Cajanus cajan</i> -planted gangue soil via high-throughput sequencing. <i>Bioengineered</i> , 2021, 12, 6981-6995.	3.2	9
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4372	Comparison of Blood Bacterial Communities in Periodontal Health and Periodontal Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 577485.	3.9	36
4373	Interaction of Intestinal Bacteria with Human Rotavirus during Infection in Children. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1010.	4.1	142

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4378	Clonal diversity of the B cell receptor repertoire in patients with coronary in-stent restenosis and type 2 diabetes. <i>Open Life Sciences</i> , 2021, 16, 884-898.	1.4	3
4379	Effect of Two Different Sugarcane Cultivars on Rhizosphere Bacterial Communities of Sugarcane and Soybean Upon Intercropping. <i>Frontiers in Microbiology</i> , 2020, 11, 596472.	3.5	28
4380	Effect of Root Diameter on the Selection and Network Interactions of Root-Associated Bacterial Microbiomes in <i>Robinia pseudoacacia</i> L. <i>Microbial Ecology</i> , 2021, 82, 391-402.	2.8	18
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4385	Development and characterization of 14 novel microsatellite markers for an invasive goby (<i>Tetraodon lineatus</i>) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 342 T	0.7	4
4386	Effect of commercially purified deoxynivalenol and zearalenone mycotoxins on microbial diversity of pig cecum contents. <i>Animal Bioscience</i> , 2021, 34, 243-255.	2.0	12
4387	Faecal bacterial composition in horses with and without free faecal liquid: a case control study. <i>Scientific Reports</i> , 2021, 11, 4745.	3.3	4
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4398	Dietary Glutamic Acid Modulates Immune Responses and Gut Health of Weaned Pigs. <i>Animals</i> , 2021, 11, 504.	2.3	13
4399	Volatile aroma composition and sensory profile of Shiraz and Cabernet Sauvignon wines produced with novel <i>Metschnikowia pulcherrima</i> yeast starter cultures. <i>Australian Journal of Grape and Wine Research</i> , 2021, 27, 406-418.	2.1	11
4400	Circulating exosomes and gut microbiome induced insulin resistance in mice exposed to intermittent hypoxia: Effects of physical activity. <i>EBioMedicine</i> , 2021, 64, 103208.	6.1	35
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4411	Cultivation and characterization of snowbound microorganisms from the South Pole. <i>Extremophiles</i> , 2021, 25, 159-172.	2.3	3
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4414	The Gut Microbial Composition Is Species-Specific and Individual-Specific in Two Species of Estrildid Finches, the Bengalese Finch and the Zebra Finch. Frontiers in Microbiology, 2021, 12, 619141.	3.5	13
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4416	High Plasticity of the Gut Microbiome and Muscle Metabolome of Chinese Mitten Crab (<i>Eriocheir</i>) Tj ETQq1 1 0.784314 rgBT /Overdo	2.1	10
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4477	Characterization of biliary microbiota dysbiosis in extrahepatic cholangiocarcinoma. <i>PLoS ONE</i> , 2021, 16, e0247798.	2.5	30
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4489	Large-scale functional network connectivity mediate the associations of gut microbiota with sleep quality and executive functions. <i>Human Brain Mapping</i> , 2021, 42, 3088-3101.	3.6	31
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4536	Holstein and Jersey Steers Differ in Rumen Microbiota and Enteric Methane Emissions Even Fed the Same Total Mixed Ration. <i>Frontiers in Microbiology</i> , 2021, 12, 601061.	3.5	18
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4558	Community Composition and Function of Bacteria in Activated Sludge of Municipal Wastewater Treatment Plants. <i>Water (Switzerland)</i> , 2021, 13, 852.	2.7	21
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4583	Effects of monobutyryn supplementation on egg production, biochemical indexes, and gut microbiota of broiler breeders. <i>Poultry Science</i> , 2021, 100, 100907.	3.4	3

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4597	The genomics of rapid climatic adaptation and parallel evolution in North American house mice. <i>PLoS Genetics</i> , 2021, 17, e1009495.	3.5	26
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4603	Plant flavones enrich rhizosphere Oxalobacteraceae to improve maize performance under nitrogen deprivation. <i>Nature Plants</i> , 2021, 7, 481-499.	9.3	247
4604	Effects of Heat Stress on Gut-Microbial Metabolites, Gastrointestinal Peptides, Glycolipid Metabolism, and Performance of Broilers. <i>Animals</i> , 2021, 11, 1286.	2.3	30
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4635	Prodigiosin of <i>Serratia marcescens</i> ZPG19 Alters the Gut Microbiota Composition of Kunming Mice. <i>Molecules</i> , 2021, 26, 2156.	3.8	9
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4643	Contrasting Composition, Diversity and Predictive Metabolic Potential of the Rhizobacterial Microbiomes Associated with Native and Invasive <i>Prosopis</i> Congeners. <i>Current Microbiology</i> , 2021, 78, 2051-2060.	2.2	8
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4666	A combination of <i>Tropilaelaps mercedesae</i> and imidacloprid negatively affects survival, pollen consumption and midgut bacterial composition of honey bee. <i>Chemosphere</i> , 2021, 268, 129368.	8.2	11
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4669	Effect of mangrove restoration on sediment properties and bacterial community. <i>Ecotoxicology</i> , 2021, 30, 1672-1679.	2.4	14
4670	Effect of Quicklime on Microbial Community in Strong Acidic Soil. <i>Journal of Soil Science and Plant Nutrition</i> , 2021, 21, 1771-1781.	3.4	8
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4672	Characterization of the B cell receptor repertoire of patients with acute coronary syndrome. <i>Genes and Genomics</i> , 2021, , 1.	1.4	1
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4674	Alterations of Gut Microbiota in Patients With Graves' Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663131.	3.9	20
4675	The Diversity and Dynamics of Fungi in <i>Dryocosmus kuriphilus</i> Community. <i>Insects</i> , 2021, 12, 426.	2.2	3
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4681	Oral administration of <i>Moringa oleifera</i> leaf powder relieves oxidative stress, modulates mucosal immune response and cecal microbiota after exposure to heat stress in New Zealand White rabbits. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 66.	5.3	17
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4804	Microbial sulfate reduction by <i>Desulfovibrio</i> is an important source of hydrogen sulfide from a large swine finishing facility. <i>Scientific Reports</i> , 2021, 11, 10720.	3.3	18
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4813	Bias of library preparation for virome characterization in untreated and treated wastewaters. <i>Science of the Total Environment</i> , 2021, 767, 144589.	8.0	12
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4823	Effects of different dissolved organic matter on microbial communities and arsenic mobilization in aquifers. <i>Journal of Hazardous Materials</i> , 2021, 411, 125146.	12.4	71
4824	Outbreaks of Root Rot Disease in Different Aged American Ginseng Plants Are Associated With Field Microbial Dynamics. <i>Frontiers in Microbiology</i> , 2021, 12, 676880.	3.5	19
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4829	Therapeutic potential of an intestinotrophic hormone, glucagon-like peptide 2, for treatment of type 2 short bowel syndrome rats with intestinal bacterial and fungal dysbiosis. <i>BMC Infectious Diseases</i> , 2021, 21, 583.	2.9	8
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4835	Printing Microbial Dark Matter: Using Single Cell Dispensing and Genomics to Investigate the Patescibacteria/Candidate Phyla Radiation. <i>Frontiers in Microbiology</i> , 2021, 12, 635506.	3.5	14
4836	Verrucomicrobial methanotrophs grow on diverse C3 compounds and use a homolog of particulate methane monooxygenase to oxidize acetone. <i>ISME Journal</i> , 2021, 15, 3636-3647.	9.8	29
4837	Response of Soil Fungal Diversity and Community Composition to Varying Levels of Bamboo Biochar in Red Soils. <i>Microorganisms</i> , 2021, 9, 1385.	3.6	29
4838	Effect of co-application of <i>Trichoderma</i> spp. with organic composts on plant growth enhancement, soil enzymes and fungal community in soil. <i>Archives of Microbiology</i> , 2021, 203, 4281-4291.	2.2	21
4839	The hepatotoxicity of altrazine exposure in mice involves the intestinal microbiota. <i>Chemosphere</i> , 2021, 272, 129572.	8.2	30
4840	Effects of dietary lipid levels on growth performance, hepatic health, lipid metabolism and intestinal microbiota on <i>Trachinotus ovatus</i> . <i>Aquaculture Nutrition</i> , 2021, 27, 1554-1568.	2.7	16
4841	A KMT2A-AFF1 gene regulatory network highlights the role of core transcription factors and reveals the regulatory logic of key downstream target genes. <i>Genome Research</i> , 2021, 31, 1159-1173.	5.5	16
4842	Bacterial community and composition of different traditional fermented dairy products in China, South Africa, and Sri Lanka by high-throughput sequencing of 16S rRNA genes. <i>LWT - Food Science and Technology</i> , 2021, 144, 111209.	5.2	12
4843	Fecal microbial composition and functional diversity of Wuzhishan pigs at different growth stages. <i>AMB Express</i> , 2021, 11, 88.	3.0	10
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4846	Antidiabetic Function of <i>Lactobacillus fermentum</i> MF423-Fermented Rice Bran and Its Effect on Gut Microbiota Structure in Type 2 Diabetic Mice. <i>Frontiers in Microbiology</i> , 2021, 12, 682290.	3.5	28
4848	APB-3 improves the adverse outcomes caused by TGEV infection by correcting the intestinal microbial disorders in piglets. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2022, 106, 69-77.	2.2	3
4849	A diverse collection of B cells responded to HIV infection in infant BG505. <i>Cell Reports Medicine</i> , 2021, 2, 100314.	6.5	6
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4855	The role of CTCF in the organization of the centromeric 11p15 imprinted domain interactome. <i>Nucleic Acids Research</i> , 2021, 49, 6315-6330.	14.5	11
4856	Shared and distinctive features of the gut microbiome of C57BL/6 mice from different vendors and production sites, and in response to a new vivarium. <i>Lab Animal</i> , 2021, 50, 185-195.	0.4	17
4857	<i>Lactobacillus acidophilus</i> LA14 Alleviates Liver Injury. <i>MSystems</i> , 2021, 6, e0038421.	3.8	30
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4859	High throughput analysis of <i>MHC-EL</i> and <i>MHC-DR</i> diversity of Brazilian cattle populations. <i>Hla</i> , 2021, 98, 93-113.	0.6	8
4860	Comparison of Diazotrophic Composition and Distribution in the South China Sea and the Western Pacific Ocean. <i>Biology</i> , 2021, 10, 555.	2.8	4
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4866	Early Alpine occupation backdates westward human migration in Late Glacial Europe. <i>Current Biology</i> , 2021, 31, 2484-2493.e7.	3.9	17
4867	Cross-taxon congruence of aquatic microbial communities across geological ages in Iceland: Stochastic and deterministic processes. <i>Science of the Total Environment</i> , 2021, 774, 145103.	8.0	2
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4874	Biomethanation of Napier Grass Mono-digestion in Single-Stage Anaerobic Completely Stirred Tank Reactors Seeded with Cow Manure and Anaerobic Sludge. <i>Bioenergy Research</i> , 2022, 15, 559-572.	3.9	4
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4878	Patterns of yeast diversity distribution and its drivers in rhizosphere soil of Hami melon orchards in different regions of Xinjiang. <i>BMC Microbiology</i> , 2021, 21, 170.	3.3	8
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4881	Correlation of Key Physiological Properties of <i>Methanosarcina</i> Isolates with Environment of Origin. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0073121.	3.1	26
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4890	Intestinal Microbiota Mediates High-Fructose and High-Fat Diets to Induce Chronic Intestinal Inflammation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 654074.	3.9	39

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4907	Quantitative evaluation of chromosomal rearrangements in gene-edited human stem cells by CAST-Seq. <i>Cell Stem Cell</i> , 2021, 28, 1136-1147.e5.	11.1	95
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4917	Evaluation of Indigenous Olive Biocontrol Rhizobacteria as Protectants against Drought and Salt Stress. <i>Microorganisms</i> , 2021, 9, 1209.	3.6	8
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4924	Comparison of fungal community composition within different intestinal segments of tilapia and bighead carp. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1961-1971.	1.3	7
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4971	Analysis of gut microbiota in three species belonging to different genera (<i>Hemitragus</i> , <i>Pseudois</i> , and) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i> 2021, 11, 12129-12140.	1.9	3
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4976	Culture-Based and Culture-Independent Assessments of Endophytic Fungal Diversity in Aquatic Plants in Southwest China. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	2.0	11
4977	Impact of microecological agents on water environment restoration and microbial community structures of trench system in a Baiyangdian wetland ecosystem. <i>Journal of Applied Microbiology</i> , 2022, 132, 2450-2463.	3.1	7
4978	<i>Ganoderma lucidum</i> promotes sleep through a gut microbiota-dependent and serotonin-involved pathway in mice. <i>Scientific Reports</i> , 2021, 11, 13660.	3.3	19
4980	Non-Lactobacillus-Dominated Vaginal Microbiota Is Associated With a Tubal Pregnancy in Symptomatic Chinese Women in the Early Stage of Pregnancy: A Nested Caseâ€“Control Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 659505.	3.9	4
4981	The Enhancement of Intestinal Immunity in Offspring Piglets by Maternal Probiotic or Synbiotic Supplementation Is Associated With the Alteration of Gut Microbiota. <i>Frontiers in Nutrition</i> , 2021, 8, 686053.	3.7	21
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4984	Caecal microbiota could effectively increase chicken growth performance by regulating fat metabolism. <i>Microbial Biotechnology</i> , 2022, 15, 844-861.	4.2	23
4985	New genetic markers for Sapotaceae phylogenomics: More than 600 nuclear genes applicable from family to population levels. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107123.	2.7	17
4986	Unveiling the Patterns of Reticulated Evolutionary Processes with Phylogenomics: Hybridization and Polyploidy in the Genus <i>Rosa</i> . <i>Systematic Biology</i> , 2022, 71, 547-569.	5.6	18

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4988	Cropland to Miscanthus conversion alters soil bacterial and archaeal communities influencing N cycle in Northern China. <i>GCB Bioenergy</i> , 2021, 13, 1528-1544.	5.6	3
4989	Environmental DNA metabarcoding uncovers environmental correlates of fish communities in spatially heterogeneous freshwater habitats. <i>Ecological Indicators</i> , 2021, 126, 107698.	6.3	22
4990	Distribution of Hydrogen-Producing Bacteria in Tibetan Hot Springs, China. <i>Frontiers in Microbiology</i> , 2021, 12, 569020.	3.5	4
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4995	Absence of Significant Off-Target Splicing Variation with a U7snRNA Vector Targeting <i>DMD</i> Exon 2 Duplications. <i>Human Gene Therapy</i> , 2021, 32, 1346-1359.	2.7	8
4996	Succession of the microbial communities and function prediction during short-term peach sawdust-based composting. <i>Bioresource Technology</i> , 2021, 332, 125079.	9.6	62
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4999	Seasonal Variation of Microbial Diversity of Coastal Sediment in Tongyeong, South Korea, Using 16S rRNA Gene Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0044621.	0.6	2
5000	Strong Replication Interference Between Hepatitis Delta Viruses in Human Liver Chimeric Mice. <i>Frontiers in Microbiology</i> , 2021, 12, 671466.	3.5	5
5001	The Microbial Community of Poultry Farm Waste and Its Role in Hydrogen Sulfide Production. <i>Microbiology</i> , 2021, 90, 507-511.	1.2	2
5002	Temporal differences in microbial composition of Poisses cheese rinds during ripening and storage. <i>Journal of Dairy Science</i> , 2021, 104, 7500-7508.	3.4	11
5003	Biparatopic single-domain antibodies against Axl achieve ultra-high affinity through intramolecular engagement. <i>Biochemical and Biophysical Research Communications</i> , 2021, 562, 154-161.	2.1	4
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5007	A sliver of the past: The decimation of the genetic diversity of the Mexican wolf. <i>Molecular Ecology</i> , 2021, 30, 6340-6354.	3.9	6
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5011	Minimal-moderate variation of human oral virome and microbiome in IgA deficiency. <i>Scientific Reports</i> , 2021, 11, 14913.	3.3	5
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5017	Warming intensifies soil pathogen negative feedback on a temperate tree. <i>New Phytologist</i> , 2021, 231, 2297-2307.	7.3	13
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5020	Characterization of Early Life Stress-Affected Gut Microbiota. <i>Brain Sciences</i> , 2021, 11, 913.	2.3	14
5021	Study on Microbial Community Succession and Protein Hydrolysis of Donkey Meat during Refrigerated Storage Based on Illumina NOVA Sequencing Technology. <i>Food Science of Animal Resources</i> , 2021, 41, 701-714.	4.1	4
5022	Alterations of Gut Microbiota in Patients With Intestinal Tuberculosis That Different From Crohn's Disease. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 673691.	4.1	9

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5027	Coupling Between the Responses of Plants, Soil, and Microorganisms Following Grazing Exclusion in an Overgrazed Grassland. <i>Frontiers in Plant Science</i> , 2021, 12, 640789.	3.6	16
5028	Alterations to arbuscular mycorrhizal fungal community composition is driven by warming at specific elevations. <i>PeerJ</i> , 2021, 9, e11792.	2.0	4
5029	Response of soil bacterial communities to organic carbon input under soil freeze-thaw in forest ecosystems. <i>European Journal of Soil Biology</i> , 2021, 105, 103333.	3.2	7
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5035	Impact of supplementary <i>Lactobacillus casei</i> K17 on growth and gut health of largemouth bass <i>Micropterus salmoides</i> . <i>Aquaculture Reports</i> , 2021, 20, 100734.	1.7	3
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5037	Effects of dietary supplementation with a laminarin-rich extract on the growth performance and gastrointestinal health in broilers. <i>Poultry Science</i> , 2021, 100, 101179.	3.4	14
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5042	Bacterial Community Spacing Is Mainly Shaped by Unique Species in the Subalpine Natural Lakes of China. <i>Frontiers in Microbiology</i> , 2021, 12, 669131.	3.5	3

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5044	Carbon sources of benthic fauna in temperate lakes across multiple trophic states. <i>Biogeosciences</i> , 2021, 18, 4369-4388.	3.3	7
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5046	Effect of a Multispecies Probiotic Mixture on the Growth and Incidence of Diarrhea, Immune Function, and Fecal Microbiota of Pre-weaning Dairy Calves. <i>Frontiers in Microbiology</i> , 2021, 12, 681014.	3.5	25
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5050	Oceanographic structure and seasonal variation contribute to high heterogeneity in mesozooplankton over small spatial scales. <i>ICES Journal of Marine Science</i> , 2021, 78, 3288-3302.	2.5	5
5051	Improved immobilization of soil cadmium by regulating soil characteristics and microbial community through reductive soil disinfestation. <i>Science of the Total Environment</i> , 2021, 778, 146222.	8.0	20
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5056	Effects of Dietary Supplementation with Protected Sodium Butyrate on Gut Microbiota in Growing-Finishing Pigs. <i>Animals</i> , 2021, 11, 2137.	2.3	15
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5062	Sensitive detection of tumor mutations from blood and its application to immunotherapy prognosis. <i>Nature Communications</i> , 2021, 12, 4172.	12.8	16

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5065	16S rRNA gene amplicon sequencing of gut microbiota in gestational diabetes mellitus and their correlation with disease risk factors. <i>Journal of Endocrinological Investigation</i> , 2022, 45, 279-289.	3.3	17
5066	How Does Pikeperch <i>Sander lucioperca</i> Respond to Dietary Insect Meal <i>Hermetia illucens</i> ? Investigation on Gut Microbiota, Histomorphology, and Antioxidant Biomarkers. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	10
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5069	Consecutive soybean (<i>Glycine max</i>) planting and covering improve acidified tea garden soil. <i>PLoS ONE</i> , 2021, 16, e0254502.	2.5	2
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5073	The inhibition effect of tea polyphenols on soil nitrification is greater than denitrification in tea garden soil. <i>Science of the Total Environment</i> , 2021, 778, 146328.	8.0	25
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5075	The metabolic process of aerobic granular sludge treating piggery wastewater: Microbial community, denitrification genes and mathematical model calculation. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 105392.	6.7	18
5076	Effects of Human, Caprine, and Bovine Milk Fat Globules on Microbiota Adhesion and Gut Microecology. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 9778-9787.	5.2	4
5077	Electrocatalytic deep dehalogenation of florfenicol using Fe-doped CoP nanotubes array for blocking resistance gene expression and microbial inhibition during biochemical treatment. <i>Water Research</i> , 2021, 201, 117361.	11.3	19
5078	Decisive Effects of Life Stage on the Gut Microbiota Discrepancy Between Two Wild Populations of Hibernating Asiatic Toads (<i>Bufo gargarizans</i>). <i>Frontiers in Microbiology</i> , 2021, 12, 665849.	3.5	6
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5081	Effects of nitrogen addition on rhizospheric soil microbial communities of poplar plantations at different ages. <i>Forest Ecology and Management</i> , 2021, 494, 119328.	3.2	28

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5084	The microbial population structure and function of peanut peanut and their effects on aflatoxin contamination. <i>LWT - Food Science and Technology</i> , 2021, 148, 111285.	5.2	4
5085	Local community assembly processes shape the diversity of soil microbial harbouring communities in the Northern Hemisphere steppes. <i>Global Ecology and Biogeography</i> , 2021, 30, 2273-2285.	5.8	19
5086	Quantitative characterization of the B cell receptor repertoires of human immunized with commercial rabies virus vaccine. <i>Human Vaccines and Immunotherapeutics</i> , 2021, 17, 2538-2546.	3.3	2
5087	Crude oil biodegradation in upper and supratidal seashores. <i>Journal of Hazardous Materials</i> , 2021, 416, 125919.	12.4	16
5088	Washed Microbiota Transplantation Lowers Blood Pressure in Patients With Hypertension. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 679624.	3.9	34
5090	Modulation of gut microbiota by chondroitin sulfate calcium complex during alleviation of osteoporosis in ovariectomized rats. <i>Carbohydrate Polymers</i> , 2021, 266, 118099.	10.2	16
5091	Inoculating with the microbial agents to start up the aerobic composting of mushroom residue and wood chips at low temperature. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 105294.	6.7	40
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5095	High-Throughput Single-Cell Technology Reveals the Contribution of Horizontal Gene Transfer to Typical Antibiotic Resistance Gene Dissemination in Wastewater Treatment Plants. <i>Environmental Science & Technology</i> , 2021, 55, 11824-11834.	10.0	33
5096	Diversity and functions of bacterial communities in water and sediment from the watershed of the Tama River flowing a highly urbanized area. <i>Fisheries Science</i> , 2021, 87, 697-715.	1.6	5
5097	The diarrhetic shellfish-poisoning toxin, okadaic acid, provokes gastropathy, dysbiosis and susceptibility to bacterial infection in a non-rodent bioassay, <i>Galleria mellonella</i> . <i>Archives of Toxicology</i> , 2021, 95, 3361-3376.	4.2	14
5098	Microbial Communities and Physicochemical Characteristics of Traditional Dajiang and Sufu in North China Revealed by High-Throughput Sequencing of 16S rRNA. <i>Frontiers in Microbiology</i> , 2021, 12, 665243.	3.5	6
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5101	Metagenomic Analysis of Bacterial Diversity in Traditional Fermented Foods Reveals Food-Specific Dominance of Specific Bacterial Taxa. <i>Fermentation</i> , 2021, 7, 167.	3.0	13

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5103	Microbial composition differs between production systems and is associated with growth performance and carcass quality in pigs. Animal Microbiome, 2021, 3, 57.	3.8	7
5104	Rumen Fermentation, Digestive Enzyme Activity, and Bacteria Composition between Pre-Weaning and Post-Weaning Dairy Calves. Animals, 2021, 11, 2527.	2.3	14
5105	Impact of biocontrol microbes on soil microbial diversity in ginger (<i>Zingiber) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622 Td (b	3.4	14
5106	Metabolic Differentiation of Co-occurring Accumilibacter Clades Revealed through Genome-Resolved Metatranscriptomics. MSystems, 2021, 6, e0047421.	3.8	15
5107	Prevotella copri increases fat accumulation in pigs fed with formula diets. Microbiome, 2021, 9, 175.	11.1	100
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5111	Folic Acid Absorption Characteristics and Effect on Cecal Microbiota of Laying Hens. Frontiers in Veterinary Science, 2021, 8, 720851.	2.2	7
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5116	Variations in bacterial and archaeal community structure and diversity along the soil profiles of a peatland in Southwest China. Environmental Science and Pollution Research, 2022, 29, 2276-2286.	5.3	5
5118	Assessment of microbial ð±-diversity in one meter squared topsoil. Soil Ecology Letters, 2022, 4, 224-236.	4.5	10
5119	The Spatial and Temporal Characterization of Gut Microbiota in Broilers. Frontiers in Veterinary Science, 2021, 8, 712226.	2.2	26
5120	The Transcriptional Response of Soil Bacteria to Long-Term Warming and Short-Term Seasonal Fluctuations in a Terrestrial Forest. Frontiers in Microbiology, 2021, 12, 666558.	3.5	8

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5121	Method for quick DNA barcode reference library construction. <i>Ecology and Evolution</i> , 2021, 11, 11627-11638.	1.9	14
5122	Microbial Reconstitution Improves Aging-Driven Lacrimal Gland Circadian Dysfunction. <i>American Journal of Pathology</i> , 2021, 191, 2091-2116.	3.8	11
5123	Gut Microbial Diversity in Female Patients With Invasive Mole and Choriocarcinoma and Its Differences Versus Healthy Controls. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 704100.	3.9	4
5124	Two community types occur in gut microbiota of large-sample wild plateau pikas (<i>Ochotona</i>) Tj ETQq1 1 0.784314 rgBT/Overlook	2.6	14
5126	Diversity and Paleodemography of the Addax (<i>Addax nasomaculatus</i>), a Saharan Antelope on the Verge of Extinction. <i>Genes</i> , 2021, 12, 1236.	2.4	8
5127	Comparative analysis of rumen fermentation parameters and bacterial profiles during adaption to different fattening stages in beef cattle fed TMR with various forage silage. <i>Animal Feed Science and Technology</i> , 2021, 278, 115006.	2.2	8
5128	Exploring prevalence of potential pathogens and fecal indicators in geographically distinct river systems through comparative metagenomics. <i>Environmental Pollution</i> , 2021, 282, 117003.	7.5	7
5129	Seasonal Dietary Shifts Alter the Gut Microbiota of Avivorous Bats: Implication for Adaptation to Energy Harvest and Nutritional Utilization. <i>MSphere</i> , 2021, 6, e0046721.	2.9	16
5130	Truffle Microbiome Is Driven by Fruit Body Compartmentalization Rather than Soils Conditioned by Different Host Trees. <i>MSphere</i> , 2021, 6, e0003921.	2.9	10
5131	Using Fecal DNA Metabarcoding to Investigate Foraging Reveals the Effects of Specific Herbage on the Improved n-3 Fatty Acid (PUFA) Composition in the Longissimus Dorsi Muscle of Grazing Tan Sheep. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 9725-9734.	5.2	1
5132	An example of DNA methylation as a means to quantify stress in wildlife using killer whales. <i>Scientific Reports</i> , 2021, 11, 16822.	3.3	5
5133	Diversity and abundance of antibiotic resistance genes in rhizosphere soil and endophytes of leafy vegetables: Focusing on the effect of the vegetable species. <i>Journal of Hazardous Materials</i> , 2021, 415, 125595.	12.4	44
5134	LYmphoid NeXt-Generation Sequencing (LYNX) Panel. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 959-974.	2.8	11
5135	Development of a tRNA-Derived Small RNA Prognostic Panel and Their Potential Functions in Osteosarcoma. <i>Frontiers in Oncology</i> , 2021, 11, 652040.	2.8	2
5136	Temporal Changes in the Function of Bacterial Assemblages Associated With Decomposing Earthworms. <i>Frontiers in Microbiology</i> , 2021, 12, 682224.	3.5	5
5137	Infection Heterogeneity and Microbiota Differences in Chicks Infected by <i>Salmonella enteritidis</i> . <i>Microorganisms</i> , 2021, 9, 1705.	3.6	8
5138	Biosorption of Copper in Swine Manure Using <i>Aspergillus</i> and Yeast: Characterization and Its Microbial Diversity Study. <i>Frontiers in Microbiology</i> , 2021, 12, 687533.	3.5	2
5139	Effects of Age, Diet CP, NDF, EE, and Starch on the Rumen Bacteria Community and Function in Dairy Cattle. <i>Microorganisms</i> , 2021, 9, 1788.	3.6	9

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5141	Deciphering the Shifts in Microbial Community Diversity From Material Pretreatment to Saccharification Process of Fuyu-Flavor Baijiu. <i>Frontiers in Microbiology</i> , 2021, 12, 705967.	3.5	16
5142	Microbial dysbiosis together with nutrient imbalance cause the replant problem of upper six flue-cured tobacco in Central Henan. <i>Journal of Plant Diseases and Protection</i> , 0, , 1.	2.9	4
5143	Linking soil bacterial diversity to satellite-derived vegetation productivity: a case study in arid and semi-arid desert areas. <i>Environmental Microbiology</i> , 2021, 23, 6137-6147.	3.8	1
5145	Bacterial Consumption of T4 Phages. <i>Microorganisms</i> , 2021, 9, 1852.	3.6	0
5146	Development of the first microsatellite markers using high-throughput sequencing for a hexaploid coastal species, <i>Tournefortia argentea</i> L. f. (Boraginaceae). <i>Molecular Biology Reports</i> , 2021, 48, 7049-7055.	2.3	1
5147	Phosphorus availability increases pathobiome abundance and invasion of rhizosphere microbial networks by <i>Ralstonia</i> . <i>Environmental Microbiology</i> , 2021, 23, 5992-6003.	3.8	28
5148	Degradation Characteristics and Microbial Community of Phosphine Biopurification Systems. <i>Environmental Engineering Science</i> , 2021, 38, 802-810.	1.6	0
5149	Exploration of the Characteristics of Intestinal Microbiota and Metabolomics in Different Rat Models of Mongolian Medicine. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	1.2	2
5150	Construction and evaluation of a bioluminescent <i>Pseudomonas aeruginosa</i> reporter for use in preservative efficacy testing. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	0
5151	Influence of different phytoremediation on soil microbial diversity and community composition in saline-alkaline land. <i>International Journal of Phytoremediation</i> , 2022, 24, 507-517.	3.1	9
5152	Impact of nisin on <i>Clostridioides difficile</i> and microbiota composition in a faecal fermentation model of the human colon. <i>Journal of Applied Microbiology</i> , 2022, 132, 1397-1408.	3.1	7
5153	Genomic insights into the diversity, virulence and resistance of <i>Klebsiella pneumoniae</i> extensively drug resistant clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	2.0	5
5154	Nasopharyngeal microbiome reveals the prevalence of opportunistic pathogens in SARS-CoV-2 infected individuals and their association with host types. <i>Microbes and Infection</i> , 2022, 24, 104880.	1.9	31
5155	Connection between the Gut Microbiota of Largemouth Bass (<i>Micropterus salmoides</i>) and Microbiota of the Pond Culture Environment. <i>Microorganisms</i> , 2021, 9, 1770.	3.6	18
5157	Probiotic supplements alleviate gestational diabetes mellitus by restoring the diversity of gut microbiota: a study based on 16S rRNA sequencing. <i>Journal of Microbiology</i> , 2021, 59, 827-839.	2.8	13
5158	Mucosal Microbiota and Metabolome in the Ileum of Hu Sheep Offered a Low-Grain, Pelleted or Non-pelleted High-Grain Diet. <i>Frontiers in Microbiology</i> , 2021, 12, 718884.	3.5	4
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5161	Seasonal Sampling of a Microbial Community in the Sediment of Geoje-Hansan Bay, Republic of Korea. <i>Microbiology Resource Announcements</i> , 2021, 10, e0056621.	0.6	1
5162	Pearl Oyster Bacterial Community Structure Is Governed by Location and Tissue-Type, but <i>Vibrio</i> Species Are Shared Among Oyster Tissues. <i>Frontiers in Microbiology</i> , 2021, 12, 723649.	3.5	6
5163	Deciphering the Endophytic and Rhizospheric Microbial Communities of a Metallophyte <i>Commelina communis</i> in Different Cu-Polluted Soils. <i>Microorganisms</i> , 2021, 9, 1689.	3.6	4
5164	Functional analysis of pristine estuarine marine sediments. <i>Science of the Total Environment</i> , 2021, 781, 146526.	8.0	16
5165	Changes of the intestinal microbiota along the gut of Japanese Eel (<i>Anguilla japonica</i>). <i>Letters in Applied Microbiology</i> , 2021, 73, 529-541.	2.2	3
5166	Change the original microbial community structure in the hydrolysis acidification tank to enhance the COD removal performance of oily wastewater. <i>Water Science and Technology</i> , 2021, 84, 1477-1486.	2.5	0
5167	Mining the Factors Driving the Evolution of the Pit Mud Microbiome under the Impact of Long-Term Production of Strong-Flavor Baijiu. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0088521.	3.1	36
5168	Impact of operational conditions on methane yield and microbial community composition during biological methanation in in situ and hybrid reactor systems. <i>Biotechnology for Biofuels</i> , 2021, 14, 170.	6.2	10
5169	Gut Microbiota Composition is Associated with Responses to Peanut Intervention in Multiple Parameters Among Adults with Metabolic Syndrome Risk. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2001051.	3.3	6
5170	Soil microbial community and network changes after long-term use of plastic mulch and nitrogen fertilization on semiarid farmland. <i>Geoderma</i> , 2021, 396, 115086.	5.1	65
5171	Mitogenome Phylogeny Including Data from Additional Subspecies Provides New Insights into the Historical Biogeography of the Eurasian lynx <i>Lynx lynx</i> . <i>Genes</i> , 2021, 12, 1216.	2.4	12
5172	Evaluation of the Dietary Black Soldier Fly Larvae Meal (<i>Hermetia illucens</i>) on Growth Performance, Intestinal Health, and Disease Resistance to <i>Vibrio parahaemolyticus</i> of the Pacific White Shrimp (<i>Litopenaeus vannamei</i>). <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	11
5173	Phylosymbiotic Structures of the Microbiota in <i>Mollitrichosiphum tenuicorpus</i> (Hemiptera: Aphididae: TJ ETQq1 1 0.784314 rgBT /Overl	2.8	5
5174	Parasitism to mutualism continuum for Joshua trees inoculated with different communities of arbuscular mycorrhizal fungi from a desert elevation gradient. <i>PLoS ONE</i> , 2021, 16, e0256068.	2.5	7
5175	Diversity and geographic variation of endosymbiotic bacteria in natural populations of the pea aphid (<i>Acyrtosiphon pisum</i>) in China. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 788-797.	0.9	5
5176	Increasing relative abundance of non-cyanobacterial photosynthetic organisms drives ecosystem multifunctionality during the succession of biological soil crusts. <i>Geoderma</i> , 2021, 395, 115052.	5.1	12
5177	Legacy effects of temporary grassland in annual crop rotation on soil ecosystem services. <i>Science of the Total Environment</i> , 2021, 780, 146140.	8.0	16

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5179	Effective control of large deletions after double-strand breaks by homology-directed repair and dsODN insertion. <i>Genome Biology</i> , 2021, 22, 236.	8.8	36
5180	The comparison of ZFNs, TALENs, and SpCas9 by GUIDE-seq in HPV-targeted gene therapy. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 1466-1478.	5.1	18
5181	Alteration of Gut Microbiota Relates to Metabolic Disorders in Primary Aldosteronism Patients. <i>Frontiers in Endocrinology</i> , 2021, 12, 667951.	3.5	21
5184	Effects of dietary forage to concentrate ratio on nutrient digestibility, ruminal fermentation and rumen bacterial composition in Angus cows. <i>Scientific Reports</i> , 2021, 11, 17023.	3.3	43
5185	Methylation of the RIN3 Promoter is Associated with Transient Ischemic Stroke/Mild Ischemic Stroke with Early Cognitive Impairment. <i>Neuropsychiatric Disease and Treatment</i> , 2021, Volume 17, 2587-2598.	2.2	5
5186	Increase in carbohydrate content and variation in microbiome are related to the drought tolerance of <i>Codonopsis pilosula</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 165, 19-35.	5.8	12
5187	An emerging chemical fumigant: two-sided effects of dazomet on soil microbial environment and plant response. <i>Environmental Science and Pollution Research</i> , 2022, 29, 3022-3036.	5.3	8
5189	Amelioration of Hepatic Steatosis in Mice through <i>Bacteroides uniformis</i> CBA7346-Mediated Regulation of High-Fat Diet-Induced Insulin Resistance and Lipogenesis. <i>Nutrients</i> , 2021, 13, 2989.	4.1	15
5190	Seasonal and annual changes in the microbial communities of Ofunato Bay, Japan, based on metagenomics. <i>Scientific Reports</i> , 2021, 11, 17277.	3.3	4
5191	Sulfidogenic Microbial Communities of the Uzen High-Temperature Oil Field in Kazakhstan. <i>Microorganisms</i> , 2021, 9, 1818.	3.6	13
5192	Replacement of fish meal with Methanotroph (<i>Methylococcus capsulatus</i> , Bath) bacteria meal in the diets of Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2021, 541, 736801.	3.5	45
5193	The fungal community outperforms the bacterial community in predicting plant health status. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 6499-6513.	3.6	18
5194	Two-stage anoxic-oxic (A/O) system for the treatment of coking wastewater: Full-scale performance and microbial community analysis. <i>Chemical Engineering Journal</i> , 2021, 417, 129204.	12.7	39
5195	Effects of sulfamethoxazole on nitrogen removal and molecular ecological network in integrated vertical-flow constructed wetland. <i>Ecotoxicology and Environmental Safety</i> , 2021, 219, 112292.	6.0	16
5196	Dynamics of the Sydney rock oyster microbiota before and during a QX disease event. <i>Aquaculture</i> , 2021, 541, 736821.	3.5	2
5197	Exploring changes in bacterioplankton community structure in response to tannic acid, a major component of mangrove litterfall of Sundarbans mangrove ecosystem: a laboratory mesocosm approach. <i>Environmental Science and Pollution Research</i> , 2022, 29, 2107-2121.	5.3	5
5198	Within-host evolutionary dynamics of seasonal and pandemic human influenza A viruses in young children. <i>ELife</i> , 2021, 10, .	6.0	8

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5200	A Study on Burrows-Wheeler Aligner's Performance Optimization for Ancient DNA Mapping. <i>Lecture Notes in Networks and Systems</i> , 2022, , 105-114.	0.7	1
5201	High salinity gradients and intermediate spatial scales shaped similar biogeographical and co-occurrence patterns of microeukaryotes in a tropical freshwater-saltwater ecosystem. <i>Environmental Microbiology</i> , 2021, 23, 4778-4796.	3.8	13
5202	Aged Ripe Pu-erh Tea Reduced Oxidative Stress-Mediated Inflammation in Dextran Sulfate Sodium-Induced Colitis Mice by Regulating Intestinal Microbes. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 10592-10605.	5.2	51
5203	Specific inhibition of <i>Streptococcus bovis</i> by endolysin LyJH307 supplementation shifts the rumen microbiota and metabolic pathways related to carbohydrate metabolism. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 93.	5.3	10
5204	Effect of intestinal microecology on postnatal weight gain in very preterm infants in intensive care units. <i>Gut Pathogens</i> , 2021, 13, 49.	3.4	2
5205	Pain after upper limb surgery under peripheral nerve block is associated with gut microbiome composition and diversity. <i>Neurobiology of Pain (Cambridge, Mass)</i> , 2021, 10, 100072.	2.5	5
5206	Effect of High Sulfur Diet on Rumen Fermentation, Microflora, and Epithelial Barrier Function in Steers. <i>Animals</i> , 2021, 11, 2545.	2.3	7
5207	Distinct bacterial community of a solid-state fermented Chinese traditional food huase sufu revealed by high-throughput sequencing. <i>Food Science and Biotechnology</i> , 2021, 30, 1233-1241.	2.6	4
5208	Application of DNA metabarcoding to characterize the diet of the moon jellyfish <i>Aurelia coerulea</i> polyps and ephyrae. <i>Acta Oceanologica Sinica</i> , 2021, 40, 160-167.	1.0	2
5209	Blended controlled-release nitrogen fertilizer with straw returning improved soil nitrogen availability, soil microbial community, and root morphology of wheat. <i>Soil and Tillage Research</i> , 2021, 212, 105045.	5.6	48
5210	Diversity, Composition, Taxa Biomarkers, and Functional Genes of Fish Gut Microbes in Peat Swamp Forests and its Converted Areas in North Selangor, Malaysia. <i>Pertanika Journal of Science and Technology</i> , 2021, 44, .	0.3	0
5211	Effect of East Asian atmospheric particulate matter deposition on bacterial activity and community structure in the oligotrophic Northwest Pacific. <i>Environmental Pollution</i> , 2021, 283, 117088.	7.5	4
5212	Plant beneficial rhizobacteria community structure changes through developmental stages of peanut and maize. <i>Rhizosphere</i> , 2021, 19, 100407.	3.0	15
5213	Comparative analysis of chicken cecal microbial diversity and taxonomic composition in response to dietary variation using 16S rRNA amplicon sequencing. <i>Molecular Biology Reports</i> , 2021, 48, 7203-7214.	2.3	3
5214	Unveiling the Gut Microbiota and Resistome of Wild Cotton Mice, <i>Peromyscus gossypinus</i> , from Heavy Metal- and Radionuclide-Contaminated Sites in the Southeastern United States. <i>Microbiology Spectrum</i> , 2021, 9, e0009721.	3.0	4
5215	Long-term organic fertilization regulates the abundance of major nitrogen-cycling-related genes in aggregates from an acidic Ultisol. <i>Applied Soil Ecology</i> , 2021, 165, 104014.	4.3	17
5216	Lactic Acid Bacteria Strains Differently Modulate Gut Microbiota and Metabolic and Immunological Parameters in High-Fat Diet-Fed Mice. <i>Frontiers in Nutrition</i> , 2021, 8, 718564.	3.7	14

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5219	Composition of the microbial communities at different body sites in women with preterm birth and their newborns. Medicine in Microecology, 2021, 9, 100046.	1.6	3
5220	Planifilum fulgidum Is the Dominant Functional Microorganism in Compost Containing Spent Mushroom Substrate. Sustainability, 2021, 13, 10002.	3.2	9
5221	Abundance and diversity of carbon-fixing bacterial communities in karst wetland soil ecosystems. Catena, 2021, 204, 105418.	5.0	40
5222	Metagenomic Analysis of Suansun, a Traditional Chinese Unsalted Fermented Food. Processes, 2021, 9, 1669.	2.8	5
5223	Draft Genome Sequence of the Anoxygenic Phototrophic Bacterium <i>Rhodomicrobium</i> sp. Strain Az07, Isolated from a Brackish Canal. Microbiology Resource Announcements, 2021, 10, e0058521.	0.6	0
5224	Unraveling the bacterial diversity of Cangar Hot Spring, Indonesia by Next Generation Sequencing of 16S rRNA gene. Biodiversitas, 2021, 22, .	0.6	0
5225	Acute oral colchicine caused gastric mucosal injury and disturbance of associated microbiota in mice. Toxicology, 2021, 461, 152908.	4.2	11
5226	Genomic Epidemiology and Strain Taxonomy of <i>Corynebacterium diphtheriae</i> . Journal of Clinical Microbiology, 2021, 59, e0158121.	3.9	12
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5228	Liquid Organic Fertilizer Amendment Alters Rhizosphere Microbial Community Structure and Co-occurrence Patterns and Improves Sunflower Yield Under Salinity-Alkalinity Stress. Microbial Ecology, 2022, 84, 423-438.	2.8	19
5229	Roots of the xerophyte Panicum turgidum host a cohort of ionizing-radiation-resistant biotechnologically-valuable bacteria. Saudi Journal of Biological Sciences, 2022, 29, 1260-1268.	3.8	4
5230	Variations in the Community Structure of Fungal Microbiota Associated with Apple Fruit Shaped by Fruit Bagging-Based Practice. Journal of Fungi (Basel, Switzerland), 2021, 7, 764.	3.5	4
5231	Sediment microbiota in polyculture of shrimp and fish pattern is distinctive from those in monoculture intensive shrimp or fish ponds. Science of the Total Environment, 2021, 787, 147594.	8.0	16
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5233	Geography-dependent symbiont communities in two oligophagous aphid species. FEMS Microbiology Ecology, 2021, 97, .	2.7	6
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5236	Rumen bacteria influence milk protein yield of yak grazing on the Qinghai-Tibet plateau. <i>Animal Bioscience</i> , 2021, 34, 1466-1478.	2.0	8
5237	Assessing the potential use of a feed additive based on biochar on broilers feeding upon productive performance, pH of digestive organs, cecum fermentation and bacterial community. <i>Animal Feed Science and Technology</i> , 2021, 279, 115039.	2.2	14
5238	Bacterial and fungal communities in the sandstone biofilms of two famous Buddhist grottoes in China. <i>International Biodeterioration and Biodegradation</i> , 2021, 163, 105267.	3.9	17
5239	Characterization of Shiga Toxin 2a Encoding Bacteriophages Isolated From High-Virulent O145:H25 Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 728116.	3.5	1
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5241	Effects of chilling rate on the freshness and microbial community composition of lamb carcasses. <i>LWT - Food Science and Technology</i> , 2022, 153, 112559.	5.2	14
5242	Different Responses of Soil Bacterial Communities to Nitrogen Addition in Moss Crust. <i>Frontiers in Microbiology</i> , 2021, 12, 665975.	3.5	6
5243	The unusual microbiota of the traditional Bulgarian dairy product Krokach – A pilot metagenomics study. <i>International Journal of Dairy Technology</i> , 2022, 75, 139-149.	2.8	8
5244	Community Structure and Function of Epiphytic Bacteria Associated With <i>Myriophyllum spicatum</i> in Baiyangdian Lake, China. <i>Frontiers in Microbiology</i> , 2021, 12, 705509.	3.5	14
5245	Effects of steam-flaked grains on foals' growth and faecal microbiota. <i>BMC Veterinary Research</i> , 2021, 17, 293.	1.9	1
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5248	Altered fecal microbiota composition in individuals who abuse methamphetamine. <i>Scientific Reports</i> , 2021, 11, 18178.	3.3	23
5249	Methane emissions and methanogenic community investigation from constructed wetlands in Chengdu City. <i>Urban Climate</i> , 2021, 39, 100956.	5.7	9
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5254	Age-Related Changes in the Ruminal Microbiota and Their Relationship With Rumen Fermentation in Lambs. <i>Frontiers in Microbiology</i> , 2021, 12, 679135.	3.5	19
5255	Gut Microbial Divergence Between Three Hadal Amphipod Species from the Isolated Hadal Trenches. <i>Microbial Ecology</i> , 2021, , 1.	2.8	5
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5257	Insights into the bacterial and fungal communities and microbiome that causes a microbe outbreak on ancient wall paintings in the Majishan Grottoes. <i>International Biodeterioration and Biodegradation</i> , 2021, 163, 105250.	3.9	38
5258	Comparison of the Bulk and Rhizosphere Soil Prokaryotic Communities Between Wild and Reintroduced <i>Manglietiastrum sinicum</i> Plants, a Threatened Species with Extremely Small Populations. <i>Current Microbiology</i> , 2021, 78, 3877-3890.	2.2	1
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5261	Influences of non-IgE-mediated cow's milk protein allergy-associated gut microbial dysbiosis on regulatory T cell-mediated intestinal immune tolerance and homeostasis. <i>Microbial Pathogenesis</i> , 2021, 158, 105020.	2.9	13
5262	New Estimation of Antibiotic Resistance Genes in Sediment Along the Haihe River and Bohai Bay in China: A Comparison Between Single and Successive DNA Extraction Methods. <i>Frontiers in Microbiology</i> , 2021, 12, 705724.	3.5	1
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5343	Dominant hyphae-associated bacteria of <i>Fusarium oxysporum</i> f. sp. <i>cucumerinum</i> in different cropping systems and insight into their functions. <i>Applied Soil Ecology</i> , 2021, 165, 103977.	4.3	7
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5374	Soil microbial and chemical responses to foliar <i>Epichloa</i> fungal infection in <i>Lolium perenne</i> , <i>Hordeum brevisubulatum</i> and <i>Achnatherum inebrians</i> . <i>Fungal Ecology</i> , 2021, 53, 101091.	1.6	3
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5378	Effect of dietary histamine on intestinal morphology, inflammatory status, and gut microbiota in yellow catfish (<i>Pelteobagrus fulvidraco</i>). <i>Fish and Shellfish Immunology</i> , 2021, 117, 95-103.	3.6	17
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5400	Rapid pathogen discovery in diseased turbot (<i>Scophthalmus maximus</i>) using 16S rRNA high throughput sequencing. <i>Aquaculture Reports</i> , 2021, 21, 100835.	1.7	3
5401	Authentication of sea cucumber products using NGS-based DNA mini-barcoding. <i>Food Control</i> , 2021, 129, 108199.	5.5	13
5402	Variations of tongue coating microbiota in children with Henoch-Schönlein purpura nephritis. <i>Microbial Pathogenesis</i> , 2021, 160, 105192.	2.9	0

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5404	Magnesium and nitrogen drive soil bacterial community structure under long-term apple orchard cultivation systems. <i>Applied Soil Ecology</i> , 2021, 167, 104103.	4.3	8
5405	Composition change and decreased diversity of microbial eukaryotes in the coastal upwelling waters of South China Sea. <i>Science of the Total Environment</i> , 2021, 795, 148892.	8.0	13
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5408	Bacterial community structure and putative nitrogen-cycling functional traits along a charosphere gradient under waterlogged conditions. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108420.	8.8	21
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5410	Fertile islands lead to more conspicuous spatial heterogeneity of bacteria than soil physicochemical properties in a desert ecosystem. <i>Catena</i> , 2021, 206, 105526.	5.0	12
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5412	Efficiency and mechanism of reducing ammonia volatilization in alkaline farmland soil using <i>Bacillus amyloliquefaciens</i> biofertilizer. <i>Environmental Research</i> , 2021, 202, 111672.	7.5	21
5413	Multi-omics revealed the effects of rumen-protected methionine on the nutrient profile of milk in dairy cows. <i>Food Research International</i> , 2021, 149, 110682.	6.2	16
5414	Pathogenic hitchhiker diversity on international ships' ballast water at West Malaysia port. <i>Marine Pollution Bulletin</i> , 2021, 172, 112850.	5.0	13
5415	Seasonal variations in soil physicochemical properties and microbial community structure influenced by <i>Spartina alterniflora</i> invasion and <i>Kandelia obovata</i> restoration. <i>Science of the Total Environment</i> , 2021, 797, 149213.	8.0	25
5416	Dynamics of soil bacterial community diversity and composition at aggregate scales in a chronosequence of tea gardens. <i>Catena</i> , 2021, 206, 105486.	5.0	3
5417	Characterization of tissue-associated bacterial community of two <i>Bathymodiolus</i> species from the adjacent cold seep and hydrothermal vent environments. <i>Science of the Total Environment</i> , 2021, 796, 149046.	8.0	7
5418	Preferential temperature and ammonia concentration for in-situ growth of <i>Candidatus Nitrospira</i> ammonia oxidising archaea. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108405.	8.8	9
5419	Salinity gradients shape the nitrifier community composition in Nanliu River Estuary sediments and the ecophysiology of comammox <i>Nitrospira inopinata</i> . <i>Science of the Total Environment</i> , 2021, 795, 148768.	8.0	22
5420	<i>Vibrio parahaemolyticus</i> alters the community composition and function of intestinal microbiota in Pacific white shrimp, <i>Penaeus vannamei</i> . <i>Aquaculture</i> , 2021, 544, 737061.	3.5	23

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5421	Biological treatment of volatile organic compounds (VOCs)-containing wastewaters from wet scrubbers in semiconductor industry. <i>Chemosphere</i> , 2021, 282, 131137.	8.2	17
5422	Chiral enantiomers of the plant growth regulator paclobutrazol selectively affect community structure and diversity of soil microorganisms. <i>Science of the Total Environment</i> , 2021, 797, 148942.	8.0	12
5423	Novel Î ² -mannanase/GLP-1 fusion peptide high effectively ameliorates obesity in a mouse model by modifying balance of gut microbiota. <i>International Journal of Biological Macromolecules</i> , 2021, 191, 753-763.	7.5	25
5424	Soil microbial community composition but not diversity is affected by land-use types in the agro-pastoral ecotone undergoing frequent conversions between cropland and grassland. <i>Geoderma</i> , 2021, 401, 115165.	5.1	14
5425	Artificial light reduces foraging opportunities in wild least horseshoe bats. <i>Environmental Pollution</i> , 2021, 288, 117765.	7.5	16
5426	Effects of design parameters, microbial community and nitrogen removal on the field-scale multi-pond constructed wetlands. <i>Science of the Total Environment</i> , 2021, 797, 148989.	8.0	14
5427	Intrauterine antibiotic exposure affected neonatal gut bacteria and infant growth speed. <i>Environmental Pollution</i> , 2021, 289, 117901.	7.5	12
5428	Evolution of innate and adaptive immune genes in a non-model waterbird, the common tern. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105069.	2.3	6
5429	UV assisted backwashing for fouling control in membrane bioreactor operation. <i>Journal of Membrane Science</i> , 2021, 639, 119751.	8.2	16
5430	Effects of anode/cathode electroactive microorganisms on arsenic removal with organic/inorganic carbon supplied. <i>Science of the Total Environment</i> , 2021, 798, 149356.	8.0	7
5431	Meadow degradation increases spatial turnover rates of the fungal community through both niche selection and dispersal limitation. <i>Science of the Total Environment</i> , 2021, 798, 149362.	8.0	24
5432	Nitrifiers drive successions of particulate organic matter and microbial community composition in a starved macrocosm. <i>Environment International</i> , 2021, 157, 106776.	10.0	8
5433	Effect of biochar applied with plant growth-promoting rhizobacteria (PGPR) on soil microbial community composition and nitrogen utilization in tomato. <i>Pedosphere</i> , 2021, 31, 872-881.	4.0	21
5434	Homogenization of reservoir eukaryotic algal and cyanobacterial communities is accelerated by dam construction and eutrophication. <i>Journal of Hydrology</i> , 2021, 603, 126842.	5.4	8
5435	Productivity and quality of banana in response to chemical fertilizer reduction with bio-organic fertilizer: Insight into soil properties and microbial ecology. <i>Agriculture, Ecosystems and Environment</i> , 2021, 322, 107659.	5.3	35
5436	The interaction of acidophiles driving community functional responses to the re-inoculated chalcophyrite bioleaching process. <i>Science of the Total Environment</i> , 2021, 798, 149186.	8.0	12
5437	Fungal community composition and diversity in the rhizosphere soils of Argentina (syn. <i>Potentilla anserina</i> , on the Qinghai Plateau. <i>Fungal Ecology</i> , 2021, 54, 101107.	1.6	5
5438	Honey bee <i>Apis mellifera</i> larvae gut microbial and immune, detoxication responses towards flumethrin stress. <i>Environmental Pollution</i> , 2021, 290, 118107.	7.5	22

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5439	Alkaline phosphatase activity mediates soil organic phosphorus mineralization in a subalpine forest ecosystem. <i>Geoderma</i> , 2021, 404, 115376.	5.1	60
5440	Bioplastic accumulates antibiotic and metal resistance genes in coastal marine sediments. <i>Environmental Pollution</i> , 2021, 291, 118161.	7.5	20
5441	Dissolved organic carbon drives nutrient cycling via microbial community in paddy soil. <i>Chemosphere</i> , 2021, 285, 131472.	8.2	13
5442	Pollution alters methanogenic and methanotrophic communities and increases dissolved methane in small ponds. <i>Science of the Total Environment</i> , 2021, 801, 149723.	8.0	8
5443	NGS-Based Metagenomic Study of Four Traditional Bulgarian Green Cheeses from Tcherni Vit. <i>LWT - Food Science and Technology</i> , 2021, 152, 112278.	5.2	9
5444	Valorization of carbon dioxide and waste (Derived from the site of Eutrophication) into syngas using a catalytic thermo-chemical platform. <i>Bioresource Technology</i> , 2021, 341, 125858.	9.6	1
5445	Evolution of PM2.5 bacterial community structure in Beijing's suburban atmosphere. <i>Science of the Total Environment</i> , 2021, 799, 149387.	8.0	10
5446	The quality of compost was improved by low concentrations of fulvic acid owing to its optimization of the exceptional microbial structure. <i>Bioresource Technology</i> , 2021, 342, 125843.	9.6	17
5447	<i>Paracoccus</i> and <i>Achromobacter</i> bacteria contribute to rapid biodegradation of imidacloprid in soils. <i>Ecotoxicology and Environmental Safety</i> , 2021, 225, 112785.	6.0	18
5448	Propamocarb exposure has the potential to accelerate the formation of atherosclerosis in both WT and ApoE ^{-/-} mice accompanied by gut microbiota dysbiosis. <i>Science of the Total Environment</i> , 2021, 800, 149602.	8.0	7
5449	Improvement of nitrogen and phosphorus availability by <i>Pseudoalteromonas</i> sp. during salt-washing in saline-alkali soil. <i>Applied Soil Ecology</i> , 2021, 168, 104117.	4.3	25
5450	<i>Lycium barbarum</i> L. (goji berry) monocropping causes microbial diversity loss and induces <i>Fusarium</i> spp. enrichment at distinct soil layers. <i>Applied Soil Ecology</i> , 2021, 168, 104107.	4.3	17
5451	Key indicators for renewal and reconstruction of perennial trees soil: Microorganisms and phloridzin. <i>Ecotoxicology and Environmental Safety</i> , 2021, 225, 112723.	6.0	22
5452	The structure and assembly mechanisms of plastisphere microbial community in natural marine environment. <i>Journal of Hazardous Materials</i> , 2022, 421, 126780.	12.4	93
5453	Gut microbiota may contribute to the postnatal male reproductive abnormalities induced by prenatal dibutyl phthalate exposure. <i>Chemosphere</i> , 2022, 287, 132046.	8.2	25
5454	Soil carbon supplementation: Improvement of root-surrounding soil bacterial communities, sugar and starch content in tobacco (<i>N. tabacum</i>). <i>Science of the Total Environment</i> , 2022, 802, 149835.	8.0	15
5455	Subsoiling and conversion to conservation tillage enriched nitrogen cycling bacterial communities in sandy soils under long-term maize monoculture. <i>Soil and Tillage Research</i> , 2022, 215, 105197.	5.6	29
5456	Restoration of organic-matter-impovertished arable soils through the application of soil conditioner prepared via short-time hydrothermal fermentation. <i>Environmental Research</i> , 2022, 204, 112088.	7.5	4

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5458	Analysis of bacterial community functional diversity in late-stage shrimp (<i>Litopenaeus vannamei</i>) ponds using Biolog EcoPlates and PICRUSt2. <i>Aquaculture</i> , 2022, 546, 737288.	3.5	14
5459	Plant and soil elemental C:N:P ratios are linked to soil microbial diversity during grassland restoration on the Loess Plateau, China. <i>Science of the Total Environment</i> , 2022, 806, 150557.	8.0	22
5460	Adaption to hydrogen sulfide-rich environments: Strategies for active detoxification in deep-sea symbiotic mussels, <i>Gigantidas platifrons</i> . <i>Science of the Total Environment</i> , 2022, 804, 150054.	8.0	19
5461	Comparative study of the anti-obesity and gut microbiota modulation effects of green tea phenolics and their oxidation products in high-fat-induced obese mice. <i>Food Chemistry</i> , 2022, 367, 130735.	8.2	24
5462	Impacts of municipal wastewater treatment plant discharge on microbial community structure and function of the receiving river in Northwest Tibetan Plateau. <i>Journal of Hazardous Materials</i> , 2022, 423, 127170.	12.4	38
5463	Remediation of soils co-contaminated with cadmium and dichlorodiphenyltrichloroethanes by king grass associated with <i>Piriformospora indica</i> : Insights into the regulation of root excretion and reshaping of rhizosphere microbial community structure. <i>Journal of Hazardous Materials</i> , 2022, 422, 126936.	12.4	20
5464	Cd and Pb immobilisation with iron oxide/lignin composite and the bacterial community response in soil. <i>Science of the Total Environment</i> , 2022, 802, 149922.	8.0	18
5465	Metal(loid)s diffusion pathway triggers distinct microbiota responses in key regions of typical karst non-ferrous smelting assembly. <i>Journal of Hazardous Materials</i> , 2022, 423, 127164.	12.4	12
5466	Little environmental adaptation and high stability of bacterial communities in rhizosphere rather than bulk soils in rice fields. <i>Applied Soil Ecology</i> , 2022, 169, 104183.	4.3	22
5467	Plastic film mulching reduces microbial interactions in black soil of northeastern China. <i>Applied Soil Ecology</i> , 2022, 169, 104187.	4.3	18
5468	Recovery patterns of soil bacterial and fungal communities in Chinese boreal forests along a fire chronosequence. <i>Science of the Total Environment</i> , 2022, 805, 150372.	8.0	15
5469	From surviving to thriving, the assembly processes of microbial communities in stone biodeterioration: A case study of the West Lake UNESCO World Heritage area in China. <i>Science of the Total Environment</i> , 2022, 805, 150395.	8.0	25
5470	The potential role of fertilizer-derived exogenous bacteria on soil bacterial community assemblage and network formation. <i>Chemosphere</i> , 2022, 287, 132338.	8.2	23
5471	Drivers of microbial beta-diversity in wastewater treatment plants in China. <i>Journal of Environmental Sciences</i> , 2022, 115, 341-349.	6.1	5
5472	Microbiota associated with the rhizosphere of <i>Paeonia lactiflora</i> Pall. (ornamental cultivar). <i>Applied Soil Ecology</i> , 2022, 169, 104214.	4.3	9
5473	Response of soil bacterial community to agricultural reclamation in the Tengger desert, northwestern China. <i>Applied Soil Ecology</i> , 2022, 169, 104189.	4.3	6
5474	Insight to bacteria community response of organic management in apple orchard-bagasse fertilizer combined with biochar. <i>Chemosphere</i> , 2022, 286, 131693.	8.2	20

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5477	Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. <i>Annals of Translational Medicine</i> , 2021, 9, 32-32.	1.7	16
5478	Reclassification of <i>Sphaerotilus natans</i> subsp. <i>sulfidivorans</i> Gridneva et al. 2011 as <i>Sphaerotilus sulfidivorans</i> sp. nov. and comparative genome analysis of the genus <i>Sphaerotilus</i> . <i>Archives of Microbiology</i> , 2021, 203, 1595-1599.	2.2	8
5480	Assessing the efficacy of eDNA metabarcoding for measuring microbial biodiversity within forest ecosystems. <i>Scientific Reports</i> , 2021, 11, 1629.	3.3	16
5481	Arbuscular mycorrhizal fungal colonization and soil pH induced by nitrogen and phosphorus additions affects leaf C:N:P stoichiometry in Chinese fir (<i>Cunninghamia lanceolata</i>) forests. <i>Plant and Soil</i> , 2021, 461, 421-440.	3.7	28
5482	<i>Amyntas corticis</i> genome reveals molecular mechanisms behind global distribution. <i>Communications Biology</i> , 2021, 4, 135.	4.4	6
5483	Effects of three different mannans on obesity and gut microbiota in high-fat diet-fed C57BL/6J mice. <i>Food and Function</i> , 2021, 12, 4606-4620.	4.6	37
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5486	Effect of host breeds on gut microbiome and serum metabolome in meat rabbits. <i>BMC Veterinary Research</i> , 2021, 17, 24.	1.9	20
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5489	The Therapeutic Efficacy of Curcumin vs. Metformin in Modulating the Gut Microbiota in NAFLD Rats: A Comparative Study. <i>Frontiers in Microbiology</i> , 2020, 11, 555293.	3.5	27
5490	Fecal microbiota composition associates with the capacity of human peripheral blood monocytes to differentiate into immunogenic dendritic cells <i>in vitro</i> . <i>Gut Microbes</i> , 2021, 13, 1-20.	9.8	9
5491	Efficient genotyping with backwards compatibility: converting a legacy microsatellite panel for muskellunge (<i>Esox masquinongy</i>) to genotyping-by-sequencing chemistry. <i>Conservation Genetics Resources</i> , 2021, 13, 151-159.	0.8	2
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5493	Comparison and interpretation of characteristics of Rhizosphere microbiomes of three blueberry varieties. <i>BMC Microbiology</i> , 2021, 21, 30.	3.3	12
5494	Plant and Animal-Type Feedstuff Shape the Gut Microbiota and Metabolic Processes of the Chinese Mitten Crab <i>Eriocheir sinensis</i> . <i>Frontiers in Veterinary Science</i> , 2021, 8, 589624.	2.2	10

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5496	Alteration of the fecal microbiota in Chinese patients with <i>Schistosoma japonicum</i> infection. <i>Parasite</i> , 2021, 28, 1.	2.0	16
5498	Tropical and temperate wastewater treatment plants assemble different and diverse microbiomes. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 853-867.	3.6	5
5499	Plant Compartments and Developmental Stages Modulate the Balance between Niche-Based and Neutral Processes in Soybean Microbiome. <i>Microbial Ecology</i> , 2021, 82, 416-428.	2.8	27
5500	Ancient DNA from the Asiatic Wild Dog (<i>Cuon alpinus</i>) from Europe. <i>Genes</i> , 2021, 12, 144.	2.4	5
5501	Complete Genome Sequence of <i>Mycobacterium bovis</i> BCG SL222 Sofia, the First WHO Reference Reagent for the M. bovis BCG Vaccine of the Russian BCG-I Substrain. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
5502	Draft Genome Sequences of <i>Idiomarina abyssalis</i> Strain KJE, <i>Marinobacter salarius</i> Strain NP2017, and <i>Marinobacter salarius</i> Strain AT3901, Isolated from Deep-Sea Sediment near the Western Flank of the Mid-Atlantic Ridge. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
5503	Bacterial diversity and lipid biomarkers in sea ice and sinking particulate organic material during the melt season in the Canadian Arctic. <i>Elementa</i> , 2021, 9, .	3.2	3
5504	<i>Limosilactobacillus fermentum</i> JL-3 isolated from Jiangshui ameliorates hyperuricemia by degrading uric acid. <i>Gut Microbes</i> , 2021, 13, 1-18.	9.8	68
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5508	Parkinson's Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
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5511	Contribution of sample processing to gut microbiome analysis in the model <i>Lepidoptera</i> , silkworm <i>Bombyx mori</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4658-4668.	4.1	16
5512	Community structure of fungal pathogens causing spikelet rot disease of naked oat from different ecological regions of China. <i>Scientific Reports</i> , 2021, 11, 1243.	3.3	5
5513	Dynamics and competition of CRISPR-Cas9 ribonucleoproteins and AAV donor-mediated NHEJ, MMEJ and HDR editing. <i>Nucleic Acids Research</i> , 2021, 49, 969-985.	14.5	90

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5517	Microbiota succession during aerobic stability of maize silage inoculated with <i>Lentilactobacillus buchneri</i> NCIMB 40788 and <i>Lentilactobacillus hilgardii</i> CNCM 4785. <i>MicrobiologyOpen</i> , 2021, 10, e1153.	3.0	31
5518	Revisiting the phosphotyrosine binding pocket of Fyn SH2 domain led to the identification of novel SH2 superbinders.. <i>Protein Science</i> , 2021, 30, 558-570.	7.6	9
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5521	Transcriptomics and Proteomics of Foodborne Bacterial Pathogens. , 2017, , 167-200.		1
5522	Metagenomic Methods: From Seawater to the Database. , 2019, , 3-16.		1
5523	Analysis of the developing gut microbiota in young dairy calvesâ€impact of colostrum microbiota and gut disturbances. <i>Tropical Animal Health and Production</i> , 2021, 53, 50.	1.4	20
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5525	Diversity and composition of microbiota during fermentation of traditional Nuodeng ham. <i>Journal of Microbiology</i> , 2021, 59, 20-28.	2.8	9
5526	The microbiome and metabolome of Napier grass silages prepared with screened lactic acid bacteria during ensiling and aerobic exposure. <i>Animal Feed Science and Technology</i> , 2020, 269, 114673.	2.2	34
5527	The Sydney rock oyster microbiota is influenced by location, season and genetics. <i>Aquaculture</i> , 2020, 527, 735472.	3.5	17
5528	Anaerobic digestion of aqueous phase from hydrothermal liquefaction of <i>Spirulina</i> using biostimulated sludge. <i>Bioresource Technology</i> , 2020, 312, 123552.	9.6	12
5529	Changes in rhizobacterial community mediating atrazine dissipation by arbuscular mycorrhiza. <i>Chemosphere</i> , 2020, 256, 127046.	8.2	27
5530	Aerobic degradation of high tetramethylammonium hydroxide (TMAH) and its impacts on nitrification and microbial community. <i>Chemosphere</i> , 2020, 258, 127146.	8.2	17
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5533	Fetal and early postnatal lead exposure measured in teeth associates with infant gut microbiota. <i>Environment International</i> , 2020, 144, 106062.	10.0	21
5534	Growth inhibition of sulfate-reducing bacteria for trichloroethylene dechlorination enhancement. <i>Environmental Research</i> , 2020, 187, 109629.	7.5	17
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5538	Integral approach using bacterial microbiome to stabilize municipal solid waste. <i>Journal of Environmental Management</i> , 2020, 265, 110528.	7.8	14
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5542	Meteorological factors had more impact on airborne bacterial communities than air pollutants. <i>Science of the Total Environment</i> , 2017, 601-602, 703-712.	8.0	138
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5546	Effects of different molecular weights of chitosan on methane production and bacterial community structure in vitro. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1644-1655.	3.5	15
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5548	Generating quantitative binding landscapes through fractional binding selections combined with deep sequencing and data normalization. <i>Nature Communications</i> , 2020, 11, 297.	12.8	10
5549	Base editors for simultaneous introduction of C-to-T and A-to-G mutations. <i>Nature Biotechnology</i> , 2020, 38, 865-869.	17.5	137

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5552	Systematic, continental scale temporal monitoring of marine pelagic microbiota by the Australian Marine Microbial Biodiversity Initiative. <i>Scientific Data</i> , 2018, 5, 180130.	5.3	41
5553	Gut dysbiosis is associated with primary hypothyroidism with interaction on gut-thyroid axis. <i>Clinical Science</i> , 2020, 134, 1521-1535.	4.3	52
5554	Early Gut Microbiota Changes in Preterm Infants with Bronchopulmonary Dysplasia: A Pilot Caseâ€“Control Study. <i>American Journal of Perinatology</i> , 2021, 38, 1142-1149.	1.4	9
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6758	Characterization of the fecal microbiota in gastrointestinal cancer patients and healthy people. <i>Clinical and Translational Oncology</i> , 2022, 24, 1134-1147.	2.4	9
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6760	Sugarcane-Peanut Intercropping System Enhances Bacteria Abundance, Diversity, and Sugarcane Parameters in Rhizospheric and Bulk Soils. <i>Frontiers in Microbiology</i> , 2021, 12, 815129.	3.5	20
6761	Microbiome Resilience and Health Implications for People in Half-Year Travel. <i>Frontiers in Immunology</i> , 2022, 13, 848994.	4.8	2
6762	Effect of g-C3N4 on biodiversity and structure of bacterial community in sediment of Xiangjiang River under tetracycline pressure. <i>Ecotoxicology</i> , 2022, 31, 503-515.	2.4	3
6763	Distinct gut microbiota profiles of Asian honey bee (<i>Apis cerana</i>) foragers. <i>Archives of Microbiology</i> , 2022, 204, 187.	2.2	2
6764	<i>Lycium barbarum</i> Polysaccharides as Antibiotic Substitutes Improve Growth Performance, Serum Immunity, Antioxidant Status, and Intestinal Health for Weaned Piglets. <i>Frontiers in Microbiology</i> , 2021, 12, 819993.	3.5	6
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6769	<i>Bacillus</i> symbiont drives alterations in intestinal microbiota and circulating metabolites of lepidopteran host. <i>Environmental Microbiology</i> , 2022, 24, 4049-4064.	3.8	13
6770	Impact of Biochar on Rhizosphere Bacterial Diversity Restoration Following Chloropicrin Fumigation of Planted Soil. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 2126.	2.6	12
6771	Murine Model for Measuring Effects of Humanized-Dosing of Antibiotics on the Gut Microbiome. <i>Frontiers in Microbiology</i> , 2022, 13, 813849.	3.5	1
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6780	Anticyclonic Eddy Driving Significant Changes in Prokaryotic and Eukaryotic Communities in the South China Sea. <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	6
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6782	Insights Into the Species-Specific Microbiota of Greenideinae (Hemiptera: Aphididae) With Evidence of Phyllosymbiosis. <i>Frontiers in Microbiology</i> , 2022, 13, 828170.	3.5	3
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6786	Effects of Sodium Hyaluronate Eye Drops With or Without Preservatives on Ocular Surface Bacterial Microbiota. <i>Frontiers in Medicine</i> , 2022, 9, 793565.	2.6	4
6787	Comparison of genetically modified insect-resistant maize and non-transgenic maize revealed changes in soil metabolomes but not in rhizosphere bacterial community. <i>GM Crops and Food</i> , 2022, 13, 1-14.	3.8	13
6788	Microbiome structure and response to watering in rhizosphere of <i>Nitrosalsola vermiculata</i> and surrounding bulk soil. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2022, 50, 12567.	1.1	1
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6791	High-Throughput Sequencing-Based Analysis of Rhizosphere and Diazotrophic Bacterial Diversity Among Wild Progenitor and Closely Related Species of Sugarcane (<i>Saccharum</i> spp. Inter-Specific) Tj ETQq0 0 0 rgBT.4 Overlook 10 Tf 50	3.4	10
6792	Effects of Ambient Microbiota on the Gut Microbiota of <i>Macrobrachium rosenbergii</i> . <i>Water (Switzerland)</i> , 2022, 14, 658.	2.7	1
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6796	Grazing by Tibetan Sheep Enhances Soil Bacterial and Fungal Diversity in Cold Season Pastures of Alpine Meadows on the Northern Qinghai-Tibetan Plateau. <i>Journal of Soil Science and Plant Nutrition</i> , 2022, 22, 2434-2456.	3.4	9
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6810	Effects of Four Antibiotics on the Diversity of the Intestinal Microbiota. <i>Microbiology Spectrum</i> , 2022, 10, e0190421.	3.0	25
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6813	HAM-ART: An optimised culture-free Hi-C metagenomics pipeline for tracking antimicrobial resistance genes in complex microbial communities. <i>PLoS Genetics</i> , 2022, 18, e1009776.	3.5	14
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6823	Intra- and interpopulation transposition of mobile genetic elements driven by antibiotic selection. <i>Nature Ecology and Evolution</i> , 2022, 6, 555-564.	7.8	37
6824	Diversity and Evolution of Pigment Types in Marine <i>Synechococcus</i> Cyanobacteria. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	15
6825	Peanut and cotton intercropping increases productivity and economic returns through regulating plant nutrient accumulation and soil microbial communities. <i>BMC Plant Biology</i> , 2022, 22, 121.	3.6	14
6826	Phosphorus Shapes Soil Microbial Community Composition and Network Properties During Grassland Expansion Into Shrubs in Tibetan Dry Valleys. <i>Frontiers in Plant Science</i> , 2022, 13, 848691.	3.6	6
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6836	Effect of rapeseed straw-derived biochar on soil bacterial community structure at tillering stage of <i>Oryza Sativa</i> . <i>Canadian Journal of Microbiology</i> , 2022, , .	1.7	1
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6839	Insights into gut microbiota communities of <i>Poecilobdella manillensis</i> , a prevalent Asian medicinal leech. <i>Journal of Applied Microbiology</i> , 2022, 133, 1402-1413.	3.1	1

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6842	Comparative microbiome analysis of <i>Diaphorina citri</i> and its associated parasitoids <i>Tamarixia radiata</i> and <i>Diaphorencyrtus aligarhensis</i> reveals <i>Wolbachia</i> as a dominant endosymbiont. <i>Environmental Microbiology</i> , 2022, 24, 1638-1652.	3.8	6
6843	High Abundance of Thaumarchaeota Found in Deep Metamorphic Subsurface in Eastern China. <i>Microorganisms</i> , 2022, 10, 542.	3.6	2
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6846	Stitchr: stitching coding TCR nucleotide sequences from V/J/CDR3 information. <i>Nucleic Acids Research</i> , 2022, 50, e68-e68.	14.5	8
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6852	Gut Microbial Characterization of Melon-Headed Whales (<i>Peponocephala electra</i>) Stranded in China. <i>Microorganisms</i> , 2022, 10, 572.	3.6	6
6853	Alleviating Soil Acidification Could Increase Disease Suppression of Bacterial Wilt by Recruiting Potentially Beneficial Rhizobacteria. <i>Microbiology Spectrum</i> , 2022, 10, e0233321.	3.0	15
6854	Normal Light-Dark and Short-Light Cycles Regulate Intestinal Inflammation, Circulating Short-chain Fatty Acids and Gut Microbiota in Period2 Gene Knockout Mice. <i>Frontiers in Immunology</i> , 2022, 13, 848248.	4.8	14
6855	Correlation analysis of the oral mucosal microbiome and diabetes mellitus using microbial DNA in elderly male subjects. <i>Oral Biology Research</i> , 2022, 46, 10-20.	0.1	1
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6860	Loss of gut microbial diversity in the cultured, agastric fish, Mexican pike silverside (<i>Chirostoma) Tj ETQq1 1 0.784314 rgBT /Overl	2.0	3
6861	Metabolic Alternations During Gestation in Dezhou Donkeys and the Link to the Gut Microbiota. Frontiers in Microbiology, 2022, 13, 801976.	3.5	2
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6880	The structure of microbial communities of activated sludge of large-scale wastewater treatment plants in the city of Moscow. <i>Scientific Reports</i> , 2022, 12, 3458.	3.3	38
6881	16S rRNA gene sequencing reveals altered composition of gut microbiota in postoperative individuals with renal stones. <i>Letters in Applied Microbiology</i> , 2022, 75, 271-280.	2.2	3
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6884	Biochar Amendment and Nitrogen Fertilizer Contribute to the Changes in Soil Properties and Microbial Communities in a Paddy Field. <i>Frontiers in Microbiology</i> , 2022, 13, 834751.	3.5	30
6885	Comparative Respiratory Tract Microbiome Between Carbapenem-Resistant <i>Acinetobacter baumannii</i> Colonization and Ventilator Associated Pneumonia. <i>Frontiers in Microbiology</i> , 2022, 13, 782210.	3.5	5
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6887	Bacterial microbiota of the contact lens surface and associated care behaviours. <i>Heliyon</i> , 2022, 8, e09038.	3.2	5
6888	Effects of Corn and Broken Rice Extrusion on the Feed Intake, Nutrient Digestibility, and Gut Microbiota of Weaned Piglets. <i>Animals</i> , 2022, 12, 818.	2.3	5
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6890	Multiple causal variants underlie genetic associations in humans. <i>Science</i> , 2022, 375, 1247-1254.	12.6	75
6891	Differences in microbiome composition and transcriptome profiles between male and female <i>Paederus fuscipes</i> harbouring pederin-producing bacteria. <i>Insect Molecular Biology</i> , 2022, 31, 457-470.	2.0	2
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6898	Effects of dietary fibre on intestinal microbiota in geese evaluated by 16SrRNA gene sequencing. <i>Journal of Applied Microbiology</i> , 2022, , .	3.1	2
6899	Effects of cadmium contamination on bacterial and fungal communities in <i>Panax ginseng</i> -growing soil. <i>BMC Microbiology</i> , 2022, 22, 77.	3.3	8
6900	Spatial Pattern of Endophytic Fungi and the Symbiotic Germination of <i>Tulasnella</i> Fungi from Wild <i>Cymbidium goeringii</i> (Orchidaceae) in China. <i>Current Microbiology</i> , 2022, 79, 139.	2.2	0
6901	Illumina MiSeq Sequencing Reveals Correlations among Fruit Ingredients, Environmental Factors, and AMF Communities in Three <i>Lycium Barbarum</i> Producing Regions of China. <i>Microbiology Spectrum</i> , 2022, 10, e0229321.	3.0	11
6902	Leveraging eDNA metabarcoding to characterize nearshore fish communities in Southeast Alaska: Do habitat and tide matter?. <i>Environmental DNA</i> , 2022, 4, 868-880.	5.8	11
6903	Assessing the Effect of Smokeless Tobacco Consumption on Oral Microbiome in Healthy and Oral Cancer Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841465.	3.9	13
6904	Long Term Influence of Fertility and Rotation on Soil Nitrification Potential and Nitrifier Communities. <i>Frontiers in Soil Science</i> , 2022, 2, .	2.2	4
6905	Nasal Bacterial Microbiome Differs Between Healthy Controls and Those With Asthma and Allergic Rhinitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841995.	3.9	16
6906	Manure fertilization enhanced microbial immigration in the wheat rhizosphere. <i>Journal of Soils and Sediments</i> , 0, , 1.	3.0	0
6907	Characterization of Distinct Microbiota Associated with Scalp Dermatitis in Patients with Atopic Dermatitis. <i>Journal of Clinical Medicine</i> , 2022, 11, 1735.	2.4	8
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6909	Comparison of changes in fecal microbiota of calves with and without dam. <i>PeerJ</i> , 2022, 10, e12826.	2.0	2
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6911	Small-sized salt-tolerant denitrifying and phosphorus removal aerobic granular sludge cultivated with mariculture waste solids to treat synthetic mariculture wastewater. <i>Biochemical Engineering Journal</i> , 2022, 181, 108396.	3.6	10
6912	The effect of inulin-type fructans on the intestinal immune function of antibiotic-treated mice. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 3265-3278.	3.6	2
6913	Infestation of Rice by Gall Midge Influences Density and Diversity of <i>Pseudomonas</i> and <i>Wolbachia</i> in the Host Plant Microbiome. <i>Current Genomics</i> , 2022, 23, 126-136.	1.6	1
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6917	Swimming Exercise Modulates Gut Microbiota in CUMS-Induced Depressed Mice. Neuropsychiatric Disease and Treatment, 2022, Volume 18, 749-760.	2.2	14
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6922	Assessing rates of parasite coinfection and spatiotemporal strain variation via metabarcoding: Insights for the conservation of European turtle doves <i>Streptopelia turtur</i>. Molecular Ecology, 2022, 31, 2730-2751.	3.9	8
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6952	Food Neophobia and scarce olfactory performances are linked to oral microbiota. <i>Food Research International</i> , 2022, 155, 111092.	6.2	3
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6954	Enhancing effect of <i>Platymonas</i> addition on water quality, microbial community diversity and shrimp performance in biofloc-based tanks for <i>Penaeus vannamei</i> nursery. <i>Aquaculture</i> , 2022, 554, 738057.	3.5	10
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6965	The host-specific resistome in environmental feces of Eurasian otters (<i>Lutra lutra</i>) and leopard cats (<i>Prionailurus bengalensis</i>) revealed by metagenomic sequencing. <i>One Health</i> , 2022, 14, 100385.	3.4	1
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6967	Combined effects of oxytetracycline and microplastic on wheat seedling growth and associated rhizosphere bacterial communities and soil metabolite profiles. <i>Environmental Pollution</i> , 2022, 302, 119046.	7.5	39
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6973	Effects of choline chloride on intestinal microbiota and its association with liver fat accumulation in zebrafish. <i>Aquaculture Reports</i> , 2022, 24, 101096.	1.7	0
6974	Diversity and community composition of nirS-type denitrifying bacteria and ammonia-oxidizing archaea in biofilm samples attached to bio-substrate and abio-substrates in integrated ecological floating bed systems. <i>Ecological Engineering</i> , 2022, 180, 106641.	3.6	4
6975	Topographic attributes override impacts of agronomic practices on prokaryotic community structure. <i>Applied Soil Ecology</i> , 2022, 175, 104446.	4.3	2
6976	Temporal variation of management effects on soil microbial communities. <i>Geoderma</i> , 2022, 418, 115828.	5.1	6
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6982	Long-term metal pollution shifts microbial functional profiles of nitrification and denitrification in agricultural soils. <i>Science of the Total Environment</i> , 2022, 830, 154732.	8.0	15
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6991	Spatial dynamics of active microeukaryotes along a latitudinal gradient: Diversity, assembly process, and co-occurrence relationships. <i>Environmental Research</i> , 2022, 212, 113234.	7.5	5
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6993	Distribution and Genetic Diversity of Hepatitis E Virus in Wild and Domestic Rabbits in Australia. <i>Pathogens</i> , 2021, 10, 1637.	2.8	6
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6995	Lignans dramatically enhance the resistance of <i>Fraxinus velutina</i> Torr. by adjusting the dominant bacterium group of <i>Agrilus planipennis</i> Fairmaire. <i>Pest Management Science</i> , 2022, 78, 1386-1397.	3.4	6
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7006	Mulberry (<i>Morus alba</i> L.) leaf polysaccharide ameliorates insulin resistance and adipose deposition associated gut microbiota and lipid metabolites in high fat diet induced obese mice. <i>Food Science and Nutrition</i> , 2022, 10, 617-630.	3.4	14
7007	Governor Vessel Moxibustion Therapy Improves Microbiota Structure in Ankylosing Spondylitis Patients. <i>Disease Markers</i> , 2021, 2021, 1-8.	1.3	2
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8651	Changes in Microbial Diversity and Nutritional Components of Mare Milk Before and After Traditional Fermentation. <i>Frontiers in Sustainable Food Systems</i> , 0, 6, .	3.9	1
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8699	The interplay of gut microbiota between donors and recipients determines the efficacy of fecal microbiota transplantation. Gut Microbes, 2022, 14, .	9.8	19
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8885	Linking the bacterial microbiome between gut and habitat soil of Tibetan macaque (<i>Macaca</i>) Tj ETQq1 1 0.784314 rgBT /Qoverlock 10	1.9	2
8887	Structural and compositional segregation of the gut microbiota in HCV and liver cirrhotic patients: A clinical pilot study. <i>Microbial Pathogenesis</i> , 2022, 171, 105739.	2.9	4
8888	Plant Growth-Promoting Rhizobacteria Promote Growth of Seedlings, Regulate Soil Microbial Community, and Alleviate Damping-Off Disease Caused by <i>Rhizoctonia solani</i> on <i>Pinus sylvestris</i> var. <i>mongolica</i> . <i>Plant Disease</i> , 2022, 106, 2730-2740.	1.4	4
8889	Protective effect of methionine on the intestinal oxidative stress and microbiota change induced by nickel. <i>Ecotoxicology and Environmental Safety</i> , 2022, 244, 114037.	6.0	2
8890	Enrichment of Methylosinus-dominant consortia from mangroves for polyhydroxybutyrate (PHB) production. <i>Journal of Environmental Chemical Engineering</i> , 2022, 10, 108490.	6.7	5
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8896	Impact of golden mussel (<i>Limnoperna fortunei</i>) colonization on bacterial communities and potential risk to water quality. <i>Ecological Indicators</i> , 2022, 144, 109499.	6.3	3
8897	Oral exposure to Ag or TiO2 nanoparticles perturbed gut transcriptome and microbiota in a mouse model of ulcerative colitis. <i>Food and Chemical Toxicology</i> , 2022, 169, 113368.	3.6	6
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8901	Implications of environmentally shaped microbial communities for insecticide resistance in <i>Sitobion miscanthi</i> . <i>Environmental Research</i> , 2022, 215, 114409.	7.5	4
8902	Field-aged biochar enhances soil organic carbon by increasing recalcitrant organic carbon fractions and making microbial communities more conducive to carbon sequestration. <i>Agriculture, Ecosystems and Environment</i> , 2022, 340, 108177.	5.3	17

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8929	Analysis of endophyte diversity of <i>Gentiana officinalis</i> among different tissue types and ages and their association with four medicinal secondary metabolites. <i>PeerJ</i> , 0, 10, e13949.	2.0	5
8930	Structural Characteristics and Formation Mechanism of Microbiota Related to Fermentation Ability and Alcohol Production Ability in Nongxiang Daqu. <i>Foods</i> , 2022, 11, 2602.	4.3	8
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8935	FXR Signaling-Mediated Bile Acid Metabolism Is Critical for Alleviation of Cholesterol Gallstones by <i>Lactobacillus</i> Strains. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	17
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8941	The Comparison of Antioxidant Performance, Immune Performance, IIS Activity and Gut Microbiota Composition between Queen and Worker Bees Revealed the Mechanism of Different Lifespan of Female Casts in the Honeybee. <i>Insects</i> , 2022, 13, 772.	2.2	3
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8943	Long-Term Fertilization Strategy Impacts <i>Rhizoctonia solani</i> –Microbe Interactions in Soil and Rhizosphere and Defense Responses in Lettuce. <i>Microorganisms</i> , 2022, 10, 1717.	3.6	5
8945	Correlation in endophytic fungi community diversity and bioactive compounds of <i>Sophora alopecuroides</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	8
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8953	Comparison of Gut Bacterial Communities of <i>Locusta migratoria manilensis</i> (Meyen) Reared on Different Food Plants. <i>Biology</i> , 2022, 11, 1347.	2.8	6
8954	Effects of sodium humate and probiotics on growth performance enzyme activity and microbial environment of <i>Litopenaeus vannamei</i> in high-density zero-water exchange systems. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	3
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8957	<i>Strongyloides stercoralis</i> infection induces gut dysbiosis in chronic kidney disease patients. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010302.	3.0	5
8958	Sheep fecal transplantation affects growth performance in mouse models by altering gut microbiota. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	1
8959	Effect of continuous cropping of konjac (<i>Amorphophallus konjac</i>) on soil bacterial communities as evaluated by Illumina high-throughput sequencing. <i>Archives of Agronomy and Soil Science</i> , 0, , 1-15.	2.6	0

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8966	Long-term cultivation alter soil bacterial community in a forest-grassland transition zone. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
8967	Diversity and assembly processes of microbial eukaryotic communities in Fildes Peninsula Lakes (West) Tj ETQq1 1 0,784314,rgBT /Over	3.3	4
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8972	Delayed application of N fertilizer mitigates the carbon emissions of pea/maize intercropping via altering soil microbial diversity. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
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8976	Comparison and interpretation of freshwater bacterial structure and interactions with organic to nutrient imbalances in restored wetlands. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
8977	In-Forest Planting of High-Value Herb <i>Sarcandra glabra</i> Enhances Soil Carbon Storage without Affecting the Diversity of the Arbuscular Mycorrhiza Fungal Community and Composition of <i>Cunninghamia lanceolata</i> . <i>Microorganisms</i> , 2022, 10, 1844.	3.6	1

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8982	5300â€Yearâ€old soil carbon is less primed than young soil organic matter. <i>Global Change Biology</i> , 2023, 29, 260-275.	9.5	13
8983	Uncovering the biogeography of the microbial community and its association with nutrient metabolism in the intestinal tract using a pig model. <i>Frontiers in Nutrition</i> , 0, 9, .	3.7	1
8984	The impact of pelvic floor electrical stimulation on vaginal microbiota and immunity. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	2
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8988	Absciscic acid-polyacrylamide (ABA-PAM) treatment enhances forage grass growth and soil microbial diversity under drought stress. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
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8996	Characteristics of soil microbiota and organic carbon distribution in jackfruit plantation under different fertilization regimes. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
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9008	Effects of g-C ₃ N ₄ on bacterial community and tetracycline resistance genes in two typical sediments in tetracycline pollution remediation. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
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9016	Metabarcoding and Metabolome Analyses Reveal Mechanisms of <i>Leymus chinensis</i> Growth Promotion by Fairy Ring of <i>Leucocalocybe mongolica</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 944.	3.5	6
9017	Effects of Dietary Supplementation of Solubles from Shredded, Steam-Exploded Pine Particles on the Performance and Cecum Microbiota of Acute Heat-Stressed Broilers. <i>Microorganisms</i> , 2022, 10, 1795.	3.6	6

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9018	Factors structuring microbial communities in highly impacted coastal marine sediments (Mar Menor) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	3.5	4
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9023	Microbiological characteristics of different tongue coatings in adults. BMC Microbiology, 2022, 22, .	3.3	3
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9032	High fat diet-induced hyperlipidemia and tissue steatosis in rabbits through modulating ileal microbiota. Applied Microbiology and Biotechnology, 2022, 106, 7187-7207.	3.6	5
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9035	Comparative Analysis of In Situ Eukaryotic Food Sources in Three Tropical Sea Cucumber Species by Metabarcoding. Animals, 2022, 12, 2303.	2.3	2
9036	Modulating effect of Xuanfei Baidu granule on host metabolism and gut microbiome in rats. Frontiers in Pharmacology, 0, 13, .	3.5	3
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9039	Anthocyanin Addition to Kefir: Metagenomic Analysis of Microbial Community Structure. <i>Current Microbiology</i> , 2022, 79, .	2.2	4
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9041	Diversity of bacterial community in Jerusalem artichoke (<i>Helianthus tuberosus</i> L.) during storage is associated with the genotype and carbohydrates. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
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9058	Influence of planting yellowhorn (<i>Xanthoceras sorbifolium</i> Bunge) on the bacterial and fungal diversity of fly ash. <i>PeerJ</i> , 0, 10, e14015.	2.0	0

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9062	Different outer membrane c-type cytochromes are involved in direct interspecies electron transfer to <i>Geobacter</i> or <i>Methanosarcina</i> species. , 2022, 1, 272-286.		15
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9067	Supplementation with paraformic acid in the diet improved intestinal development through modulating intestinal inflammation and microbiota in broiler chickens. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	7
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9131	Gut microbiota modulation by plant polyphenols in koi carp (<i>Cyprinus carpio</i> L.). <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5
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9186	Coal Mining Activities Driving the Changes in Microbial Community and Hydrochemical Characteristics of Underground Mine Water. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 13359.	2.6	6
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9188	Long-term nitrogen fertilization alters phylogenetic structure of arbuscular mycorrhizal fungal community in plant roots across fine spatial scales. <i>Plant and Soil</i> , 2023, 483, 427-440.	3.7	2
9189	Changes in soil fungal communities after onset of wheat yellow mosaic virus disease. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	4.1	4
9190	Dephenolization pyrolysis fluid improved physicochemical properties and microbial community structure of saline-alkali soils. <i>Environmental Science and Pollution Research</i> , 0, , .	5.3	0

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9204	Comprehensive analysis and accurate quantification of unintended large gene modifications induced by CRISPR-Cas9 gene editing. <i>Science Advances</i> , 2022, 8, .	10.3	25
9205	Effects of combined aerobic and resistance training on gut microbiota and cardiovascular risk factors in physically active elderly women: A randomized controlled trial. <i>Frontiers in Physiology</i> , 0, 13, .	2.8	5
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9209	Effects of rice–crayfish co-culture on ammonia-oxidizing microbial abundance and community structure. <i>Aquatic Ecology</i> , 0, , .	1.5	0

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9218	The impact of genetic modified Ma bamboo on soil microbiome. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
9219	Unraveling potential enzymes and their functional role in fine cocoa beans fermentation using temporal shotgun metagenomics. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
9220	Lake sediments from littoral and profundal zones are heterogeneous but equivalent sources of methane produced by distinct methanogenic communities – a case study from Lake Remoray. <i>Journal of Geophysical Research G: Biogeosciences</i> , 0, .	3.0	0
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9231	Changes in the gut microbial community of larvae of the harlequin lady beetle in response to cannibalism and intraguild predation. <i>Biological Control</i> , 2022, 176, 105090.	3.0	3
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9238	Acute polyethylene microplastic (PE-MPs) exposure activates the intestinal mucosal immune network pathway in adult zebrafish (<i>Danio rerio</i>). <i>Chemosphere</i> , 2023, 311, 137048.	8.2	9
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9246	A novel endophytic bacterial strain improves potato storage characteristics by degrading glycoalkaloids and regulating microbiota. <i>Postharvest Biology and Technology</i> , 2023, 196, 112176.	6.0	1
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9249	Dietary selenium regulates the diversity and stability of microbial communities in stomach and intestine of rabbitfish (<i>Siganus oramin</i>). <i>Aquaculture</i> , 2023, 563, 738979.	3.5	2
9250	Effects of secondary release of chromium and vanadium on soil properties, nutrient cycling and bacterial communities in contaminated acidic paddy soil. <i>Journal of Environmental Management</i> , 2023, 326, 116725.	7.8	4
9251	Adaptive bacterial and fungal matching between a parasitic plant and its host: A case of <i>Cistanche deserticola</i> and <i>Haloxylon ammodendron</i> . <i>Industrial Crops and Products</i> , 2023, 191, 115932.	5.2	2
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9259	Amoxicillin impact on pathophysiology induced by short term high salt diet in mice. <i>Scientific Reports</i> , 2022, 12, .	3.3	4
9260	Diversity of soil faunal community as influenced by crop straw combined with different synthetic fertilizers in upland purple soil. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
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9265	Association of intestinal microbiota markers and dietary pattern in Chinese patients with type 2 diabetes: The Henan rural cohort study. <i>Frontiers in Public Health</i> , 0, 10, .	2.7	2

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9271	Short-term head-down bed rest microgravity simulation alters salivary microbiome in young healthy men. Frontiers in Microbiology, 0, 13, .	3.5	3
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9281	Phyllosphere microbial community of cigar tobacco and its corresponding metabolites. Frontiers in Microbiology, 0, 13, .	3.5	8
9282	The Impact of <i>Vairimorpha</i> (<i>Nosema</i>) <i>ceranae</i> Natural Infection on Honey Bee (<i>Apis mellifera</i>) and Bee Bread Microbiota. Applied Sciences (Switzerland), 2022, 12, 11476.	2.5	2
9283	Effect of Mulberry Leaf Powder of Varying Levels on Growth Performance, Immuno-Antioxidant Status, Meat Quality and Intestinal Health in Finishing Pigs. Antioxidants, 2022, 11, 2243.	5.1	2
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9305	Genetic mutation and tumor microbiota determine heterogeneity of tumor immune signature: Evidence from gastric and colorectal synchronous cancers. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	4
9306	Microbial Community Structure of Colostrum in Women with Antibiotic Exposure Immediately After Delivery. <i>Breastfeeding Medicine</i> , 2022, 17, 940-946.	1.7	0
9308	Effects of combined addition of 3-nitrooxypropanol and vitamin B12 on methane and propionate production in dairy cows by in vitro-simulated fermentation. <i>Journal of Dairy Science</i> , 2023, 106, 219-232.	3.4	2
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10431	Exploring the effects of silver nanoparticles on the bacterial microbiota composition of normal human skin. , 2023, 1, 100009.		0
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11549	A multi-omics study reveals the therapeutic effect of <i>Linderae Radix</i> water extract on irritable bowel syndrome (IBS-D). <i>Journal of Ethnopharmacology</i> , 2024, 328, 118050.	4.1	0
11550	Enhancing soil health and strawberry disease resistance: the impact of calcium cyanamide treatment on soil microbiota and physicochemical properties. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
11551	Enriched rhizospheric functional microbiome may enhance adaptability of <i>Artemisia lavandulaefolia</i> and <i>Betula luminifera</i> in antimony mining areas. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
11553	Heritable microbiome variation is correlated with source environment in locally adapted maize varieties. <i>Nature Plants</i> , 2024, 10, 598-617.	9.3	0
11555	Responses of Nutrients and Bacterial Communities to Temperature and Nitrogen Addition in Rhizosphere Soil for <i>Malus sieversii</i> Seedlings. <i>Journal of Soil Science and Plant Nutrition</i> , 0, , .	3.4	0
11556	Intestinal microbial profiling and immune responses of hybrid snakehead (<i>Channa maculata</i> × <i>Channa</i>) Tj ETQg1 1 0.784314 rgBT	1.7	0
11557	Strong associations between dissolved organic matter and microbial communities in the sediments of Qinghai-Tibetan Plateau lakes depend on salinity. <i>Science of the Total Environment</i> , 2024, 926, 171857.	8.0	0
11558	Impact of climate zones and seasons on indoor airborne microbial communities: Insights from a comprehensive analysis. <i>Science of the Total Environment</i> , 2024, 926, 171879.	8.0	0
11559	Using meta-analysis to understand the impacts of dietary protein and fat content on the composition of fecal microbiota of domestic dogs (<i>Canis lupus familiaris</i>): A pilot study. <i>MicrobiologyOpen</i> , 2024, 13, .	3.0	0
11560	Comparison of Rhizosphere Bacterial Communities of <i>Pinus squamata</i> , a Plant Species with Extremely Small Populations (PSESP) in Different Conservation Sites. <i>Microorganisms</i> , 2024, 12, 638.	3.6	0
11561	A New 4-Thiazolidinone Derivative (Les-6490) as a Gut Microbiota Modulator: Antimicrobial and Prebiotic Perspectives. <i>Antibiotics</i> , 2024, 13, 291.	3.7	0
11562	Folic Acid and Taurine Alleviate the Impairment of Redox Status, Immunity, Rumen Microbial Composition and Fermentation of Lambs under Heat Stress. <i>Animals</i> , 2024, 14, 998.	2.3	0
11563	Inflammatory response in dairy cows caused by heat stress and biological mechanisms for maintaining homeostasis. <i>PLoS ONE</i> , 2024, 19, e0300719.	2.5	0
11564	Diversity and distribution analysis of eukaryotic communities in the Xiangshan Bay, East China sea by metabarcoding approach. <i>Marine Environmental Research</i> , 2024, 197, 106451.	2.5	0
11565	Changes in the bacterial communities of <i>Harmonia axyridis</i> (Coleoptera: Coccinellidae) in response to long-term cold storage and progressive loss of egg viability in cold-stored beetles. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
11566	Profiling of fungal communities in functional food <i>Cistanches herba</i> using high-throughput sequencing. <i>Food Bioscience</i> , 2024, 59, 103869.	4.4	0
11567	Sugar transporters spatially organize microbiota colonization along the longitudinal root axis of <i>Arabidopsis</i> . <i>Cell Host and Microbe</i> , 2024, 32, 543-556.e6.	11.0	0
11568	Biological soil crust elicits microbial community and extracellular polymeric substances restructuring to reduce the soil erosion on tropical island, South China Sea. <i>Marine Environmental Research</i> , 2024, 197, 106449.	2.5	0

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11569	Dietary metabarcoding reveals the simplification of birdâ€™pest interaction networks across a gradient of agricultural cover. Molecular Ecology, 2024, 33, .	3.9	0
11570	Characteristics of cervicovaginal microflora at different cervical maturity during late pregnancy: A nested case-control study. PLoS ONE, 2024, 19, e0300510.	2.5	0
11571	Clinical Efficacy and Gut Microbiota Regulating-Related Effect of Si-Jun-Zi Decoction in Postoperative Non-Small Cell Lung Cancer Patients: A Prospective Observational Study. Integrative Cancer Therapies, 2024, 23, .	2.0	0
11572	DNA metabarcoding reveals ecological patterns and driving mechanisms of archaeal, bacterial, and eukaryotic communities in sediments of the Sansha Yongle Blue Hole. Scientific Reports, 2024, 14, .	3.3	0
11573	Diet replacement with whole insect larvae affects intestinal morphology and microbiota of broiler chickens. Scientific Reports, 2024, 14, .	3.3	0