

Introducing mothur: Open-Source, Platform-Independent for Describing and Comparing Microbial Communities

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Citation Report

#	ARTICLE	IF	CITATIONS
18	Molecular Biological Detection of Anaerobic Gut Fungi (Neocallimastigales) from Landfill Sites. Applied and Environmental Microbiology, 2006, 72, 5659-5661.	1.4	64
19	A Semantic Web Management Model for Integrative Biomedical Informatics. PLoS ONE, 2008, 3, e2946.	1.1	26
20	A High-Throughput DNA Sequence Aligner for Microbial Ecology Studies. PLoS ONE, 2009, 4, e8230.	1.1	280
21	arrayQualityMetrics—a bioconductor package for quality assessment of microarray data. Bioinformatics, 2009, 25, 415-416.	1.8	885
22	Molecular Methods in Biological Systems. Water Environment Research, 2010, 82, 908-930.	1.3	7
23	A Molecular Survey of the Diversity of Microbial Communities in Different Amazonian Agricultural Model Systems. Diversity, 2010, 2, 787-809.	0.7	64
24	Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14691-14696.	3.3	4,561
25	Pyrosequencing Reveals a Highly Diverse and Cultivar-Specific Bacterial Endophyte Community in Potato Roots. Microbial Ecology, 2010, 60, 157-166.	1.4	256
26	Bacterial Diversity of Weathered Terrestrial Icelandic Volcanic Glasses. Microbial Ecology, 2010, 60, 740-752.	1.4	66
27	Analysis of Oral Microbiota in Children with Dental Caries by PCR-DGGE and Barcoded Pyrosequencing. Microbial Ecology, 2010, 60, 677-690.	1.4	240
28	Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. Applied Microbiology and Biotechnology, 2010, 88, 389-399.	1.7	32
29	Diversity and identification of methanogenic archaea and sulphate-reducing bacteria in sediments from a pristine tropical mangrove. Antonie Van Leeuwenhoek, 2010, 97, 401-411.	0.7	80
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32	Microbial and antibiotic resistant constituents associated with biological aerosols and poultry litter within a commercial poultry house. Science of the Total Environment, 2010, 408, 4770-4777.	3.9	64
33	Metaproteomic characterization of a soil microbial community following carbon amendment. Soil Biology and Biochemistry, 2010, 42, 1148-1156.	4.2	45
34	Structural and functional diversity of soil bacterial and fungal communities following woody plant encroachment in the southern Great Plains. Soil Biology and Biochemistry, 2010, 42, 1816-1824.	4.2	72
35	Introducing W.A.T.E.R.S.: a Workflow for the Alignment, Taxonomy, and Ecology of Ribosomal Sequences. BMC Bioinformatics, 2010, 11, 317.	1.2	29

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36	TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. BMC Bioinformatics, 2010, 11, 341.	1.2	207
37	Molecular analysis of the diversity of vaginal microbiota associated with bacterial vaginosis. BMC Genomics, 2010, 11, 488.	1.2	284
38	Effects of polymerase, template dilution and cycle number on PCR based 16 S rRNA diversity analysis using the deep sequencing method. BMC Microbiology, 2010, 10, 255.	1.3	105
39	Planctomycetes dominate biofilms on surfaces of the kelp <i>Laminaria hyperborea</i> . BMC Microbiology, 2010, 10, 261.	1.3	221
40	Short-term changes in the composition of active marine bacterial assemblages in response to diesel oil pollution. Microbial Biotechnology, 2010, 3, 607-621.	2.0	26
41	Evaluation of the bacterial diversity of Pressure ulcers using bTEFAP pyrosequencing. BMC Medical Genomics, 2010, 3, 41.	0.7	108
42	454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. New Phytologist, 2010, 188, 291-301.	3.5	484
43	The bacterial community in "taberna"™ a traditional beverage of Southern Mexico. Letters in Applied Microbiology, 2010, 51, 558-563.	1.0	45
44	Isolated communities of Epsilonproteobacteria in hydrothermal vent fluids of the Mariana Arc seamounts. FEMS Microbiology Ecology, 2010, 73, no-no.	1.3	99
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47	Concurrent hexachlorobenzene and chloroethene transformation by endogenous dechlorinating microorganisms in the Ebro River sediment. FEMS Microbiology Ecology, 2010, 74, 682-692.	1.3	7
48	Influence of indigenous eukaryotic microbial communities on the reduction of <i>Escherichia coli</i> O157:H7 in compost slurry. FEMS Microbiology Letters, 2010, 313, 148-154.	0.7	11
49	Quantifying microbial communities with 454 pyrosequencing: does read abundance count?. Molecular Ecology, 2010, 19, 5555-5565.	2.0	468
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55	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
56	Intensity normalization improves color calling in SOLiD sequencing. <i>Nature Methods</i> , 2010, 7, 336-337.	9.0	31
57	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. <i>Nature Methods</i> , 2010, 7, 668-669.	9.0	647
58	The effect of nutrient deposition on bacterial communities in Arctic tundra soil. <i>Environmental Microbiology</i> , 2010, 12, 1842-1854.	1.8	323
59	Ironing out the wrinkles in the rare biosphere through improved OTU clustering. <i>Environmental Microbiology</i> , 2010, 12, 1889-1898.	1.8	1,226
60	GeneFISH â€“ an <i>in situ</i> technique for linking gene presence and cell identity in environmental microorganisms. <i>Environmental Microbiology</i> , 2010, 12, 3057-3073.	1.8	75
61	Temporal dynamics and genetic diversity of chemotacticâ€œcompetent microbial populations in the rhizosphere. <i>Environmental Microbiology</i> , 2010, 12, 3171-3184.	1.8	33
62	An Insect Herbivore Microbiome with High Plant Biomass-Degrading Capacity. <i>PLoS Genetics</i> , 2010, 6, e1001129.	1.5	213
63	CRISPR Associated Diversity within a Population of <i>Sulfolobus islandicus</i> . <i>PLoS ONE</i> , 2010, 5, e12988.	1.1	112
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69	Extraction of high molecular weight DNA from microbial mats. <i>BioTechniques</i> , 2010, 49, 631-640.	0.8	22
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71	Bacterial diversity in biofilms formed on condenser tube surfaces in a nuclear power plant. <i>Biofouling</i> , 2010, 26, 953-959.	0.8	15

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141	Composition of bacterial and archaeal communities in freshwater sediments with different contamination levels (Lake Geneva, Switzerland). <i>Water Research</i> , 2011, 45, 1213-1228.	5.3	192
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152	Diversity of cultivated and metabolically active aerobic anoxygenic phototrophic bacteria along an oligotrophic gradient in the Mediterranean Sea. <i>Biogeosciences</i> , 2011, 8, 1955-1970.	1.3	23
153	Diversity and Vertical Distribution of Microbial Eukaryotes in the Snow, Sea Ice and Seawater Near the North Pole at the End of the Polar Night. <i>Frontiers in Microbiology</i> , 2011, 2, 106.	1.5	95
154	The Deep Biosphere in Terrestrial Sediments in the Chesapeake Bay Area, Virginia, USA. <i>Frontiers in Microbiology</i> , 2011, 2, 156.	1.5	46
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1691	Comparisons of the composition and biogeographic distribution of the bacterial communities occupying South African thermal springs with those inhabiting deep subsurface fracture water. <i>Frontiers in Microbiology</i> , 2014, 5, 679.	1.5	72
1692	Diversity of cultivable bacteria involved in the formation of macroscopic microbial colonies (cave) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 6	0.4	17
1693	Investigations of potential microbial methanogenic and carbon monoxide utilization pathways in ultra-basic reducing springs associated with present-day continental serpentinization: the Tablelands, NL, CAN. <i>Frontiers in Microbiology</i> , 2014, 5, 613.	1.5	45
1694	Temporal changes in the diazotrophic bacterial communities associated with Caribbean sponges <i>Ircinia strobilina</i> and <i>Mycale laxissima</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 561.	1.5	20
1695	Microbial Dysbiosis Is Associated with Human Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e83744.	1.1	384
1696	Draft Genome Sequence of <i>Sphingobacterium</i> sp. Strain PM2-P1-29, a Tetracycline-Degrading TetX-Expressing Aerobic Bacterium Isolated from Agricultural Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
1697	Structural and functional diversity of free-living microorganisms in reef surface, Kra island, Thailand. <i>BMC Genomics</i> , 2014, 15, 607.	1.2	25
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1699	Photosynthetic picoeukaryote assemblages in the South China Sea from the Pearl River estuary to the SEATS station. <i>Aquatic Microbial Ecology</i> , 2014, 71, 271-284.	0.9	39
1700	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. <i>Genome Biology</i> , 2014, 15, R76.	13.9	219
1701	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. <i>MicrobiologyOpen</i> , 2014, 3, 910-921.	1.2	89
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1703	Infectious Microecology. <i>Advanced Topics in Science and Technology in China</i> , 2014, , .	0.0	5
1704	Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for <i>Clostridium difficile</i> susceptibility. <i>Microbiome</i> , 2014, 2, 42.	4.9	128
1705	Linking Geology and Microbiology: Inactive Pockmarks Affect Sediment Microbial Community Structure. <i>PLoS ONE</i> , 2014, 9, e85990.	1.1	14
1706	Fast dendrogram-based OTU clustering using sequence embedding. , 2014, , .		3
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1715	Bacteria diversity, distribution and insight into their role in <i>S</i> and <i>F</i> biogeochemical cycling during black shale weathering. <i>Environmental Microbiology</i> , 2014, 16, 3533-3547.	1.8	50
1716	Microbial community in anoxic-oxic settling anaerobic sludge reduction process revealed by 454 pyrosequencing analysis. <i>Canadian Journal of Microbiology</i> , 2014, 60, 799-809.	0.8	16
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1718	Effects of ultrasonic pretreatment on quantity and composition of bacterial DNA recovered from granular activated carbon used for drinking water treatment. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2014, 49, 609-616.	0.9	5
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1722	Stability of airborne microbes in the Louvre Museum over time. <i>Indoor Air</i> , 2014, 24, 29-40.	2.0	31
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1725	Changes in the composition and diversity of the bacterial microbiota associated with oysters (<i>Crassostrea corteziensis</i> , <i>Crassostrea gigas</i> and <i>Crassostrea sikamea</i>) during commercial production. <i>FEMS Microbiology Ecology</i> , 2014, 88, 69-83.	1.3	114

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1727	Correlates of gut community composition across an ant species (<i>Cephalotes</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i> 1284-1300.	2.0	82
1728	Altered Duodenal Microbiota Composition in Celiac Disease Patients Suffering From Persistent Symptoms on a Long-Term Gluten-Free Diet. <i>American Journal of Gastroenterology</i> , 2014, 109, 1933-1941.	0.2	156
1729	Microbial community of the bottom sediments of the brackish Lake Beloe (Transbaikal region). <i>Microbiology</i> , 2014, 83, 861-868.	0.5	14
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1733	<i>Bdellovibrio</i> and Like Organisms. , 2014, Chapter 7, 3-17.		46
1734	Identifying the core microbial community in the gut of fungus-growing termites. <i>Molecular Ecology</i> , 2014, 23, 4631-4644.	2.0	151
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1738	Shifts in microbial community structure and function in light- and dark-grown biofilms driven by warming. <i>Environmental Microbiology</i> , 2014, 16, 2550-2567.	1.8	38
1739	An analysis of geothermal and carbonic springs in the western United States sustained by deep fluid inputs. <i>Geobiology</i> , 2014, 12, 83-98.	1.1	8
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1741	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. <i>ISME Journal</i> , 2014, 8, 1153-1165.	4.4	139
1742	Water Stratification Affects the Microeukaryotic Community in a Subtropical Deep Reservoir. <i>Journal of Eukaryotic Microbiology</i> , 2014, 61, 126-133.	0.8	15
1743	Coprophagous behavior of rabbit pups affects implantation of cecal microbiota and health status. <i>Journal of Animal Science</i> , 2014, 92, 652-665.	0.2	46

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1753	Analysis of the factors affecting the formation of the microbiome associated with chronic osteomyelitis of the jaw. <i>Clinical Microbiology and Infection</i> , 2014, 20, O309-O317.	2.8	21
1754	Temporal changes in particle-associated microbial communities after interception by nonlethal sediment traps. <i>FEMS Microbiology Ecology</i> , 2014, 87, 153-163.	1.3	50
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1757	Impact of drinking water conditions and copper materials on downstream biofilm microbial communities and <i>Legionella pneumophila</i> colonization. <i>Journal of Applied Microbiology</i> , 2014, 117, 905-918.	1.4	55
1758	Contrasting soil fungal community responses to experimental nitrogen addition using the large subunit <i>rRNA</i> taxonomic marker and cellobiohydrolase I functional marker. <i>Molecular Ecology</i> , 2014, 23, 4406-4417.	2.0	36
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1760	Human Microbiota Characterization in the Course of Renal Transplantation. <i>American Journal of Transplantation</i> , 2014, 14, 416-427.	2.6	142
1762	Pyrosequencing assessment of rhizosphere fungal communities from a soybean field. <i>Canadian Journal of Microbiology</i> , 2014, 60, 687-690.	0.8	21

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1764	Methyl coenzyme <i>M</i> reductase (<i>mcrA</i>) gene abundance correlates with activity measurements of methanogenic <i>H₂</i> enriched anaerobic biomass. <i>Microbial Biotechnology</i> , 2014, 7, 77-84.	2.0	89
1765	Resident Microbiota Affect <i>Bordetella pertussis</i> Infectious Dose and Host Specificity. <i>Journal of Infectious Diseases</i> , 2014, 209, 913-921.	1.9	50
1766	Iron-Manganese Nodules Harbor Lower Bacterial Diversity and Greater Proportions of <i>Proteobacteria</i> Compared to Bulk Soils in Four Locations Spanning from North to South China. <i>Geomicrobiology Journal</i> , 2014, 31, 562-577.	1.0	17
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1768	Exploring <i>Symbiodinium</i> diversity and host specificity in <i>Acropora</i> corals from geographical extremes of <i>Western Australia</i> with 454 amplicon pyrosequencing. <i>Molecular Ecology</i> , 2014, 23, 3113-3126.	2.0	143
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1775	Symbiotic archaea in marine sponges show stability and host specificity in community structure and ammonia oxidation functionality. <i>FEMS Microbiology Ecology</i> , 2014, 90, 699-707.	1.3	34
1776	Diversity and abundance of phyllosphere bacteria are linked to insect herbivory. <i>Molecular Ecology</i> , 2014, 23, 1497-1515.	2.0	84
1777	Ribosomal Database Project: data and tools for high throughput rRNA analysis. <i>Nucleic Acids Research</i> , 2014, 42, D633-D642.	6.5	3,768
1778	Diversity of rhizosphere bacteria associated with different soybean cultivars in two soil conditions. <i>Soil Science and Plant Nutrition</i> , 2014, 60, 630-639.	0.8	17
1779	StreamingTrim 1.0: a Java software for dynamic trimming of 16S rRNA sequence data from metagenetic studies. <i>Molecular Ecology Resources</i> , 2014, 14, 426-434.	2.2	44
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1782	Land-use influences the distribution and activity of high affinity CO-oxidizing bacteria associated to type I-coxL genotype in soil. <i>Frontiers in Microbiology</i> , 2014, 5, 271.	1.5	36
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1784	Community Dynamics and Activity of Ammonia-Oxidizing Prokaryotes in Intertidal Sediments of the Yangtze Estuary. <i>Applied and Environmental Microbiology</i> , 2014, 80, 408-419.	1.4	140
1785	Phylogenetic signal in the community structure of host-specific microbiomes of tropical marine sponges. <i>Frontiers in Microbiology</i> , 2014, 5, 532.	1.5	174
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1787	Molecular Diversity of Eukaryotes in Municipal Wastewater Treatment Processes as Revealed by 18S rRNA Gene Analysis. <i>Microbes and Environments</i> , 2014, 29, 401-407.	0.7	53
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1791	High-throughput sequencing of 16S RNA genes of soil bacterial communities from a naturally occurring CO ₂ gas vent. <i>International Journal of Greenhouse Gas Control</i> , 2014, 29, 176-184.	2.3	67
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1794	ITScan: a web-based analysis tool for Internal Transcribed Spacer (ITS) sequences. <i>BMC Research Notes</i> , 2014, 7, 857.	0.6	9
1795	Molecular analysis of bacterial diversity in mudflats along the salinity gradient of an acidified tropical Bornean estuary (South East Asia). <i>Aquatic Biosystems</i> , 2014, 10, 10.	1.8	16
1796	Characterization and comparison of bacterial communities in benign vocal fold lesions. <i>Microbiome</i> , 2014, 2, 43.	4.9	30
1797	SÅ©ance: reference-based phylogenetic analysis for 18S rRNA studies. <i>BMC Evolutionary Biology</i> , 2014, 14, 235.	3.2	8
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1802	Evaluation of the impact of refrigeration on next generation sequencing-based assessment of the canine and feline fecal microbiota. BMC Veterinary Research, 2014, 10, 230.	0.7	18
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1805	The Bio-Community Perl toolkit for microbial ecology. Bioinformatics, 2014, 30, 1926-1927.	1.8	16
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1807	Molecular and phenetic characterization of the bacterial assemblage of Hot Lake, WA, an environment with high concentrations of magnesium sulphate, and its relevance to Mars. International Journal of Astrobiology, 2014, 13, 69-80.	0.9	24
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1812	Intestinal Microbial Diversity and Perioperative Complications. Journal of Parenteral and Enteral Nutrition, 2014, 38, 392-399.	1.3	56
1813	Sampling locality is more detectable than taxonomy or ecology in the gut microbiota of the brood-parasitic Brown-headed Cowbird (<i>Molothrus ater</i>). PeerJ, 2014, 2, e321.	0.9	126
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1819	Microbial community structure and nitrogenase gene diversity of sediment from a deep-sea hydrothermal vent field on the Southwest Indian Ridge. <i>Acta Oceanologica Sinica</i> , 2014, 33, 94-104.	0.4	9
1820	Iron supplementation promotes gut microbiota metabolic activity but not colitis markers in human gut microbiota-associated rats. <i>British Journal of Nutrition</i> , 2014, 111, 2135-2145.	1.2	58
1821	Intravenous lipopolysaccharide challenge alters ruminal bacterial microbiota and disrupts ruminal metabolism in dairy cattle. <i>British Journal of Nutrition</i> , 2014, 112, 170-182.	1.2	25
1822	Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. <i>PLoS ONE</i> , 2014, 9, e95567.	1.1	218
1824	Competitive interactions between methane- and ammonia-oxidizing bacteria modulate carbon and nitrogen cycling in paddy soil. <i>Biogeosciences</i> , 2014, 11, 3353-3368.	1.3	75
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1828	Spatial Diversity of Bacterioplankton Communities in Surface Water of Northern South China Sea. <i>PLoS ONE</i> , 2014, 9, e113014.	1.1	17
1829	Application of Bioinformatics in Microbial Ecology. <i>Advanced Materials Research</i> , 0, 955-959, 276-280.	0.3	0
1830	Characterization of Intestinal Bacteria in Wild and Domesticated Adult Black Tiger Shrimp (<i>Penaeus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.1	213
1831	Soil Acidobacterial 16S rRNA Gene Sequences Reveal Subgroup Level Differences between Savanna-Like Cerrado and Atlantic Forest Brazilian Biomes. <i>International Journal of Microbiology</i> , 2014, 2014, 1-12.	0.9	30
1832	Effects of Elevated Carbon Dioxide and Salinity on the Microbial Diversity in Lithifying Microbial Mats. <i>Minerals (Basel, Switzerland)</i> , 2014, 4, 145-169.	0.8	11
1833	Analysis of Run-to-Run Variation of Bar-Coded Pyrosequencing for Evaluating Bacterial Community Shifts and Individual Taxa Dynamics. <i>PLoS ONE</i> , 2014, 9, e99414.	1.1	10
1834	Variations of Bacterial Community Structure and Composition in Mangrove Sediment at Different Depths in Southeastern Brazil. <i>Diversity</i> , 2014, 6, 827-843.	0.7	59
1835	MPI-blastn and NCBI-TaxCollector: Improving metagenomic analysis with high performance classification and wide taxonomic attachment. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1450013.	0.3	7

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1837	Archaeal Diversity and Spatial Distribution in the Surface Sediment of the South China Sea. <i>Geomicrobiology Journal</i> , 2014, 31, 1-11.	1.0	11
1838	Reprogrammed and transmissible intestinal microbiota confer diminished susceptibility to induced colitis in TMF ^{+/+} mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4964-4969.	3.3	51
1839	The bacterial microbiota of <i>Stolotermes ruficeps</i> (<i>Stolotermitidae</i>), a phylogenetically basal termite endemic to New Zealand. <i>FEMS Microbiology Ecology</i> , 2014, 90, 678-688.	1.3	11
1840	Spatially tracking ¹³ C-labelled substrate (bicarbonate) accumulation in microbial communities using laser ablation isotope ratio mass spectrometry. <i>Environmental Microbiology Reports</i> , 2014, 6, 786-791.	1.0	17
1841	Active Ammonia Oxidizers in an Acidic Soil Are Phylogenetically Closely Related to Neutrophilic Archaeon. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1684-1691.	1.4	49
1842	Impact of feed restriction on health, digestion and faecal microbiota of growing pigs housed in good or poor hygiene conditions. <i>Animal</i> , 2014, 8, 1632-1642.	1.3	52
1843	Leaf-associated fungal diversity in acidified streams: insights from combining traditional and molecular approaches. <i>Environmental Microbiology</i> , 2014, 16, 2145-2156.	1.8	21
1844	Viscera-Associated Bacterial Diversity Among Intertidal Gastropods from Northern-Atlantic Coast of Portugal. <i>Current Microbiology</i> , 2014, 68, 140-148.	1.0	6
1845	Resistance and resilience of the forest soil microbiome to logging-associated compaction. <i>ISME Journal</i> , 2014, 8, 226-244.	4.4	293
1846	Resilience of soil bacterial community to irrigation with water of different qualities under Mediterranean climate. <i>Environmental Microbiology</i> , 2014, 16, 559-569.	1.8	72
1847	Overfeeding and genetics affect the composition of intestinal microbiota in <i>Anas platyrhynchos</i> (Pekin) and <i>Cairina moschata</i> (Muscovy) ducks. <i>FEMS Microbiology Ecology</i> , 2014, 87, 204-216.	1.3	46
1848	Response of the methanogenic microbial communities in Amazonian oxbow lake sediments to desiccation stress. <i>Environmental Microbiology</i> , 2014, 16, 1682-1694.	1.8	60
1849	Bacterial diversity associated with the tunic of the model chordate <i>Ciona intestinalis</i> . <i>ISME Journal</i> , 2014, 8, 309-320.	4.4	48
1850	Barcoding the Collembola of Churchill: a molecular taxonomic reassessment of species diversity in a subarctic area. <i>Molecular Ecology Resources</i> , 2014, 14, 249-261.	2.2	32
1851	Commercial DNA extraction kits impact observed microbial community composition in permafrost samples. <i>FEMS Microbiology Ecology</i> , 2014, 87, 217-230.	1.3	89
1852	Characterization of bacterial communities in soil and sediment of a created riverine wetland complex using high-throughput 16S rRNA amplicon sequencing. <i>Ecological Engineering</i> , 2014, 72, 56-66.	1.6	166
1853	Early Empiric Antibiotic Use in Preterm Infants Is Associated with Lower Bacterial Diversity and Higher Relative Abundance of Enterobacter. <i>Journal of Pediatrics</i> , 2014, 165, 23-29.	0.9	306

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1855	The anti-obesity effect of <i>Ephedra sinica</i> through modulation of gut microbiota in obese Korean women. <i>Journal of Ethnopharmacology</i> , 2014, 152, 532-539.	2.0	76
1856	Bacterial communities in chitin-amended soil as revealed by 16S rRNA gene based pyrosequencing. <i>Soil Biology and Biochemistry</i> , 2014, 76, 5-11.	4.2	32
1857	Microbial community composition of a down-flow hanging sponge (DHS) reactor combined with an up-flow anaerobic sludge blanket (UASB) reactor for the treatment of municipal sewage. <i>Bioresource Technology</i> , 2014, 151, 144-150.	4.8	56
1858	Characterization of the oral microbiota of healthy cats using next-generation sequencing. <i>Veterinary Journal</i> , 2014, 201, 223-229.	0.6	64
1859	“Core species”™ in three sources of indoor air belonging to the human micro-environment to the exclusion of outdoor air. <i>Science of the Total Environment</i> , 2014, 485-486, 508-517.	3.9	23
1860	Influence of <i>Panax ginseng</i> on obesity and gut microbiota in obese middle-aged Korean women. <i>Journal of Ginseng Research</i> , 2014, 38, 106-115.	3.0	75
1861	Transfer of antibiotic resistance plasmids in pure and activated sludge cultures in the presence of environmentally representative micro-contaminant concentrations. <i>Science of the Total Environment</i> , 2014, 468-469, 813-820.	3.9	92
1862	Response of ammonia oxidizing microbes to the stresses of arsenic and copper in two acidic alfisols. <i>Applied Soil Ecology</i> , 2014, 77, 59-67.	2.1	39
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1864	Successional development of biofilms in moving bed biofilm reactor (MBBR) systems treating municipal wastewater. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1429-1440.	1.7	99
1865	Sulphur-oxidizing and sulphate-reducing communities in Brazilian mangrove sediments. <i>Environmental Microbiology</i> , 2014, 16, 845-855.	1.8	126
1866	Distribution of <i>actA</i> and <i>ctrA</i> genes in <i>Baltic Sea</i> salinity gradients indicates adaptation of facultative freshwater photoheterotrophs to brackish waters. <i>Environmental Microbiology</i> , 2014, 16, 586-597.	1.8	19
1867	Endophytic and mycorrhizal fungi associated with roots of endangered native orchids from the Atlantic Forest, Brazil. <i>Mycorrhiza</i> , 2014, 24, 55-64.	1.3	57
1868	Vertical mother-to-neonate transfer of maternal gut bacteria via breastfeeding. <i>Environmental Microbiology</i> , 2014, 16, 2891-2904.	1.8	432
1869	Genus-wide acid tolerance accounts for the biogeographical distribution of soil <i>Burkholderia</i> populations. <i>Environmental Microbiology</i> , 2014, 16, 1503-1512.	1.8	105
1870	Distribution of antibiotic-resistant bacteria in chicken manure and manure-fertilized vegetables. <i>Environmental Science and Pollution Research</i> , 2014, 21, 1231-1241.	2.7	89
1871	Molecular phylogenetic analyses reveal three new <i>Ceratocystis</i> species and provide evidence for geographic differentiation of the genus in Africa. <i>Mycological Progress</i> , 2014, 13, 219-240.	0.5	20

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1873	Effects of temperature on microbial succession and metabolite change during saeu-jeot fermentation. <i>Food Microbiology</i> , 2014, 38, 16-25.	2.1	79
1874	The importance of species sorting differs between habitat generalists and specialists in bacterial communities. <i>FEMS Microbiology Ecology</i> , 2014, 87, 102-112.	1.3	166
1875	Community differentiation and population enrichment of <i>Sargasso sea</i> bacterioplankton in the euphotic zone of a mesoscale mode-2 water eddy. <i>Environmental Microbiology</i> , 2014, 16, 871-887.	1.8	66
1876	Effects of water temperature and backwashing on bacterial population and community in a biological activated carbon process at a water treatment plant. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1417-1427.	1.7	52
1877	Bronchial microbiome of severe COPD patients colonised by <i>Pseudomonas aeruginosa</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2014, 33, 1101-1111.	1.3	112
1878	Interactive influence of light intensity and soil fertility on root-associated arbuscular mycorrhizal fungi. <i>Plant and Soil</i> , 2014, 378, 173-188.	1.8	53
1879	Comparison of bacterial community in aqueous and oil phases of water-flooded petroleum reservoirs using pyrosequencing and clone library approaches. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4209-4221.	1.7	79
1880	Molecular Characterization of Skin Microbiota Between Cancer Cachexia Patients and Healthy Volunteers. <i>Microbial Ecology</i> , 2014, 67, 679-689.	1.4	21
1881	16S rDNA Pyrosequencing Analysis of Bacterial Community in Heavy Metals Polluted Soils. <i>Microbial Ecology</i> , 2014, 67, 635-647.	1.4	235
1882	Establishing a core microbiome in acetate-fed microbial fuel cells. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4187-4196.	1.7	65
1883	Application of DNA barcoding in biodiversity studies of shallow-water octocorals: molecular proxies agree with morphological estimates of species richness in Palau. <i>Coral Reefs</i> , 2014, 33, 275.	0.9	50
1884	Analysis of bacterial diversity in sponges collected from chuuk and kosrae islands in micronesia. <i>Journal of Microbiology</i> , 2014, 52, 20-26.	1.3	4
1885	Specific Archaeal Communities are Selected on the Root Surfaces of <i>Ruppia</i> spp. and <i>Phragmites australis</i> . <i>Wetlands</i> , 2014, 34, 403-411.	0.7	17
1886	Conversion from natural wetlands to paddy field alters the composition of soil bacterial communities in Sanjiang Plain, Northeast China. <i>Annals of Microbiology</i> , 2014, 64, 1395-1403.	1.1	15
1887	Unique picoeukaryotic algal community under multiple environmental stress conditions in a shallow, alkaline pan. <i>Extremophiles</i> , 2014, 18, 111-119.	0.9	30
1888	Abundance and diversity based on amoA genes of ammonia-oxidizing archaea and bacteria in ten wastewater treatment systems. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3339-3354.	1.7	95
1889	Assessing the diversity of arbuscular mycorrhizal fungi in semiarid shrublands dominated by <i>Artemisia tridentata</i> ssp. <i>wyomingensis</i> . <i>Mycorrhiza</i> , 2014, 24, 301-314.	1.3	12

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1891	Microbiome of prebiotic-treated mice reveals novel targets involved in host response during obesity. <i>ISME Journal</i> , 2014, 8, 2116-2130.	4.4	491
1892	Prokaryote populations of extant microbialites along a depth gradient in Pavilion Lake, British Columbia, Canada. <i>Geobiology</i> , 2014, 12, 250-264.	1.1	33
1893	Atmospheric methane oxidizers are present and active in Canadian high Arctic soils. <i>FEMS Microbiology Ecology</i> , 2014, 89, 257-269.	1.3	45
1894	<i>Lactobacillus sakei</i> modulates mule duck microbiota in ileum and ceca during overfeeding. <i>Poultry Science</i> , 2014, 93, 916-925.	1.5	26
1895	Effects of Water-Saving Irrigation on Emissions of Greenhouse Gases and Prokaryotic Communities in Rice Paddy Soil. <i>Microbial Ecology</i> , 2014, 68, 271-283.	1.4	39
1896	Influence of soil properties on archaeal diversity and distribution in the McMurdo Dry Valleys, Antarctica. <i>FEMS Microbiology Ecology</i> , 2014, 89, 347-359.	1.3	44
1897	Genetic analysis on <i>Dolichospermum</i> (Cyanobacteria; sensu <i>Anabaena</i>) populations based on the culture-independent clone libraries revealed the dominant genotypes existing in Lake Taihu, China. <i>Harmful Algae</i> , 2014, 31, 76-81.	2.2	14
1898	Bacterial communities in a bioelectrochemical denitrification system: The effects of supplemental electron acceptors. <i>Water Research</i> , 2014, 51, 25-36.	5.3	144
1899	<i>Environmental Microbiology. Methods in Molecular Biology</i> , 2014, , .	0.4	14
1900	Analysis of microbial diversity by pyrosequencing the small-subunit ribosomal RNA without PCR amplification. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3777-3789.	1.7	16
1901	The counteractive effects of nitrogen addition and watering on soil bacterial communities in a steppe ecosystem. <i>Soil Biology and Biochemistry</i> , 2014, 72, 26-34.	4.2	88
1902	Effect of intermittent aeration cycle on nutrient removal and microbial community in a fluidized bed reactor-membrane bioreactor combo system. <i>Bioresource Technology</i> , 2014, 156, 195-205.	4.8	63
1903	Analysis of the Gull Fecal Microbial Community Reveals the Dominance of <i>Catellibacoccus marimammalium</i> in Relation to Culturable Enterococci. <i>Applied and Environmental Microbiology</i> , 2014, 80, 757-765.	1.4	30
1904	Identification of key nitrous oxide production pathways in aerobic partial nitrifying granules. <i>Environmental Microbiology</i> , 2014, 16, 3168-3180.	1.8	49
1905	Determining the diet of larvae of the red rock lobster (<i>Jasus edwardsii</i>) using high-throughput DNA sequencing techniques. <i>Marine Biology</i> , 2014, 161, 551-563.	0.7	41
1906	Bacterial community of sediments from the Australian-Antarctic ridge. <i>Polar Biology</i> , 2014, 37, 587-593.	0.5	10
1907	Comparisons of the Fungal and Protistan Communities among Different Marine Sponge Holobionts by Pyrosequencing. <i>Microbial Ecology</i> , 2014, 67, 951-961.	1.4	38

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1910	Comparative metagenomic analysis of bacterial populations in three full-scale mesophilic anaerobic manure digesters. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2709-2717.	1.7	121
1911	Eukaryotic microbial communities in hypersaline soils and sediments from the alkaline hypersaline Huama Lake as revealed by 454 pyrosequencing. <i>Antonie Van Leeuwenhoek</i> , 2014, 105, 871-880.	0.7	19
1912	Niche Differentiation of Ammonia-Oxidising Archaea (AOA) and Bacteria (AOB) in Response to Paper and Pulp Mill Effluent. <i>Microbial Ecology</i> , 2014, 67, 758-768.	1.4	8
1913	Distinct Bacterial Communities Dominate Tropical and Temperate Zone Leaf Litter. <i>Microbial Ecology</i> , 2014, 67, 837-848.	1.4	50
1914	Response of the Archaeal Community to Simulated Petroleum Hydrocarbon Contamination in Marine and Hypersaline Ecosystems. <i>Water, Air, and Soil Pollution</i> , 2014, 225, 1.	1.1	12
1915	Genotypic and Phenotypic Diversity of Cyanobacteria in Biological Soil Crusts of the Succulent Karoo and Nama Karoo of Southern Africa. <i>Microbial Ecology</i> , 2014, 67, 286-301.	1.4	60
1916	Influence of the Changjiang River Flood on <i>Synechococcus</i> Ecology in the Surface Waters of the East China Sea. <i>Microbial Ecology</i> , 2014, 67, 273-285.	1.4	16
1917	Changes in the Soil Bacterial Communities in a Cedar Plantation Invaded by Moso Bamboo. <i>Microbial Ecology</i> , 2014, 67, 421-429.	1.4	62
1918	Detecting the Nonviable and Heat-Tolerant Bacteria in Activated Sludge by Minimizing DNA from Dead Cells. <i>Microbial Ecology</i> , 2014, 67, 829-836.	1.4	22
1919	Pyrosequencing Reveals Contrasting Soil Bacterial Diversity and Community Structure of Two Main Winter Wheat Cropping Systems in China. <i>Microbial Ecology</i> , 2014, 67, 443-453.	1.4	186
1920	Survival of prokaryotes in a polluted waste dump during remediation by alkaline hydrolysis. <i>Ecotoxicology</i> , 2014, 23, 404-418.	1.1	9
1921	Performance and bacterial communities of successive alkalinity-producing systems (SAPSs) in passive treatment processes treating mine drainages differing in acidity and metal levels. <i>Environmental Science and Pollution Research</i> , 2014, 21, 3722-3732.	2.7	11
1922	VAMPS: a website for visualization and analysis of microbial population structures. <i>BMC Bioinformatics</i> , 2014, 15, 41.	1.2	189
1923	Environmental selection of marine stramenopile clades in the Arctic Ocean and coastal waters. <i>Polar Biology</i> , 2014, 37, 347-357.	0.5	13
1924	Multiple ITS Haplotypes in the Genome of the Lichenized Basidiomycete <i>Cora inversa</i> (Hygrophoraceae): Fact or Artifact?. <i>Journal of Molecular Evolution</i> , 2014, 78, 148-162.	0.8	31
1925	Stability of the Maternal Gut Microbiota During Late Pregnancy and Early Lactation. <i>Current Microbiology</i> , 2014, 68, 419-427.	1.0	126

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1927	Diversity and abundance of Bacteria and nirS-encoding denitrifiers associated with the Juan de Fuca Ridge hydrothermal system. <i>Annals of Microbiology</i> , 2014, 64, 1691-1705.	1.1	20
1928	Genetic data generated from virus-host complexes obtained by membrane co-immobilization are equivalent to data obtained from tangential filtrate virus concentrates and virus cultures. <i>Virus Genes</i> , 2014, 48, 160-167.	0.7	2
1929	The Possible Role of Cyanobacterial Filaments in Coral Black Band Disease Pathology. <i>Microbial Ecology</i> , 2014, 67, 177-185.	1.4	21
1930	Comparison of microbial communities involved in souring and corrosion in offshore and onshore oil production facilities in Nigeria. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 665-678.	1.4	46
1931	Biochar addition affected the dynamics of ammonia oxidizers and nitrification in microcosms of a coastal alkaline soil. <i>Biology and Fertility of Soils</i> , 2014, 50, 321-332.	2.3	158
1932	High-Throughput DNA Sequencing of the Ruminant Bacteria from Moose (<i>Alces alces</i>) in Vermont, Alaska, and Norway. <i>Microbial Ecology</i> , 2014, 68, 185-195.	1.4	49
1933	Extracellular DNA can preserve the genetic signatures of present and past viral infection events in deep hypersaline anoxic basins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20133299.	1.2	69
1934	Bacterial diversity and community structure along different peat soils in boreal forest. <i>Applied Soil Ecology</i> , 2014, 74, 37-45.	2.1	89
1935	Changes in methane oxidation activity and methanotrophic community composition in saline alkaline soils. <i>Extremophiles</i> , 2014, 18, 561-571.	0.9	21
1936	Bacterial metal resistance genes and metal bioavailability in contaminated sediments. <i>Environmental Pollution</i> , 2014, 189, 143-151.	3.7	123
1937	Analyses of ITS and LSU gene regions provide congruent results on fungal community responses. <i>Fungal Ecology</i> , 2014, 9, 65-68.	0.7	44
1938	Genetic Diversity Patterns and Functional Traits of Bradyrhizobium Strains Associated with <i>Pterocarpus officinalis</i> Jacq. in Caribbean Islands and Amazonian Forest (French Guiana). <i>Microbial Ecology</i> , 2014, 68, 329-338.	1.4	8
1939	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. <i>ISME Journal</i> , 2014, 8, 493-503.	4.4	40
1940	Respiratory Microbiota Dynamics following <i>Streptococcus pneumoniae</i> Acquisition in Young and Elderly Mice. <i>Infection and Immunity</i> , 2014, 82, 1725-1731.	1.0	26
1941	Plant age and genotype affect the bacterial community composition in the tuber rhizosphere of field-grown sweet potato plants. <i>FEMS Microbiology Ecology</i> , 2014, 88, 424-435.	1.3	150
1942	The fibre-associated cellulolytic bacterial community in the hindgut of wood-feeding higher termites (<i>Nasutitermes</i> spp.). <i>Environmental Microbiology</i> , 2014, 16, 2711-2722.	1.8	57
1943	Resilience of the Natural Phyllosphere Microbiota of the Grapevine to Chemical and Biological Pesticides. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3585-3596.	1.4	144

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1945	Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. <i>Journal of Biotechnology</i> , 2014, 190, 30-39.	1.9	34
1946	Fish gut microbiota analysis differentiates physiology and behavior of invasive Asian carp and indigenous American fish. <i>ISME Journal</i> , 2014, 8, 541-551.	4.4	251
1947	Specific Microbial Attachment to Root Knot Nematodes in Suppressive Soil. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2679-2686.	1.4	103
1948	Comparative metagenome analysis of an Alaskan glacier. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1441003.	0.3	15
1949	Novel integrons and gene cassettes from a Cascadian submarine gas-hydrate-bearing core. <i>FEMS Microbiology Ecology</i> , 2014, 87, 343-356.	1.3	13
1950	<i>Burkholderia cordobensis</i> sp. nov., from agricultural soils. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2003-2008.	0.8	28
1951	Dynamics and associations of microbial community types across the human body. <i>Nature</i> , 2014, 509, 357-360.	13.7	723
1952	Large-scale fungal diversity assessment in the Andean Yungas forests reveals strong community turnover among forest types along an altitudinal gradient. <i>Molecular Ecology</i> , 2014, 23, 2452-2472.	2.0	151
1953	Bacterial Community Structure in Two Permafrost Wetlands on the Tibetan Plateau and Sanjiang Plain, China. <i>Microbial Ecology</i> , 2014, 68, 360-369.	1.4	52
1954	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i> . <i>Science</i> , 2014, 344, 416-420.	6.0	506
1955	Subgingival microbiota of Sri Lankan tea labourers naïve to oral hygiene measures. <i>Journal of Clinical Periodontology</i> , 2014, 41, 433-441.	2.3	16
1956	Meta'omic Analytic Techniques for Studying the Intestinal Microbiome. <i>Gastroenterology</i> , 2014, 146, 1437-1448.e1.	0.6	137
1957	Black truffle-associated bacterial communities during the development and maturation of <i>Sclerotinia sclerotiorum</i> ascocarps and putative functional roles. <i>Environmental Microbiology</i> , 2014, 16, 2831-2847.	1.8	133
1958	DNA barcoding of xeniid soft corals (Octocorallia: Alcyonacea: Xeniidae) from Indonesia: species richness and phylogenetic relationships. <i>Systematics and Biodiversity</i> , 2014, 12, 247-257.	0.5	30
1959	Ammonia oxidation-dependent growth of group I.1b <i>Thaumarchaeota</i> in acidic red soil microcosms. <i>FEMS Microbiology Ecology</i> , 2014, 89, 127-134.	1.3	17
1960	Altered Fecal Microbiota Composition Associated with Food Allergy in Infants. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2546-2554.	1.4	295
1961	Barcoded pyrosequencing analysis of the bacterial community of Daqu for light-flavour Chinese liquor. <i>Letters in Applied Microbiology</i> , 2014, 58, 549-555.	1.0	52

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1963	Nitrogen and phosphorus additions impact arbuscular mycorrhizal abundance and molecular diversity in a tropical montane forest. <i>Global Change Biology</i> , 2014, 20, 3646-3659.	4.2	194
1964	Taxonomic relatedness shapes bacterial assembly in activated sludge of globally distributed wastewater treatment plants. <i>Environmental Microbiology</i> , 2014, 16, 2421-2432.	1.8	333
1965	Biochar enhances the microbial and chemical transformation of pentachlorophenol in paddy soil. <i>Soil Biology and Biochemistry</i> , 2014, 70, 142-150.	4.2	170
1966	An analysis of the ruminal bacterial microbiota in West African Dwarf sheep fed grass- and tree-based diets. <i>Journal of Applied Microbiology</i> , 2014, 116, 1094-1105.	1.4	23
1967	Pyrosequencing survey of intestinal microbiota diversity in cultured sea bass (<i>Dicentrarchus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 119	1.3	119
1968	Diffuse symbioses: roles of plant-plant, plant-microbe and microbe-microbe interactions in structuring the soil microbiome. <i>Molecular Ecology</i> , 2014, 23, 1571-1583.	2.0	143
1969	The effects of read length, quality and quantity on microsatellite discovery and primer development: from Illumina to PacBio. <i>Molecular Ecology Resources</i> , 2014, 14, 953-965.	2.2	28
1970	Microbial Community Dynamics and Stability during an Ammonia-Induced Shift to Syntrophic Acetate Oxidation. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3375-3383.	1.4	118
1971	Global biogeography of <i>Streptomyces</i> antibiotic inhibition, resistance, and resource use. <i>FEMS Microbiology Ecology</i> , 2014, 88, 386-397.	1.3	47
1972	Plant-associated bacteria degrade defense chemicals and reduce their adverse effects on an insect defoliator. <i>Oecologia</i> , 2014, 175, 901-910.	0.9	106
1973	Methane emission and dynamics of methanotrophic and methanogenic communities in a flooded rice field ecosystem. <i>FEMS Microbiology Ecology</i> , 2014, 88, 195-212.	1.3	110
1974	Archaeal diversity and the extent of iron and manganese pyritization in sediments from a tropical mangrove creek (Cardoso Island, Brazil). <i>Estuarine, Coastal and Shelf Science</i> , 2014, 146, 1-13.	0.9	18
1975	Performance comparison of genetic markers for high-throughput sequencing-based biodiversity assessment in complex communities. <i>Molecular Ecology Resources</i> , 2014, 14, 1049-1059.	2.2	86
1976	Ancient DNA sheds new light on the Svalbard foraminiferal fossil record of the last millennium. <i>Geobiology</i> , 2014, 12, 277-288.	1.1	39
1977	Antibiotic Resistance is Widespread in Urban Aquatic Environments of Rio de Janeiro, Brazil. <i>Microbial Ecology</i> , 2014, 68, 441-452.	1.4	33
1978	Atmospheric N Deposition Increases Bacterial Laccase-Like Multicopper Oxidases: Implications for Organic Matter Decay. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4460-4468.	1.4	46
1979	The genetic potential for key biogeochemical processes in Arctic frost flowers and young sea ice revealed by metagenomic analysis. <i>FEMS Microbiology Ecology</i> , 2014, 89, 376-387.	1.3	25

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1980	Dynamics of bacterial and fungal communities associated with eggshells during incubation. <i>Ecology and Evolution</i> , 2014, 4, 1140-1157.	0.8	43
1981	Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. <i>ISME Journal</i> , 2014, 8, 1566-1576.	4.4	377
1982	River organic matter shapes microbial communities in the sediment of the Rhône prodelta. <i>ISME Journal</i> , 2014, 8, 2327-2338.	4.4	64
1983	Mathematical modeling of primary succession of murine intestinal microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 439-444.	3.3	183
1984	Metatranscriptomic Analyses of Plankton Communities Inhabiting Surface and Subpycnocline Waters of the Chesapeake Bay during Oxidic-Anoxic-Oxidic Transitions. <i>Applied and Environmental Microbiology</i> , 2014, 80, 328-338.	1.4	47
1985	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	4.7	123
1986	Characterization of the gut microbiota of three commercially valuable warmwater fish species. <i>Journal of Applied Microbiology</i> , 2014, 116, 1396-1404.	1.4	346
1987	Community fingerprinting in a sequencing world. <i>FEMS Microbiology Ecology</i> , 2014, 89, 316-330.	1.3	140
1988	Effects of cultivation and return of <i>Bacillus thuringiensis</i> (Bt) maize on the diversity of the arbuscular mycorrhizal community in soils and roots of subsequently cultivated conventional maize. <i>Soil Biology and Biochemistry</i> , 2014, 75, 254-263.	4.2	26
1989	Cultivation-independent analysis of microbial communities on Austrian raw milk hard cheese rinds. <i>International Journal of Food Microbiology</i> , 2014, 180, 88-97.	2.1	74
1990	Comparative analysis of the microbial communities in agricultural soil amended with enhanced biochars or traditional fertilisers. <i>Agriculture, Ecosystems and Environment</i> , 2014, 191, 73-82.	2.5	171
1991	Differentiation between sediment and hypolimnion methanogen communities in humic lakes. <i>Environmental Microbiology</i> , 2014, 16, 1411-1423.	1.8	21
1992	Microbial activity and community structure in two terrace-type wetlands constructed for the treatment of domestic wastewater. <i>Ecological Engineering</i> , 2014, 67, 198-205.	1.6	14
1993	Inhibition of sulfate reducing bacteria in aquifer sediment by iron nanoparticles. <i>Water Research</i> , 2014, 51, 64-72.	5.3	96
1994	Diversity and structure of bacterial communities associated with <i>Panerochaete chrysosporium</i> during wood decay. <i>Environmental Microbiology</i> , 2014, 16, 2238-2252.	1.8	51
1995	Interactions between Thaumarchaea, <i>Nitrospira</i> and methanotrophs modulate autotrophic nitrification in volcanic grassland soil. <i>ISME Journal</i> , 2014, 8, 2397-2410.	4.4	121
1996	Is the omega-3 index a valid marker of intestinal membrane phospholipid EPA+DHA content?. <i>Prostaglandins Leukotrienes and Essential Fatty Acids</i> , 2014, 91, 87-96.	1.0	39
1997	Response of Free-Living Nitrogen-Fixing Microorganisms to Land Use Change in the Amazon Rainforest. <i>Applied and Environmental Microbiology</i> , 2014, 80, 281-288.	1.4	104

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1998	Complex patterns in phytoplankton and microeukaryote diversity along the estuarine continuum. <i>Hydrobiologia</i> , 2014, 726, 155-178.	1.0	20
1999	Successful bioremediation of an aged and heavily contaminated soil using a microbial/plant combination strategy. <i>Journal of Hazardous Materials</i> , 2014, 264, 430-438.	6.5	87
2000	Seasonal changes in microbial community structure and activity imply winter production is linked to summer hypoxia in a large lake. <i>FEMS Microbiology Ecology</i> , 2014, 87, 475-485.	1.3	86
2001	Specificity and transcriptional activity of microbiota associated with low and high microbial abundance sponges from the Red Sea. <i>Molecular Ecology</i> , 2014, 23, 1348-1363.	2.0	139
2002	Detection of a novel intracellular microbiome hosted in arbuscular mycorrhizal fungi. <i>ISME Journal</i> , 2014, 8, 257-270.	4.4	128
2003	Meta-analysis of deep-sequenced fungal communities indicates limited taxon sharing between studies and the presence of biogeographic patterns. <i>New Phytologist</i> , 2014, 201, 623-635.	3.5	106
2004	Airborne Bacterial Populations Above Desert Soils of the McMurdo Dry Valleys, Antarctica. <i>Microbial Ecology</i> , 2014, 67, 120-128.	1.4	104
2005	Analysis of biofilm bacterial communities responsible for carbon removal through a reactor cascade treating wastewater. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 977-987.	1.7	8
2006	Antibiotic-induced shifts in the mouse gut microbiome and metabolome increase susceptibility to <i>Clostridium difficile</i> infection. <i>Nature Communications</i> , 2014, 5, 3114.	5.8	817
2007	Genome sequencing and characterization of an extensively drug-resistant sequence type 111 serotype O12 hospital outbreak strain of <i>Pseudomonas aeruginosa</i> . <i>Clinical Microbiology and Infection</i> , 2014, 20, O609-O618.	2.8	57
2008	Phylogenetic Differences in Attached and Free-Living Bacterial Communities in a Temperate Coastal Lagoon during Summer, Revealed via High-Throughput 16S rRNA Gene Sequencing. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2071-2083.	1.4	104
2009	Ultrastructure and Phylogenetic Position of <i>Regin rotiferus</i> and <i>Otto terricolus</i> Genera et Species Novae (Bicosoecida, Heterokonta/Stramenopiles). <i>Protist</i> , 2014, 165, 144-160.	0.6	10
2010	Characterization of tobermolite as a bed material for selective growth of methanotrophs in biofiltration. <i>Journal of Biotechnology</i> , 2014, 173, 90-97.	1.9	16
2011	Multistate assessment of wetland restoration on CO ₂ and N ₂ O emissions and soil bacterial communities. <i>Applied Soil Ecology</i> , 2014, 76, 87-94.	2.1	14
2012	Characterisation of the soil bacterial community structure and composition of natural and constructed wetlands. <i>Science of the Total Environment</i> , 2014, 473-474, 63-71.	3.9	220
2013	Rifaximin Alters Intestinal Bacteria and Prevents Stress-Induced Gut Inflammation and Visceral Hyperalgesia in Rats. <i>Gastroenterology</i> , 2014, 146, 484-496.e4.	0.6	212
2014	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , 2014, 8, 841-853.	4.4	137
2015	Rhizosphere microbiome assemblage is affected by plant development. <i>ISME Journal</i> , 2014, 8, 790-803.	4.4	1,128

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2017	Extracellular Electron Transport-Mediated Fe(III) Reduction by a Community of Alkaliphilic Bacteria That Use Flavins as Electron Shuttles. <i>Applied and Environmental Microbiology</i> , 2014, 80, 128-137.	1.4	86
2018	Winterâ€“Summer Succession of Unicellular Eukaryotes in a Meso-eutrophic Coastal System. <i>Microbial Ecology</i> , 2014, 67, 13-23.	1.4	39
2019	Mineral Microniches Control the Diversity of Subsurface Microbial Populations. <i>Geomicrobiology Journal</i> , 2014, 31, 246-261.	1.0	68
2020	Bacterial and Fungal Diversity of Quaternary Cave Sediment Deposits. <i>Geomicrobiology Journal</i> , 2014, 31, 116-127.	1.0	22
2021	Comparison of Bacterial Diversity in Azorean and Hawai'ian Lava Cave Microbial Mats. <i>Geomicrobiology Journal</i> , 2014, 31, 205-220.	1.0	63
2022	Diversity of Ammonia Oxidation (<i>amoA</i>) and Nitrogen Fixation (<i>nifH</i>) Genes in Lava Caves of Terceira, Azores, Portugal. <i>Geomicrobiology Journal</i> , 2014, 31, 221-235.	1.0	26
2023	<i>Nipharagus</i> and <i>Thiothrix</i> associations may be widespread in sulphidic groundwater ecosystems: evidence from southeastern Romania. <i>Molecular Ecology</i> , 2014, 23, 1405-1417.	2.0	47
2024	Community structure and distribution of planktonic ammonia-oxidizing archaea and bacteria in the Dongjiang River, China. <i>Research in Microbiology</i> , 2014, 165, 657-670.	1.0	15
2025	Ribonucleotide reductases reveal novel viral diversity and predict biological and ecological features of unknown marine viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15786-15791.	3.3	56
2026	Sensitive, Efficient Quantitation of ¹³ C-Enriched Nucleic Acids via Ultrahigh-Performance Liquid Chromatographyâ€“Tandem Mass Spectrometry for Applications in Stable Isotope Probing. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7206-7211.	1.4	20
2027	Probiotic <i>L. reuteri</i> Treatment Prevents Bone Loss in a Menopausal Ovariectomized Mouse Model. <i>Journal of Cellular Physiology</i> , 2014, 229, 1822-1830.	2.0	374
2028	Alkaline phosphatases in microbialites and bacterioplankton from Alchichica soda lake, Mexico. <i>FEMS Microbiology Ecology</i> , 2014, 90, n/a-n/a.	1.3	33
2029	Instrumenting Genomic Sequence Analysis Pipeline Mothur on Shared Memory Architecture. , 2014, , .		1
2030	Isolated faecal bacterial communities found for Weddell seals, <i>Leptonychotes weddellii</i> , at White Island, McMurdo Sound, Antarctica. <i>Polar Biology</i> , 2014, 37, 1857-1864.	0.5	14
2031	Simultaneous profiling of seed-associated bacteria and fungi reveals antagonistic interactions between microorganisms within a shared epiphytic microbiome on <i>Triticum</i> and <i>Bassica</i> seeds. <i>New Phytologist</i> , 2014, 202, 542-553.	3.5	149
2032	Close association of active nitrifiers with <i>Beggiatoa</i> mats covering deep-sea hydrothermal sediments. <i>Environmental Microbiology</i> , 2014, 16, 1612-1626.	1.8	29
2033	Alterations in cecal microbiota of Jinhua piglets fostered by a Yorkshire sow. <i>Science Bulletin</i> , 2014, 59, 4304-4311.	1.7	9

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2035	Characterization of the bacterioplankton community and its antibiotic resistance genes in the Baltic Sea. <i>Biotechnology and Applied Biochemistry</i> , 2014, 61, 23-32.	1.4	13
2036	Partner associations across sympatric broad-headed bug species and their environmentally acquired bacterial symbionts. <i>Molecular Ecology</i> , 2014, 23, 1333-1347.	2.0	39
2037	Spatial-Temporal Survey and Occupancy-Abundance Modeling To Predict Bacterial Community Dynamics in the Drinking Water Microbiome. <i>MBio</i> , 2014, 5, e01135-14.	1.8	160
2038	Microbially enhanced oil recovery from miniature model columns through stimulation of indigenous microflora with nitrate. <i>International Biodeterioration and Biodegradation</i> , 2014, 96, 135-143.	1.9	25
2039	Characterisation of bacterioplankton communities in the meltwater ponds of Bratina Island, Victoria Land, Antarctica. <i>FEMS Microbiology Ecology</i> , 2014, 89, 451-464.	1.3	20
2040	Bacterial community dynamics during the early stages of biofilm formation in a chlorinated experimental drinking water distribution system: implications for drinking water discoloration. <i>Journal of Applied Microbiology</i> , 2014, 117, 286-301.	1.4	84
2041	Forestry impacts on the hidden fungal biodiversity associated with bryophytes. <i>FEMS Microbiology Ecology</i> , 2014, 90, 313-325.	1.3	20
2042	Can the freshwater bacterial communities shift to the marine-like taxa?. <i>Journal of Basic Microbiology</i> , 2014, 54, 1264-1272.	1.8	16
2043	Impact of a hormone-releasing intrauterine system on the vaginal microbiome: a prospective baboon model. <i>Journal of Medical Primatology</i> , 2014, 43, 89-99.	0.3	21
2044	Dietary differences are reflected on the gut prokaryotic community structure of wild and commercially reared sea bream (<i>Sparus aurata</i>). <i>MicrobiologyOpen</i> , 2014, 3, 718-728.	1.2	116
2045	Changes in free-living bacterial community diversity reflect the magnitude of environmental variability. <i>FEMS Microbiology Ecology</i> , 2014, 87, 291-301.	1.3	40
2046	Shifts in archaeoplankton community structure along ecological gradients of Pearl Estuary. <i>FEMS Microbiology Ecology</i> , 2014, 90, n/a-n/a.	1.3	41
2047	Abundance, diversity and seasonal dynamics of predatory bacteria in aquaculture zero discharge systems. <i>FEMS Microbiology Ecology</i> , 2014, 89, 149-161.	1.3	65
2048	Gene-targeted microfluidic cultivation validated by isolation of a gut bacterium listed in Human Microbiome Project's Most Wanted taxa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9768-9773.	3.3	126
2049	Spatial patterns of microbial diversity and activity in an aged creosote-contaminated site. <i>ISME Journal</i> , 2014, 8, 2131-2142.	4.4	99
2050	The communities of tomato (<i>Solanum lycopersicum</i> L.) leaf endophytic bacteria, analyzed by 16S-ribosomal RNA gene pyrosequencing. <i>FEMS Microbiology Letters</i> , 2014, 351, 187-194.	0.7	121
2051	Molecular diversity of indigenous arbuscular mycorrhizal fungi in three different agricultural regions of Turkey. <i>Soil Science and Plant Nutrition</i> , 2014, 60, 367-376.	0.8	4

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2052	Tissue storage and primer selection influence pyrosequencing-based inferences of diversity and community composition of endolichenic and endophytic fungi. <i>Molecular Ecology Resources</i> , 2014, 14, 1032-1048.	2.2	83
2053	Free-Living and Particle-Associated Bacterioplankton in Large Rivers of the Mississippi River Basin Demonstrate Biogeographic Patterns. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7186-7195.	1.4	60
2054	Directly Sampling the Lung of a Young Child with Cystic Fibrosis Reveals Diverse Microbiota. <i>Annals of the American Thoracic Society</i> , 2014, 11, 1049-1055.	1.5	65
2055	<i>Pezizomycotina</i> dominates the fungal communities of South China Sea Sponges <i>Theonella swinhoei</i> and <i>Xestospongia testudinaria</i> . <i>FEMS Microbiology Ecology</i> , 2014, 90, 935-945.	1.3	16
2056	Integration of Clustering and Multidimensional Scaling to Determine Phylogenetic Trees as Spherical Phylograms Visualized in 3 Dimensions. , 2014, , .		7
2057	Microbial diversity and biogenic methane potential of a thermogenic-gas coal mine. <i>International Journal of Coal Geology</i> , 2014, 134-135, 96-107.	1.9	51
2058	Substrate-Specific Development of Thermophilic Bacterial Consortia by Using Chemically Pretreated Switchgrass. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7423-7432.	1.4	27
2059	Technology and Techniques for Microbial Ecology via DNA Sequencing. <i>Annals of the American Thoracic Society</i> , 2014, 11, S16-S20.	1.5	8
2060	CO ₂ concentration and pH alters subsurface microbial ecology at reservoir temperature and pressure. <i>RSC Advances</i> , 2014, 4, 17443-17453.	1.7	12
2061	Recovery of the Gut Microbiome following Fecal Microbiota Transplantation. <i>MBio</i> , 2014, 5, e00893-14.	1.8	267
2062	Early Respiratory Microbiota Composition Determines Bacterial Succession Patterns and Respiratory Health in Children. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014, 190, 1283-1292.	2.5	451
2063	Prebiotic effects of cassava bagasse in TNO's in vitro model of the colon in lean versus obese microbiota. <i>Journal of Functional Foods</i> , 2014, 11, 210-220.	1.6	48
2064	Comparative pyrosequencing analysis of bacterial community change in biofilm formed on seawater reverse osmosis membrane. <i>Environmental Technology (United Kingdom)</i> , 2014, 35, 125-136.	1.2	14
2065	Comparative survey of bacterial and archaeal communities in high arsenic shallow aquifers using 454 pyrosequencing and traditional methods. <i>Ecotoxicology</i> , 2014, 23, 1878-1889.	1.1	12
2066	Microbiota transplantation restores normal fecal bile acid composition in recurrent <i>Clostridium difficile</i> infection. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 306, G310-G319.	1.6	341
2067	The cellular community in the intestine of the shrimp <i>Penaeus penicillatus</i> and its culture environments. <i>Fisheries Science</i> , 2014, 80, 1001-1007.	0.7	49
2068	New insights into <i>Oculina patagonica</i> coral diseases and their associated <i>Vibrio</i> spp. communities. <i>ISME Journal</i> , 2014, 8, 1794-1807.	4.4	54
2069	Internal transcribed spacer rRNA gene sequencing analysis of fungal diversity in Kansas City indoor environments. <i>Environmental Sciences: Processes and Impacts</i> , 2014, 16, 33-43.	1.7	40

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2070	Ectomycorrhizal fungi contribute to soil organic matter cycling in sub-boreal forests. <i>ISME Journal</i> , 2014, 8, 699-713.	4.4	132
2071	Combination of Metagenomics and Culture-Based Methods to Study the Interaction Between Ochratoxin A and Gut Microbiota. <i>Toxicological Sciences</i> , 2014, 141, 314-323.	1.4	80
2072	<i>Methyloceanibacter caenitepidi</i> gen. nov., sp. nov., a facultatively methylotrophic bacterium isolated from marine sediments near a hydrothermal vent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 462-468.	0.8	54
2073	The pathogen <i>Batrachochytrium dendrobatidis</i> disturbs the frog skin microbiome during a natural epidemic and experimental infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5049-58.	3.3	264
2074	Effect of wastewater disposal on the bacterial and archaeal community of sea sediment in an industrial area in China. <i>FEMS Microbiology Ecology</i> , 2014, 88, 320-332.	1.3	41
2075	Bacterial epibionts of <i>Daphnia</i> : a potential route for the transfer of dissolved organic carbon in freshwater food webs. <i>ISME Journal</i> , 2014, 8, 1808-1819.	4.4	65
2076	Construction of aligned database of <i>dsrA</i> , a gene encoding dissimilatory sulfite reductase alpha subunit, for metagenomic studies of sulfate-reducing bacteria. <i>Journal of the Korean Society for Applied Biological Chemistry</i> , 2014, 57, 419-427.	0.9	2
2077	Single-Molecule Long-Read 16S Sequencing To Characterize the Lung Microbiome from Mechanically Ventilated Patients with Suspected Pneumonia. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3913-3921.	1.8	69
2078	Scale-up of sediment microbial fuel cells. <i>Journal of Power Sources</i> , 2014, 272, 311-319.	4.0	110
2079	Decreased diversity of nasal microbiota and their secreted extracellular vesicles in patients with chronic rhinosinusitis based on a metagenomic analysis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2014, 69, 517-526.	2.7	129
2080	Microbial Community Composition Is Unaffected by Anode Potential. <i>Environmental Science & Technology</i> , 2014, 48, 1352-1358.	4.6	171
2081	Assessing <i>Symbiodinium</i> diversity in scleractinian corals via next-generation sequencing-based genotyping of the ITS2 rDNA region. <i>Molecular Ecology</i> , 2014, 23, 4418-4433.	2.0	284
2082	An Illumina metabarcoding pipeline for fungi. <i>Ecology and Evolution</i> , 2014, 4, 2642-2653.	0.8	107
2083	Identification of Mn(II)-Oxidizing Bacteria from a Low-pH Contaminated Former Uranium Mine. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5086-5097.	1.4	91
2084	Cultivation-based multiplex phenotyping of human gut microbiota allows targeted recovery of previously uncultured bacteria. <i>Nature Communications</i> , 2014, 5, 4714.	5.8	123
2085	Effects of a nutrient additive on the density of functional bacteria and the microbial community structure of bioorganic fertilizer. <i>Bioresource Technology</i> , 2014, 172, 328-334.	4.8	13
2086	Psychrotrophic lactic acid bacteria associated with production batch recalls and sporadic cases of early spoilage in Belgium between 2010 and 2014. <i>International Journal of Food Microbiology</i> , 2014, 191, 157-163.	2.1	41
2087	Effect of pine bark on the biotransformation of trinitrotoluene and on the bacterial community structure in a batch experiment. <i>Environmental Technology (United Kingdom)</i> , 2014, 35, 2456-2465.	1.2	2

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2088	Biodegradation in Waters from Hydraulic Fracturing: Chemistry, Microbiology, and Engineering. <i>Journal of Environmental Engineering, ASCE</i> , 2014, 140, .	0.7	70
2089	Diversity of bacterial community and detection of nirS- and nirK-encoding denitrifying bacteria in sandy intertidal sediments along Laizhou Bay of Bohai Sea, China. <i>Marine Pollution Bulletin</i> , 2014, 88, 215-223.	2.3	54
2090	Dynamics of antibiotic resistance genes and presence of putative pathogens during ambient temperature anaerobic digestion. <i>Journal of Applied Microbiology</i> , 2014, 117, 1689-1699.	1.4	50
2091	Microbial genome-enabled insights into plant-microorganism interactions. <i>Nature Reviews Genetics</i> , 2014, 15, 797-813.	7.7	187
2092	Diversity and Abundance of Ammonia-Oxidizing Archaea and Bacteria in Diverse Chinese Paddy Soils. <i>Geomicrobiology Journal</i> , 2014, 31, 12-22.	1.0	23
2093	<i>In Vitro</i> Fermentability of Sugar Beet Pulp Derived Oligosaccharides Using Human and Pig Fecal Inocula. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 1079-1087.	2.4	66
2094	Effect of plankton-derived organic matter on the microbial community of coastal marine sediments. <i>Journal of Experimental Marine Biology and Ecology</i> , 2014, 461, 257-266.	0.7	19
2095	Microbial Abundance and Community Composition Influence Production Performance in a Low-Temperature Petroleum Reservoir. <i>Environmental Science & Technology</i> , 2014, 48, 5336-5344.	4.6	61
2096	Latitudinal Distribution of Ammonia-Oxidizing Bacteria and Archaea in the Agricultural Soils of Eastern China. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5593-5602.	1.4	60
2097	Research on Neonatal Microbiomes: What Neonatologists Need to Know. <i>Neonatology</i> , 2014, 105, 14-24.	0.9	12
2098	Interleukin-22 Regulates the Complement System to Promote Resistance against Pathobionts after Pathogen-Induced Intestinal Damage. <i>Immunity</i> , 2014, 41, 620-632.	6.6	124
2099	Biofouling of reverse-osmosis membranes under different shear rates during tertiary wastewater desalination: Microbial community composition. <i>Water Research</i> , 2014, 67, 86-95.	5.3	39
2100	Bacterial community characterization in the soils of native and restored rainforest fragments. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 947-957.	0.7	2
2101	Niche specificity of ammonia-oxidizing archaeal and bacterial communities in a freshwater wetland receiving municipal wastewater in Daqing, Northeast China. <i>Ecotoxicology</i> , 2014, 23, 2081-2091.	1.1	9
2102	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. <i>Nature</i> , 2014, 514, 508-512.	13.7	366
2103	Off-site impacts of agricultural composting: role of terrestrially derived organic matter in structuring aquatic microbial communities and their metabolic potential. <i>FEMS Microbiology Ecology</i> , 2014, 90, 622-632.	1.3	17
2104	Viruses in a 14th-Century Coprolite. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2648-2655.	1.4	58
2105	Biofilm Community Dynamics in Bench-Scale Annular Reactors Simulating Arrestment of Chloraminated Drinking Water Nitrification. <i>Environmental Science & Technology</i> , 2014, 48, 5448-5457.	4.6	30

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2106	Design and Validation of Four New Primers for Next-Generation Sequencing To Target the 18S rRNA Genes of Gastrointestinal Ciliate Protozoa. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5515-5521.	1.4	36
2107	Down under the tunic: bacterial biodiversity hotspots and widespread ammonia-oxidizing archaea in coral reef ascidians. <i>ISME Journal</i> , 2014, 8, 575-588.	4.4	88
2108	Discrimination of Plant-Parasitic Nematodes from Complex Soil Communities Using Ecometagenetics. <i>Phytopathology</i> , 2014, 104, 749-761.	1.1	10
2109	Arsenite Oxidation by the Phyllosphere Bacterial Community Associated with <i>Wolffia australiana</i> . <i>Environmental Science & Technology</i> , 2014, 48, 9668-9674.	4.6	31
2110	Effect of acid-pretreatment on hydrogen fermentation of food waste: Microbial community analysis by next generation sequencing. <i>International Journal of Hydrogen Energy</i> , 2014, 39, 16302-16309.	3.8	67
2111	Shifts in the Microbial Community, Nitrifiers and Denitrifiers in the Biofilm in a Full-scale Rotating Biological Contactor. <i>Environmental Science & Technology</i> , 2014, 48, 8044-8052.	4.6	99
2112	Revealing the microbial community structure of clogging materials in dewatering wells differing in physico-chemical parameters in an open-cast mining area. <i>Water Research</i> , 2014, 63, 222-233.	5.3	25
2113	Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets. <i>Bioinformatics</i> , 2014, 30, 629-635.	1.8	186
2114	Improved performance of the PacBio SMRT technology for 16S rDNA sequencing. <i>Journal of Microbiological Methods</i> , 2014, 104, 59-60.	0.7	89
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2119	Arbuscular mycorrhizal fungal communities are phylogenetically clustered at small scales. <i>ISME Journal</i> , 2014, 8, 2231-2242.	4.4	88
2120	A comprehensive insight into bacterial virulence in drinking water using 454 pyrosequencing and Illumina high-throughput sequencing. <i>Ecotoxicology and Environmental Safety</i> , 2014, 109, 15-21.	2.9	74
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2130	Microbiome investigation in the ecological speciation context of lake whitefish (<i>Coregonus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50 1029-1046.	0.8	35
2131	Getting Started with Microbiome Analysis: Sample Acquisition to Bioinformatics. <i>Current Protocols in Human Genetics</i> , 2014, 82, 18.8.1-29.	3.5	111
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2133	Bacterial communities and greenhouse gas emissions of shallow ponds in the High Arctic. <i>Polar Biology</i> , 2014, 37, 1669-1683.	0.5	30
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2144	pH-dominated niche segregation of ammonia-oxidising microorganisms in Chinese agricultural soils. <i>FEMS Microbiology Ecology</i> , 2014, 90, 290-299.	1.3	72
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2154	Data analysis for 16S microbial profiling from different benchtop sequencing platforms. <i>Journal of Microbiological Methods</i> , 2014, 107, 30-37.	0.7	221
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2173	Life in extreme environments: microbial diversity in Great Salt Lake, Utah. <i>Extremophiles</i> , 2014, 18, 525-535.	0.9	67
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2217	Communities of sediment ammonia-oxidizing bacteria along a coastal pollution gradient in the East China Sea. <i>Marine Pollution Bulletin</i> , 2014, 86, 147-153.	2.3	15
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2222	Host signature effect on plant root-associated microbiomes revealed through analyses of resident vs. active communities. <i>Environmental Microbiology</i> , 2014, 16, 2157-2167.	1.8	158
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2235	Alteration of the Murine Gastrointestinal Microbiota by Tigecycline Leads to Increased Susceptibility to <i>Clostridium difficile</i> Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2767-2774.	1.4	61
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2249	Correlating Microbial Diversity Patterns with Geochemistry in an Extreme and Heterogeneous Environment of Mine Tailings. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3677-3686.	1.4	175
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2253	Development of a growth medium suitable for exopolysaccharide production and structural characterisation by <i>Bifidobacterium animalis</i> ssp. <i>lactis</i> ADO11. <i>Journal of Microbiological Methods</i> , 2014, 100, 93-98.	0.7	16
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2406	Spliced leader RNA trans-splicing discovered in copepods. <i>Scientific Reports</i> , 2015, 5, 17411.	1.6	9
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2408	End-product inhibition and acidification limit biowaste fermentation efficiency. <i>Bioresource Technology</i> , 2015, 198, 540-549.	4.8	5
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2530	Microbiome composition and geochemical characteristics of deep subsurface high-pressure environment, Pyh�asalmi mine Finland. <i>Frontiers in Microbiology</i> , 2015, 6, 1203.	1.5	53
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2541	Bacterial Exchange in Household Washing Machines. <i>Frontiers in Microbiology</i> , 2015, 6, 1381.	1.5	64
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2543	Comparative Gut Microbiota of 59 Neotropical Bird Species. <i>Frontiers in Microbiology</i> , 2015, 6, 1403.	1.5	216
2544	Ubiquitous Presence and Novel Diversity of Anaerobic Alkane Degraders in Cold Marine Sediments. <i>Frontiers in Microbiology</i> , 2015, 6, 1414.	1.5	30
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2700	Genetic diversity and population structure in <i>Physalis peruviana</i> and related taxa based on InDels and SNPs derived from COSII and IRG markers. <i>Plant Gene</i> , 2015, 4, 29-37.	1.4	30
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2705	<i>Carpoglyphus lactis</i> (Acari: Astigmata) from various dried fruits differed in associated micro-organisms. <i>Journal of Applied Microbiology</i> , 2015, 118, 470-484.	1.4	18
2706	<i>Spirochaeta lutea</i> sp. nov., isolated from marine habitats and emended description of the genus <i>Spirochaeta</i> . <i>Systematic and Applied Microbiology</i> , 2015, 38, 110-114.	1.2	35
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2988	Patterns and Determinants of Halophilic Archaea (Class Halobacteria) Diversity in Tunisian Endorheic Salt Lakes and Sebkhet Systems. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4432-4441.	1.4	35
2989	Human Adenovirus Diversity in Water Samples Using a Next-Generation Amplicon Sequencing Approach. <i>Food and Environmental Virology</i> , 2015, 7, 112-121.	1.5	46
2990	Effect of biofertilizer for suppressing <i>Fusarium</i> wilt disease of banana as well as enhancing microbial and chemical properties of soil under greenhouse trial. <i>Applied Soil Ecology</i> , 2015, 93, 111-119.	2.1	97

#	ARTICLE	IF	CITATIONS
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2996	Changes in human gut microbiota influenced by probiotic fermented milk ingestion. <i>Journal of Dairy Science</i> , 2015, 98, 3568-3576.	1.4	60
2997	Evaluating variation in human gut microbiota profiles due to DNA extraction method and inter-subject differences. <i>Frontiers in Microbiology</i> , 2015, 6, 130.	1.5	152
2998	Characterization of airborne ice-nucleation-active bacteria and bacterial fragments. <i>Atmospheric Environment</i> , 2015, 109, 105-117.	1.9	81
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3000	The pig gut microbial diversity: Understanding the pig gut microbial ecology through the next generation high throughput sequencing. <i>Veterinary Microbiology</i> , 2015, 177, 242-251.	0.8	218
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3005	Physicochemical conditions, metabolites and community structure of the bacterial microbiota in the gut of wood-feeding cockroaches (Blaberidae: Panesthiinae). <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-14.	1.3	50
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3007	Analysis of swine fecal microbiota at various growth stages. <i>Archives of Microbiology</i> , 2015, 197, 753-759.	1.0	68
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3011	The Gut Microbiota of Workers of the Litter-Feeding Termite <i>Syntermes wheeleri</i> (Termitidae: Termitidae). <i>Journal of Insect Science and Technology</i> , 2015, 10, 662-667.	1.4	26
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3038	Deciphering chicken gut microbial dynamics based on high-throughput 16S rRNA metagenomics analyses. <i>Gut Pathogens</i> , 2015, 7, 4.	1.6	230
3039	The oral and conjunctival microbiotas in cats with and without feline immunodeficiency virus infection. <i>Veterinary Research</i> , 2015, 46, 21.	1.1	29
3040	The daily dynamics of cystic fibrosis airway microbiota during clinical stability and at exacerbation. <i>Microbiome</i> , 2015, 3, 12.	4.9	122
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3049	Evaluation of water sampling methodologies for amplicon-based characterization of bacterial community structure. <i>Journal of Microbiological Methods</i> , 2015, 114, 43-50.	0.7	42
3050	Microbiota implications for immunity and transplantation. <i>Nature Reviews Nephrology</i> , 2015, 11, 342-353.	4.1	47
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3061	Parental material and cultivation determine soil bacterial community structure and fertility. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-10.	1.3	37
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3071	Alamethicin Suppresses Methanogenesis and Promotes Acetogenesis in Bioelectrochemical Systems. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3863-3868.	1.4	25
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3073	Illumina MiSeq sequencing investigation on the contrasting soil bacterial community structures in different iron mining areas. <i>Environmental Science and Pollution Research</i> , 2015, 22, 10788-10799.	2.7	188
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3077	Impacts of bulk soil microbial community structure on rhizosphere microbiomes of <i>Zea mays</i> . <i>Plant and Soil</i> , 2015, 392, 115-126.	1.8	155
3078	The abundance of functional genes, <i>cbbL</i> , <i>nifH</i> , <i>amoA</i> and <i>apsA</i> , and bacterial community structure of intertidal soil from Arabian Sea. <i>Microbiological Research</i> , 2015, 175, 57-66.	2.5	50
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3098	Microbial diversity and community respiration in freshwater sediments influenced by artificial light at night. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140130.	1.8	107
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3103	Le mycobiome humain : actualités et perspectives. <i>Revue Francophone Des Laboratoires</i> , 2015, 2015, 67-73.	0.0	2
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3116	Dietary calcium concentration and cereals differentially affect mineral balance and tight junction proteins expression in jejunum of weaned pigs. <i>British Journal of Nutrition</i> , 2015, 113, 1019-1031.	1.2	13
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3119	Metatranscriptomic Analysis of Diminutive Thiomargarita-Like Bacteria (â€œCandidatus Thiopilulaâ€-spp.) from Abyssal Cold Seeps of the Barbados Accretionary Prism. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3142-3156.	1.4	20
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3125	Physicochemical impacts associated with natural gas development on methanogenesis in deep sand aquifers. <i>ISME Journal</i> , 2015, 9, 436-446.	4.4	19
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3282	Inconsistent Denoising and Clustering Algorithms for Amplicon Sequence Data. <i>Journal of Computational Biology</i> , 2015, 22, 743-751.	0.8	15
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3284	Steps in Metagenomics: Let's Avoid Garbage in and Garbage Out. , 2015, , 1-23.		2
3285	Isolation and characterization of bacteria from the rhizosphere and bulk soil of <i>Stellera chamaejasme</i> L.. <i>Canadian Journal of Microbiology</i> , 2015, 61, 171-181.	0.8	9
3286	Characterization of the bacterial biodiversity in Pico cheese (an artisanal Azorean food). <i>International Journal of Food Microbiology</i> , 2015, 192, 86-94.	2.1	80
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3426	Archaeal Community Changes Associated with Cultivation of Amazon Forest Soil with Oil Palm. <i>Archaea</i> , 2016, 2016, 1-14.	2.3	10
3427	Effects of Betaine Aldehyde Dehydrogenase-Transgenic Soybean on Phosphatase Activities and Rhizospheric Bacterial Community of the Saline-Alkali Soil. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	2
3428	The Gut Microbial Community of Antarctic Fish Detected by 16S rRNA Gene Sequence Analysis. <i>BioMed Research International</i> , 2016, 2016, 1-7.	0.9	37
3429	Co-occurrence patterns in aquatic bacterial communities across changing permafrost landscapes. <i>Biogeosciences</i> , 2016, 13, 175-190.	1.3	64
3430	Controls on microalgal community structures in cryoconite holes upon high-Arctic glaciers, Svalbard. <i>Biogeosciences</i> , 2016, 13, 659-674.	1.3	35
3431	<i>Lactobacillus fermentum</i> CRL1446 Ameliorates Oxidative and Metabolic Parameters by Increasing Intestinal Feruloyl Esterase Activity and Modulating Microbiota in Caloric-Restricted Mice. <i>Nutrients</i> , 2016, 8, 415.	1.7	37
3432	Microbial Community Structure in the Rhizosphere of Rice Plants. <i>Frontiers in Microbiology</i> , 2015, 6, 1537.	1.5	148
3433	Diversity and Temporal Dynamics of the Epiphytic Bacterial Communities Associated with the Canopy-Forming Seaweed <i>Cystoseira compressa</i> (Esper) Gerloff and Nizamuddin. <i>Frontiers in Microbiology</i> , 2016, 7, 476.	1.5	112
3434	Spatio-Temporal Detection of the <i>Thiomonas</i> Population and the <i>Thiomonas</i> Arsenite Oxidase Involved in Natural Arsenite Attenuation Processes in the Carnoulès Acid Mine Drainage. <i>Frontiers in Cell and Developmental Biology</i> , 2016, 4, 3.	1.8	15
3435	Effect of Plant Harvesting on the Performance of Constructed Wetlands during Summer. <i>Water (Switzerland)</i> , 2016, 8, 24.	1.2	27
3436	Dynamics of Bacterial Community Abundance and Structure in Horizontal Subsurface Flow Wetland Mesocosms Treating Municipal Wastewater. <i>Water (Switzerland)</i> , 2016, 8, 457.	1.2	12
3437	Human microbiome studies in Korea. <i>Allergy Asthma & Respiratory Disease</i> , 2016, 4, 311.	0.3	4
3438	<i>Bacillus</i> sp. QSI-1 Modulate Quorum Sensing Signals Reduce <i>Aeromonas hydrophila</i> Level and Alter Gut Microbial Community Structure in Fish. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 184.	1.8	42
3439	The Effects of Various Land Reclamation Scenarios on the Succession of Soil Bacteria, Archaea, and Fungi Over the Short and Long Term. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	16
3440	Social Environment Has a Primary Influence on the Microbial and Odor Profiles of a Chemically Signaling Songbird. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	45
3441	Spatial Variations of Prokaryotic Communities in Surface Water from India Ocean to Chinese Marginal Seas and their Underlying Environmental Determinants. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	11
3442	Benchmarking DNA Metabarcoding for Biodiversity-Based Monitoring and Assessment. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	157

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3444	Shifts in Microbial Community Structure and Activity in the Ultra-Oligotrophic Eastern Mediterranean Sea Driven by the Deposition of Saharan Dust and European Aerosols. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	24
3445	Evaluating the Impact of Atmospheric Depositions on Springtime Dinitrogen Fixation in the Cretan Sea (Eastern Mediterranean)â€™A Mesocosm Approach. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	19
3446	Dark Production of Extracellular Superoxide by the Coral <i>Porites astreoides</i> and Representative Symbionts. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	32
3447	Distinct Bacterial Communities Associated with the Coral Model <i>Aiptasia</i> in Aposymbiotic and Symbiotic States with <i>Symbiodinium</i> . <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	67
3448	Methanotrophic Community Dynamics in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	17
3449	Dynamics of Viral Abundance and Diversity in a Sphagnum-Dominated Peatland: Temporal Fluctuations Prevail Over Habitat. <i>Frontiers in Microbiology</i> , 2015, 6, 1494.	1.5	14
3450	Novel Barite Chimneys at the Loki's Castle Vent Field Shed Light on Key Factors Shaping Microbial Communities and Functions in Hydrothermal Systems. <i>Frontiers in Microbiology</i> , 2015, 6, 1510.	1.5	36
3451	High Diversity of Anaerobic Alkane-Degrading Microbial Communities in Marine Seep Sediments Based on (1-methylalkyl)succinate Synthase Genes. <i>Frontiers in Microbiology</i> , 2015, 6, 1511.	1.5	47
3452	Structural Iron (II) of Basaltic Glass as an Energy Source for Zetaproteobacteria in an Abyssal Plain Environment, Off the Mid Atlantic Ridge. <i>Frontiers in Microbiology</i> , 2015, 6, 1518.	1.5	48
3453	Bacterial Diversity in Submarine Groundwater along the Coasts of the Yellow Sea. <i>Frontiers in Microbiology</i> , 2015, 6, 1519.	1.5	21
3454	Expanding the World of Marine Bacterial and Archaeal Clades. <i>Frontiers in Microbiology</i> , 2015, 6, 1524.	1.5	122
3455	Microbial Methane Production Associated with Carbon Steel Corrosion in a Nigerian Oil Field. <i>Frontiers in Microbiology</i> , 2015, 6, 1538.	1.5	30
3456	Exploration of Microbial Diversity and Community Structure of Lonar Lake: The Only Hypersaline Meteorite Crater Lake within Basalt Rock. <i>Frontiers in Microbiology</i> , 2015, 6, 1553.	1.5	100
3457	Ecophysiology of Zetaproteobacteria Associated with Shallow Hydrothermal Iron-Oxyhydroxide Deposits in Nagahama Bay of Satsuma Iwo-Jima, Japan. <i>Frontiers in Microbiology</i> , 2015, 6, 1554.	1.5	20
3458	Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. <i>Frontiers in Microbiology</i> , 2016, 7, 17.	1.5	72
3459	Metabolic Capabilities of Microorganisms Involved in and Associated with the Anaerobic Oxidation of Methane. <i>Frontiers in Microbiology</i> , 2016, 7, 46.	1.5	99
3460	Comparison of Fungal Community in Black Pepper-Vanilla and Vanilla Monoculture Systems Associated with <i>Vanilla Fusarium</i> Wilt Disease. <i>Frontiers in Microbiology</i> , 2016, 7, 117.	1.5	78

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3462	Bacterial Community Succession in Pine-Wood Decomposition. <i>Frontiers in Microbiology</i> , 2016, 7, 231.	1.5	106
3463	Distinct Spatial Patterns of SAR11, SAR86, and Actinobacteria Diversity along a Transect in the Ultra-oligotrophic South Pacific Ocean. <i>Frontiers in Microbiology</i> , 2016, 7, 234.	1.5	45
3464	Effect of Biostimulation Using Sewage Sludge, Soybean Meal, and Wheat Straw on Oil Degradation and Bacterial Community Composition in a Contaminated Desert Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 240.	1.5	45
3465	Spatial-Temporal Changes of Bacterioplankton Community along an Exhorheic River. <i>Frontiers in Microbiology</i> , 2016, 7, 250.	1.5	32
3466	Mucus Sugar Content Shapes the Bacterial Community Structure in Thermally Stressed <i>Acropora muricata</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 371.	1.5	86
3467	Distinctive Tropical Forest Variants Have Unique Soil Microbial Communities, But Not Always Low Microbial Diversity. <i>Frontiers in Microbiology</i> , 2016, 7, 376.	1.5	44
3468	In Search of Alternative Antibiotic Drugs: Quorum-Quenching Activity in Sponges and their Bacterial Isolates. <i>Frontiers in Microbiology</i> , 2016, 7, 416.	1.5	66
3469	Restructuring of Epibacterial Communities on <i>Fucus vesiculosus</i> forma <i>mytili</i> in Response to Elevated pCO ₂ and Increased Temperature Levels. <i>Frontiers in Microbiology</i> , 2016, 7, 434.	1.5	57
3470	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 459.	1.5	659
3471	Protist-Bacteria Associations: Gammaproteobacteria and Alphaproteobacteria Are Prevalent as Digestion-Resistant Bacteria in Ciliated Protozoa. <i>Frontiers in Microbiology</i> , 2016, 7, 498.	1.5	88
3472	Sample Processing Impacts the Viability and Cultivability of the Sponge Microbiome. <i>Frontiers in Microbiology</i> , 2016, 7, 499.	1.5	49
3473	Carbon and Sulfur Cycling below the Chemocline in a Meromictic Lake and the Identification of a Novel Taxonomic Lineage in the FCB Superphylum, Candidate Aegiribacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 598.	1.5	51
3474	Performance of 16s rDNA Primer Pairs in the Study of Rhizosphere and Endosphere Bacterial Microbiomes in Metabarcoding Studies. <i>Frontiers in Microbiology</i> , 2016, 7, 650.	1.5	237
3475	Molecular Characterization and Meta-Analysis of Gut Microbial Communities Illustrate Enrichment of <i>Prevotella</i> and <i>Megasphaera</i> in Indian Subjects. <i>Frontiers in Microbiology</i> , 2016, 7, 660.	1.5	110
3476	Identification of Free-Living and Particle-Associated Microbial Communities Present in Hadal Regions of the Mariana Trench. <i>Frontiers in Microbiology</i> , 2016, 7, 665.	1.5	99
3477	Superimposed Pristine Limestone Aquifers with Marked Hydrochemical Differences Exhibit Distinct Fungal Communities. <i>Frontiers in Microbiology</i> , 2016, 7, 666.	1.5	24
3478	Concentration of Petroleum-Hydrocarbon Contamination Shapes Fungal Endophytic Community Structure in Plant Roots. <i>Frontiers in Microbiology</i> , 2016, 7, 685.	1.5	19

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3479	The Ability of Microbial Community of Lake Baikal Bottom Sediments Associated with Gas Discharge to Carry Out the Transformation of Organic Matter under Thermobaric Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 690.	1.5	11
3480	Comparison of Microbial Communities Isolated from Feces of Asymptomatic Salmonella-Shedding and Non-Salmonella Shedding Dairy Cows. <i>Frontiers in Microbiology</i> , 2016, 7, 691.	1.5	7
3481	Unearthing the Ecology of Soil Microorganisms Using a High Resolution DNA-SIP Approach to Explore Cellulose and Xylose Metabolism in Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 703.	1.5	154
3482	Isolation and Characterization of Electrochemically Active Subsurface Delftia and Azonexus Species. <i>Frontiers in Microbiology</i> , 2016, 7, 756.	1.5	65
3483	In Situ Microbial Community Succession on Mild Steel in Estuarine and Marine Environments: Exploring the Role of Iron-Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 767.	1.5	66
3484	Size Matters: Assessing Optimum Soil Sample Size for Fungal and Bacterial Community Structure Analyses Using High Throughput Sequencing of rRNA Gene Amplicons. <i>Frontiers in Microbiology</i> , 2016, 7, 824.	1.5	58
3485	Differential Impacts of Willow and Mineral Fertilizer on Bacterial Communities and Biodegradation in Diesel Fuel Oil-Contaminated Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 837.	1.5	26
3486	Bacterial Dormancy Is More Prevalent in Freshwater than Hypersaline Lakes. <i>Frontiers in Microbiology</i> , 2016, 7, 853.	1.5	39
3487	Population Dynamics and Community Composition of Ammonia Oxidizers in Salt Marshes after the Deepwater Horizon Oil Spill. <i>Frontiers in Microbiology</i> , 2016, 7, 854.	1.5	22
3488	Responses of Aquatic Bacteria to Terrestrial Runoff: Effects on Community Structure and Key Taxonomic Groups. <i>Frontiers in Microbiology</i> , 2016, 7, 889.	1.5	18
3489	Isolation and Genomic Characterization of <i>Desulfuromonas soudanensis</i> WTL TM , a Metal- and Electrode-Respiring Bacterium from Anoxic Deep Subsurface Brine. <i>Frontiers in Microbiology</i> , 2016, 7, 913.	1.5	53
3490	Microbiomes of <i>Muricea californica</i> and <i>M. fruticosa</i> : Comparative Analyses of Two Co-occurring Eastern Pacific Octocorals. <i>Frontiers in Microbiology</i> , 2016, 7, 917.	1.5	33
3491	Indirect Evidence Link PCB Dehalogenation with Geobacteraceae in Anaerobic Sediment-Free Microcosms. <i>Frontiers in Microbiology</i> , 2016, 7, 933.	1.5	38
3492	Fungal Community Associated with <i>Dactylopius</i> (Hemiptera: Coccoidea: Dactylopiidae) and Its Role in Uric Acid Metabolism. <i>Frontiers in Microbiology</i> , 2016, 7, 954.	1.5	27
3493	Flow Cytometric and 16S Sequencing Methodologies for Monitoring the Physiological Status of the Microbiome in Powdered Infant Formula Production. <i>Frontiers in Microbiology</i> , 2016, 7, 968.	1.5	12
3494	Biogeographic Variation in Host Range Phenotypes and Taxonomic Composition of Marine Cyanophage Isolates. <i>Frontiers in Microbiology</i> , 2016, 7, 983.	1.5	26
3495	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. <i>Frontiers in Microbiology</i> , 2016, 7, 987.	1.5	61
3496	Plants Rather than Mineral Fertilization Shape Microbial Community Structure and Functional Potential in Legacy Contaminated Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 995.	1.5	43

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3497	Distribution and Composition of Thiotrophic Mats in the Hypoxic Zone of the Black Sea (150â€“170 m) Tj ETQq0 0,0,rgBT /Oyerlock 10	1.5	15
3498	Unanticipated Geochemical and Microbial Community Structure under Seasonal Ice Cover in a Dilute, Dimictic Arctic Lake. <i>Frontiers in Microbiology</i> , 2016, 7, 1035.	1.5	33
3499	Endozoicomonas Are Specific, Facultative Symbionts of Sea Squirts. <i>Frontiers in Microbiology</i> , 2016, 7, 1042.	1.5	43
3500	Populations of Stored Product Mite Tyrophagus putrescentiae Differ in Their Bacterial Communities. <i>Frontiers in Microbiology</i> , 2016, 7, 1046.	1.5	43
3501	A Metaproteomic Analysis of the Response of a Freshwater Microbial Community under Nutrient Enrichment. <i>Frontiers in Microbiology</i> , 2016, 7, 1172.	1.5	28
3502	Rumen Bacterial Community Composition in Holstein and Jersey Cows Is Different under Same Dietary Condition and Is Not Affected by Sampling Method. <i>Frontiers in Microbiology</i> , 2016, 07, 1206.	1.5	155
3503	Wheat and Rice Growth Stages and Fertilization Regimes Alter Soil Bacterial Community Structure, But Not Diversity. <i>Frontiers in Microbiology</i> , 2016, 7, 1207.	1.5	86
3504	Chronic Polyaromatic Hydrocarbon (PAH) Contamination Is a Marginal Driver for Community Diversity and Prokaryotic Predicted Functioning in Coastal Sediments. <i>Frontiers in Microbiology</i> , 2016, 7, 1303.	1.5	39
3505	Aboveground Whitefly Infestation-Mediated Reshaping of the Root Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 1314.	1.5	74
3506	Composition of Ileal Bacterial Community in Grazing Goats Varies across Non-rumination, Transition and Rumination Stages of Life. <i>Frontiers in Microbiology</i> , 2016, 07, 1364.	1.5	46
3507	Spatial and Temporal Dynamics of Pacific Oyster Hemolymph Microbiota across Multiple Scales. <i>Frontiers in Microbiology</i> , 2016, 7, 1367.	1.5	83
3508	Riverine Bacterial Communities Reveal Environmental Disturbance Signatures within the Betaproteobacteria and Verrucomicrobia. <i>Frontiers in Microbiology</i> , 2016, 7, 1441.	1.5	52
3509	Mineral vs. Organic Amendments: Microbial Community Structure, Activity and Abundance of Agriculturally Relevant Microbes Are Driven by Long-Term Fertilization Strategies. <i>Frontiers in Microbiology</i> , 2016, 7, 1446.	1.5	462
3510	Microbial Community Structure of Subglacial Lake Whillans, West Antarctica. <i>Frontiers in Microbiology</i> , 2016, 7, 1457.	1.5	74
3511	Evaluation of the Microbial Diversity in Amyotrophic Lateral Sclerosis Using High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2016, 7, 1479.	1.5	145
3512	Persistent Infection by Wolbachia wAlbB Has No Effect on Composition of the Gut Microbiota in Adult Female Anopheles stephensi. <i>Frontiers in Microbiology</i> , 2016, 7, 1485.	1.5	28
3513	Niche Filtering of Bacteria in Soil and Rock Habitats of the Colorado Plateau Desert, Utah, USA. <i>Frontiers in Microbiology</i> , 2016, 7, 1489.	1.5	51
3514	Effects of Dietary Forage and Calf Starter Diet on Ruminal pH and Bacteria in Holstein Calves during Weaning Transition. <i>Frontiers in Microbiology</i> , 2016, 7, 1575.	1.5	80

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3515	Summer Abundance and Distribution of Proteorhodopsin Genes in the Western Arctic Ocean. <i>Frontiers in Microbiology</i> , 2016, 7, 1584.	1.5	10
3516	The Madeira Archipelago As a Significant Source of Marine-Derived Actinomycete Diversity with Anticancer and Antimicrobial Potential. <i>Frontiers in Microbiology</i> , 2016, 7, 1594.	1.5	32
3517	Interactions between Obesity Status and Dietary Intake of Monounsaturated and Polyunsaturated Oils on Human Gut Microbiome Profiles in the Canola Oil Multicenter Intervention Trial (COMIT). <i>Frontiers in Microbiology</i> , 2016, 7, 1612.	1.5	64
3518	Microbial Mat Compositional and Functional Sensitivity to Environmental Disturbance. <i>Frontiers in Microbiology</i> , 2016, 7, 1632.	1.5	21
3519	Response of Core Microbial Consortia to Chronic Hydrocarbon Contaminations in Coastal Sediment Habitats. <i>Frontiers in Microbiology</i> , 2016, 7, 1637.	1.5	76
3520	Community Composition and Abundance of Bacterial, Archaeal and Nitrifying Populations in Savanna Soils on Contrasting Bedrock Material in Kruger National Park, South Africa. <i>Frontiers in Microbiology</i> , 2016, 7, 1638.	1.5	34
3521	Assessing Marine Microbial Induced Corrosion at Santa Catalina Island, California. <i>Frontiers in Microbiology</i> , 2016, 7, 1679.	1.5	37
3522	Gradual Changes of Gut Microbiota in Weaned Miniature Piglets. <i>Frontiers in Microbiology</i> , 2016, 7, 1727.	1.5	164
3523	Characterization of Electricity Generated by Soil in Microbial Fuel Cells and the Isolation of Soil Source Exoelectrogenic Bacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 1776.	1.5	75
3524	Non-selective Separation of Bacterial Cells with Magnetic Nanoparticles Facilitated by Varying Surface Charge. <i>Frontiers in Microbiology</i> , 2016, 7, 1891.	1.5	12
3525	Antibacterial Compounds-Macrolactin Alters the Soil Bacterial Community and Abundance of the Gene Encoding PKS. <i>Frontiers in Microbiology</i> , 2016, 7, 1904.	1.5	28
3526	Intraclade Heterogeneity in Nitrogen Utilization by Marine Prokaryotes Revealed Using Stable Isotope Probing Coupled with Tag Sequencing (Tag-SIP). <i>Frontiers in Microbiology</i> , 2016, 7, 1932.	1.5	24
3527	The Relationship between pH and Bacterial Communities in a Single Karst Ecosystem and Its Implication for Soil Acidification. <i>Frontiers in Microbiology</i> , 2016, 7, 1955.	1.5	134
3528	Diverse Profiles of AI-1 Type Quorum Sensing Molecules in Cultivable Bacteria from the Mangrove (<i>Kandelia obovata</i>) Rhizosphere Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 1957.	1.5	22
3529	Diversity of Phototrophic Genes Suggests Multiple Bacteria May Be Able to Exploit Sunlight in Exposed Soils from the SÅr Rondane Mountains, East Antarctica. <i>Frontiers in Microbiology</i> , 2016, 7, 2026.	1.5	20
3530	Trace Elements Induce Predominance among Methanogenic Activity in Anaerobic Digestion. <i>Frontiers in Microbiology</i> , 2016, 7, 2034.	1.5	78
3531	Fine Spatial Scale Variation of Soil Microbial Communities under European Beech and Norway Spruce. <i>Frontiers in Microbiology</i> , 2016, 7, 2067.	1.5	74
3532	Effect of Different Lignocellulosic Diets on Bacterial Microbiota and Hydrolytic Enzyme Activities in the Gut of the Cotton Boll Weevil (<i>Anthonomus grandis</i>). <i>Frontiers in Microbiology</i> , 2016, 07, 2093.	1.5	27

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3533	Evaluating the Contribution of Gut Microbiota to the Variation of Porcine Fatness with the Cecum and Fecal Samples. <i>Frontiers in Microbiology</i> , 2016, 07, 2108.	1.5	66
3534	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. <i>Frontiers in Nutrition</i> , 2016, 3, 26.	1.6	40
3535	Extremophiles in an Antarctic Marine Ecosystem. <i>Microorganisms</i> , 2016, 4, 8.	1.6	18
3536	Highly Variable Bacterial Communities Associated with the Octocoral <i>Antilloorgia elisabethae</i> . <i>Microorganisms</i> , 2016, 4, 23.	1.6	29
3537	MMinte: an application for predicting metabolic interactions among the microbial species in a community. <i>BMC Bioinformatics</i> , 2016, 17, 343.	1.2	67
3538	Household air pollution and the lung microbiome of healthy adults in Malawi: a cross-sectional study. <i>BMC Microbiology</i> , 2016, 16, 182.	1.3	49
3539	Longitudinal survey of <i>Clostridium difficile</i> presence and gut microbiota composition in a Belgian nursing home. <i>BMC Microbiology</i> , 2016, 16, 229.	1.3	36
3540	The impact of albendazole treatment on the incidence of viral- and bacterial-induced diarrhea in school children in southern Vietnam: study protocol for a randomized controlled trial. <i>Trials</i> , 2016, 17, 279.	0.7	2
3541	An adaptive association test for microbiome data. <i>Genome Medicine</i> , 2016, 8, 56.	3.6	69
3542	Vitamin A deficiency impacts the structural segregation of gut microbiota in children with persistent diarrhea. <i>Journal of Clinical Biochemistry and Nutrition</i> , 2016, 59, 113-121.	0.6	49
3543	Bacterial Communities of Three Saline Meromictic Lakes in Central Asia. <i>PLoS ONE</i> , 2016, 11, e0150847.	1.1	56
3544	Microbiota in Breast Milk of Chinese Lactating Mothers. <i>PLoS ONE</i> , 2016, 11, e0160856.	1.1	92
3545	Effect of <i>Saccharomyces boulardii</i> and Mode of Delivery on the Early Development of the Gut Microbial Community in Preterm Infants. <i>PLoS ONE</i> , 2016, 11, e0150306.	1.1	29
3546	The Effect of Dietary Replacement of Ordinary Rice with Red Yeast Rice on Nutrient Utilization, Enteric Methane Emission and Rumen Archaeal Diversity in Goats. <i>PLoS ONE</i> , 2016, 11, e0160198.	1.1	16
3547	Influences of Plant Species, Season and Location on Leaf Endophytic Bacterial Communities of Non-Cultivated Plants. <i>PLoS ONE</i> , 2016, 11, e0150895.	1.1	96
3548	First Comparative Analysis of the Community Structures and Carbon Metabolic Pathways of the Bacteria Associated with <i>Alvinocaris longirostris</i> in a Hydrothermal Vent of Okinawa Trough. <i>PLoS ONE</i> , 2016, 11, e0154359.	1.1	15
3549	Effects of Propidium Monoazide (PMA) Treatment on Mycobiome and Bacteriome Analysis of Cystic Fibrosis Airways during Exacerbation. <i>PLoS ONE</i> , 2016, 11, e0168860.	1.1	21
3550	Unbiased Characterization of Anopheles Mosquito Blood Meals by Targeted High-Throughput Sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004512.	1.3	61

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3551	Clonal Evolution of <i>Enterocytozoon bieneusi</i> Populations in Swine and Genetic Differentiation in Subpopulations between Isolates from Swine and Humans. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004966.	1.3	26
3552	The Microbiome of Ehrlichia-Infected and Uninfected Lone Star Ticks (<i>Amblyomma americanum</i>). <i>PLoS ONE</i> , 2016, 11, e0146651.	1.1	49
3553	Supragingival Microbial Profiles of Permanent and Deciduous Teeth in Children with Mixed Dentition. <i>PLoS ONE</i> , 2016, 11, e0146938.	1.1	52
3554	Diversity and Stability of Lactic Acid Bacteria in Rye Sourdoughs of Four Bakeries with Different Propagation Parameters. <i>PLoS ONE</i> , 2016, 11, e0148325.	1.1	46
3555	Reassessment of Species Diversity of the Subfamily Denticollinae (Coleoptera: Elateridae) through DNA Barcoding. <i>PLoS ONE</i> , 2016, 11, e0148602.	1.1	27
3556	Soil Respiration and Bacterial Structure and Function after 17 Years of a Reciprocal Soil Transplant Experiment. <i>PLoS ONE</i> , 2016, 11, e0150599.	1.1	60
3557	Gut Bacterial Community of the Xylophagous Cockroaches <i>Cryptocercus punctulatus</i> and <i>Parasphaeria boleiriana</i> . <i>PLoS ONE</i> , 2016, 11, e0152400.	1.1	32
3558	Age-Related Differences in the Gastrointestinal Microbiota of Chinstrap Penguins (<i>Pygoscelis</i>) Tj ETQq1 1 0.784314 rrgBT /Overlock 10 T	1.1	79
3559	Specific Microbial Communities Associate with the Rhizosphere of <i>Welwitschia mirabilis</i> , a Living Fossil. <i>PLoS ONE</i> , 2016, 11, e0153353.	1.1	41
3560	Response of Spring Diatoms to CO ₂ Availability in the Western North Pacific as Determined by Next-Generation Sequencing. <i>PLoS ONE</i> , 2016, 11, e0154291.	1.1	12
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3562	Spatial Variations of the Methanogenic Communities in the Sediments of Tropical Mangroves. <i>PLoS ONE</i> , 2016, 11, e0161065.	1.1	19
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3754	Laboratory maintained and wild populations of <i>Hydra</i> differ in their microbiota. <i>Annals of Microbiology</i> , 2016, 66, 931-935.	1.1	2
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3803	Bacterial community analysis of Tatsoi cultivated by hydroponics. <i>Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes</i> , 2016, 51, 490-496.	0.7	3
3804	Bacterial populations on brewery filling hall surfaces as revealed by next-generation sequencing. <i>Biofouling</i> , 2016, 32, 571-581.	0.8	6

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3806	Low-strength ultrasonication positively affects methanogenic granules toward higher AD performance: Implications from microbial community shift. <i>Ultrasonics Sonochemistry</i> , 2016, 32, 198-203.	3.8	12
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4000	Reflection on Molecular Approaches Influencing State-of-the-Art Bioremediation Design: Culturing to Microbial Community Fingerprinting to Omics. <i>Journal of Environmental Engineering, ASCE</i> , 2016, 142, .	0.7	28
4001	DOMINO: development of informative molecular markers for phylogenetic and genome-wide population genetic studies in non-model organisms. <i>Bioinformatics</i> , 2016, 32, 3753-3759.	1.8	8
4002	The importance of neutral and niche processes for bacterial community assembly differs between habitat generalists and specialists. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw174.	1.3	123
4003	Coping with copper: legacy effect of copper on potential activity of soil bacteria following a century of exposure. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw175.	1.3	126
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4012	Hyperoxaluria leads to dysbiosis and drives selective enrichment of oxalate metabolizing bacterial species in recurrent kidney stone endures. <i>Scientific Reports</i> , 2016, 6, 34712.	1.6	84
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4155	A distinct microbiota composition is associated with protection from food allergy in an oral mouse immunization model. <i>Clinical Immunology</i> , 2016, 173, 10-18.	1.4	52
4156	Genomic and enzymatic evidence for acetogenesis among multiple lineages of the archaeal phylum Bathyarchaeota widespread in marine sediments. <i>Nature Microbiology</i> , 2016, 1, 16035.	5.9	256
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4159	Role of the Gut Microbiome in Modulating Arthritis Progression in Mice. <i>Scientific Reports</i> , 2016, 6, 30594.	1.6	169
4160	Structural modulation of the gut microbiota and the relationship with body weight: compared evaluation of liraglutide and saxagliptin treatment. <i>Scientific Reports</i> , 2016, 6, 33251.	1.6	117
4161	Construction of a Species-Level Tree of Life for the Insects and Utility in Taxonomic Profiling. <i>Systematic Biology</i> , 2016, 66, syw099.	2.7	29
4162	Phylogenetic congruence between subtropical trees and their associated fungi. <i>Ecology and Evolution</i> , 2016, 6, 8412-8422.	0.8	16
4164	Preliminary analysis of salivary microbiome and their potential roles in oral lichen planus. <i>Scientific Reports</i> , 2016, 6, 22943.	1.6	99
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4175	Distinguishing between Microbial Habitats Unravels Ecological Complexity in Coral Microbiomes. <i>MSystems</i> , 2016, 1, .	1.7	90
4176	Metagenomics, Metatranscriptomics, and Metabolomics Approaches for Microbiome Analysis. <i>Evolutionary Bioinformatics</i> , 2016, 12s1, EBO.S36436.	0.6	227
4177	Bayesian nonparametric dependent model for partially replicated data: The influence of fuel spills on species diversity. <i>Annals of Applied Statistics</i> , 2016, 10, .	0.5	16
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4181	Functional Responses of Bacterioplankton Diversity and Metabolism to Experimental Bottom-Up and Top-Down Forcings. <i>Microbial Ecology</i> , 2016, 72, 347-358.	1.4	16
4182	Illumina sequencing-based community analysis of bacteria associated with different bryophytes collected from Tibet, China. <i>BMC Microbiology</i> , 2016, 16, 276.	1.3	20
4183	A method for automated pathogenic content estimation with application to rheumatoid arthritis. <i>BMC Systems Biology</i> , 2016, 10, 107.	3.0	9
4184	Enhancement and Biological Characteristics Related to Aerobic Biodegradation of Toluene with Co-Existence of Benzene. <i>Water, Air, and Soil Pollution</i> , 2016, 227, 1.	1.1	13
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4197	Nitrogen-fixing bacterial communities in invasive legume nodules and associated soils are similar across introduced and native range populations in Australia. <i>Journal of Biogeography</i> , 2016, 43, 1631-1644.	1.4	23
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4202	Metagenomic analysis of microbial consortia enriched from compost: new insights into the role of Actinobacteria in lignocellulose decomposition. <i>Biotechnology for Biofuels</i> , 2016, 9, 22.	6.2	237
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4229	Microbial Reconstitution Reverses Maternal Diet-Induced Social and Synaptic Deficits in Offspring. <i>Cell</i> , 2016, 165, 1762-1775.	13.5	840
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4231	Ecological differentiation in planktonic and sediment-associated chemotrophic microbial populations in Yellowstone hot springs. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw137.	1.3	60
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4281	Metagenomic assessment of the microbial diversity in ground pork products from markets in the North Central Region of South Korea. <i>Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes</i> , 2016, 51, 622-627.	0.7	7
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4283	Relationship of Bacterial Richness to Organic Degradation Rate and Sediment Age in Subseafloor Sediment. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4994-4999.	1.4	47
4284	A Brief Review on the Ecological Network Analysis with Applications in the Emerging Medical Ecology. <i>Springer Protocols</i> , 2016, , 7-39.	0.1	7
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4287	Analysis of bacterial diversity of Chinese Luzhou-flavor liquor brewed in different seasons by Illumina Miseq sequencing. <i>Annals of Microbiology</i> , 2016, 66, 1293-1301.	1.1	56
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4298	Distribution and diversity of bacterial communities and sulphate-reducing bacteria in a paddy soil irrigated with acid mine drainage. <i>Journal of Applied Microbiology</i> , 2016, 121, 196-206.	1.4	26
4299	Biogeographic patterns of soil diazotrophic communities across six forests in the North America. <i>Molecular Ecology</i> , 2016, 25, 2937-2948.	2.0	76
4300	Variability of the Sheep Lung Microbiota. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3225-3238.	1.4	43
4301	nirS-Encoding denitrifier community composition, distribution, and abundance along the coastal wetlands of China. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8573-8582.	1.7	57
4302	Deterministic processes dominate nematode community structure in the Fynbos Mediterranean heathland of South Africa. <i>Evolutionary Ecology</i> , 2016, 30, 685-701.	0.5	24
4303	Estimating genetic structure and diversity of cyanobacterial communities in Atlantic forest phyllosphere. <i>Canadian Journal of Microbiology</i> , 2016, 62, 953-960.	0.8	19
4304	16S rRNA gene sequencing of mock microbial populations- impact of DNA extraction method, primer choice and sequencing platform. <i>BMC Microbiology</i> , 2016, 16, 123.	1.3	241
4305	Millions of reads, thousands of taxa: microbial community structure and associations analyzed via marker genes. <i>FEMS Microbiology Reviews</i> , 2016, 40, 686-700.	3.9	159
4306	Mitigation of ammonia inhibition by internal dilution in high-rate anaerobic digestion of food waste leachate and evidences of microbial community response. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1892-1901.	1.7	23
4307	Microbiome Survey of the Inflamed and Noninflamed Gut at Different Compartments Within the Gastrointestinal Tract of Inflammatory Bowel Disease Patients. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 817-825.	0.9	114
4308	Microbiome change by symbiotic invasion in lichens. <i>Environmental Microbiology</i> , 2016, 18, 1428-1439.	1.8	41
4309	Bacterial responses to environmental change on the Tibetan plateau over the past half century. <i>Environmental Microbiology</i> , 2016, 18, 1930-1941.	1.8	34
4310	Phylogenetic conservation of freshwater lake habitat preference varies between abundant bacterioplankton phyla. <i>Environmental Microbiology</i> , 2016, 18, 1212-1226.	1.8	70
4311	The <i>rpb2</i> gene represents a viable alternative molecular marker for the analysis of environmental fungal communities. <i>Molecular Ecology Resources</i> , 2016, 16, 388-401.	2.2	66
4312	Measuring the biodiversity of microbial communities by flow cytometry. <i>Methods in Ecology and Evolution</i> , 2016, 7, 1376-1385.	2.2	161
4313	The longitudinal effect of a multi-strain probiotic on the intestinal bacterial microbiota of neonatal foals. <i>Equine Veterinary Journal</i> , 2016, 48, 689-696.	0.9	30
4314	Growth dynamics of a laminated microbial mat in response to variable irradiance in an Antarctic lake. <i>Freshwater Biology</i> , 2016, 61, 396-410.	1.2	17

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4316	Decoupled distanceâ€“decay patterns between <i>dsrA</i> and <i>16S rRNA</i> genes among salt marsh sulfate-reducing bacteria. <i>Environmental Microbiology</i> , 2016, 18, 75-86.	1.8	35
4317	Microbial abundance and community in subsurface flow constructed wetland microcosms: role of plant presence. <i>Environmental Science and Pollution Research</i> , 2016, 23, 4036-4045.	2.7	80
4318	Examining the diversity of microbes in a deep-sea coral community impacted by the Deepwater Horizon oil spill. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 129, 157-166.	0.6	32
4319	Characteristics of actinomycetes producing geosmin in Paldang Lake, Korea. <i>Desalination and Water Treatment</i> , 2016, 57, 888-899.	1.0	6
4320	Geographical patterns of the standing and active human gut microbiome in health and IBD. <i>Gut</i> , 2016, 65, 238-248.	6.1	143
4321	Complete mitochondrial genome sequences of Atlantic sturgeon, <i>Acipenser oxyrinchus oxyrinchus</i> , Gulf sturgeon, <i>A. o. desotoi</i> and European sturgeon <i>A. sturio</i> (Acipenseriformes: Acipenseridae) obtained through next generation sequencing. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2549-2551.	0.7	5
4322	Dysbiosis of the fecal microbiota in the TNBS-induced Crohnâ€™s disease mouse model. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 4485-4494.	1.7	33
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4324	The microbiome and functions of black soils are altered by dibutyl phthalate contamination. <i>Applied Soil Ecology</i> , 2016, 99, 51-61.	2.1	62
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4326	Deterministic Assembly of Complex Bacterial Communities in Guts of Germ-Free Cockroaches. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1256-1263.	1.4	59
4327	Application of slow-release phosphorus fertilizers increases arbuscular mycorrhizal fungal diversity in the roots of apple trees. <i>Plant and Soil</i> , 2016, 402, 291-301.	1.8	40
4328	Empowering a mesophilic inoculum for thermophilic nitrification: Growth mode and temperature pattern as critical proliferation factors for archaeal ammonia oxidizers. <i>Water Research</i> , 2016, 92, 94-103.	5.3	17
4329	Evaluation of microbial diversity of activated sludge in a municipal wastewater treatment plant of northern China by high-throughput sequencing technology. <i>Desalination and Water Treatment</i> , 2016, 57, 23516-23521.	1.0	24
4330	Microbial Environmental Genomics (MEG). <i>Methods in Molecular Biology</i> , 2016, , .	0.4	6
4331	Use of functional gene expression and respirometry to study wastewater nitrification activity after exposure to low doses of copper. <i>Environmental Science and Pollution Research</i> , 2016, 23, 6443-6450.	2.7	18
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4336	Chemical Signals in Vertebrates 13. , 2016, , .		1
4337	Response of gut microbiota to salinity change in two euryhaline aquatic animals with reverse salinity preference. <i>Aquaculture</i> , 2016, 454, 72-80.	1.7	188
4338	Soil Bacteria Population Dynamics Following Stimulation for Ureolytic Microbial-Induced CaCO ₃ Precipitation. <i>Environmental Science & Technology</i> , 2016, 50, 616-624.	4.6	78
4339	Evidences for Microbial Precipitation of Calcite in Speleothems from Krem Syndai in Jaintia Hills, Meghalaya, India. <i>Geomicrobiology Journal</i> , 2016, 33, 906-933.	1.0	18
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4345	Conversion of methane-derived carbon and microbial community in enrichment cultures in response to O ₂ availability. <i>Environmental Science and Pollution Research</i> , 2016, 23, 7517-7528.	2.7	20
4346	The impact of sampling, PCR, and sequencing replication on discerning changes in drinking water bacterial community over diurnal time-scales. <i>Water Research</i> , 2016, 90, 216-224.	5.3	45
4347	The dual oxidase gene <i>BdDuoX</i> regulates the intestinal bacterial community homeostasis of <i>Bactrocera dorsalis</i> . <i>ISME Journal</i> , 2016, 10, 1037-1050.	4.4	118
4348	The effects of the growth substrate on cultivable and total endophytic assemblages of <i>Arabidopsis thaliana</i> . <i>Plant and Soil</i> , 2016, 405, 325-336.	1.8	22
4349	Bacterial concentration and diversity in fresh tropical shrimps (<i>Penaeus notialis</i>) and the surrounding brackish waters and sediment. <i>International Journal of Food Microbiology</i> , 2016, 218, 96-104.	2.1	36
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4352	A New N -Acyl Homoserine Lactone Synthase in an Uncultured Symbiont of the Red Sea Sponge <i>Theonella swinhoei</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 1274-1285.	1.4	30
4353	Molecular analysis of microbial community structures in Nigerian oil production and processing facilities in order to access souring corrosion and methanogenesis. <i>Corrosion Science</i> , 2016, 103, 242-254.	3.0	27
4354	Microbial community structure and methane-cycling activity of subsurface sediments at Mississippi Canyon 118 before the Deepwater Horizon disaster. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 129, 148-156.	0.6	15
4355	Nitrogen fertilization induced changes in ammonia oxidation are attributable mostly to bacteria rather than archaea in greenhouse-based high N input vegetable soil. <i>Soil Biology and Biochemistry</i> , 2016, 93, 150-159.	4.2	73
4356	Novel phenazine crystals enable direct electron transfer to methanogens in anaerobic digestion by redox potential modulation. <i>Energy and Environmental Science</i> , 2016, 9, 644-655.	15.6	69
4357	Practical survey on antibiotic-resistant bacterial communities in livestock manure and manure-amended soil. <i>Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes</i> , 2016, 51, 14-23.	0.7	30
4358	Temporal, regional and geochemical drivers of microbial community variation in the melt ponds of the Ross Sea region, Antarctica. <i>Polar Biology</i> , 2016, 39, 267-282.	0.5	6
4359	Impact of microbial communities on floral nectar chemistry: Potential implications for biological control of pest insects. <i>Basic and Applied Ecology</i> , 2016, 17, 189-198.	1.2	30
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4361	Analysis of <i>cbbL</i> , <i>nifH</i> , and <i>pufLM</i> in Soils from the Sør Rondane Mountains, Antarctica, Reveals a Large Diversity of Autotrophic and Phototrophic Bacteria. <i>Microbial Ecology</i> , 2016, 71, 131-149.	1.4	28
4362	Effects of Volcanic Pumice Inputs on Microbial Community Composition and Dissolved C/P Ratios in Lake Waters: an Experimental Approach. <i>Microbial Ecology</i> , 2016, 71, 18-28.	1.4	11
4363	Characterization of Bacterial Communities in Deep-Sea Hydrothermal Vents from Three Oceanic Regions. <i>Marine Biotechnology</i> , 2016, 18, 232-241.	1.1	22
4364	Colonization of new land by arbuscular mycorrhizal fungi. <i>Fungal Ecology</i> , 2016, 20, 22-29.	0.7	49
4365	Dietary nitrate improves vascular function in patients with hypercholesterolemia: a randomized, double-blind, placebo-controlled study. <i>American Journal of Clinical Nutrition</i> , 2016, 103, 25-38.	2.2	206
4366	Microbial profiling of South African acid mine water samples using next generation sequencing platform. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6069-6079.	1.7	7
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4371	Bacterial communities of an agricultural soil amended with solid pig and dairy manures, and urea fertilizer. <i>Applied Soil Ecology</i> , 2016, 103, 61-71.	2.1	56
4372	Gut microbiome-derived metabolites modulate intestinal epithelial cell damage and mitigate graft-versus-host disease. <i>Nature Immunology</i> , 2016, 17, 505-513.	7.0	536
4373	Rumen bacterial communities shift across a lactation in Holstein, Jersey and Holstein \times Jersey dairy cows and correlate to rumen function, bacterial fatty acid composition and production parameters. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv059.	1.3	62
4374	Microbial Diversity of Ground Beef Products in South Korean Retail Market Analyzed by PCR-DGGE and 454 Pyrosequencing. <i>Food Biotechnology</i> , 2016, 30, 63-77.	0.6	11
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4377	Absence of MHC class II on cDCs results in microbial-dependent intestinal inflammation. <i>Journal of Experimental Medicine</i> , 2016, 213, 517-534.	4.2	110
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4388	The impact of tropical forest logging and oil palm agriculture on the soil microbiome. <i>Molecular Ecology</i> , 2016, 25, 2244-2257.	2.0	99
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4390	Do shifts in life strategies explain microbial community responses to increasing nitrogen in tundra soil?. <i>Soil Biology and Biochemistry</i> , 2016, 96, 216-228.	4.2	62
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4394	Functional maintenance and structural flexibility of microbial communities perturbed by simulated intense rainfall in a pilot-scale membrane bioreactor. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6447-6456.	1.7	23
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4401	Nearing the cold-arid limits of microbial life in permafrost of an upper dry valley, Antarctica. <i>ISME Journal</i> , 2016, 10, 1613-1624.	4.4	144
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4427	Short-term effects of mechanical drainage on fungal and bacterial community structure in a managed grassland soil. <i>Applied Soil Ecology</i> , 2016, 101, 93-100.	2.1	8
4428	Effects of varying CO ₂ flows on bacterial communities in mesocosms created from two soils. <i>International Journal of Greenhouse Gas Control</i> , 2016, 46, 205-214.	2.3	19
4429	Profiling microbial community in a watershed heavily contaminated by an active antimony (Sb) mine in Southwest China. <i>Science of the Total Environment</i> , 2016, 550, 297-308.	3.9	104
4430	Intestinal microbiome analyses identify melanoma patients at risk for checkpoint-blockade-induced colitis. <i>Nature Communications</i> , 2016, 7, 10391.	5.8	784
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4432	Molecular Identification of Soil Eukaryotes and Focused Approaches Targeting Protist and Faunal Groups Using High-Throughput Metabarcoding. <i>Methods in Molecular Biology</i> , 2016, 1399, 125-140.	0.4	11
4433	Assessing Antibacterial Potential of Components of <i>Phyllomedusa distincta</i> Skin and its Associated Dermal Microbiota. <i>Journal of Chemical Ecology</i> , 2016, 42, 139-148.	0.9	13
4434	The diversity of iron reducing bacteria communities in subtropical paddy soils of China. <i>Applied Soil Ecology</i> , 2016, 101, 20-27.	2.1	63
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4457	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	1.7	308
4458	Isolation and characterization of bacteria from the feathers of wild Dark-eyed Juncos (<i>Junco</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.7	23

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4468	Characterization of bacterial communities in lithobionts and soil niches from Victoria Valley, Antarctica. <i>FEMS Microbiology Ecology</i> , 2016, 92, f1w051.	1.3	69
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4478	Characterization of the gut microbiome in epidemiologic studies: the multiethnic cohort experience. <i>Annals of Epidemiology</i> , 2016, 26, 373-379.	0.9	42
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4529	Failure of biohydrogen production by low levels of substrate and lactic acid accumulation. <i>Renewable Energy</i> , 2016, 86, 889-894.	4.3	33
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4533	The biogeography of the atlantic salmon (<i>Salmo salar</i>) gut microbiome. <i>ISME Journal</i> , 2016, 10, 1280-1284.	4.4	301
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4535	Characterization of the bacterial communities of casts from <i>Eisenia andrei</i> fed with different substrates. <i>Applied Soil Ecology</i> , 2016, 98, 103-111.	2.1	56
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4543	Drivers of bacterial beta diversity in two temperate forests. <i>Ecological Research</i> , 2016, 31, 57-64.	0.7	17
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4551	The complete mitochondrial genome of <i>Chaenogobius gulosus</i> (Gobiidae, Perciformes) from the South Sea, Korea. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4207-4208.	0.7	3
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4563	Insights in the ecology and evolutionary history of the <i>Miscellaneous Crenarchaeotic Group</i> lineage. ISME Journal, 2016, 10, 665-677.	4.4	100
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4565	Experimental insights into the importance of aquatic bacterial community composition to the degradation of dissolved organic matter. ISME Journal, 2016, 10, 533-545.	4.4	418
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4568	Rhizospheric fungi of <i>Panax notoginseng</i> : diversity and antagonism to host phytopathogens. <i>Journal of Ginseng Research</i> , 2016, 40, 127-134.	3.0	101
4569	Molecular Ecology of <i>nifH</i> Genes and Transcripts Along a Chronosequence in Revegetated Areas of the Tengger Desert. <i>Microbial Ecology</i> , 2016, 71, 150-163.	1.4	28
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4575	The contribution of endophytic bacteria to <i>Albizia lebbeck</i> -mediated phytoremediation of tannery effluent contaminated soil. <i>International Journal of Phytoremediation</i> , 2016, 18, 77-86.	1.7	4
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4578	Bacterial Diversity in the Hyperalkaline Allas Springs (Cyprus), a Natural Analogue for Cementitious Radioactive Waste Repository. <i>Geomicrobiology Journal</i> , 2016, 33, 73-84.	1.0	29
4579	Evaluation of bacterial communities by bacteriome analysis targeting 16S rRNA genes and quantitative analysis of ammonia monooxygenase gene in different types of compost. <i>Journal of Bioscience and Bioengineering</i> , 2016, 121, 57-65.	1.1	22
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4725	Linking the community structure of arbuscular mycorrhizal fungi and plants: a story of interdependence?. <i>ISME Journal</i> , 2017, 11, 1400-1411.	4.4	78
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4727	Endophytic root bacteria associated with the natural vegetation growing at the hydrocarbon-contaminated Bitumount Provincial Historic site. <i>Canadian Journal of Microbiology</i> , 2017, 63, 502-515.	0.8	32
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4731	MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580.	6.5	328
4732	Increasing the frequency of pulses in crop rotations reduces soil fungal diversity and increases the proportion of fungal pathotrophs in a semiarid agroecosystem. <i>Agriculture, Ecosystems and Environment</i> , 2017, 240, 206-214.	2.5	76
4733	Next-Generation Sequencing Analyses of Bacterial Community Structures in Soybean Pastes Produced in Northeast China. <i>Journal of Food Science</i> , 2017, 82, 960-968.	1.5	13
4734	Plant diversity and plant identity influence <i>Fusarium</i> communities in soil. <i>Mycologia</i> , 2017, 109, 128-139.	0.8	21
4735	Loss of cutaneous microbial diversity during first 3 weeks of life in very low birthweight infants. <i>Experimental Dermatology</i> , 2017, 26, 861-867.	1.4	21
4736	Gut symbiont enhances insecticide resistance in a significant pest, the oriental fruit fly <i>Bactrocera dorsalis</i> (Hendel). <i>Microbiome</i> , 2017, 5, 13.	4.9	318
4737	Local-scale spatial structure and community composition of orchid mycorrhizal fungi in semi-natural grasslands. <i>Mycorrhiza</i> , 2017, 27, 355-367.	1.3	21
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4739	Barcode-based species delimitation in the marine realm: a test using Hexanauplia (Multicrustacea: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.9	11
4740	Short timescale dynamics of phytoplankton in Fildes Bay, Antarctica. <i>Antarctic Science</i> , 2017, 29, 217-228.	0.5	10
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4742	Resistant starch can improve insulin sensitivity independently of the gut microbiota. <i>Microbiome</i> , 2017, 5, 12.	4.9	113
4743	Fermentation of model hemicelluloses by <i>Prevotella</i> strains and <i>Butyrivibrio fibrisolvens</i> in pure culture and in ruminal enrichment cultures. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4269-4278.	1.7	110
4744	Deep Sequencing Reveals Highly Variable Gut Microbial Composition of Invasive Fish <i>Mossambicus Tilapia</i> (<i>Oreochromis mossambicus</i>) Collected from Two Different Habitats. <i>Indian Journal of Microbiology</i> , 2017, 57, 235-240.	1.5	10
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4748	Bacterial community diversity associated with different levels of dietary nutrition in the rumen of sheep. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3717-3728.	1.7	55
4749	Wildfire impact: Natural experiment reveals differential short-term changes in soil microbial communities. <i>Soil Biology and Biochemistry</i> , 2017, 109, 1-13.	4.2	68
4750	Biodegradation of Phenanthrene in Polycyclic Aromatic Hydrocarbon-Contaminated Wastewater Revealed by Coupling Cultivation-Dependent and -Independent Approaches. <i>Environmental Science & Technology</i> , 2017, 51, 3391-3401.	4.6	93
4751	Microbial taxa and functional genes shift in degraded soil with bacterial wilt. <i>Scientific Reports</i> , 2017, 7, 39911.	1.6	63
4752	Response of microbial communities to roxarsone under different culture conditions. <i>Canadian Journal of Microbiology</i> , 2017, 63, 661-670.	0.8	8
4753	Bacterial community dynamics are linked to patterns of coral heat tolerance. <i>Nature Communications</i> , 2017, 8, 14213.	5.8	529
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4759	Microbiome dynamic modulation through functional diets based on pre- and probiotics (mannan-oligosaccharides and <i>Saccharomyces cerevisiae</i>) in juvenile rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Journal of Applied Microbiology</i> , 2017, 122, 1333-1347.	1.4	52
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4762	Secondary bile acid-induced dysbiosis promotes intestinal carcinogenesis. <i>International Journal of Cancer</i> , 2017, 140, 2545-2556.	2.3	164
4763	Acidobacteria Community Responses to Nitrogen Dose and Form in Chinese Fir Plantations in Southern China. <i>Current Microbiology</i> , 2017, 74, 396-403.	1.0	35
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4768	Microbiota Disruption Induced by Early Use of Broad-Spectrum Antibiotics Is an Independent Risk Factor of Outcome after Allogeneic Stem Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2017, 23, 845-852.	2.0	183
4769	Response of gut health and microbiota to sulfide exposure in Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2017, 63, 87-96.	1.6	117
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4771	<i>Paenibacillus polymyxa</i> NSY50 suppresses <i>Fusarium</i> wilt in cucumbers by regulating the rhizospheric microbial community. <i>Scientific Reports</i> , 2017, 7, 41234.	1.6	60
4772	Microbial fouling and corrosion of carbon steel in deep anoxic alkaline groundwater. <i>Biofouling</i> , 2017, 33, 195-209.	0.8	21
4773	Soil microbial community responses to contamination with silver, aluminium oxide and silicon dioxide nanoparticles. <i>Ecotoxicology</i> , 2017, 26, 449-458.	1.1	111
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4775	Successful Resolution of Recurrent <i>Clostridium difficile</i> Infection using Freeze-Dried, Encapsulated Fecal Microbiota; Pragmatic Cohort Study. <i>American Journal of Gastroenterology</i> , 2017, 112, 940-947.	0.2	164
4776	Comparison of Archaeal Populations in Soil and Their Encapsulated Iron-Manganese Nodules in Four Locations Spanning from North to South China. <i>Geomicrobiology Journal</i> , 2017, 34, 811-822.	1.0	3
4778	Bacterial communities on facial skin of teenage and elderly Thai females. <i>Archives of Microbiology</i> , 2017, 199, 1035-1042.	1.0	21
4779	Targeted deep sequencing reveals high diversity and variable dominance of bloom-forming cyanobacteria in eutrophic lakes. <i>Harmful Algae</i> , 2017, 64, 42-50.	2.2	20
4780	Microbiota in Exhaled Breath Condensate and the Lung. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	16
4781	Impact of Next-Generation Sequencing Technology in Plant-Microbe Interaction Study. , 2017, , 269-294.		5
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4787	Changes in richness and community composition of ectomycorrhizal fungi among altitudinal vegetation types on Mount Kinabalu in Borneo. <i>New Phytologist</i> , 2017, 215, 454-468.	3.5	64
4788	Functional soil metagenomics: elucidation of polycyclic aromatic hydrocarbon degradation potential following 12 years of <i>in situ</i> bioremediation. <i>Environmental Microbiology</i> , 2017, 19, 2992-3011.	1.8	39
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4805	Isolation and identification of culturable bacteria, capable of heterotrophic growth, from rapid sand filters of drinking water treatment plants. <i>Research in Microbiology</i> , 2017, 168, 594-607.	1.0	31
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4822	Comparative profiling of microbial community of three economically important fishes reared in sea cages under tropical offshore environment. <i>Marine Genomics</i> , 2017, 34, 57-65.	0.4	23
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4855	Interactive microbial distribution analysis using BioAtlas. <i>Nucleic Acids Research</i> , 2017, 45, W509-W513.	6.5	8
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4860	Microbial community function in the bleaching disease of the marine macroalgae <i>Delisea pulchra</i> . <i>Environmental Microbiology</i> , 2017, 19, 3012-3024.	1.8	42
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4869	Development and Characterization of 18 Polymorphic SSR Markers for <i>Barthea barthei</i> (Melastomataceae). <i>Applications in Plant Sciences</i> , 2017, 5, 1600149.	0.8	1
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5019	Factors influencing ruminal bacterial community diversity and composition and microbial fibrolytic enzyme abundance in lactating dairy cows with a focus on the role of active dry yeast. <i>Journal of Dairy Science</i> , 2017, 100, 4377-4393.	1.4	53
5020	Methylphosphonate metabolism by <i>Pseudomonas</i> sp. populations contributes to the methane oversaturation paradox in an oxic freshwater lake. <i>Environmental Microbiology</i> , 2017, 19, 2366-2378.	1.8	55

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5022	Pasture flock chicken cecal microbiome responses to prebiotics and plum fiber feed amendments. <i>Poultry Science</i> , 2017, 96, 1820-1830.	1.5	29
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5024	Cassava foliage affects the microbial diversity of Chinese indigenous geese caecum using 16S rRNA sequencing. <i>Scientific Reports</i> , 2017, 7, 45697.	1.6	40
5025	<i>Propionibacterium acnes</i> phylogenetic type III is associated with progressive macular hypomelanosis. <i>European Journal of Microbiology and Immunology</i> , 2017, 7, 37-45.	1.5	42
5026	Relative Abundance and Strain Diversity in the Bacterial Endosymbiont Community of a Sap-Feeding Insect Across Its Native and Introduced Geographic Range. <i>Microbial Ecology</i> , 2017, 74, 722-734.	1.4	13
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5028	Endophytic bacterial communities in in vitro shoot cultures derived from embryonic tissue of hybrid walnut (<i>Juglans</i> – <i>intermedia</i>). <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 130, 153-165.	1.2	19
5029	In-depth analysis of core methanogenic communities from high elevation permafrost-affected wetlands. <i>Soil Biology and Biochemistry</i> , 2017, 111, 66-77.	4.2	36
5030	Characterization of the Fecal Bacterial Microbiota of Healthy and Diarrheic Dairy Calves. <i>Journal of Veterinary Internal Medicine</i> , 2017, 31, 928-939.	0.6	123
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5032	The influence of environmental factors on communities of arbuscular mycorrhizal fungi associated with <i>Chenopodium ambrosioides</i> revealed by MiSeq sequencing investigation. <i>Scientific Reports</i> , 2017, 7, 45134.	1.6	70
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5037	Inoculation of a phenanthrene-degrading endophytic bacterium reduces the phenanthrene level and alters the bacterial community structure in wheat. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5199-5212.	1.7	14
5038	Cross-talk among metabolic parameters, esophageal microbiota, and host gene expression following chronic exposure to an obesogenic diet. <i>Scientific Reports</i> , 2017, 7, 45753.	1.6	24
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5041	Effects of cellulase-producing bacteria on bacterial community structure and diversity during fermentation of Chinese liquor grains. <i>Journal of the Institute of Brewing</i> , 2017, 123, 130-137.	0.8	7
5042	Distribution of anaerobic carbon monoxide dehydrogenase genes in deep subseafloor sediments. <i>Letters in Applied Microbiology</i> , 2017, 64, 355-363.	1.0	18
5043	Assessing the colonic microbiome, hydrogenogenic and hydrogenotrophic genes, transit and breath methane in constipation. <i>Neurogastroenterology and Motility</i> , 2017, 29, 1-9.	1.6	23
5044	Bacterial diversity of the rhizosphere and nearby surface soil of rice (<i>Oryza sativa</i>) growing in the Camargue (France). <i>Rhizosphere</i> , 2017, 3, 112-122.	1.4	29
5045	Exploring the under-investigated "microbial dark matter" of drinking water treatment plants. <i>Scientific Reports</i> , 2017, 7, 44350.	1.6	41
5046	Community analysis of microbial sharing and specialization in a Costa Rican ant-plant-hemipteran symbiosis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162770.	1.2	19
5047	<i>Sulfolobus islandicus</i> meta-populations in Yellowstone National Park hot springs. <i>Environmental Microbiology</i> , 2017, 19, 2334-2347.	1.8	19
5048	RNA virus receptor Rig-I monitors gut microbiota and inhibits colitis-associated colorectal cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2017, 36, 2.	3.5	42
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5050	Variability of airborne bacteria in an urban Mediterranean area (Thessaloniki, Greece). <i>Atmospheric Environment</i> , 2017, 157, 101-110.	1.9	62
5051	The Introduction of Woody Plants for Freshwater Wetland Restoration Alters the Archaeal Community Structure in Soil. <i>Land Degradation and Development</i> , 2017, 28, 1933-1942.	1.8	7
5052	Striking alterations in the soil bacterial community structure and functioning of the biological N cycle induced by <i>Pennisetum setaceum</i> invasion in a semiarid environment. <i>Soil Biology and Biochemistry</i> , 2017, 109, 176-187.	4.2	50
5053	Global Distribution Patterns and Pangenomic Diversity of the Candidate Phylum "Latescibacteria" (WS3). <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	107
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5056	Changes in bacterial diversity associated with bioremediation of used lubricating oil in tropical soils. <i>Archives of Microbiology</i> , 2017, 199, 839-851.	1.0	13
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5059	Diel-scale temporal dynamics recorded for bacterial groups in Namib Desert soil. <i>Scientific Reports</i> , 2017, 7, 40189.	1.6	42
5060	Distribution of Bathyarchaeota Communities Across Different Terrestrial Settings and Their Potential Ecological Functions. <i>Scientific Reports</i> , 2017, 7, 45028.	1.6	88
5061	Oral Biology. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	2
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5067	Identifying the plant-associated microbiome across aquatic and terrestrial environments: the effects of amplification method on taxa discovery. <i>Molecular Ecology Resources</i> , 2017, 17, 931-942.	2.2	25
5068	Design and composition of synthetic fungal-bacterial microbial consortia that improve lignocellulolytic enzyme activity. <i>Bioresource Technology</i> , 2017, 227, 247-255.	4.8	48
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5071	Mineral Types and Tree Species Determine the Functional and Taxonomic Structures of Forest Soil Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	39
5072	Preliminary data on antibacterial activity of <i>Echinacea purpurea</i> -associated bacterial communities against <i>Burkholderia cepacia</i> complex strains, opportunistic pathogens of Cystic Fibrosis patients. <i>Microbiological Research</i> , 2017, 196, 34-43.	2.5	35
5073	Mercury-methylating genes <i>dsrB</i> and <i>hgcA</i> in soils/sediments of the Three Gorges Reservoir. <i>Environmental Science and Pollution Research</i> , 2017, 24, 5001-5011.	2.7	47
5074	Characterization and identification of microbial communities in bovine necrotic vulvovaginitis. <i>Veterinary Journal</i> , 2017, 219, 34-39.	0.6	10
5075	Cyanobacterial harmful algal blooms are a biological disturbance to Western Lake Erie bacterial communities. <i>Environmental Microbiology</i> , 2017, 19, 1149-1162.	1.8	193

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5077	Microbial diversity in degraded and non-degraded petroleum samples and comparison across oil reservoirs at local and global scales. <i>Extremophiles</i> , 2017, 21, 211-229.	0.9	34
5078	Contrasting effects of grassland management modes on species-abundance distributions of multiple groups. <i>Agriculture, Ecosystems and Environment</i> , 2017, 237, 143-153.	2.5	26
5079	Lake bacterioplankton dynamics over diurnal timescales. <i>Freshwater Biology</i> , 2017, 62, 191-204.	1.2	11
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5084	Sex and diversity: The mutualistic and parasitic fungi of a fungus-growing termite differ in genetic diversity and reproductive strategy. <i>Fungal Ecology</i> , 2017, 26, 20-27.	0.7	6
5085	A Review of Bacterial Interactions With Blow Flies (Diptera: Calliphoridae) of Medical, Veterinary, and Forensic Importance. <i>Annals of the Entomological Society of America</i> , 2017, 110, 19-36.	1.3	71
5086	Interaction Between Atypical Antipsychotics and the Gut Microbiome in a Bipolar Disease Cohort. <i>Pharmacotherapy</i> , 2017, 37, 261-267.	1.2	207
5087	Hydrocarbon and Lipid Microbiology Protocols. <i>Springer Protocols</i> , 2017, , .	0.1	1
5088	Effects of diet type, developmental stage, and gut compartment in the gut bacterial communities of two Cerambycidae species (Coleoptera). <i>Journal of Microbiology</i> , 2017, 55, 21-30.	1.3	66
5089	Shifts in microbial community structure and function in surface waters impacted by unconventional oil and gas wastewater revealed by metagenomics. <i>Science of the Total Environment</i> , 2017, 580, 1205-1213.	3.9	39
5090	Overcoming the Law of the Hidden in Cyberinfrastructures. <i>Trends in Plant Science</i> , 2017, 22, 117-123.	4.3	10
5091	Ericoid Roots and Mycospheres Govern Plant-Specific Bacterial Communities in Boreal Forest Humus. <i>Microbial Ecology</i> , 2017, 73, 939-953.	1.4	45
5092	Arbuscular mycorrhizal fungal community composition is altered by long-term litter removal but not litter addition in a lowland tropical forest. <i>New Phytologist</i> , 2017, 214, 455-467.	3.5	45
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5095	Salinity Affects the Composition of the Aerobic Methanotroph Community in Alkaline Lake Sediments from the Tibetan Plateau. <i>Microbial Ecology</i> , 2017, 73, 101-110.	1.4	38
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5102	Response of the microbial community to bioturbation by benthic macrofauna on intertidal flats. <i>Journal of Experimental Marine Biology and Ecology</i> , 2017, 488, 44-51.	0.7	31
5103	Patterns of bacterial diversity in the marine planktonic particulate matter continuum. <i>ISME Journal</i> , 2017, 11, 999-1010.	4.4	128
5104	Expression of eukaryotic-like protein in the microbiome of sponges. <i>Molecular Ecology</i> , 2017, 26, 1432-1451.	2.0	55
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5106	Effects of a bacterial consortium from acid mine drainage on cadmium phytoextraction and indigenous soil microbial community. <i>Plant and Soil</i> , 2017, 415, 347-358.	1.8	14
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5108	Tobacco bacterial wilt suppression with biochar soil addition associates to improved soil physiochemical properties and increased rhizosphere bacteria abundance. <i>Applied Soil Ecology</i> , 2017, 112, 90-96.	2.1	109
5109	Enhanced treatment performance of coking wastewater and reduced membrane fouling using a novel EMBR. <i>Bioresource Technology</i> , 2017, 229, 39-45.	4.8	37
5110	Analysis of gut microbiota – An ever changing landscape. <i>Gut Microbes</i> , 2017, 8, 268-275.	4.3	25
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5113	Bacterial community collapse: a meta-analysis of the sinonasal microbiota in chronic rhinosinusitis. <i>Environmental Microbiology</i> , 2017, 19, 381-392.	1.8	174
5114	Comparative community structure of archaea in rumen of buffaloes and cattle. <i>Journal of the Science of Food and Agriculture</i> , 2017, 97, 3284-3293.	1.7	16
5116	Imbalance of bacteriome profiles within the Finnish Diabetes Prediction and Prevention study: Parallel use of 16S profiling and virome sequencing in stool samples from children with islet autoimmunity and matched controls. <i>Pediatric Diabetes</i> , 2017, 18, 588-598.	1.2	44
5117	Influences of pH and Iron Concentration on the Salivary Microbiome in Individual Humans with and without Caries. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	38
5118	Cellular and humoral biomarkers of Bronchopulmonary Dysplasia. <i>Early Human Development</i> , 2017, 105, 35-39.	0.8	23
5119	Haptophyte Diversity and Vertical Distribution Explored by 18S and 28S Ribosomal <i>scp>RNA</scp></i> Gene Metabarcoding and Scanning Electron Microscopy. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 514-532.	0.8	35
5120	Unravelling the active microbial community in a thermophilic anaerobic digester-microbial electrolysis cell coupled system under different conditions. <i>Water Research</i> , 2017, 110, 192-201.	5.3	55
5121	Vegetation type and layer depth influence nitrite-dependent methane-oxidizing bacteria in constructed wetland. <i>Archives of Microbiology</i> , 2017, 199, 505-511.	1.0	14
5122	Arbuscular mycorrhizal fungal community differences among European long-term observatories. <i>Mycorrhiza</i> , 2017, 27, 331-343.	1.3	14
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5124	An improved protocol with a highly degenerate primer targeting copper-containing membrane-bound monooxygenase genes for community analysis of methane- and ammonia-oxidizing bacteria. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw244.	1.3	35
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5130	Metabarcoding Analyses Enable Differentiation of Both Interspecific Assemblages and Intraspecific Divergence in Habitats With Differing Management Practices. <i>Environmental Entomology</i> , 2017, 46, 1381-1389.	0.7	9

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5133	Effect of maltitol-containing chewing gum use on the composition of dental plaque microbiota in subjects with active dental caries. <i>Journal of Oral Microbiology</i> , 2017, 9, 1374152.	1.2	13
5134	A dysbiotic mycobiome dominated by <i>Candida albicans</i> is identified within oral squamous-cell carcinomas. <i>Journal of Oral Microbiology</i> , 2017, 9, 1385369.	1.2	71
5135	Impact of hydraulic retention time (HRT) and pH on dark fermentative hydrogen production from glycerol. <i>Energy</i> , 2017, 141, 358-367.	4.5	39
5136	The influence of e-waste recycling on the molecular ecological network of soil microbial communities in Pakistan and China. <i>Environmental Pollution</i> , 2017, 231, 173-181.	3.7	50
5137	Ammonia exposure alters the expression of immune-related and antioxidant enzymes-related genes and the gut microbial community of crucian carp (<i>Carassius auratus</i>). <i>Fish and Shellfish Immunology</i> , 2017, 70, 485-492.	1.6	88
5138	A formation water-based nutrient recipe for potentially increasing methane release from coal in situ. <i>Fuel</i> , 2017, 209, 498-508.	3.4	26
5139	Biologically induced formation of realgar deposits in soil. <i>Geochimica Et Cosmochimica Acta</i> , 2017, 218, 237-256.	1.6	23
5140	Limited influence of primary treated sewage waters on bacterial abundance, production and community composition in coastal seawaters. <i>Marine Environmental Research</i> , 2017, 131, 215-226.	1.1	8
5141	Revision of the Genus <i>Micromonas</i> Manton et Parke (Chlorophyta, Mamiellophyceae), of the Type Species <i>M. pusilla</i> (Butcher) Manton & Parke and of the Species <i>M. commoda</i> van Baren, Bachy and Worden and Description of Two New Species Based on the Genetic and Phenotypic Characterization of Cultured Isolates. <i>Protist</i> , 2017, 168, 612-635.	0.6	62
5142	Molecular divergence of fungal communities in soil, roots and hyphae highlight the importance of sampling strategies. <i>Rhizosphere</i> , 2017, 4, 104-111.	1.4	14
5143	Impact of β -1 fructan on faecal community change: results from a placebo-controlled, randomised, double-blinded, cross-over study in healthy adults. <i>British Journal of Nutrition</i> , 2017, 118, 441-453.	1.2	18
5144	Pyrosequencing reveals profiles of soil bacterial communities after 12 years of conservation management on irrigated crop rotations. <i>Applied Soil Ecology</i> , 2017, 121, 65-73.	2.1	35
5145	Stepwise impact of urban wastewater treatment on the bacterial community structure, antibiotic contents, and prevalence of antimicrobial resistance. <i>Environmental Pollution</i> , 2017, 231, 1578-1585.	3.7	59
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5147	Root-associated fungal microbiota of nonmycorrhizal <i>Arabidopsis thaliana</i> and its contribution to plant phosphorus nutrition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9403-E9412.	3.3	239
5148	Diversity and succession of pelagic microorganism communities in a newly restored Illinois River floodplain lake. <i>Hydrobiologia</i> , 2017, 804, 35-58.	1.0	12
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5151	Diversity and co-occurrence network of soil fungi are more responsive than those of bacteria to shifts in precipitation seasonality in a subtropical forest. <i>Soil Biology and Biochemistry</i> , 2017, 115, 499-510.	4.2	134
5152	Photochemical alteration of organic carbon draining permafrost soils shifts microbial metabolic pathways and stimulates respiration. <i>Nature Communications</i> , 2017, 8, 772.	5.8	112
5153	Exploring the Plant Microbiome Through Multi-omics Approaches. , 2017, , 233-268.		11
5154	Transformation of anaerobic granules into aerobic granules and the succession of bacterial community. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7703-7713.	1.7	28
5155	Differences in root-associated bacterial communities among fine root branching orders of poplar (<i>Populus euramericana</i> (Dode) Guinier.). <i>Plant and Soil</i> , 2017, 421, 123-135.	1.8	17
5156	Analysis of the bacterial microbiome in the small octopus, <i>Octopus variabilis</i> , from South Korea to detect the potential risk of foodborne illness and to improve product management. <i>Food Research International</i> , 2017, 102, 51-60.	2.9	11
5157	Utilizing ion-exchange resin to improve recovery from organic shock-loading in an AnMBR treating sewage sludge. <i>Water Research</i> , 2017, 126, 285-298.	5.3	8
5158	Algorithm for post-clustering curation of DNA amplicon data yields reliable biodiversity estimates. <i>Nature Communications</i> , 2017, 8, 1188.	5.8	451
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5162	Modulating Effects of Dicafeoylquinic Acids from <i>Ilex kudingcha</i> on Intestinal Microecology in Vitro. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 10185-10196.	2.4	56
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5339	Occurrence and expression of novel methyl-coenzyme M reductase gene (<i>mcrA</i>) variants in hot spring sediments. <i>Scientific Reports</i> , 2017, 7, 7252.	1.6	37
5340	High diversity and unique composition of gut microbiomes in pygmy (<i>Kogia breviceps</i>) and dwarf (K.) Tj ETQq1 1 0.784314 rgBT /Overlo	1.6	31
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5369	The use of nemabiome metabarcoding to explore gastro-intestinal nematode species diversity and anthelmintic treatment effectiveness in beef calves. <i>International Journal for Parasitology</i> , 2017, 47, 893-902.	1.3	91
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5381	Transcriptional Variation of Diverse Enteropathogenic <i>Escherichia coli</i> Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017, 2, .	1.7	12
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5409	Evaluating the contribution of gut microbiome to the variance of porcine serum glucose and lipid concentration. <i>Scientific Reports</i> , 2017, 7, 14928.	1.6	15
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5413	Gut microbiomes and reproductive isolation in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12767-12772.	3.3	71
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5431	Effects of endocrine disrupting chemicals (EDCs) on bacterial communities in mangrove sediments. <i>Marine Pollution Bulletin</i> , 2017, 122, 122-128.	2.3	23
5432	Diversity and abundance of microbial eukaryotes in stream sediments from Svalbard. <i>Polar Biology</i> , 2017, 40, 1835-1843.	0.5	4
5433	Effect of experimental soil disturbance and recovery on structure and function of soil community: a metagenomic and metagenetic approach. <i>Scientific Reports</i> , 2017, 7, 2260.	1.6	18
5434	Microbial biodiversity of meadows under different modes of land use: catabolic and genetic fingerprinting. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 154.	1.7	23
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5437	Effects of oral antibiotics and isotretinoin on the murine gut microbiota. <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 342-351.	1.1	27
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5458	Emerging microbiota during cold storage and temperature abuse of ready-to-eat salad. <i>Infection Ecology and Epidemiology</i> , 2017, 7, 1328963.	0.5	21
5459	Greater diversity of soil fungal communities and distinguishable seasonal variation in temperate deciduous forests compared with subtropical evergreen forests of eastern China. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	57
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5478	Spatiotemporal and species variations in prokaryotic communities associated with sediments from surface-flow constructed wetlands for treating swine wastewater. <i>Chemosphere</i> , 2017, 185, 1-10.	4.2	19
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5489	Targeted metagenomic sequencing data of human gut microbiota associated with <i>Blastocystis</i> colonization. <i>Scientific Data</i> , 2017, 4, 170081.	2.4	8
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5514	Changes in the Bacteriome of Honey Bees Associated with the Parasite <i>Varroa destructor</i> , and Pathogens <i>Nosema</i> and <i>Lotmaria passim</i> . <i>Microbial Ecology</i> , 2017, 73, 685-698.	1.4	55
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5537	Cellulose accessibility and microbial community in solid state anaerobic digestion of rape straw. <i>Bioresource Technology</i> , 2017, 223, 192-201.	4.8	28
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5550	Human milk oligosaccharide effects on intestinal function and inflammation after preterm birth in pigs. <i>Journal of Nutritional Biochemistry</i> , 2017, 40, 141-154.	1.9	52
5551	Structure and diversity of bacterial communities in two large sanitary landfills in China as revealed by high-throughput sequencing (MiSeq). <i>Waste Management</i> , 2017, 63, 41-48.	3.7	117
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5567	Prokaryotic community composition in alkaline-fermented skate (<i>RajaÂpulchra</i>). <i>Food Microbiology</i> , 2017, 61, 72-82.	2.1	19
5568	Ammonia-Oxidizing Archaea Dominate Ammonia-Oxidizing Communities within Alkaline Cave Sediments. <i>Geomicrobiology Journal</i> , 2017, 34, 511-523.	1.0	17
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5760	Diversity of Extremely Halophilic Archaeal and Bacterial Communities from Commercial Salts. <i>Frontiers in Microbiology</i> , 2017, 8, 799.	1.5	29
5761	From Vineyard Soil to Wine Fermentation: Microbiome Approximations to Explain the "œterroir" Concept. <i>Frontiers in Microbiology</i> , 2017, 8, 821.	1.5	155
5762	Host Immune Selection of Rumen Bacteria through Salivary Secretory IgA. <i>Frontiers in Microbiology</i> , 2017, 8, 848.	1.5	19
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5780	Microbial Populations of Stony Meteorites: Substrate Controls on First Colonizers. <i>Frontiers in Microbiology</i> , 2017, 8, 1227.	1.5	22
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5789	Influence of Igneous Basement on Deep Sediment Microbial Diversity on the Eastern Juan de Fuca Ridge Flank. <i>Frontiers in Microbiology</i> , 2017, 8, 1434.	1.5	52
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5837	Increased Denitrification Rates Associated with Shifts in Prokaryotic Community Composition Caused by Varying Hydrologic Connectivity. <i>Frontiers in Microbiology</i> , 2017, 8, 2304.	1.5	22
5838	Soil Bacterial Community Structure and Co-occurrence Pattern during Vegetation Restoration in Karst Rocky Desertification Area. <i>Frontiers in Microbiology</i> , 2017, 8, 2377.	1.5	158
5839	The Microbiome of Potentially Malignant Oral Leukoplakia Exhibits Enrichment for <i>Fusobacterium</i> , <i>Leptotrichia</i> , <i>Campylobacter</i> , and <i>Rothia</i> Species. <i>Frontiers in Microbiology</i> , 2017, 8, 2391.	1.5	95
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5891	The abundance and diversity of arbuscular mycorrhizal fungi are linked to the soil chemistry of screes and to slope in the Alpic paleo-endemic <i>Berardia subacaulis</i> . <i>PLoS ONE</i> , 2017, 12, e0171866.	1.1	39
5892	Microbiomes associated with infective stages of root-knot and lesion nematodes in soil. <i>PLoS ONE</i> , 2017, 12, e0177145.	1.1	113
5893	Habitat and indigenous gut microbes contribute to the plasticity of gut microbiome in oriental river prawn during rapid environmental change. <i>PLoS ONE</i> , 2017, 12, e0181427.	1.1	67
5894	Assembling metagenomes, one community at a time. <i>BMC Genomics</i> , 2017, 18, 521.	1.2	89
5895	Bile acid is a significant host factor shaping the gut microbiome of diet-induced obese mice. <i>BMC Biology</i> , 2017, 15, 120.	1.7	208
5896	The effect of storage at ambient temperature on the feline fecal microbiota. <i>BMC Veterinary Research</i> , 2017, 13, 256.	0.7	26
5897	Exposure to ambient particulate matter alters the microbial composition and induces immune changes in rat lung. <i>Respiratory Research</i> , 2017, 18, 143.	1.4	49
5898	Flow cytometric quantification, sorting and sequencing of methanogenic archaea based on F420 autofluorescence. <i>Microbial Cell Factories</i> , 2017, 16, 180.	1.9	39
5899	Ileal antimicrobial peptide expression is dysregulated in old age. <i>Immunity and Ageing</i> , 2017, 14, 19.	1.8	22
5900	From grass to gas: microbiome dynamics of grass biomass acidification under mesophilic and thermophilic temperatures. <i>Biotechnology for Biofuels</i> , 2017, 10, 171.	6.2	43
5901	The effect of temperature and retention time on methane production and microbial community composition in staged anaerobic digesters fed with food waste. <i>Biotechnology for Biofuels</i> , 2017, 10, 302.	6.2	80
5902	Bacterial microbiota associated with <i>Rhipicephalus sanguineus</i> (s.l.) ticks from France, Senegal and Arizona. <i>Parasites and Vectors</i> , 2017, 10, 416.	1.0	40
5903	The plant pathogen <i>Gluconobacter cerinus</i> strain CDF1 is beneficial to the fruit fly <i>Bactrocera dorsalis</i> . <i>AMB Express</i> , 2017, 7, 207.	1.4	12
5904	Human presence impacts fungal diversity of inflated lunar/Mars analog habitat. <i>Microbiome</i> , 2017, 5, 62.	4.9	25
5905	Influence of the pneumococcal conjugate vaccines on the temporal variation of pneumococcal carriage and the nasal microbiota in healthy infants: a longitudinal analysis of a case-control study. <i>Microbiome</i> , 2017, 5, 85.	4.9	28
5906	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	4.9	138
5907	Microbes and associated soluble and volatile chemicals on periodically wet household surfaces. <i>Microbiome</i> , 2017, 5, 128.	4.9	45

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5909	Comparing microbiotas in the upper aerodigestive and lower respiratory tracts of lambs. <i>Microbiome</i> , 2017, 5, 145.	4.9	23
5910	Dietary energy drives the dynamic response of bovine rumen viral communities. <i>Microbiome</i> , 2017, 5, 155.	4.9	81
5911	Relations among epiphytic microbial communities from soil, leaves and grapes of the grapevine. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2017, 10, 73-83.	1.1	19
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5914	Evaluating the accuracy of amplicon-based microbiome computational pipelines on simulated human gut microbial communities. <i>BMC Bioinformatics</i> , 2017, 18, 283.	1.2	51
5915	Visibiome: an efficient microbiome search engine based on a scalable, distributed architecture. <i>BMC Bioinformatics</i> , 2017, 18, 353.	1.2	0
5916	MetaComp: comprehensive analysis software for comparative meta-omics including comparative metagenomics. <i>BMC Bioinformatics</i> , 2017, 18, 434.	1.2	13
5917	CONSTAX: a tool for improved taxonomic resolution of environmental fungal ITS sequences. <i>BMC Bioinformatics</i> , 2017, 18, 538.	1.2	72
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5928	Decoding Complex Soil Microbial Communities through New Age "Omics". <i>Journal of Microbial & Biochemical Technology</i> , 2017, 09, .	0.2	3
5929	Functional diversity of microbial communities in pristine aquifers inferred by PLFA- and sequencing-based approaches. <i>Biogeosciences</i> , 2017, 14, 2697-2714.	1.3	72
5930	Strand-specific transcriptomes of Enterohemorrhagic <i>Escherichia coli</i> in response to interactions with ground beef microbiota: interactions between microorganisms in raw meat. <i>BMC Genomics</i> , 2017, 18, 574.	1.2	10
5931	Optimization of a metatranscriptomic approach to study the lignocellulolytic potential of the higher termite gut microbiome. <i>BMC Genomics</i> , 2017, 18, 681.	1.2	29
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6024	The impact of storage buffer, DNA extraction method, and polymerase on microbial analysis. <i>Scientific Reports</i> , 2018, 8, 6292.	1.6	46
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6038	Comparative biogeography of the gut microbiome between Jinhua and Landrace pigs. <i>Scientific Reports</i> , 2018, 8, 5985.	1.6	101
6039	Nitrogen enrichment suppresses other environmental drivers and homogenizes salt marsh leaf microbiome. <i>Ecology</i> , 2018, 99, 1411-1418.	1.5	13
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6044	Dung application increases CH ₄ production potential and alters the composition and abundance of methanogen community in restored peatland soils from Europe. <i>Biology and Fertility of Soils</i> , 2018, 54, 533-547.	2.3	10
6045	High-throughput sequencing for algal systematics. <i>European Journal of Phycology</i> , 2018, 53, 256-272.	0.9	33
6046	Bacterial communities associated with honeybee food stores are correlated with land use. <i>Ecology and Evolution</i> , 2018, 8, 4743-4756.	0.8	52
6047	The influences of thorny bamboo growth on the bacterial community in badland soils of southwestern Taiwan. <i>Land Degradation and Development</i> , 2018, 29, 2728-2738.	1.8	3
6048	Insights into microbial communities mediating the bioremediation of hydrocarbon-contaminated soil from an Alpine former military site. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4409-4421.	1.7	85
6049	Comparison of heterotrophic and autotrophic denitrification processes for nitrate removal from phosphorus-limited surface water. <i>Environmental Pollution</i> , 2018, 238, 562-572.	3.7	26
6050	Seasonal metabolic analysis of marine sediments collected from Moreton Bay in South East Queensland, Australia, using a multi-omics-based approach. <i>Science of the Total Environment</i> , 2018, 631-632, 1328-1341.	3.9	20
6051	Antibiotic distribution, risk assessment, and microbial diversity in river water and sediment in Hong Kong. <i>Environmental Geochemistry and Health</i> , 2018, 40, 2191-2203.	1.8	41
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6053	Rumen bacterial community structure impacts feed efficiency in beef cattle. <i>Journal of Animal Science</i> , 2018, 96, 1045-1058.	0.2	71
6054	Future warming and acidification result in multiple ecological impacts to a temperate coralline alga. <i>Environmental Microbiology</i> , 2018, 20, 2769-2782.	1.8	24
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6057	Effect of daidzein on fermentation parameters and bacterial community of finishing Xianan cattle. <i>Italian Journal of Animal Science</i> , 2018, 17, 950-958.	0.8	7
6058	Yeast culture dietary supplementation modulates gut microbiota, growth and biochemical parameters of grass carp. <i>Microbial Biotechnology</i> , 2018, 11, 551-565.	2.0	36
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6060	Metagenomic analysis of ssDNA viruses in surface seawater of Yangshan Deep-Water Harbor, Shanghai, China. <i>Marine Genomics</i> , 2018, 41, 50-53.	0.4	5
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6063	Cultivation and genomics of the first freshwater SAR11 (LD12) isolate. <i>ISME Journal</i> , 2018, 12, 1846-1860.	4.4	123
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6065	Impact of tart cherries polyphenols on the human gut microbiota and phenolic metabolites in vitro and in vivo. <i>Journal of Nutritional Biochemistry</i> , 2018, 59, 160-172.	1.9	80
6066	Drinking water microbiome assembly induced by water stagnation. <i>ISME Journal</i> , 2018, 12, 1520-1531.	4.4	172
6067	Bacterial community succession and degradation patterns of hydrocarbons in seawater at low temperature. <i>Journal of Hazardous Materials</i> , 2018, 353, 127-134.	6.5	21
6068	The effects of feeding monensin on rumen microbial communities and methanogenesis in bred heifers fed in a drylot. <i>Livestock Science</i> , 2018, 212, 131-136.	0.6	10
6069	High-throughput sequencing reveals microbial communities in drinking water treatment sludge from six geographically distributed plants, including potentially toxic cyanobacteria and pathogens. <i>Science of the Total Environment</i> , 2018, 634, 769-779.	3.9	40
6070	Fecal bacterial diversity of wild Sichuan snub-nosed monkeys (<i>Rhinopithecus roxellana</i>). <i>American Journal of Primatology</i> , 2018, 80, e22753.	0.8	17
6071	High diversity of potential nitrate-reducing Fe(II)-oxidizing bacteria enriched from activated sludge. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4975-4985.	1.7	17
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6079	Structure and co-occurrence patterns in microbial communities under acute environmental stress reveal ecological factors fostering resilience. <i>Scientific Reports</i> , 2018, 8, 5875.	1.6	123
6080	Anaerobic methanotrophic communities thrive in deep submarine permafrost. <i>Scientific Reports</i> , 2018, 8, 1291.	1.6	58
6081	Novel staged anaerobic fluidized bed ceramic membrane bioreactor: Energy reduction, fouling control and microbial characterization. <i>Journal of Membrane Science</i> , 2018, 553, 200-208.	4.1	84
6082	Nitrifying activity and ammonia-oxidizing microorganisms in a constructed wetland treating polluted surface water. <i>Science of the Total Environment</i> , 2018, 628-629, 310-318.	3.9	32
6083	Amphibian chytridiomycosis outbreak dynamics are linked with host skin bacterial community structure. <i>Nature Communications</i> , 2018, 9, 693.	5.8	126
6084	CO ₂ leakage alters biogeochemical and ecological functions of submarine sands. <i>Science Advances</i> , 2018, 4, eaao2040.	4.7	27
6085	Anthropogenic N Deposition Alters the Composition of Expressed Class II Fungal Peroxidases. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	19
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6087	Characterization of the nasopharyngeal and middle ear microbiota in gastroesophageal reflux-prone versus gastroesophageal reflux non-prone children. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 851-857.	1.3	17
6088	Do we similarly assess diversity with microscopy and high-throughput sequencing? Case of microalgae in lakes. <i>Organisms Diversity and Evolution</i> , 2018, 18, 51-62.	0.7	46
6089	Comparative study on intestinal bacterial communities of <i>Boleophthalmus pectinirostris</i> and <i>Periophthalmus magnuspinnatus</i> with different sexes and feeding strategies. <i>Annals of Microbiology</i> , 2018, 68, 123-133.	1.1	9
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6096	The Madness of Microbiome: Attempting To Find Consensus "Best Practice" for 16S Microbiome Studies. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	422
6097	Impacts of quaternary ammonium compounds on membrane bioreactor performance: Acute and chronic responses of microorganisms. <i>Water Research</i> , 2018, 134, 153-161.	5.3	43
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6099	Free-living bacteria and potential bacterial pathogens in sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2455-2464.	1.7	47
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6103	Interactive effects between tetracycline and nitrosifying sludge microbiota in a nitrification membrane bioreactor. <i>Chemical Engineering Journal</i> , 2018, 341, 556-564.	6.6	34
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6112	Association of gut microbial communities with plasma lipopolysaccharide-binding protein (LBP) in premenopausal women. <i>ISME Journal</i> , 2018, 12, 1631-1641.	4.4	49
6113	Melanization of mycorrhizal fungal necromass structures microbial decomposer communities. <i>Journal of Ecology</i> , 2018, 106, 468-479.	1.9	66
6114	Metabolomics-based chemotaxonomy of root endophytic fungi for natural products discovery. <i>Environmental Microbiology</i> , 2018, 20, 1253-1270.	1.8	24
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6120	Vaccination Against <i>Lawsonia intracellularis</i> Decreases Shedding of <i>Salmonella enterica</i> serovar Typhimurium in Co-Infected Pigs and Alters the Gut Microbiome. <i>Scientific Reports</i> , 2018, 8, 2857.	1.6	24
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6126	Early microbial colonization affects DNA methylation of genes related to intestinal immunity and metabolism in preterm pigs. <i>DNA Research</i> , 2018, 25, 287-296.	1.5	48
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6129	Comammox Functionality Identified in Diverse Engineered Biological Wastewater Treatment Systems. <i>Environmental Science and Technology Letters</i> , 2018, 5, 110-116.	3.9	118
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6133	Changes in bacterial and archaeal communities during the concentration of brine at the graduation towers in Ciechocinek spa (Poland). <i>Extremophiles</i> , 2018, 22, 233-246.	0.9	12
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6143	Sex dependent effects of silver nanoparticles on the zebrafish gut microbiota. <i>Environmental Science: Nano</i> , 2018, 5, 740-751.	2.2	55
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6147	High resolution time series reveals cohesive but short-lived communities in coastal plankton. <i>Nature Communications</i> , 2018, 9, 266.	5.8	122
6148	Kudingcha and Fuzhuan Brick Tea Prevent Obesity and Modulate Gut Microbiota in High-Fat Diet Fed Mice. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1700485.	1.5	161
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6154	Social status shapes the bacterial and fungal gut communities of the honey bee. <i>Scientific Reports</i> , 2018, 8, 2019.	1.6	64
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6158	Functional biogeography and host specificity of bacterial communities associated with the Marine Green Alga <i>Ulva</i> spp.. <i>Molecular Ecology</i> , 2018, 27, 1952-1965.	2.0	71
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6161	Investigation on microbial diversity of industrial Zhacai paocai during fermentation using high-throughput sequencing and their functional characterization. <i>LWT - Food Science and Technology</i> , 2018, 91, 460-466.	2.5	86
6162	Influence of metal contamination in soil on metabolic profiles of <i>Miscanthus x giganteus</i> belowground parts and associated bacterial communities. <i>Applied Soil Ecology</i> , 2018, 125, 240-249.	2.1	13
6163	Rampant Host Switching Shaped the Termite Gut Microbiome. <i>Current Biology</i> , 2018, 28, 649-654.e2.	1.8	101

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6167	Diversity of root-associated microbial populations of <i>Tamarix parviflora</i> cultivated under various conditions. <i>Applied Soil Ecology</i> , 2018, 125, 264-272.	2.1	16
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6169	Coastal urbanisation affects microbial communities on a dominant marine holobiont. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 1.	2.9	82
6170	Distinct responses of soil bacterial and fungal communities to changes in fertilization regime and crop rotation. <i>Geoderma</i> , 2018, 319, 156-166.	2.3	203
6171	Top-down effects of a grazing, omnivorous minnow (<i>Campostoma anomalum</i>) on stream microbial communities. <i>Freshwater Science</i> , 2018, 37, 121-133.	0.9	7
6172	Influence of Pig Farming on the Human Nasal Microbiota: Key Role of Airborne Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	65
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6175	The nasal microbiome mirrors and potentially shapes olfactory function. <i>Scientific Reports</i> , 2018, 8, 1296.	1.6	76
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6177	Occurrence and Distribution of Urban Dust-Associated Bacterial Antibiotic Resistance in Northern China. <i>Environmental Science and Technology Letters</i> , 2018, 5, 50-55.	3.9	42
6178	Arabinoxylo-Oligosaccharides and Inulin Impact Inter-Individual Variation on Microbial Metabolism and Composition, Which Immunomodulates Human Cells. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 1121-1130.	2.4	63
6179	Nonalcoholic fatty liver disease is associated with dysbiosis independent of body mass index and insulin resistance. <i>Scientific Reports</i> , 2018, 8, 1466.	1.6	196
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6184	Shift in the subgingival microbiome following scaling and root planing in generalized aggressive periodontitis. <i>Journal of Clinical Periodontology</i> , 2018, 45, 440-452.	2.3	36
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6186	Quantitative analyses of denitrifying bacterial diversity from a seasonally hypoxic monsoon governed tropical coastal region. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 156, 34-43.	0.6	11
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6188	Autochthonous facility-specific microbiota dominates washed-rind Austrian hard cheese surfaces and its production environment. <i>International Journal of Food Microbiology</i> , 2018, 267, 54-61.	2.1	31
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6195	Characterization of the bacterial community in shower water before and after chlorination. <i>Journal of Water and Health</i> , 2018, 16, 233-243.	1.1	5
6196	Short communication: Signs of host genetic regulation in the microbiome composition in 2 dairy breeds: Holstein and Brown Swiss. <i>Journal of Dairy Science</i> , 2018, 101, 2285-2292.	1.4	36
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6198	Ethyl Carbamate Formation Regulated by Lactic Acid Bacteria and Nonconventional Yeasts in Solid-State Fermentation of Chinese <i>Moutai</i> -Flavor Liquor. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 387-392.	2.4	34
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6201	Bacterial community structure and functional potential of rhizosphere soils as influenced by nitrogen addition and bacterial wilt disease under continuous sesame cropping. <i>Applied Soil Ecology</i> , 2018, 125, 117-127.	2.1	59
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6204	Changes in mouse gut bacterial community in response to different types of drinking water. <i>Water Research</i> , 2018, 132, 79-89.	5.3	47
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6216	Effects of high-concentration influent suspended solids on aerobic granulation in pilot-scale sequencing batch reactors treating real domestic wastewater. <i>Water Research</i> , 2018, 131, 74-89.	5.3	68
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6222	Field study reveals core plant microbiota and relative importance of their drivers. <i>Environmental Microbiology</i> , 2018, 20, 124-140.	1.8	255
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6256	Metabarcoding for the parallel identification of several hundred predators and their prey: Application to bat species diet analysis. <i>Molecular Ecology Resources</i> , 2018, 18, 474-489.	2.2	118
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6262	Isolation and characterization of phosphofungi, and screening of their plant growth-promoting activities. <i>AMB Express</i> , 2018, 8, 63.	1.4	59
6263	Microbial community and diversity in the feces of Sichuan takin (<i>Budorcas taxicolor tibetana</i>) as revealed by Illumina Miseq sequencing and quantitative real-time PCR. <i>AMB Express</i> , 2018, 8, 68.	1.4	5
6264	Gut microbiota trajectory in early life may predict development of celiac disease. <i>Microbiome</i> , 2018, 6, 36.	4.9	107
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6268	Impact of nutrient addition on diversity and fate of fecal bacteria. <i>Science of the Total Environment</i> , 2018, 636, 717-726.	3.9	9
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6273	Fecal Microbiota Transplantation in Experimental Ulcerative Colitis Reveals Associated Gut Microbial and Host Metabolic Reprogramming. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
6274	Metagenome, metatranscriptome, and metaproteome approaches unraveled compositions and functional relationships of microbial communities residing in biogas plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5045-5063.	1.7	128
6275	Reanalysis of microbiomes in soils affected by apple replant disease (ARD): Old foes and novel suspects lead to the proposal of extended model of disease development. <i>Applied Soil Ecology</i> , 2018, 129, 24-33.	2.1	30
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6277	The distribution of active iron-cycling bacteria in marine and freshwater sediments is decoupled from geochemical gradients. <i>Environmental Microbiology</i> , 2018, 20, 2483-2499.	1.8	76
6278	Marine-influenced microbial communities inhabit terrestrial hot springs on a remote island volcano. <i>Extremophiles</i> , 2018, 22, 687-698.	0.9	10
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6281	Co-application of wood ash and <i>Paenibacillus mucilaginosus</i> to soil: the effect on maize nutritional status, root exudation and composition of soil solution. <i>Plant and Soil</i> , 2018, 428, 105-122.	1.8	14
6282	The effects of sequencing platforms on phylogenetic resolution in 16S rRNA gene profiling of human feces. <i>Scientific Data</i> , 2018, 5, 180068.	2.4	22
6283	Differential susceptibility of whitefly-associated bacteria to antibiotic as revealed by metagenomics analysis. <i>Infection, Genetics and Evolution</i> , 2018, 63, 24-29.	1.0	11
6284	Bacterial diversity in the feces of dogs with CPV infection. <i>Microbial Pathogenesis</i> , 2018, 121, 70-76.	1.3	19
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6287	Long-Term Coffee Monoculture Alters Soil Chemical Properties and Microbial Communities. <i>Scientific Reports</i> , 2018, 8, 6116.	1.6	102
6288	Bacterial Community in Water and Air of Two Sub-Alpine Lakes in Taiwan. <i>Microbes and Environments</i> , 2018, 33, 120-126.	0.7	17
6289	Concentration-dependent responses of soil bacterial, fungal and nitrifying communities to silver nano and micron particles. <i>Environmental Science and Pollution Research</i> , 2018, 25, 18693-18704.	2.7	27

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6291	Integrative metabolic and microbial profiling on patients with Spleen-yang-deficiency syndrome. <i>Scientific Reports</i> , 2018, 8, 6619.	1.6	73
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6294	Endophyte-enhanced phytoremediation of DDE-contaminated using <i>Cucurbita pepo</i> : A field trial. <i>International Journal of Phytoremediation</i> , 2018, 20, 301-310.	1.7	16
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6296	Long-term spatial and temporal microbial community dynamics in a large-scale drinking water distribution system with multiple disinfectant regimes. <i>Water Research</i> , 2018, 139, 406-419.	5.3	106
6297	Investigating Colonization of the Healthy Adult Gastrointestinal Tract by Fungi. <i>MSphere</i> , 2018, 3, .	1.3	173
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6299	Effects of dietary black soldier fly larvae on performance of broilers mediated or not through changes in microbiota. <i>Journal of Insects As Food and Feed</i> , 2018, 4, 31-42.	2.1	13
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6303	Microbial degradation of Cold Lake Blend and Western Canadian select dilbits by freshwater enrichments. <i>Journal of Hazardous Materials</i> , 2018, 352, 111-120.	6.5	38
6304	Cultivated bacterial diversity associated with the carnivorous plant <i>Utricularia breviscapa</i> (Lentibulariaceae) from floodplains in Brazil. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 714-722.	0.8	9
6305	Constructing lightweight and flexible pipelines using Plugin-Based Microbiome Analysis (PluMA). <i>Bioinformatics</i> , 2018, 34, 2881-2888.	1.8	5
6306	The Lung Microbiota of Healthy Mice Are Highly Variable, Cluster by Environment, and Reflect Variation in Baseline Lung Innate Immunity. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 497-508.	2.5	189
6307	Diversity of microbial communities potentially involved in mercury methylation in rice paddies surrounding typical mercury mining areas in China. <i>MicrobiologyOpen</i> , 2018, 7, e00577.	1.2	20

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6309	Benthic phototrophic community from Kiran soda lake, south-eastern Siberia. <i>Extremophiles</i> , 2018, 22, 211-220.	0.9	9
6310	Host range of antibiotic resistance genes in wastewater treatment plant influent and effluent. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	148
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6312	Importance of soil legacy effects and successful mutualistic interactions during Australian acacia invasions in nutrient-poor environments. <i>Journal of Ecology</i> , 2018, 106, 2071-2081.	1.9	46
6313	A microbial perspective on the life-history evolution of marine invertebrate larvae: If, where and when to feed. <i>Marine Ecology</i> , 2018, 39, e12490.	0.4	15
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6315	Impact of soil pedogenesis on the diversity and composition of fungal communities across the California soil chronosequence of Mendocino. <i>Mycorrhiza</i> , 2018, 28, 343-356.	1.3	10
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6317	Cervical microbiome is altered in cervical intraepithelial neoplasia after loop electrosurgical excision procedure in china. <i>Scientific Reports</i> , 2018, 8, 4923.	1.6	32
6318	Earthworm-induced shifts in microbial diversity in soils with rare versus established invasive earthworm populations. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	19
6319	Bacterial and Archaeal Community Structure in the Surface Diatom Sediments of Deep Freshwater Lake Baikal (Eastern Siberia). <i>Geomicrobiology Journal</i> , 2018, 35, 635-647.	1.0	5
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6321	Salinity is a key factor driving the nitrogen cycling in the mangrove sediment. <i>Science of the Total Environment</i> , 2018, 631-632, 1342-1349.	3.9	120
6322	Earthworms differentially modify the microbiome of arable soils varying in residue management. <i>Soil Biology and Biochemistry</i> , 2018, 121, 120-129.	4.2	38
6323	Long- and short-term effects of mercury pollution on the soil microbiome. <i>Soil Biology and Biochemistry</i> , 2018, 120, 191-199.	4.2	84
6324	Shifts of Sediment Microbial Community Structure along a Salinized and Degraded River Continuum. <i>Journal of Coastal Research</i> , 2018, 342, 443-450.	0.1	5
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6327	Current Perspectives of the Chicken Gastrointestinal Tract and Its Microbiome. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 131-139.	1.9	181
6328	Characterization of functional microbial communities involved in diazo dyes decolorization and mineralization stages. <i>International Biodeterioration and Biodegradation</i> , 2018, 132, 166-177.	1.9	18
6329	Male spiders control offspring sex ratio through greater production of female-determining sperm. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172887.	1.2	15
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6331	Development and evaluation of a culture-free microbiota profiling platform (MYcrobiota) for clinical diagnostics. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 1081-1089.	1.3	13
6332	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.	1.6	37
6333	Plant sterols and human gut microbiota relationship: An in vitro colonic fermentation study. <i>Journal of Functional Foods</i> , 2018, 44, 322-329.	1.6	27
6334	Reproducibility and repeatability of six high-throughput 16S rDNA sequencing protocols for microbiota profiling. <i>Journal of Microbiological Methods</i> , 2018, 147, 76-86.	0.7	30
6335	Assessment of Passive Traps Combined with High-Throughput Sequencing To Study Airborne Fungal Communities. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	39
6336	Highlighting Clinical Metagenomics for Enhanced Diagnostic Decision-making: A Step Towards Wider Implementation. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 108-120.	1.9	79
6337	Biogeochemical cycling of gold: Transforming gold particles from arctic Finland. <i>Chemical Geology</i> , 2018, 483, 511-529.	1.4	24
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6341	Sulfide inhibition of nitrite oxidation in activated sludge depends on microbial community composition. <i>Water Research</i> , 2018, 138, 241-249.	5.3	69
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6350	Antibiotics-induced modulation of large intestinal microbiota altered aromatic amino acid profile and expression of neurotransmitters in the hypothalamus of piglets. <i>Journal of Neurochemistry</i> , 2018, 146, 219-234.	2.1	71
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6352	The Bacterial Population of Neutral Mine Drainage Water of Elizabeth's Shaft (Slovinky, Slovakia). <i>Current Microbiology</i> , 2018, 75, 988-996.	1.0	13
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6354	The influence of aggregate size fraction and horizon position on microbial community composition. <i>Applied Soil Ecology</i> , 2018, 127, 19-29.	2.1	43
6355	Successful aerobic bioremediation of groundwater contaminated with higher chlorinated phenols by indigenous degrader bacteria. <i>Water Research</i> , 2018, 138, 118-128.	5.3	30
6356	Influence of fecal collection conditions and 16S rRNA gene sequencing at two centers on human gut microbiota analysis. <i>Scientific Reports</i> , 2018, 8, 4386.	1.6	46
6357	Below-ground processes control the success of an invasive seaweed. <i>Journal of Ecology</i> , 2018, 106, 2082-2095.	1.9	20
6358	A different gut microbial community between larvae and adults of a wild bumblebee nest (<i>Bombus</i>) Tj ETQq0 0 Q rgeBT /Overlock 10 T	1.5	23
6359	Effects of heap-bioleaching plant on microbial community of the nearby river. <i>International Biodeterioration and Biodegradation</i> , 2018, 128, 36-40.	1.9	7
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6364	Vertical and Horizontal Distribution of Bacterial Communities in Alluvial Groundwater of the Nakdong River Bank. <i>Geomicrobiology Journal</i> , 2018, 35, 74-80.	1.0	9
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6373	Power and sample size calculations for high-throughput sequencing-based experiments. <i>Briefings in Bioinformatics</i> , 2018, 19, 1247-1255.	3.2	32
6374	Effect of rhizobacteria on arsenic uptake by macrophyte <i>Eichhornia crassipes</i> (Mart.) Solms. <i>International Journal of Phytoremediation</i> , 2018, 20, 114-120.	1.7	53
6375	The Microbiome of Eucalyptus Roots under Different Management Conditions and Its Potential for Biological Nitrogen Fixation. <i>Microbial Ecology</i> , 2018, 75, 183-191.	1.4	45
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6377	Shift in Cyanobacteria Community Diversity in Hot Springs of India. <i>Geomicrobiology Journal</i> , 2018, 35, 141-147.	1.0	11
6378	Effect of Sweetened Dried Cranberry Consumption on Urinary Proteome and Fecal Microbiome in Healthy Human Subjects. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 145-153.	1.0	34
6379	Inhibitory effect of high phenol concentration in treating coal gasification wastewater in anaerobic biofilter. <i>Journal of Environmental Sciences</i> , 2018, 64, 207-215.	3.2	36

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6381	Inference for Empirical Wasserstein Distances on Finite Spaces. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2018, 80, 219-238.	1.1	68
6382	Opportunities and challenges in metabarcoding approaches for helminth community identification in wild mammals. <i>Parasitology</i> , 2018, 145, 608-621.	0.7	28
6383	Gastrointestinal Colonization of <i>Candida Albicans</i> Increases Serum (1 \rightarrow 3)- β -D-Glucan, without Candidemia, and Worsens Cecal Ligature and Puncture Sepsis in Murine Model. <i>Shock</i> , 2018, 49, 62-70.	1.0	50
6384	Variation of <i>Synechococcus</i> Pigment Genetic Diversity Along Two Turbidity Gradients in the China Seas. <i>Microbial Ecology</i> , 2018, 75, 10-21.	1.4	19
6385	Extensive Overlap of Tropical Rainforest Bacterial Endophytes between Soil, Plant Parts, and Plant Species. <i>Microbial Ecology</i> , 2018, 75, 88-103.	1.4	37
6386	Solid-State Co-digestion of NaOH-Pretreated Corn Straw and Chicken Manure Under Mesophilic Condition. <i>Waste and Biomass Valorization</i> , 2018, 9, 1027-1035.	1.8	19
6387	Skin Bacterial Community Reorganization Following Metamorphosis of the Fire-Bellied Toad (<i>Bombina</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.4	18
6388	Peaks of in situ N ₂ O emissions are influenced by N ₂ O-producing and reducing microbial communities across arable soils. <i>Global Change Biology</i> , 2018, 24, 360-370.	4.2	109
6389	Bacterial and Archaeal Diversity in Hypersaline Cyanobacterial Mats Along a Transect in the Intertidal Flats of the Sultanate of Oman. <i>Microbial Ecology</i> , 2018, 75, 331-347.	1.4	24
6390	An Exploration into the Bacterial Community under Different Pasteurization Conditions during Substrate Preparation (Composting "Phase II") for <i>Agaricus bisporus</i> Cultivation. <i>Microbial Ecology</i> , 2018, 75, 318-330.	1.4	42
6391	Metabarcoding: A powerful tool to investigate microbial communities and shape future plant protection strategies. <i>Biological Control</i> , 2018, 120, 1-10.	1.4	115
6392	Electro-fermentation triggering population selection in mixed-culture glycerol fermentation. <i>Microbial Biotechnology</i> , 2018, 11, 74-83.	2.0	58
6393	Validating novel oligonucleotide primers targeting three classes of bacterial non-specific acid phosphatase genes in grassland soils. <i>Plant and Soil</i> , 2018, 427, 39-51.	1.8	24
6394	Strategies for managing rival bacterial communities: Lessons from burying beetles. <i>Journal of Animal Ecology</i> , 2018, 87, 414-427.	1.3	57
6395	Introducing DNA-based methods to compare fungal microbiota and concentrations in indoor, outdoor, and personal air. <i>Aerobiologia</i> , 2018, 34, 1-12.	0.7	20
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6399	Understanding bacterial communities of partial nitrification and nitrification reactors at ambient and low temperature. <i>Chemical Engineering Journal</i> , 2018, 337, 755-763.	6.6	16
6400	Bioaugmentation of thiabendazole-contaminated soils from a wastewater disposal site: Factors driving the efficacy of this strategy and the diversity of the indigenous soil bacterial community. <i>Environmental Pollution</i> , 2018, 233, 16-25.	3.7	26
6401	From vineyard to winery: a source map of microbial diversity driving wine fermentation. <i>Environmental Microbiology</i> , 2018, 20, 75-84.	1.8	102
6402	The taxonomic composition of the donor intestinal microbiota is a major factor influencing the efficacy of faecal microbiota transplantation in therapy refractory ulcerative colitis. <i>Alimentary Pharmacology and Therapeutics</i> , 2018, 47, 67-77.	1.9	154
6403	Estimating Population Turnover Rates by Relative Quantification Methods Reveals Microbial Dynamics in Marine Sediment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	31
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6405	Habitability analyses of aquatic bacteria. <i>Journal of Oceanography</i> , 2018, 74, 197-207.	0.7	5
6406	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. <i>Nucleic Acids Research</i> , 2018, 46, D127-D132.	6.5	31
6407	Biofilm biodiversity in French and Swiss show caves using the metabarcoding approach: First data. <i>Science of the Total Environment</i> , 2018, 615, 1207-1217.	3.9	51
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6409	The effects of warming and ocean acidification on growth, photosynthesis, and bacterial communities for the marine invasive macroalga <i>Caulerpa taxifolia</i> . <i>Limnology and Oceanography</i> , 2018, 63, 459-471.	1.6	22
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6414	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018, 359, 97-103.	6.0	3,126
6415	Brown Rot Syndrome and Changes in the Bacterial Community of the Baikal Sponge <i>Lubomirskia baicalensis</i> . <i>Microbial Ecology</i> , 2018, 75, 1024-1034.	1.4	24

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6417	Membrane bioreactor and hybrid moving bed biofilm reactor-membrane bioreactor for the treatment of variable salinity wastewater: Influence of biomass concentration and hydraulic retention time. <i>Chemical Engineering Journal</i> , 2018, 336, 102-111.	6.6	61
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6419	The role of the microbiome in psoriasis: moving from disease description to treatment selection?. <i>British Journal of Dermatology</i> , 2018, 178, 1020-1027.	1.4	54
6420	Microbial community differentiation between active and inactive sulfide chimneys of the Kolumbo submarine volcano, Hellenic Volcanic Arc. <i>Extremophiles</i> , 2018, 22, 13-27.	0.9	21
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6422	Gut microbiome in gestational diabetes: a cross-sectional study of mothers and offspring 5 years postpartum. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2018, 97, 38-46.	1.3	51
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6424	Impact of DNA extraction, sample dilution, and reagent contamination on 16S rRNA gene sequencing of human feces. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 403-411.	1.7	43
6425	New barcoded primers for efficient retrieval of cercozoan sequences in high-throughput environmental diversity surveys, with emphasis on worldwide biological soil crusts. <i>Molecular Ecology Resources</i> , 2018, 18, 229-239.	2.2	71
6426	Microbiological, chemical and sensory spoilage analysis of raw Atlantic cod (<i>Gadus morhua</i>) stored under modified atmospheres. <i>Food Microbiology</i> , 2018, 70, 232-244.	2.1	90
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6428	Freshwater fisheries assessment using environmental DNA: A primer on the method, its potential, and shortcomings as a conservation tool. <i>Fisheries Research</i> , 2018, 197, 60-66.	0.9	82
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6430	Blackwater treatment using vertical greening: Efficiency and microbial community structure. <i>Bioresource Technology</i> , 2018, 249, 175-181.	4.8	22
6431	Metagenomic insights into zooplankton-associated bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 492-505.	1.8	57
6432	Cyanobacteria of the Wadden Sea: seasonality and sediment influence on community composition. <i>Hydrobiologia</i> , 2018, 811, 103-117.	1.0	13
6433	Biocrust morphology is linked to marked differences in microbial community composition. <i>Plant and Soil</i> , 2018, 429, 65-75.	1.8	46

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6435	Polymorphism of antibiotic-inactivating enzyme driven by ecology expands the environmental resistome. <i>ISME Journal</i> , 2018, 12, 267-276.	4.4	19
6436	Flow cytometric monitoring of bacterioplankton phenotypic diversity predicts high population-specific feeding rates by invasive dreissenid mussels. <i>Environmental Microbiology</i> , 2018, 20, 521-534.	1.8	31
6437	Application of stable isotope labelling techniques for the detection of active diazotrophs. <i>Environmental Microbiology</i> , 2018, 20, 44-61.	1.8	44
6438	Characterization of iron and manganese minerals and their associated microbiota in different mine sites to reveal the potential interactions of microbiota with mineral formation. <i>Chemosphere</i> , 2018, 191, 245-252.	4.2	14
6439	Excess labile carbon promotes the expression of virulence factors in coral reef bacterioplankton. <i>ISME Journal</i> , 2018, 12, 59-76.	4.4	58
6440	Aquatic urban ecology at the scale of a capital: community structure and interactions in street gutters. <i>ISME Journal</i> , 2018, 12, 253-266.	4.4	11
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6443	Effects of nitrate and sulfate on the performance and bacterial community structure of membrane-less single-chamber air-cathode microbial fuel cells. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2018, 53, 13-24.	0.9	18
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6445	Overall bacterial community composition and abundance of nitrifiers and denitrifiers in a typical macrotidal estuary. <i>Marine Pollution Bulletin</i> , 2018, 126, 540-548.	2.3	8
6446	Bacteria alone establish the chemical basis of the wood-fall chemosynthetic ecosystem in the deep-sea. <i>ISME Journal</i> , 2018, 12, 367-379.	4.4	28
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6448	Application of compost and clay under water-stressed conditions influences functional diversity of rhizosphere bacteria. <i>Biology and Fertility of Soils</i> , 2018, 54, 55-70.	2.3	53
6449	Persistence of Halophilic Methanogens and Oil-Degrading Bacteria in an Offshore Oil-Producing Facility. <i>Geomicrobiology Journal</i> , 2018, 35, 323-333.	1.0	3
6450	Assembly of seed-associated microbial communities within and across successive plant generations. <i>Plant and Soil</i> , 2018, 422, 67-79.	1.8	91
6451	Next generation of microbiological risk assessment: Potential of omics data for exposure assessment. <i>International Journal of Food Microbiology</i> , 2018, 287, 18-27.	2.1	54

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6452	Metabarcoding of lake benthic diatoms: from structure assemblages to ecological assessment. <i>Hydrobiologia</i> , 2018, 807, 37-51.	1.0	90
6453	Influence of arbuscular mycorrhizal fungi on antimony phyto-uptake and compartmentation in vegetables cultivated in urban gardens. <i>Chemosphere</i> , 2018, 191, 272-279.	4.2	18
6454	Comparative analysis of microbial communities associated with bacteriomes, reproductive organs and eggs of the cicada <i>Subsalstria yangi</i> . <i>Archives of Microbiology</i> , 2018, 200, 227-235.	1.0	15
6455	Taxonomic and Functional Analyses of the Supragingival Microbiome from Caries-Affected and Caries-Free Hosts. <i>Microbial Ecology</i> , 2018, 75, 543-554.	1.4	23
6456	Characterization of microbial community composition and pathogens risk assessment in typical Italian-style salami by high-throughput sequencing technology. <i>Food Science and Biotechnology</i> , 2018, 27, 241-249.	1.2	22
6457	Biodiversity and ecology of flower-associated actinomycetes in different flowering stages of <i>Protea repens</i> . <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 209-226.	0.7	4
6458	Genetic Diversity of Benthic Microbial Eukaryotes in Response to Spatial Heterogeneity of Sediment Geochemistry in a Mangrove Ecosystem. <i>Estuaries and Coasts</i> , 2018, 41, 751-764.	1.0	27
6459	A comparative study of composting the solid fraction of dairy manure with or without bulking material: Performance and microbial community dynamics. <i>Bioresource Technology</i> , 2018, 247, 443-452.	4.8	135
6460	Temporal dynamics and metabolic correlation between lactate-producing and hydrogen-producing bacteria in sugarcane vinasse dark fermentation: The key role of lactate. <i>Bioresource Technology</i> , 2018, 247, 426-433.	4.8	104
6461	Effect of extracellular electron shuttles on arsenic-mobilizing activities in soil microbial communities. <i>Journal of Hazardous Materials</i> , 2018, 342, 571-578.	6.5	56
6462	Archaea and bacteria respectively dominate nitrification in lightly and heavily grazed soil in a grassland system. <i>Biology and Fertility of Soils</i> , 2018, 54, 41-54.	2.3	52
6463	Do different probing depths exhibit striking differences in microbial profiles?. <i>Journal of Clinical Periodontology</i> , 2018, 45, 26-37.	2.3	49
6464	<i>Cryptosporidium</i> infecting wild cricetid rodents from the subfamilies Arvicolinae and Neotominae. <i>Parasitology</i> , 2018, 145, 326-334.	0.7	14
6465	The diversity and biogeography of abundant and rare intertidal marine microeukaryotes explained by environment and dispersal limitation. <i>Environmental Microbiology</i> , 2018, 20, 462-476.	1.8	112
6466	Reduced obesity, diabetes, and steatosis upon cinnamon and grape pomace are associated with changes in gut microbiota and markers of gut barrier. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 314, E334-E352.	1.8	119
6467	Biodiversity analysis of the unique geothermal microbial ecosystem of the Blue Lagoon (Iceland) using next-generation sequencing (NGS). <i>Hydrobiologia</i> , 2018, 811, 93-102.	1.0	13
6468	Fungal diversity during fermentation correlates with thiol concentration in wine. <i>Australian Journal of Grape and Wine Research</i> , 2018, 24, 105-112.	1.0	21
6469	Methanogenic community compositions in surface sediment of freshwater aquaculture ponds and the influencing factors. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 115-124.	0.7	8

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6470	Effect of barley supplementation on the fecal microbiota, caecal biochemistry, and key biomarkers of obesity and inflammation in obese db/db mice. <i>European Journal of Nutrition</i> , 2018, 57, 2513-2528.	1.8	28
6471	Principal component analysis for interaction of nitrifiers and wastewater environments at a full-scale activated sludge plant. <i>International Journal of Environmental Science and Technology</i> , 2018, 15, 1477-1490.	1.8	14
6472	Maternal obesity is associated with gut microbial metabolic potential in offspring during infancy. <i>Journal of Physiology and Biochemistry</i> , 2018, 74, 159-169.	1.3	29
6473	Diversity of bacterial communities in French chicken cuts stored under modified atmosphere packaging. <i>Food Microbiology</i> , 2018, 70, 7-16.	2.1	65
6474	Nutrient and acetate amendment leads to acetoclastic methane production and microbial community change in a non-producing Australian coal well. <i>Microbial Biotechnology</i> , 2018, 11, 626-638.	2.0	30
6475	Photosynthetic Picoeukaryotes in the Land-Fast Ice of the White Sea, Russia. <i>Microbial Ecology</i> , 2018, 75, 582-597.	1.4	22
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6486	Microbial diversity and composition in different gut locations of hyperlipidemic mice receiving krill oil. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 355-366.	1.7	14
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6767	A nearly uniform distributional pattern of heterotrophic bacteria in the Mariana Trench interior. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2018, 142, 116-126.	0.6	27
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6773	A salamander's top down effect on fungal communities in a detritivore ecosystem. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	7
6774	Oral probiotic combination of <i>Lactobacillus</i> and <i>Bifidobacterium</i> alters the gastrointestinal microbiota during antibiotic treatment for <i>Clostridium difficile</i> infection. <i>PLoS ONE</i> , 2018, 13, e0204253.	1.1	45
6775	Progress of analytical tools and techniques for human gut microbiome research. <i>Journal of Microbiology</i> , 2018, 56, 693-705.	1.3	49
6776	Diversity of nitrogen fixing bacterial communities in the coastal sediments of southeastern Arabian Sea (SEAS). <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 156, 51-59.	0.6	14
6777	Toward Integrative Bacterial Monitoring of Metolachlor Toxicity in Groundwater. <i>Frontiers in Microbiology</i> , 2018, 9, 2053.	1.5	4
6778	Antibiotic Effects on Microbial Communities Responsible for Denitrification and N ₂ O Production in Grassland Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 2121.	1.5	55
6779	Nitrate reduced arsenic redox transformation and transfer in flooded paddy soil-rice system. <i>Environmental Pollution</i> , 2018, 243, 1015-1025.	3.7	33

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6781	Natural Secretory Immunoglobulins Promote Enteric Viral Infections. <i>Journal of Virology</i> , 2018, 92, .	1.5	18
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6783	Single-Cell Genomics Reveals a Diverse Metabolic Potential of Uncultivated Desulfatiglans-Related Deltaproteobacteria Widely Distributed in Marine Sediment. <i>Frontiers in Microbiology</i> , 2018, 9, 2038.	1.5	69
6784	Determinants of Deadwood-Inhabiting Fungal Communities in Temperate Forests: Molecular Evidence From a Large Scale Deadwood Decomposition Experiment. <i>Frontiers in Microbiology</i> , 2018, 9, 2120.	1.5	43
6785	Mucin degradation niche as a driver of microbiome composition and <i>Akkermansia muciniphila</i> abundance in a dynamic gut model is donor independent. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	51
6786	Intestinal microbiota profiling and predicted metabolic dysregulation in psoriasis patients. <i>Experimental Dermatology</i> , 2018, 27, 1336-1343.	1.4	79
6787	Differences in the Gut Microbiota Establishment and Metabolome Characteristics Between Low- and Normal-Birth-Weight Piglets During Early-Life. <i>Frontiers in Microbiology</i> , 2018, 9, 1798.	1.5	74
6788	Possible aplanochytrid (Labyrinthulea) prey detected using 18S metagenetic diet analysis in the key copepod species <i>Calanus sinicus</i> in the coastal waters of the subtropical western North Pacific. <i>Plankton and Benthos Research</i> , 2018, 13, 75-82.	0.2	12
6789	Biofouling Formation and Bacterial Community Structure in Hybrid Moving Bed Biofilm Reactor-Membrane Bioreactors: Influence of Salinity Concentration. <i>Water (Switzerland)</i> , 2018, 10, 1133.	1.2	8
6790	Effects of an oral synbiotic on the gastrointestinal immune system and microbiota in patients with diarrhea-predominant irritable bowel syndrome. <i>European Journal of Nutrition</i> , 2018, 58, 2767-2778.	1.8	21
6791	<i>Bifidobacterium pseudocatenulatum</i> CECT 7765 supplementation improves inflammatory status in insulin-resistant obese children. <i>European Journal of Nutrition</i> , 2018, 58, 2789-2800.	1.8	35
6792	Historical DNA Metabarcoding of the Prey and Microbiome of Trematomid Fishes Using Museum Samples. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	16
6793	Urinary microbes and postoperative urinary tract infection risk in urogynecologic surgical patients. <i>International Urogynecology Journal</i> , 2018, 29, 1797-1805.	0.7	91
6794	Denitrifying Microbial Communities in Heavy-Metal-Contaminated Paddy Soils near Electronic-Waste Processing Centers. <i>Water, Air, and Soil Pollution</i> , 2018, 229, 1.	1.1	13
6795	Microbial electrosynthesis (MES) from CO ₂ is resilient to fluctuations in renewable energy supply. <i>Energy Conversion and Management</i> , 2018, 177, 272-279.	4.4	110
6796	Association of metformin administration with gut microbiome dysbiosis in healthy volunteers. <i>PLoS ONE</i> , 2018, 13, e0204317.	1.1	96
6797	Development of the Tonsil Microbiome in Pigs and Effects of Stress on the Microbiome. <i>Frontiers in Veterinary Science</i> , 2018, 5, 220.	0.9	13

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6799	Alterations in gut bacterial and fungal microbiomes are associated with bacterial Keratitis, an inflammatory disease of the human eye. <i>Journal of Biosciences</i> , 2018, 43, 835-856.	0.5	47
6800	Consumption of Mediterranean versus Western Diet Leads to Distinct Mammary Gland Microbiome Populations. <i>Cell Reports</i> , 2018, 25, 47-56.e3.	2.9	114
6801	Inhibitory effects of ammonia on syntrophic propionate oxidation in anaerobic digester sludge. <i>Water Research</i> , 2018, 146, 275-287.	5.3	41
6802	Viable cyanobacteria in the deep continental subsurface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10702-10707.	3.3	124
6803	Detection of <i>Diplodia corticola</i> spores in Ontario and Québec based on High Throughput Sequencing (HTS) methods. <i>Canadian Journal of Plant Pathology</i> , 2018, 40, 378-386.	0.8	20
6804	Monitoring of microbial dynamics in a drinking water distribution system using the culture-free, user-friendly, MYcrobiota platform. <i>Scientific Reports</i> , 2018, 8, 14727.	1.6	12
6805	Seasonal and Sexual Differences in the Microbiota of the Hoopoe Uropygial Secretion. <i>Genes</i> , 2018, 9, 407.	1.0	19
6806	Molecular analysis of oral microflora in patients with primary Sjögren's syndrome by using high-throughput sequencing. <i>PeerJ</i> , 2018, 6, e5649.	0.9	26
6807	Soil amendment with sewage sludge affects soil prokaryotic community composition, mobilome and resistome. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	12
6808	A Simple <i>In Vitro</i> Gut Model for Studying the Interaction between <i>Escherichia coli</i> and the Intestinal Commensal Microbiota in Cecal Mucus. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	6
6809	Pediatric asthma comprises different phenotypic clusters with unique nasal microbiotas. <i>Microbiome</i> , 2018, 6, 179.	4.9	45
6810	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. <i>Nature Communications</i> , 2018, 9, 3891.	5.8	313
6811	Recovering cellular biomass from fluids using chemical flocculation. <i>Environmental Microbiology Reports</i> , 2018, 10, 686-694.	1.0	2
6812	Methanogens and Iron-Reducing Bacteria: the Overlooked Members of Mercury-Methylating Microbial Communities in Boreal Lakes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	46
6813	Systematic Comparison of Bacterial Colonization of Endometrial Tissue and Fluid Samples in Recurrent Miscarriage Patients: Implications for Future Endometrial Microbiome Studies. <i>Clinical Chemistry</i> , 2018, 64, 1743-1752.	1.5	45
6814	Microbial responses to combined oxidation and catalysis treatment of 1,4-dioxane and co-contaminants in groundwater and soil. <i>Frontiers of Environmental Science and Engineering</i> , 2018, 12, 1.	3.3	12
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6818	Short-term microbial effects of a large-scale mine-tailing storage facility collapse on the local natural environment. PLoS ONE, 2018, 13, e0196032.	1.1	12
6819	The genome sequence of <i>Enterococcus faecium</i> 8S3, lactic acid-producing bacterium from Slovak cheese "bryndza" with biotechnological potential. Biologia (Poland), 2018, 73, 1159-1162.	0.8	1
6820	Microbiome Analysis. Methods in Molecular Biology, 2018, , .	0.4	13
6821	Normalization of Microbiome Profiling Data. Methods in Molecular Biology, 2018, 1849, 143-168.	0.4	10
6822	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. Methods in Molecular Biology, 2018, 1849, 169-177.	0.4	155
6823	Characterization of Eukaryotic Microbiome Using 18S Amplicon Sequencing. Methods in Molecular Biology, 2018, 1849, 29-48.	0.4	10
6824	Culture and Molecular Profiling of the Respiratory Tract Microbiota. Methods in Molecular Biology, 2018, 1849, 49-61.	0.4	2
6825	Processing a 16S rRNA Sequencing Dataset with the Microbiome Helper Workflow. Methods in Molecular Biology, 2018, 1849, 131-141.	0.4	5
6826	Bioinformatic Analysis of Microbiome Data. ICSA Book Series in Statistics, 2018, , 1-27.	0.0	6
6827	Introductory Overview of Statistical Analysis of Microbiome Data. ICSA Book Series in Statistics, 2018, , 43-75.	0.0	7
6828	Quinoa whole grain diet compromises the changes of gut microbiota and colonic colitis induced by dextran Sulfate sodium in C57BL/6 mice. Scientific Reports, 2018, 8, 14916.	1.6	48
6829	Diversity and dynamic succession of microorganisms during <i>Daqu</i> preparation for <i>Luzhou</i> flavour liquor using second-generation sequencing technology. Journal of the Institute of Brewing, 2018, 124, 498-507.	0.8	32
6830	Transkingdom Networks: A Systems Biology Approach to Identify Causal Members of Host-Microbiota Interactions. Methods in Molecular Biology, 2018, 1849, 227-242.	0.4	23
6831	What Are Microbiome Data?. ICSA Book Series in Statistics, 2018, , 29-41.	0.0	9
6832	Upland soil cluster $\hat{3}$ dominates the methanotroph communities in the karst Heshang Cave. FEMS Microbiology Ecology, 2018, 94, .	1.3	31
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6837	Petroleum hydrocarbon rich oil refinery sludge of North-East India harbours anaerobic, fermentative, sulfate-reducing, syntrophic and methanogenic microbial populations. <i>BMC Microbiology</i> , 2018, 18, 151.	1.3	41
6838	Evaluation of the ribosomal DNA internal transcribed spacer (ITS), specifically ITS1 and ITS2, for the analysis of fungal diversity by deep sequencing. <i>PLoS ONE</i> , 2018, 13, e0206428.	1.1	96
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6840	Diet induced obesity is independent of metabolic endotoxemia and TLR4 signalling, but markedly increases hypothalamic expression of the acute phase protein, SerpinA3N. <i>Scientific Reports</i> , 2018, 8, 15648.	1.6	51
6841	Maximum Influent Salinity Affects the Diversity of Mineral-Precipitation-Mediating Bacterial Communities in Membrane Biofilm of Hybrid Moving Bed Biofilm Reactor-Membrane Bioreactor. <i>Water, Air, and Soil Pollution</i> , 2018, 229, 1.	1.1	15
6842	Complete mitochondrial genome of <i>Penaeus acehensis</i> (Crustacea, Decapoda, Penaeidae) from Aceh province, Indonesia. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 898-899.	0.2	4
6843	Biochemical Changes and Biological Origin of Key Odor Compound Generations in Pig Slurry during Indoor Storage Periods: A Pyrosequencing Approach. <i>BioMed Research International</i> , 2018, 2018, 1-13.	0.9	17
6844	Variations of the lung microbiome and immune response in mechanically ventilated surgical patients. <i>PLoS ONE</i> , 2018, 13, e0205788.	1.1	7
6845	Distinct mucosal microbial communities in infants with surgical necrotizing enterocolitis correlate with age and antibiotic exposure. <i>PLoS ONE</i> , 2018, 13, e0206366.	1.1	14
6846	Molecular and Microbiological Insights on the Enrichment Procedures for the Isolation of Petroleum Degrading Bacteria and Fungi. <i>Frontiers in Microbiology</i> , 2018, 9, 2543.	1.5	56
6847	Toxicity responses of bacterial community as a biological indicator after repeated exposure to lead (Pb) in the presence of decabromodiphenyl ether (BDE209). <i>Environmental Science and Pollution Research</i> , 2018, 25, 36278-36286.	2.7	3
6848	<i>Clostridium perfringens</i> -mediated necrotic enteritis is not influenced by the pre-existing microbiota but is promoted by large changes in the post-challenge microbiota. <i>Veterinary Microbiology</i> , 2018, 227, 119-126.	0.8	25
6849	The endangered northern bettong, <i>Bettongia tropica</i> , performs a unique and potentially irreplaceable dispersal function for ectomycorrhizal truffle fungi. <i>Molecular Ecology</i> , 2018, 27, 4960-4971.	2.0	13
6850	Dosing Regimen of Enrofloxacin Impacts Intestinal Pharmacokinetics and the Fecal Microbiota in Steers. <i>Frontiers in Microbiology</i> , 2018, 9, 2190.	1.5	14
6851	Safety and preliminary efficacy of orally administered lyophilized fecal microbiota product compared with frozen product given by enema for recurrent <i>Clostridium difficile</i> infection: A randomized clinical trial. <i>PLoS ONE</i> , 2018, 13, e0205064.	1.1	77

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6853	Assessing Pathogen Presence in an Intensively Tile Drained, Agricultural Watershed. <i>Journal of Environmental Quality</i> , 2018, 47, 1033-1042.	1.0	14
6854	Biofilm Microbiome (Re)Growth Dynamics in Drinking Water Distribution Systems Are Impacted by Chlorine Concentration. <i>Frontiers in Microbiology</i> , 2018, 9, 2519.	1.5	62
6855	Supplemental <i>Bacillus subtilis</i> DSM 32315 manipulates intestinal structure and microbial composition in broiler chickens. <i>Scientific Reports</i> , 2018, 8, 15358.	1.6	86
6856	Two Populations of Mites (<i>Tyrophagus putrescentiae</i>) Differ in Response to Feeding on Feces-Containing Diets. <i>Frontiers in Microbiology</i> , 2018, 9, 2590.	1.5	18
6857	A Comparative Study of Fungal Community Structure, Diversity and Richness between the Soil and the Phyllosphere of Native Grass Species in a Copper Tailings Dam in Shanxi Province, China. <i>Applied Sciences (Switzerland)</i> , 2018, 8, 1297.	1.3	23
6858	Fecal source identification using random forest. <i>Microbiome</i> , 2018, 6, 185.	4.9	88
6859	Soil microbial response following wildfires in thermic oak-pine forests. <i>Biology and Fertility of Soils</i> , 2018, 54, 985-997.	2.3	17
6860	Biology and Taxonomy of crAss-like Bacteriophages, the Most Abundant Virus in the Human Gut. <i>Cell Host and Microbe</i> , 2018, 24, 653-664.e6.	5.1	233
6861	Changes in ruminal and reticular pH and bacterial communities in Holstein cattle fed a high-grain diet. <i>BMC Veterinary Research</i> , 2018, 14, 310.	0.7	46
6862	Impact of carbohydrate substrate complexity on the diversity of the human colonic microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	28
6863	In situ responses of the sponge microbiome to ocean acidification. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	6
6864	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dysbiosis and alteration of community structure. <i>Microbiome</i> , 2018, 6, 180.	4.9	23
6865	Mitigating Sulfidogenesis With Simultaneous Perchlorate and Nitrate Treatments. <i>Frontiers in Microbiology</i> , 2018, 9, 2305.	1.5	13
6866	Community profiling of the urinary microbiota: considerations for low-biomass samples. <i>Nature Reviews Urology</i> , 2018, 15, 735-749.	1.9	87
6867	In Vitro Fermentation of Selected Prebiotics and Their Effects on the Composition and Activity of the Adult Gut Microbiota. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3097.	1.8	126
6868	Changes in bacterial communities during two agricultural solid wastesâ€™ co-composting processes. <i>Annals of Microbiology</i> , 2018, 68, 743-754.	1.1	9
6869	Daily HIV pre-exposure prophylaxis (PrEP) with tenofovir disoproxil fumarate-emtricitabine reduced <i>Streptococcus</i> and increased <i>Erysipelotrichaceae</i> in rectal microbiota. <i>Scientific Reports</i> , 2018, 8, 15212.	1.6	24

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6871	Effects of Chloramine and Coupon Material on Biofilm Abundance and Community Composition in Bench-Scale Simulated Water Distribution Systems and Comparison with Full-Scale Water Mains. <i>Environmental Science & Technology</i> , 2018, 52, 13077-13088.	4.6	42
6872	Structural and Functional Interrogation of Selected Biological Nitrogen Removal Systems in the United States, Denmark, and Singapore Using Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 2544.	1.5	7
6873	Upgrading lignocellulosic ethanol for caproate production via chain elongation fermentation. <i>International Biodeterioration and Biodegradation</i> , 2018, 135, 103-109.	1.9	28
6874	Bacterial Carbon Cycling in the River Plume in the Northern South China Sea During Summer. <i>Journal of Geophysical Research: Oceans</i> , 2018, 123, 8106-8121.	1.0	15
6875	Organic Matter Regulates Ammonia-Oxidizing Bacterial and Archaeal Communities in the Surface Sediments of <i>Ctenopharyngodon idellus</i> Aquaculture Ponds. <i>Frontiers in Microbiology</i> , 2018, 9, 2290.	1.5	28
6876	Significant microbial nitrogen loss from denitrification and anammox in the land-sea interface of low permeable sediments. <i>International Biodeterioration and Biodegradation</i> , 2018, 135, 80-89.	1.9	31
6877	Protists Within Corals: The Hidden Diversity. <i>Frontiers in Microbiology</i> , 2018, 9, 2043.	1.5	39
6878	Diversity and characteristics of colonization of root-associated fungi of <i>Vaccinium uliginosum</i> . <i>Scientific Reports</i> , 2018, 8, 15283.	1.6	27
6879	Anaerobic lignocellulolytic microbial consortium derived from termite gut: enrichment, lignocellulose degradation and community dynamics. <i>Biotechnology for Biofuels</i> , 2018, 11, 284.	6.2	32
6880	Reindeer grazing alter soil fungal community structure and litter decomposition related enzyme activities in boreal coniferous forests in Finnish Lapland. <i>Applied Soil Ecology</i> , 2018, 132, 74-82.	2.1	20
6881	Bacterial community structure in the Bohai Strait provides insights into organic matter niche partitioning. <i>Continental Shelf Research</i> , 2018, 169, 46-54.	0.9	13
6882	The biological role of N-acyl-homoserine lactone-based quorum sensing (QS) in EPS production and microbial community assembly during anaerobic granulation process. <i>Scientific Reports</i> , 2018, 8, 15793.	1.6	45
6884	Species-level bacterial community profiling of the healthy sinonasal microbiome using Pacific Biosciences sequencing of full-length 16S rRNA genes. <i>Microbiome</i> , 2018, 6, 190.	4.9	117
6885	De novo transcriptome based on next-generation sequencing reveals candidate genes with sex-specific expression in <i>Arapaima gigas</i> (Schinz, 1822), an ancient Amazonian freshwater fish. <i>PLoS ONE</i> , 2018, 13, e0206379.	1.1	13
6886	Bacterial Microbiota Response in <i>Graptemys pseudogeographica</i> to Captivity and Roundup [®] Exposure. <i>Copeia</i> , 2018, 106, 580-588.	1.4	7
6887	Community composition and functions of endophytic bacteria of Bt maize. <i>South African Journal of Science</i> , 2018, 114, .	0.3	12
6888	Nutrients removal performance of a denitrifying phosphorus removal process in alternate anaerobic/anoxic-aerobic double membrane bioreactors (A2N-DMBR). <i>Water Science and Technology</i> , 2018, 78, 1741-1752.	1.2	11

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6890	Over 2.5 million COI sequences in GenBank and growing. <i>PLoS ONE</i> , 2018, 13, e0200177.	1.1	125
6891	Genetic structure of the grey side-gilled sea slug (<i>Pleurobranchaea maculata</i>) in coastal waters of New Zealand. <i>PLoS ONE</i> , 2018, 13, e0202197.	1.1	7
6892	Differentiated Mechanisms of Biochar Mitigating Straw-Induced Greenhouse Gas Emissions in Two Contrasting Paddy Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 2566.	1.5	46
6893	Phylogenetic trait conservatism predicts patterns of plant-soil feedback. <i>Ecosphere</i> , 2018, 9, e02409.	1.0	7
6894	Arbuscular Mycorrhizal Fungal Communities in Organic and Conventional Onion Crops in the Columbia Basin of the Pacific Northwest United States. <i>Phytobiomes Journal</i> , 2018, 2, 194-207.	1.4	5
6895	Abundance and diversity of iron reducing bacteria communities in the sediments of a heavily polluted freshwater lake. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10791-10801.	1.7	29
6896	MetaHCR: a web-enabled metagenome data management system for hydrocarbon resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-10.	1.4	1
6897	TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution. <i>MSphere</i> , 2018, 3, .	1.3	60
6898	The microbiome of Crohn's disease aphthous ulcers. <i>Gut Pathogens</i> , 2018, 10, 44.	1.6	8
6899	Effects of red clover isoflavones on tall fescue seed fermentation and microbial populations in vitro. <i>PLoS ONE</i> , 2018, 13, e0201866.	1.1	11
6900	Experimental Evidence of Functional Group-Dependent Effects of Tree Diversity on Soil Fungi in Subtropical Forests. <i>Frontiers in Microbiology</i> , 2018, 9, 2312.	1.5	28
6901	Short-term effect of Eucalyptus plantations on soil microbial communities and soil-atmosphere methane and nitrous oxide exchange. <i>Scientific Reports</i> , 2018, 8, 15133.	1.6	25
6902	Porcine circovirus 2 (PCV-2) genetic variability under natural infection scenario reveals a complex network of viral quasispecies. <i>Scientific Reports</i> , 2018, 8, 15469.	1.6	22
6903	A comparative analysis of gut microbiota disturbances in the Gottingen minipig and rhesus macaque models of acute radiation syndrome following bioequivalent radiation exposures. <i>Radiation and Environmental Biophysics</i> , 2018, 57, 419-426.	0.6	12
6904	Functional modulation of caecal fermentation and microbiota in rat by feeding bean husk as a dietary fibre supplement. <i>Beneficial Microbes</i> , 2018, 9, 963-974.	1.0	16
6905	Insight into Bacterial Community Diversity and Monthly Fluctuations of <i>Medicago sativa</i> Rhizosphere Soil in Response to Hydrogen Gas Using Illumina High-Throughput Sequencing. <i>Current Microbiology</i> , 2018, 75, 1626-1633.	1.0	7
6906	Physiological and genomic properties of <i>Thermus tenuipunicus</i> sp. nov., a novel slight reddish color member isolated from a terrestrial geothermal spring. <i>Systematic and Applied Microbiology</i> , 2018, 41, 611-618.	1.2	12

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6908	Microbial Communities of the Gut and Nest of the Humus- and Litter-Feeding Termite <i>Procornitermes araujoi</i> (Syntermitinae). <i>Current Microbiology</i> , 2018, 75, 1609-1618.	1.0	13
6909	Influence of Physicochemical Factors on Bacterial Communities Along the Lower Mekong River Assessed by Illumina Next-Generation Sequencing. <i>Water, Air, and Soil Pollution</i> , 2018, 229, 1.	1.1	7
6910	Smoking is associated with quantifiable differences in the human lung DNA virome and metabolome. <i>Respiratory Research</i> , 2018, 19, 174.	1.4	28
6911	Bacterial community composition in the salivary glands of triatomines (Hemiptera: Reduviidae). <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006739.	1.3	20
6912	Naturally Fermented Milk From Northern Senegal: Bacterial Community Composition and Probiotic Enrichment With <i>Lactobacillus rhamnosus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2218.	1.5	50
6913	Microbial community analysis of sulfate-reducing passive bioreactor for treating acid mine drainage under failure conditions after long-term continuous operation. <i>Journal of Environmental Chemical Engineering</i> , 2018, 6, 5795-5800.	3.3	15
6914	Bipolar dispersal of red-snow algae. <i>Nature Communications</i> , 2018, 9, 3094.	5.8	75
6915	Intestinal probiotics restore the ecological fitness decline of <i>Bactrocera dorsalis</i> by irradiation. <i>Evolutionary Applications</i> , 2018, 11, 1946-1963.	1.5	64
6916	The variation profile of intestinal microbiota in blunt snout bream (<i>Megalobrama amblycephala</i>) during feeding habit transition. <i>BMC Microbiology</i> , 2018, 18, 99.	1.3	24
6917	HmmUFOtu: An HMM and phylogenetic placement based ultra-fast taxonomic assignment and OTU picking tool for microbiome amplicon sequencing studies. <i>Genome Biology</i> , 2018, 19, 82.	3.8	32
6918	A Single Vibrionales 16S rRNA Oligotype Dominates the Intestinal Microbiome in Two Geographically Separated Atlantic cod Populations. <i>Frontiers in Microbiology</i> , 2018, 9, 1561.	1.5	18
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6932	Bacterial communities under long-term conventional and transgenic cotton farming systems using V3-V5 and V5-V9 of 16s rDNA. <i>Ecotoxicology and Environmental Safety</i> , 2018, 164, 618-628.	2.9	5
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7058	Alterations to the Intestinal Microbiome and Metabolome of <i>Pimephales promelas</i> and <i>Mus musculus</i> Following Exposure to Dietary Methylmercury. <i>Environmental Science & Technology</i> , 2018, 52, 8774-8784.	4.6	77
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7215	The Effect of Hydrostatic Pressure on Enrichments of Hydrocarbon Degrading Microbes From the Gulf of Mexico Following the Deepwater Horizon Oil Spill. <i>Frontiers in Microbiology</i> , 2018, 9, 808.	1.5	40
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7218	Trichoderma Biofertilizer Links to Altered Soil Chemistry, Altered Microbial Communities, and Improved Grassland Biomass. <i>Frontiers in Microbiology</i> , 2018, 9, 848.	1.5	89
7219	Low-Light Anoxygenic Photosynthesis and Fe-S-Biogeochemistry in a Microbial Mat. <i>Frontiers in Microbiology</i> , 2018, 9, 858.	1.5	19
7220	Killing Effects of an Isolated <i>Serratia marcescens</i> KH-001 on <i>Diaphorina citri</i> via Lowering the Endosymbiont Numbers. <i>Frontiers in Microbiology</i> , 2018, 9, 860.	1.5	7
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7222	Pig Farmers' Homes Harbor More Diverse Airborne Bacterial Communities Than Pig Stables or Suburban Homes. <i>Frontiers in Microbiology</i> , 2018, 9, 870.	1.5	33
7223	Impact of Microbial Composition of Cambodian Traditional Dried Starters (Dombea) on Flavor Compounds of Rice Wine: Combining Amplicon Sequencing With HP-SPME-GCMS. <i>Frontiers in Microbiology</i> , 2018, 9, 894.	1.5	37
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7225	Effect of Limit-Fed Diets With Different Forage to Concentrate Ratios on Fecal Bacterial and Archaeal Community Composition in Holstein Heifers. <i>Frontiers in Microbiology</i> , 2018, 9, 976.	1.5	37
7226	Metagenomic Approaches to Investigate the Contribution of the Vineyard Environment to the Quality of Wine Fermentation: Potentials and Difficulties. <i>Frontiers in Microbiology</i> , 2018, 9, 991.	1.5	90
7227	Microscale Biosignatures and Abiotic Mineral Authigenesis in Little Hot Creek, California. <i>Frontiers in Microbiology</i> , 2018, 9, 997.	1.5	35
7228	Water Masses and Depth Structure Prokaryotic and T4-Like Viral Communities Around Hydrothermal Systems of the Nordic Seas. <i>Frontiers in Microbiology</i> , 2018, 9, 1002.	1.5	6
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7230	CowPI: A Rumen Microbiome Focussed Version of the PICRUSt Functional Inference Software. <i>Frontiers in Microbiology</i> , 2018, 9, 1095.	1.5	132
7231	In Vitro Modeling of Bile Acid Processing by the Human Fecal Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 1153.	1.5	36

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7233	Canola Root-Associated Microbiomes in the Canadian Prairies. <i>Frontiers in Microbiology</i> , 2018, 9, 1188.	1.5	85
7234	Microbial Community Structure and Associations During a Marine Dinoflagellate Bloom. <i>Frontiers in Microbiology</i> , 2018, 9, 1201.	1.5	103
7235	Comparative Analysis of Gut Microbiota Changes in Père David's Deer Populations in Beijing Milu Park and Shishou, Hubei Province in China. <i>Frontiers in Microbiology</i> , 2018, 9, 1258.	1.5	22
7236	Effectiveness of Interventions to Modulate the Rumen Microbiota Composition and Function in Pre-ruminant and Ruminant Lambs. <i>Frontiers in Microbiology</i> , 2018, 9, 1273.	1.5	52
7237	Microbial Community Structure-Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. <i>Frontiers in Microbiology</i> , 2018, 9, 1282.	1.5	48
7238	Metformin Alters Gut Microbiota of Healthy Mice: Implication for Its Potential Role in Gut Microbiota Homeostasis. <i>Frontiers in Microbiology</i> , 2018, 9, 1336.	1.5	57
7239	Cultivation of Drought-Tolerant and Insect-Resistant Rice Affects Soil Bacterial, but Not Fungal, Abundances and Community Structures. <i>Frontiers in Microbiology</i> , 2018, 9, 1390.	1.5	25
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7242	The influence of bioregenerative life-support system dietary structure and lifestyle on the gut microbiota: a 105-day ground-based space simulation in Lunar Palace 1. <i>Environmental Microbiology</i> , 2018, 20, 3643-3656.	1.8	35
7243	Effects of the Artificial Sweetener Neotame on the Gut Microbiome and Fecal Metabolites in Mice. <i>Molecules</i> , 2018, 23, 367.	1.7	75
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7245	Diversification of Secondary Metabolite Biosynthetic Gene Clusters Coincides with Lineage Divergence in <i>Streptomyces</i> . <i>Antibiotics</i> , 2018, 7, 12.	1.5	46
7246	High-Throughput Sequencing Analysis of the Actinobacterial Spatial Diversity in Moonmilk Deposits. <i>Antibiotics</i> , 2018, 7, 27.	1.5	22
7247	Massive Sequencing: A New Tool for the Control of Alcoholic Fermentation in Wine?. <i>Fermentation</i> , 2018, 4, 7.	1.4	10
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7254	Impacts of long-term nitrogen addition, watering and mowing on ammonia oxidizers, denitrifiers and plant communities in a temperate steppe. <i>Applied Soil Ecology</i> , 2018, 130, 241-250.	2.1	22
7255	Soil aggregate size mediates the responses of microbial communities to crop rotation. <i>European Journal of Soil Biology</i> , 2018, 88, 48-56.	1.4	25
7256	Impacts of experimentally accelerated forest succession on belowground plant and fungal communities. <i>Soil Biology and Biochemistry</i> , 2018, 125, 44-53.	4.2	4
7257	Refinery and concentration of nutrients from urine with electrodialysis enabled by upstream precipitation and nitrification. <i>Water Research</i> , 2018, 144, 76-86.	5.3	51
7258	Responses of Active Ammonia Oxidizers to Eutrophication and Oxygen Statuses in Taihu Freshwater Sediments. <i>Geomicrobiology Journal</i> , 2018, 35, 829-839.	1.0	4
7259	Fast start-up of the cold-anammox process with different inoculums at low temperature (13°C) in innovative reactor. <i>Bioresource Technology</i> , 2018, 267, 696-703.	4.8	50
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7262	Manipulation of microbial community in the rhizosphere alleviates the replanting issues in <i>Panax ginseng</i> . <i>Soil Biology and Biochemistry</i> , 2018, 125, 64-74.	4.2	64
7263	The maternal vaginal microbiome partially mediates the effects of prenatal stress on offspring gut and hypothalamus. <i>Nature Neuroscience</i> , 2018, 21, 1061-1071.	7.1	141
7264	Sjögren-Like Lacrimal Keratoconjunctivitis in Germ-Free Mice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 565.	1.8	57
7265	Pasture Feeding Changes the Bovine Rumen and Milk Metabolome. <i>Metabolites</i> , 2018, 8, 27.	1.3	70
7266	Bacterial Microbiota of Rice Roots: 16S-Based Taxonomic Profiling of Endophytic and Rhizospheric Diversity, Endophytes Isolation and Simplified Endophytic Community. <i>Microorganisms</i> , 2018, 6, 14.	1.6	75
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7269	Greater health risk in wet season than in dry season in the Yellow River of the Lanzhou region. <i>Science of the Total Environment</i> , 2018, 644, 873-883.	3.9	31
7270	Producing desulfurized biogas using two-stage domesticated shear-loop anaerobic contact stabilization system. <i>Waste Management</i> , 2018, 78, 770-780.	3.7	1
7271	Effects of dietary energy levels on rumen bacterial community composition in Holstein heifers under the same forage to concentrate ratio condition. <i>BMC Microbiology</i> , 2018, 18, 69.	1.3	103
7272	Responses and successions of sulfonamides, tetracyclines and fluoroquinolones resistance genes and bacterial community during the short-term storage of biogas residue and organic manure under the incubator and natural conditions. <i>Environmental Pollution</i> , 2018, 242, 749-759.	3.7	21
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7274	The effect of the timing of exposure to <i>Campylobacter jejuni</i> on the gut microbiome and inflammatory responses of broiler chickens. <i>Microbiome</i> , 2018, 6, 88.	4.9	104
7275	Selection of validated hypervariable regions is crucial in 16S-based microbiota studies of the female genital tract. <i>Scientific Reports</i> , 2018, 8, 9678.	1.6	108
7276	Exploring temporal patterns of bacterial and fungal DNA accumulation on a ventilation system filter for a Singapore university library. <i>PLoS ONE</i> , 2018, 13, e0200820.	1.1	9
7277	The cecal microbiome of commercial broiler chickens varies significantly by season. <i>Poultry Science</i> , 2018, 97, 3635-3644.	1.5	26
7278	Bacterial community composition responds to changes in copepod abundance and alters ecosystem function in an Arctic mesocosm study. <i>ISME Journal</i> , 2018, 12, 2694-2705.	4.4	22
7279	Characterization of Microbial Communities Hosted in Quartzofeldspathic and Serpentinite Lithologies in Jeffrey Mine, Canada. <i>Astrobiology</i> , 2018, 18, 1008-1022.	1.5	2
7280	Analysis of temporal fecal microbiota dynamics in weaner pigs with and without exposure to enterotoxigenic <i>Escherichia coli</i> 1,2. <i>Journal of Animal Science</i> , 2018, 96, 3777-3790.	0.2	35
7281	Robust Microbial Markers for Non-Invasive Inflammatory Bowel Disease Identification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 16, 1-1.	1.9	7
7282	Soil microbial community and activity are affected by integrated agricultural practices in China. <i>European Journal of Soil Science</i> , 2018, 69, 924-935.	1.8	27
7283	A microbial community snapshot of windrows from a commercial composting facility. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8069-8077.	1.7	14
7284	Bio-cord plays a similar role as submerged macrophytes in harboring bacterial assemblages in an eco-ditch. <i>Environmental Science and Pollution Research</i> , 2018, 25, 26550-26561.	2.7	10
7285	<i>Arabidopsis thaliana</i> and <i>Pseudomonas</i> Pathogens Exhibit Stable Associations over Evolutionary Timescales. <i>Cell Host and Microbe</i> , 2018, 24, 168-179.e4.	5.1	145

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7287	Functional exploration of natural networks and ecological communities. <i>Methods in Ecology and Evolution</i> , 2018, 9, 2028-2033.	2.2	5
7288	The canine gut microbiome is associated with higher risk of gastric dilatation-volvulus and high risk genetic variants of the immune system. <i>PLoS ONE</i> , 2018, 13, e0197686.	1.1	13
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7293	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	1.8	39
7294	Bacterial communities of decaying Norway spruce follow distinct slope exposure and time-dependent trajectories. <i>Environmental Microbiology</i> , 2018, 20, 3657-3670.	1.8	30
7295	Reduced microbiome alpha diversity in young patients with ADHD. <i>PLoS ONE</i> , 2018, 13, e0200728.	1.1	178
7296	Reduction of Gibbs free energy and enhancement of Methanosaeta by bicarbonate to promote anaerobic syntrophic butyrate oxidation. <i>Bioresource Technology</i> , 2018, 267, 209-217.	4.8	33
7297	The composition of the perinatal intestinal microbiota in cattle. <i>Scientific Reports</i> , 2018, 8, 10437.	1.6	138
7298	Fungal communities and functions response to long-term fertilization in paddy soils. <i>Applied Soil Ecology</i> , 2018, 130, 251-258.	2.1	59
7299	Electron donor-driven bacterial and archaeal community patterns along forest ring edges in Ontario, Canada. <i>Environmental Microbiology Reports</i> , 2018, 10, 663-672.	1.0	4
7300	A year of monitoring 20 mesophilic full-scale bioreactors reveals the existence of stable but different core microbiomes in bio-waste and wastewater anaerobic digestion systems. <i>Biotechnology for Biofuels</i> , 2018, 11, 196.	6.2	138
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7303	Experimentally induced metamorphosis in highly regenerative axolotl (<i>Ambystoma mexicanum</i>) under constant diet restructures microbiota. <i>Scientific Reports</i> , 2018, 8, 10974.	1.6	31

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7306	Removal of antibiotic resistance genes in an anaerobic membrane bioreactor treating primary clarifier effluent at 20 °C. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 1783-1793.	1.2	35
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7310	Black water collected from the septic tank treated with a living machine system: HRT effect and microbial community structure. <i>Chemosphere</i> , 2018, 210, 745-752.	4.2	23
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7313	Gastrointestinal microbial community changes in Atlantic cod (<i>Gadus morhua</i>) exposed to crude oil. <i>BMC Microbiology</i> , 2018, 18, 25.	1.3	36
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7315	Chronic fertilization of 37 years alters the phylogenetic structure of soil arbuscular mycorrhizal fungi in Chinese Mollisols. <i>AMB Express</i> , 2018, 8, 57.	1.4	20
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7318	Rapid isolation of fast-growing methanotrophs from environmental samples using continuous cultivation with gradually increased dilution rates. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5707-5715.	1.7	20
7319	Physicochemical differences between malanga (<i>Xanthosoma sagittifolium</i>) and potato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overl... Functional Foods, 2018, 45, 268-276.	1.6	11
7320	Diversity and distribution of Archaea in global estuarine ecosystems. <i>Science of the Total Environment</i> , 2018, 637-638, 349-358.	3.9	62
7321	Microbial Nitrogen Cycle Hotspots in the Plant-Bed/Ditch System of a Constructed Wetland with N ₂ O Mitigation. <i>Environmental Science & Technology</i> , 2018, 52, 6226-6236.	4.6	61

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7323	An obesity-associated gut microbiome reprograms the intestinal epigenome and leads to altered colonic gene expression. <i>Genome Biology</i> , 2018, 19, 7.	3.8	117
7324	Enhancing methane production from lignocellulosic biomass by combined steam-explosion pretreatment and bioaugmentation with cellulolytic bacterium <i>Caldicellulosiruptor bescii</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 19.	6.2	78
7325	Transcriptome analysis of pig intestinal cell monolayers infected with <i>Cryptosporidium parvum</i> asexual stages. <i>Parasites and Vectors</i> , 2018, 11, 176.	1.0	49
7326	Age and fecal microbial strain-specific differences in patients with spondyloarthritis. <i>Arthritis Research and Therapy</i> , 2018, 20, 14.	1.6	58
7327	The influence of oxygen and methane on nitrogen fixation in subarctic <i>Sphagnum</i> mosses. <i>AMB Express</i> , 2018, 8, 76.	1.4	16
7328	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. <i>Microbiome</i> , 2018, 6, 16.	4.9	208
7329	Development of the tonsillar microbiome in pigs from newborn through weaning. <i>BMC Microbiology</i> , 2018, 18, 35.	1.3	25
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7332	Different effects of nano-scale and micro-scale zero-valent iron particles on planktonic microorganisms from natural reservoir water. <i>Environmental Science: Nano</i> , 2018, 5, 1117-1129.	2.2	27
7333	The antibiotic resistome of free-living and particle-attached bacteria under a reservoir cyanobacterial bloom. <i>Environment International</i> , 2018, 117, 107-115.	4.8	95
7334	Gut microbiota promotes production of aromatic metabolites through degradation of barley leaf fiber. <i>Journal of Nutritional Biochemistry</i> , 2018, 58, 49-58.	1.9	21
7335	Characterization of odor emissions and microbial community structure during degradation of pig carcasses using the soil burial-composting method. <i>Waste Management</i> , 2018, 77, 30-42.	3.7	14
7336	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.	2.9	45
7337	Chloromethane formation and degradation in the fern phyllosphere. <i>Science of the Total Environment</i> , 2018, 634, 1278-1287.	3.9	13
7338	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
7339	Combined effects of phosphate-solubilizing bacterium XMT-5 (<i>Rhizobium</i> sp.) and submerged macrophyte <i>Ceratophyllum demersum</i> on phosphorus release in eutrophic lake sediments. <i>Environmental Science and Pollution Research</i> , 2018, 25, 18990-19000.	2.7	6

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7341	Progressive biogeochemical transformation of placer gold particles drives compositional changes in associated biofilm communities. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
7342	Contrasting prevalence of selection and drift in the community structuring of bacteria and microbial eukaryotes. <i>Environmental Microbiology</i> , 2018, 20, 2231-2240.	1.8	153
7343	Crown-of-Thorns Sea Star <i>Acanthaster cf. solaris</i> Has Tissue-Characteristic Microbiomes with Potential Roles in Health and Reproduction. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	29
7344	Response of the denitrifier community and its relationship with multiple N ₂ O emission peaks after mature compost addition into dairy manure compost with forced aeration. <i>Chemosphere</i> , 2018, 206, 310-319.	4.2	35
7345	Gut microbiota profiling in Han Chinese with type 1 diabetes. <i>Diabetes Research and Clinical Practice</i> , 2018, 141, 256-263.	1.1	68
7346	Actinobacteria associated with Chinaberry tree are diverse and show antimicrobial activity. <i>Scientific Reports</i> , 2018, 8, 11103.	1.6	12
7347	Microbiomes of gall-inducing copepod crustaceans from the corals <i>Stylophora pistillata</i> (Scleractinia) and <i>Gorgonia ventalina</i> (Alcyonacea). <i>Scientific Reports</i> , 2018, 8, 11563.	1.6	13
7348	Diversity and composition of bacterial endophytes among plant parts of <i>Panax notoginseng</i> . <i>Chinese Medicine</i> , 2018, 13, 41.	1.6	53
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7350	Interaction between ferruginous clay sediment and an iron-reducing hyperthermophilic <i>Pyrobaculum</i> sp. in a terrestrial hot spring. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	2
7351	Genome Analyses of the Microalga <i>Picochlorum</i> Provide Insights into the Evolution of Thermotolerance in the Green Lineage. <i>Genome Biology and Evolution</i> , 2018, 10, 2347-2365.	1.1	36
7352	<i>Klebsiella oxytoca</i> expands in cancer cachexia and acts as a gut pathobiont contributing to intestinal dysfunction. <i>Scientific Reports</i> , 2018, 8, 12321.	1.6	71
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7503	Distributions and environmental drivers of archaea and bacteria in paddy soils. <i>Journal of Soils and Sediments</i> , 2019, 19, 23-37.	1.5	39
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7505	Compositional and structural dynamics of the ruminal microbiota in dairy heifers and its relationship to methane production. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 210-218.	1.7	18
7506	Rapid Microbial Community Changes During Initial Stages of Pine Litter Decomposition. <i>Microbial Ecology</i> , 2019, 77, 56-75.	1.4	40
7507	Metagenomic Analysis and its Applications. , 2019, , 184-193.		24
7508	The Mite <i>Tyrophagus putrescentiae</i> Hosts Population-Specific Microbiomes That Respond Weakly to Starvation. <i>Microbial Ecology</i> , 2019, 77, 488-501.	1.4	15
7509	Ectomycorrhizal community composition and function in a spruce forest transitioning between nitrogen and phosphorus limitation. <i>Fungal Ecology</i> , 2019, 40, 20-31.	0.7	38
7510	Magnesium lithospermate B improves the gut microbiome and bile acid metabolic profiles in a mouse model of diabetic nephropathy. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 507-513.	2.8	33
7511	Core bacterial community composition of a cryptoendolithic ecosystem in the Grand Staircase-Escalante National Monument, Utah. <i>MicrobiologyOpen</i> , 2019, 8, e00707.	1.2	3
7512	Soil bacterial communities exhibit systematic spatial variation with landform across a commercial potato field. <i>Geoderma</i> , 2019, 335, 112-122.	2.3	13
7513	A diet rich in C 3 plants reveals the sensitivity of an alpine mammal to climate change. <i>Molecular Ecology</i> , 2019, 28, 250-265.	2.0	31
7514	Co-occurrence of Anaerobes in Human Chronic Wounds. <i>Microbial Ecology</i> , 2019, 77, 808-820.	1.4	40
7515	Characteristics of microbial community indicate anthropogenic impact on the sediments along the Yangtze Estuary and its coastal area, China. <i>Science of the Total Environment</i> , 2019, 648, 306-314.	3.9	70
7516	Vermicompost addition influences symbiotic fungi communities associated with leek cultivated in metal-rich soils. <i>Environmental Science and Pollution Research</i> , 2019, 26, 20040-20051.	2.7	2
7517	High contribution of ammonia-oxidizing archaea (AOA) to ammonia oxidation related to a potential active AOA species in various arable land soils. <i>Journal of Soils and Sediments</i> , 2019, 19, 1077-1087.	1.5	23
7518	Responses of soil bacterial communities, enzyme activities, and nutrients to agricultural-to-natural ecosystem conversion in the Loess Plateau, China. <i>Journal of Soils and Sediments</i> , 2019, 19, 1427-1440.	1.5	51
7519	Assessment of fungi proliferation and diversity in cultural heritage: Reactions to UV-C treatment. <i>Science of the Total Environment</i> , 2019, 647, 905-913.	3.9	11

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7521	Glucose electro-fermentation as main driver for efficient H ₂ -producing bacteria selection in mixed cultures. <i>International Journal of Hydrogen Energy</i> , 2019, 44, 2230-2238.	3.8	24
7522	Effect of dietary fiber levels on bacterial composition with age in the cecum of meat rabbits. <i>MicrobiologyOpen</i> , 2019, 8, e00708.	1.2	9
7523	Effects of experimental harvesting of an invasive hybrid cattail on wetland structure and function. <i>Restoration Ecology</i> , 2019, 27, 389-398.	1.4	17
7524	Profiling the Gut Microbiome: Practice and Potential. , 2019, , 200-217.		0
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7527	Analysis of the bacterial community from high alkaline (pH > 13) drainage water at a brown mud disposal site near Āziar nad Hronom (BanskĀj Bystrica region, Slovakia) using 454 pyrosequencing. <i>Folia Microbiologica</i> , 2019, 64, 83-90.	1.1	7
7528	Batch effects correction for microbiome data with Dirichlet-multinomial regression. <i>Bioinformatics</i> , 2019, 35, 807-814.	1.8	23
7529	Do composition and diversity of bacterial communities and abiotic conditions of spring water reflect characteristics of groundwater ecosystems exposed to different agricultural activities?. <i>MicrobiologyOpen</i> , 2019, 8, e00681.	1.2	5
7530	Inoculation of <i>Pseudomonas</i> sp. GHD-4 and mushroom residue carrier increased the soil enzyme activities and microbial community diversity in Pb-contaminated soils. <i>Journal of Soils and Sediments</i> , 2019, 19, 1064-1076.	1.5	24
7531	<i>scn</i> DNA metabarcoding reveals changes in the contents of carnivorous plants along an elevation gradient. <i>Molecular Ecology</i> , 2019, 28, 281-292.	2.0	6
7532	Metagenomic assessment of the microbial community and methanogenic pathways in biosolids from a municipal wastewater treatment plant in MedellĀn, Colombia. <i>Science of the Total Environment</i> , 2019, 648, 572-581.	3.9	26
7533	Functional metagenomics reveals abundant polysaccharide-degrading gene clusters and cellobiose utilization pathways within gut microbiota of a wood-feeding higher termite. <i>ISME Journal</i> , 2019, 13, 104-117.	4.4	93
7534	Combined use of eDNA metabarcoding and video surveillance for the assessment of fish biodiversity. <i>Conservation Biology</i> , 2019, 33, 196-205.	2.4	178
7535	The role of the microbiome in nonhealing diabetic wounds. <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 79-92.	1.8	79
7536	Effects of Long-Term Application of Vinasse on Physicochemical Properties, Heavy Metals Content and Microbial Diversity in Sugarcane Field Soil. <i>Sugar Tech</i> , 2019, 21, 62-70.	0.9	16
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7539	Improved hemodynamic and liver function in portal hypertensive cirrhotic rats after administration of <i>B. pseudocatenulatum</i> CECT 7765. <i>European Journal of Nutrition</i> , 2019, 58, 1647-1658.	1.8	13
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7543	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.	1.4	13
7544	Selection for antimicrobial resistance is reduced when embedded in a natural microbial community. <i>ISME Journal</i> , 2019, 13, 2927-2937.	4.4	102
7545	Gut microbiota alterations associated with reduced bone mineral density in older adults. <i>Rheumatology</i> , 2019, 58, 2295-2304.	0.9	106
7546	High Diversity in Iron Cycling Microbial Communities in Acidic, Iron-Rich Water of the Pyh�asalmi Mine, Finland. <i>Geofluids</i> , 2019, 2019, 1-17.	0.3	27
7547	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.	1.5	50
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7549	Prokaryote Communities at Active Chimney and <i>In Situ</i> Colonization Devices After a Magmatic Degassing Event (37�N MAR, EMSO�Azores Deep�Sea Observatory). <i>Geochemistry, Geophysics, Geosystems</i> , 2019, 20, 3065-3089.	1.0	6
7550	Suppression of <i>Phytophthora</i> blight of pepper by biochar amendment is associated with improved soil bacterial properties. <i>Biology and Fertility of Soils</i> , 2019, 55, 813-824.	2.3	26
7551	Maternal dietary resveratrol alleviates weaning-associated diarrhea and intestinal inflammation in pig offspring by changing intestinal gene expression and microbiota. <i>Food and Function</i> , 2019, 10, 5626-5643.	2.1	62
7552	Genomic and physiological analyses reveal that extremely thermophilic <i>Caldicellulosiruptor changbaiensis</i> deploys uncommon cellulose attachment mechanisms. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1251-1263.	1.4	4
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7554	Temporal variation in indoor transfer of dirt-associated environmental bacteria in agricultural and urban areas. <i>Environment International</i> , 2019, 132, 105069.	4.8	34
7555	Bacterial community rather than metals shaping metal resistance genes in water, sediment and biofilm in lakes from arid northwestern China. <i>Environmental Pollution</i> , 2019, 254, 113041.	3.7	41

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7558	Large-scale identification of pathogen essential genes during coinfection with sympatric and allopatric microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19685-19694.	3.3	30
7559	Development of amplicon sequencing for the analysis of benzimidazole resistance allele frequencies in field populations of gastrointestinal nematodes. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2019, 10, 92-100.	1.4	25
7560	Salt-Tolerant Halophyte Rhizosphere Bacteria Stimulate Growth of Alfalfa in Salty Soil. <i>Frontiers in Microbiology</i> , 2019, 10, 1849.	1.5	103
7561	A protective mechanism of probiotic <i>Lactobacillus</i> against hepatic steatosis via reducing host intestinal fatty acid absorption. <i>Experimental and Molecular Medicine</i> , 2019, 51, 1-14.	3.2	50
7562	Environmental latitudinal gradients and host-specificity shape Symbiodiniaceae distribution in Red Sea <i>Porites</i> corals. <i>Journal of Biogeography</i> , 2019, 46, 2323-2335.	1.4	39
7563	Marine Bacterial Diversity in Coastal Sichang Island, the Upper Gulf of Thailand, in 2011 Wet Season. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	5
7564	High-throughput 16S rRNA gene sequencing reveals that 6-hydroxydopamine affects gut microbial environment. <i>PLoS ONE</i> , 2019, 14, e0217194.	1.1	16
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7566	Microbiota in Human Periodontal Abscess Revealed by 16S rDNA Sequencing. <i>Frontiers in Microbiology</i> , 2019, 10, 1723.	1.5	10
7567	Microbial Exposure Enhances Immunity to Pathogens Recognized by TLR2 but Increases Susceptibility to Cytokine Storm through TLR4 Sensitization. <i>Cell Reports</i> , 2019, 28, 1729-1743.e5.	2.9	74
7568	The microbiology, pH, and oxidation reduction potential of larval masses in decomposing carcasses on Oahu, Hawaii. <i>Journal of Clinical Forensic and Legal Medicine</i> , 2019, 67, 37-48.	0.5	19
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7572	The microbiome of the <i>Melitaea cinxia</i> butterfly shows marked variation but is only little explained by the traits of the butterfly or its host plant. <i>Environmental Microbiology</i> , 2019, 21, 4253-4269.	1.8	21
7573	Complete mitochondrial genome of green shrimp, <i>Chlorotocus crassicornis</i> (Crustacea: Decapoda:) Tj ETQq1 1 0.784314 rgBJ /Overl	0.2	2

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7575	Amplicon-based microbiome study highlights the loss of diversity and the establishment of a set of species in patients with dentin caries. <i>PLoS ONE</i> , 2019, 14, e0219714.	1.1	24
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7578	Biorefinery for heterogeneous organic waste using microbial electrochemical technology. <i>Bioresource Technology</i> , 2019, 292, 121943.	4.8	15
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7581	Bacterial diversity in Korean temple kimchi fermentation. <i>Food Research International</i> , 2019, 126, 108592.	2.9	34
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7685	Contrasting responses of diazotrophic specialists, opportunists, and generalists to steppe types in Inner Mongolia. <i>Catena</i> , 2019, 182, 104168.	2.2	8
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7738	Hydrothermal vent protistan distribution along the Mariana arc suggests vent endemics may be rare and novel. <i>Environmental Microbiology</i> , 2019, 21, 3796-3815.	1.8	23
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7781	Characterization of Distinct CyanoHABs-Related Modules in Microbial Recurrent Association Network. <i>Frontiers in Microbiology</i> , 2019, 10, 1637.	1.5	33
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7797	Deciphering Underlying Drivers of Disease Suppressiveness Against Pathogenic <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2535.	1.5	38
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7808	Evaluation of Human Milk Microbiota by 16S rRNA Gene Next-Generation Sequencing (NGS) and Cultivation/MALDI-TOF Mass Spectrometry Identification. <i>Frontiers in Microbiology</i> , 2019, 10, 2612.	1.5	25
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7814	Latitudinal gradient of cyanobacterial diversity in tidal flats. <i>PLoS ONE</i> , 2019, 14, e0224444.	1.1	4
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7831	Korean Traditional Medicine (Jakyakgamcho-tang) Ameliorates Colitis by Regulating Gut Microbiota. <i>Metabolites</i> , 2019, 9, 226.	1.3	11
7832	Influence of Human Activities on Broad-Scale Estuarine-Marine Habitats Using Omics-Based Approaches Applied to Marine Sediments. <i>Microorganisms</i> , 2019, 7, 419.	1.6	11
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7891	Dynamics and environmental importance of anaerobic ammonium oxidation (anammox) bacteria in urban river networks. <i>Environmental Pollution</i> , 2019, 254, 112998.	3.7	22
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7907	Groundwater microbial communities and their connection to hydrochemical environment in Golmud, Northwest China. <i>Science of the Total Environment</i> , 2019, 695, 133848.	3.9	47
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7918	Statistical Analysis of Metagenomics Data. <i>Genomics and Informatics</i> , 2019, 17, e6.	0.4	166
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7923	Taste perception and oral microbiota are associated with obesity in children and adolescents. <i>PLoS ONE</i> , 2019, 14, e0221656.	1.1	46
7924	The respiratory microbiota: associations with influenza symptomatology and viral shedding. <i>Annals of Epidemiology</i> , 2019, 37, 51-56.e6.	0.9	16
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7933	In-silico Design of DNA Oligonucleotides: Challenges and Approaches. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1056-1065.	1.9	15
7934	Bacterial Profiling and Dynamic Succession Analysis of <i>Phlebotopus portentosus</i> Casing Soil Using MiSeq Sequencing. <i>Frontiers in Microbiology</i> , 2019, 10, 1927.	1.5	28
7935	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. <i>Microbiome</i> , 2019, 7, 131.	4.9	65
7936	Rapid and Cost-Efficient Enterovirus Genotyping from Clinical Samples Using Flongle Flow Cells. <i>Genes</i> , 2019, 10, 659.	1.0	37
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7942	Increased abundance of proteobacteria in aggressive Crohn's disease seven years after diagnosis. <i>Scientific Reports</i> , 2019, 9, 13473.	1.6	83
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7947	A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. <i>Cell Host and Microbe</i> , 2019, 26, 542-550.e5.	5.1	94
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8034	Effects of temperature on bacterial microbiome composition in <i>Ixodes scapularis</i> ticks. <i>MicrobiologyOpen</i> , 2019, 8, e00719.	1.2	58
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8053	Mycobacterial species and their contribution to cholesterol degradation in wastewater treatment plants. <i>Scientific Reports</i> , 2019, 9, 836.	1.6	24
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8062	Effects of urea plus nitrate pretreated rice straw and corn oil supplementation on fiber digestibility, nitrogen balance, rumen fermentation, microbiota and methane emissions in goats. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 6.	2.1	18
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8073	Metagenomics a modern approach to reveal the secrets of unculturable microbes. , 2019, , 177-195.		1
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8075	Evidence for fungi and gold redox interaction under Earth surface conditions. <i>Nature Communications</i> , 2019, 10, 2290.	5.8	25
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8082	Intestinal parasitic infection alters bacterial gut microbiota in children. <i>PeerJ</i> , 2019, 7, e6200.	0.9	49
8083	Vertical distribution of microbial communities in chromium-contaminated soil and isolation of Cr(VI)-Reducing strains. <i>Ecotoxicology and Environmental Safety</i> , 2019, 180, 242-251.	2.9	63

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8086	The response of methanotrophs to additions of either ammonium, nitrate or urea in alpine swamp meadow soil as revealed by stable isotope probing. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	26
8087	Gut microbiome identifies risk for colorectal polyps. <i>BMJ Open Gastroenterology</i> , 2019, 6, e000297.	1.1	33
8088	Microbiome-Metabolomics Analysis Investigating the Impacts of Dietary Starch Types on the Composition and Metabolism of Colonic Microbiota in Finishing Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 1143.	1.5	37
8089	Arsenite Oxidation by a Newly Isolated Betaproteobacterium Possessing <i>ars</i> Genes and Diversity of the <i>ars</i> Gene Cluster in Bacterial Genomes. <i>Frontiers in Microbiology</i> , 2019, 10, 1210.	1.5	11
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8091	Integrated Analysis of Clinical and Microbiome Risk Factors Associated with the Development of Oral Candidiasis during Cancer Chemotherapy. <i>Journal of Fungi (Basel, Switzerland)</i> , 2019, 5, 49.	1.5	25
8092	Comparison of community composition between <i>Microcystis</i> colony-attached and free-living bacteria, and among bacteria attached with <i>Microcystis</i> colonies of various sizes in culture. <i>Aquatic Ecology</i> , 2019, 53, 465-481.	0.7	11
8093	Farm-like indoor microbiota in non-farm homes protects children from asthma development. <i>Nature Medicine</i> , 2019, 25, 1089-1095.	15.2	219
8094	Analysis of functional gene transcripts suggests active CO ₂ assimilation and CO oxidation by diverse bacteria in marine sponges. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	7
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8096	Identification of respiratory microbiota markers in ventilator-associated pneumonia. <i>Intensive Care Medicine</i> , 2019, 45, 1082-1092.	3.9	49
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8106	Effects of dietary supplementation with lysozyme on the structure and function of the cecal microbiota in broiler chickens. <i>PLoS ONE</i> , 2019, 14, e0216748.	1.1	20
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8111	Endocrine disruption and commensal bacteria alteration associated with gaseous and soil PAH contamination among daycare children. <i>Environment International</i> , 2019, 130, 104894.	4.8	32
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8113	Microbial indicators of environmental perturbations in coral reef ecosystems. <i>Microbiome</i> , 2019, 7, 94.	4.9	126
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8122	Patterns and assembly processes of planktonic and sedimentary bacterial community differ along a trophic gradient in freshwater lakes. <i>Ecological Indicators</i> , 2019, 106, 105491.	2.6	78
8123	How the bacterial community of a tannery effluent responds to bioaugmentation with the consortium SFC 500-1. Impact of environmental variables. <i>Journal of Environmental Management</i> , 2019, 247, 46-56.	3.8	5
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8127	The Pedological Context Modulates the Response of Soil Microbial Communities to Agroecological Management. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	13
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8133	Anthropogenic nitrogen enrichment enhances soil carbon accumulation by impacting saprotrophs rather than ectomycorrhizal fungal activity. <i>Global Change Biology</i> , 2019, 25, 2900-2914.	4.2	68
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8137	Highly diverse fungal communities in carbon-rich aquifers of two contrasting lakes in Northeast Germany. <i>Fungal Ecology</i> , 2019, 41, 116-125.	0.7	9
8138	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.	2.3	100

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8141	Emission and dispersal of antibiotic resistance genes through bioaerosols generated during the treatment of municipal sewage. <i>Science of the Total Environment</i> , 2019, 686, 402-412.	3.9	70
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8149	Inhibition mitigation and ecological mechanism of mesophilic methanogenesis triggered by supplement of ferrous oxide in sulfate-containing systems. <i>Bioresource Technology</i> , 2019, 288, 121546.	4.8	56
8150	The Fungal and Bacterial Rhizosphere Microbiome Associated With Grapevine Rootstock Genotypes in Mature and Young Vineyards. <i>Frontiers in Microbiology</i> , 2019, 10, 1142.	1.5	123
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8152	Could benthic biofilm analyses be used as a reliable proxy for freshwater environmental health?. <i>Environmental Pollution</i> , 2019, 252, 440-449.	3.7	20
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8155	Association of breast and gut microbiota dysbiosis and the risk of breast cancer: a case-control clinical study. <i>BMC Cancer</i> , 2019, 19, 495.	1.1	75
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8168	Experimental warming alters the community composition, diversity, and N ₂ fixation activity of peat moss (<i>Sphagnum fallax</i>) microbiomes. <i>Global Change Biology</i> , 2019, 25, 2993-3004.	4.2	89
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8171	Key sub-community dynamics of medium-chain carboxylate production. <i>Microbial Cell Factories</i> , 2019, 18, 92.	1.9	56
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8177	<i>Euonymus japonicus</i> phyllosphere microbiome is significantly changed by powdery mildew. <i>Archives of Microbiology</i> , 2019, 201, 1099-1109.	1.0	15
8178	The effect of <i>Codonopsis bulleyana</i> Forest ex Diels on chronically constipated mice. <i>Saudi Journal of Biological Sciences</i> , 2019, 26, 402-412.	1.8	4
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8181	Microbial community evolution and fate of antibiotic resistance genes during sludge treatment in two full-scale anaerobic digestion plants with thermal hydrolysis pretreatment. <i>Bioresource Technology</i> , 2019, 288, 121575.	4.8	44
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8183	Microbiota alter metabolism and mediate neurodevelopmental toxicity of 17 β -estradiol. <i>Scientific Reports</i> , 2019, 9, 7064.	1.6	23
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8191	Understanding microbial community dynamics to improve optimal microbiome selection. <i>Microbiome</i> , 2019, 7, 85.	4.9	233
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8194	A eukaryotic community succession based method for postmortem interval (PMI) estimation of decomposing porcine remains. <i>Forensic Science International</i> , 2019, 302, 109838.	1.3	17
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8196	The effects of chemical and organic fertilizer usage on rhizosphere soil in tea orchards. <i>PLoS ONE</i> , 2019, 14, e0217018.	1.1	188
8197	Microbial communities in a former pilot-scale uranium mine in Eastern Finland – Association with radium immobilization. <i>Science of the Total Environment</i> , 2019, 686, 619-640.	3.9	12
8198	Dynamic and Asymmetric Changes of the Microbial Communities after Cohousing in Laboratory Mice. <i>Cell Reports</i> , 2019, 27, 3401-3412.e3.	2.9	72
8199	Archaeal Communities in Deep Terrestrial Subsurface Underneath the Deccan Traps, India. <i>Frontiers in Microbiology</i> , 2019, 10, 1362.	1.5	15
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8212	Propionate-Producing Consortium Restores Antibiotic-Induced Dysbiosis in a Dynamic in vitro Model of the Human Intestinal Microbial Ecosystem. <i>Frontiers in Microbiology</i> , 2019, 10, 1206.	1.5	84
8213	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.	1.1	24
8214	Diversity and shifts of the bacterial community associated with Baikal sponge mass mortalities. <i>PLoS ONE</i> , 2019, 14, e0213926.	1.1	45
8215	Microbial Consortia versus Single-Strain Inoculants: An Advantage in PGPM-Assisted Tomato Production?. <i>Agronomy</i> , 2019, 9, 105.	1.3	99
8216	Evaluation of microbial communities in peels of Brazilian tropical fruits by amplicon sequence analysis. <i>Brazilian Journal of Microbiology</i> , 2019, 50, 739-748.	0.8	12
8217	Soil alkaline phosphatase activity and bacterial <i>phoD</i> gene abundance and diversity under long-term nitrogen and manure inputs. <i>Geoderma</i> , 2019, 349, 36-44.	2.3	72
8218	Impact of maternal intrapartum antibiotics on the initial oral microbiome of neonates. <i>Pediatrics and Neonatology</i> , 2019, 60, 654-661.	0.3	18
8219	Comparative analysis of intestinal bacteria among venom secretion and non-secretion snakes. <i>Scientific Reports</i> , 2019, 9, 6335.	1.6	10
8220	Bacterial Insights into the Formation of Opaline Stromatolites from the Chimalacatepec Lava Tube System, Mexico. <i>Geomicrobiology Journal</i> , 2019, 36, 694-704.	1.0	3
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8328	Effects of a diet based on inulin-rich vegetables on gut health and nutritional behavior in healthy humans. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 1683-1695.	2.2	121
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8354	Insight into the microbial world of <i>Bemisia tabaci</i> cryptic species complex and its relationships with its host. <i>Scientific Reports</i> , 2019, 9, 6568.	1.6	23
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8365	Bacillus-Dominant Airborne Bacterial Communities Identified During Asian Dust Events. <i>Microbial Ecology</i> , 2019, 78, 677-687.	1.4	13
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8791	Biodiversity and dynamics of cyanobacterial communities during blooms in temperate lake (Harsha) Tj ETQq1 1 0.784314 rgBT /Overl	2.2	15
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8805	Effects of Dicafeoylquinic Acids from <i>Ilex kudingcha</i> on Lipid Metabolism and Intestinal Microbiota in High-Fat-Diet-Fed Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 171-183.	2.4	41
8806	Response of Colonic Mucosa-Associated Microbiota Composition, Mucosal Immune Homeostasis, and Barrier Function to Early Life Galactooligosaccharides Intervention in Suckling Piglets. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 578-588.	2.4	60
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8810	Effects of ridge-furrow mulching on soil CO ₂ efflux in a maize field in the Chinese Loess Plateau. <i>Agricultural and Forest Meteorology</i> , 2019, 264, 200-212.	1.9	36
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8813	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.	1.1	8
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8817	Spatially and temporally variable sulfur cycling in shallow-sea hydrothermal vents, Milos, Greece. <i>Marine Chemistry</i> , 2019, 208, 83-94.	0.9	12
8818	Bioremediation of contaminated urban river sediment with methanol stimulation: Metabolic processes accompanied with microbial community changes. <i>Science of the Total Environment</i> , 2019, 653, 649-657.	3.9	43
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8827	Exploring the Human Microbiome: The Potential Future Role of Next-Generation Sequencing in Disease Diagnosis and Treatment. <i>Frontiers in Immunology</i> , 2018, 9, 2868.	2.2	207
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8838	The use of next generation sequencing for improving food safety: Translation into practice. <i>Food Microbiology</i> , 2019, 79, 96-115.	2.1	225
8839	Trace metals supplementation enhanced microbiota and biohythane production by two-stage thermophilic fermentation. <i>International Journal of Hydrogen Energy</i> , 2019, 44, 3325-3338.	3.8	17
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8845	The evolution of abdominal microbiomes in fungus-growing ants. <i>Molecular Ecology</i> , 2019, 28, 879-899.	2.0	25
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8850	Detection of Human Enteric Viruses in French Polynesian Wastewaters, Environmental Waters and Giant Clams. <i>Food and Environmental Virology</i> , 2019, 11, 52-64.	1.5	12
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8859	Identification of microorganisms producing lactic acid during solid-state fermentation of <i>Maotai</i> flavour liquor. <i>Journal of the Institute of Brewing</i> , 2019, 125, 171-177.	0.8	32
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8864	Population and Culture Age Influence the Microbiome Profiles of House Dust Mites. <i>Microbial Ecology</i> , 2019, 77, 1048-1066.	1.4	28
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8878	The complex interactions between novel DEHP-metabolising bacteria and the microbes in agricultural soils. <i>Science of the Total Environment</i> , 2019, 660, 733-740.	3.9	34
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8880	Response of soil microbial communities to the application of a formulated <i>Metarhizium brunneum</i> biocontrol strain. <i>Biocontrol Science and Technology</i> , 2019, 29, 547-564.	0.5	11
8881	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. <i>American Journal of Epidemiology</i> , 2019, 188, 1023-1026.	1.6	30
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8884	Kinetic and microbial response of activated sludge community to acute and chronic exposure to tetracycline. <i>Journal of Hazardous Materials</i> , 2019, 367, 418-426.	6.5	24

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8888	Genome of the candidate phylum Aminicenantes bacterium from a deep subsurface thermal aquifer revealed its fermentative saccharolytic lifestyle. <i>Extremophiles</i> , 2019, 23, 189-200.	0.9	74
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8891	Characterization of the bacterial community composition in water of drinking water production and distribution systems in Flanders, Belgium. <i>MicrobiologyOpen</i> , 2019, 8, e00726.	1.2	18
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8905	Effects of salinity on microbialite-associated production in Great Salt Lake, Utah. <i>Ecology</i> , 2019, 100, e02611.	1.5	24
8906	Shifts in the Skin-Associated Microbiota of Hatchery-Reared Common Snook <i>Centropomus undecimalis</i> During Acclimation to the Wild. <i>Microbial Ecology</i> , 2019, 77, 770-781.	1.4	43
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8910	Responses of soil aggregates and bacterial communities to soil-Pb immobilization induced by biofertilizer. <i>Chemosphere</i> , 2019, 220, 828-836.	4.2	39
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8919	Metabolomics and bacterial diversity of packaged yellowfin tuna (<i>Thunnus albacares</i>) and salmon (<i>Salmo salar</i>) show fish species-specific spoilage development during chilled storage. <i>International Journal of Food Microbiology</i> , 2019, 293, 44-52.	2.1	80
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8925	Diversity of Bacterial Biota in <i>Capnodis tenebrionis</i> (Coleoptera: Buprestidae) Larvae. <i>Pathogens</i> , 2019, 8, 4.	1.2	9
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8929	Comamonadaceae OTU as a Remnant of an Ancient Microbial Community in Sulfidic Waters. <i>Microbial Ecology</i> , 2019, 78, 85-101.	1.4	21
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8932	Impact of high-grain diet feeding on mucosa-associated bacterial community and gene expression of tight junction proteins in the small intestine of goats. <i>MicrobiologyOpen</i> , 2019, 8, e00745.	1.2	19
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8934	Bioinformatics tools to assess metagenomic data for applied microbiology. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 69-82.	1.7	43
8935	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.	2.5	47
8936	Plant-plant interactions and N fertilization shape soil bacterial and fungal communities. <i>Soil Biology and Biochemistry</i> , 2019, 128, 127-138.	4.2	94
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8940	Decreased enzyme activities, ammonification rate and ammonifiers contribute to higher nitrogen retention in hyperthermophilic pretreatment composting. <i>Bioresource Technology</i> , 2019, 272, 521-528.	4.8	58
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8943	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.	1.4	45
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8947	Soil pH rather than elevation determines bacterial phylogenetic community assembly on Mt. Norikura. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	22
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8951	Balance of saccharolysis and proteolysis underpins improvements in stool quality induced by adding a fiber bundle containing bound polyphenols to either hydrolyzed meat or grain-rich foods. <i>Gut Microbes</i> , 2019, 10, 298-320.	4.3	56
8952	Remitted affective disorders and high familial risk of affective disorders associate with aberrant intestinal microbiota. <i>Acta Psychiatrica Scandinavica</i> , 2019, 139, 174-184.	2.2	35
8953	Geospatial variation in occurrence networks of nitrifying microbial guilds. <i>Molecular Ecology</i> , 2019, 28, 293-306.	2.0	50
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8955	Developmental stage has a greater effect than Cry1Ac expression in transgenic cotton on the phyllosphere mycobiome. <i>Canadian Journal of Microbiology</i> , 2019, 65, 116-125.	0.8	2
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8960	Host Developmental Toxicity of BPA and BPA Alternatives Is Inversely Related to Microbiota Disruption in Zebrafish. <i>Toxicological Sciences</i> , 2019, 167, 468-483.	1.4	62
8961	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.	1.5	56
8962	Gut microbiota dynamics in travelers returning from India colonized with extended-spectrum cephalosporin-resistant Enterobacteriaceae: A longitudinal study. <i>Travel Medicine and Infectious Disease</i> , 2019, 27, 72-80.	1.5	26
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9095	Prokaryotic community in Pleistocene ice wedges of Mammoth Mountain. <i>Extremophiles</i> , 2020, 24, 93-105.	0.9	2
9096	Diatom metabarcoding applied to large scale monitoring networks: Optimization of bioinformatics strategies using Mothur software. <i>Ecological Indicators</i> , 2020, 109, 105775.	2.6	41
9097	Interstitial Pregnancy after Ipsilateral Salpingectomy: Analysis of 46 Cases and a Literature Review. <i>Journal of Minimally Invasive Gynecology</i> , 2020, 27, 613-617.	0.3	13
9098	Illumina sequencing of 16S rRNA tag shows disparity in rhizobial and non-rhizobial diversity associated with root nodules of mung bean (<i>Vigna radiata</i> L.) growing in different habitats in Pakistan. <i>Microbiological Research</i> , 2020, 231, 126356.	2.5	25
9099	Enhanced reductive dechlorination of trichloroethene with immobilized <i>Clostridium butyricum</i> in silica gel. <i>Chemosphere</i> , 2020, 238, 124596.	4.2	18
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9109	Relevance of plant and fungal DNA metabarcoding in aerobiology. <i>Aerobiologia</i> , 2020, 36, 9-23.	0.7	23
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9114	Diversity of endophytic bacterial community inhabiting in tropical aerobic rice under aerobic and flooded condition. <i>Archives of Microbiology</i> , 2020, 202, 17-29.	1.0	6
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9214	Applying microbial indicators of hydrocarbon toxicity to contaminated sites undergoing bioremediation on subantarctic Macquarie Island. <i>Environmental Pollution</i> , 2020, 259, 113780.	3.7	9
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9382	Digestive gland microbiome of <i>Pleurobema cordatum</i> : mesocosms induce dysbiosis. <i>Journal of Molluscan Studies</i> , 2020, 86, 280-289.	0.4	10
9383	<i>Bifidobacterium adolescentis</i> supplementation attenuates fracture-induced systemic sequelae. <i>Biomedicine and Pharmacotherapy</i> , 2020, 132, 110831.	2.5	24
9384	Low-dose Ultraviolet-A irradiation selectively eliminates nitrite oxidizing bacteria for mainstream nitrification. <i>Chemosphere</i> , 2020, 261, 128172.	4.2	13
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9496	Identification of potential markers for internal exposure to ambient ozone in oral cavity of healthy adults. <i>Environmental Research</i> , 2020, 190, 109907.	3.7	6
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9499	Impacts of anthropogenic disturbances on microbial community of coastal waters in Shenzhen, South China. <i>Ecotoxicology</i> , 2021, 30, 1652-1661.	1.1	9
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9502	Evaluating the Microbiome of Hemp. <i>Phytobiomes Journal</i> , 2020, 4, 351-363.	1.4	12
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9505	Identifying the "unidentified"™ fungi: a global-scale long-read third-generation sequencing approach. <i>Fungal Diversity</i> , 2020, 103, 273-293.	4.7	48
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9517	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. <i>Chinese Medical Journal</i> , 2020, 133, 1844-1855.	0.9	55
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9962	Variation in Near-Surface Airborne Bacterial Communities among Five Forest Types. <i>Forests</i> , 2020, 11, 561.	0.9	4
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9965	Bacterial Diversity of a High-Altitude Permafrost Thaw Pond Located on Ojos del Salado (Dry Andes,)	1.5	14
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10003	The Association between Gut Microbiota and Uremia of Chronic Kidney Disease. <i>Microorganisms</i> , 2020, 8, 907.	1.6	32
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10017	The Snowmelt Niche Differentiates Three Microbial Life Strategies That Influence Soil Nitrogen Availability During and After Winter. <i>Frontiers in Microbiology</i> , 2020, 11, 871.	1.5	32
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10023	Bacterial profiles and volatile flavor compounds in commercial Suancai with varying salt concentration from Northeastern China. <i>Food Research International</i> , 2020, 137, 109384.	2.9	47
10024	High-throughput sequencing analysis of endophytic fungal diversity in <i>Cynanchum</i> sp.. <i>South African Journal of Botany</i> , 2020, 134, 349-358.	1.2	11
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10029	A Framework for Effective Application of Machine Learning to Microbiome-Based Classification Problems. <i>MBio</i> , 2020, 11, .	1.8	118
10030	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. <i>MSystems</i> , 2020, 5, .	1.7	135
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10033	Use of bacteriophage vB_Pd_PDCC41 as biological control agent of <i>Photobacterium damsela</i> subsp. <i>damsela</i> during hatching of longfin yellowtail (<i>Seriola rivoliana</i>) eggs. <i>Journal of Applied Microbiology</i> , 2020, 129, 1497-1510.	1.4	12
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10036	Revealing links between gut microbiome and its fungal community in Type 2 Diabetes Mellitus among Emirati subjects: A pilot study. <i>Scientific Reports</i> , 2020, 10, 9624.	1.6	31
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10039	Changes in the Microbiome of Cryptosporidium-Infected Mice Correlate to Differences in Susceptibility and Infection Levels. <i>Microorganisms</i> , 2020, 8, 879.	1.6	30
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10043	Modulation of cecal microbiota in laying hens via intake of genetically modified corn with the <i>maroACC</i> or <i>mCry1Ac</i> genes. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 5450-5457.	1.7	1
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10047	Responses of arbuscular mycorrhizal fungal communities to soil core transplantation across Saskatchewan prairie climatic regions. <i>Canadian Journal of Soil Science</i> , 2020, 100, 81-96.	0.5	4
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10049	Plant Grafting Shapes Complexity and Co-occurrence of Rhizobacterial Assemblages. <i>Microbial Ecology</i> , 2020, 80, 643-655.	1.4	20
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10051	Variety features differentiate microbiota in the grape leaves. <i>Canadian Journal of Microbiology</i> , 2020, 66, 653-663.	0.8	9
10052	Effects of Italian Ryegrass (IRG) Supplementation on Animal Performance, Gut Microbial Compositions and Odor Emission from Manure in Growing Pigs. <i>Agronomy</i> , 2020, 10, 647.	1.3	9
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10058	Analysis of Marine Planktonic Cyanobacterial Assemblages From Mooriganga Estuary, Indian Sundarbans Using Molecular Approaches. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
10059	Disentangling Large- and Small-Scale Abiotic and Biotic Factors Shaping Soil Microbial Communities in an Alpine Cushion Plant System. <i>Frontiers in Microbiology</i> , 2020, 11, 925.	1.5	25
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10061	Functional and Structural Responses of Arctic and Alpine Soil Prokaryotic and Fungal Communities Under Freeze-Thaw Cycles of Different Frequencies. <i>Frontiers in Microbiology</i> , 2020, 11, 982.	1.5	31
10062	Special Features of Bat Microbiota Differ From Those of Terrestrial Mammals. <i>Frontiers in Microbiology</i> , 2020, 11, 1040.	1.5	17
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10065	Drivers of Foliar Fungal Endophytic Communities of Kudzu (<i>Pueraria montana</i> var. <i>lobata</i>) in the Southeast United States. <i>Diversity</i> , 2020, 12, 185.	0.7	8
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10071	Divergent biotic and abiotic filtering of root endosphere and rhizosphere soil fungal communities along ecological gradients. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	11
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10073	Bacterioplankton reveal years-long retention of Atlantic deep-ocean water by the Tropic Seamount. <i>Scientific Reports</i> , 2020, 10, 4715.	1.6	8
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10077	$\hat{\pm}$ -Linolenic Acid-Rich Diet Influences Microbiota Composition and Villus Morphology of the Mouse Small Intestine. <i>Nutrients</i> , 2020, 12, 732.	1.7	21
10078	Resveratrol enhances brown adipose tissue activity and white adipose tissue browning in part by regulating bile acid metabolism via gut microbiota remodeling. <i>International Journal of Obesity</i> , 2020, 44, 1678-1690.	1.6	55
10079	Responses of Intertidal Bacterial Biofilm Communities to Increasing pCO ₂ . <i>Marine Biotechnology</i> , 2020, 22, 727-738.	1.1	11
10080	Bacterial analysis in the early developmental stages of the black tiger shrimp (<i>Penaeus monodon</i>). <i>Scientific Reports</i> , 2020, 10, 4896.	1.6	38
10081	Resource availability drives bacterial succession during leaf-litter decomposition in a bromeliad ecosystem. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9

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10083	The Bacterial Microbiome of Meloidogyne-Based Disease Complex in Coffee and Tomato. <i>Frontiers in Plant Science</i> , 2020, 11, 136.	1.7	34
10084	Differences in Gut Microbial Diversity are Driven by Drug Use and Drug Cessation by Either Compulsory Detention or Methadone Maintenance Treatment. <i>Microorganisms</i> , 2020, 8, 411.	1.6	11
10085	Host Genetic and Environmental Factors Shape the Composition and Function of Gut Microbiota in Populations Living at High Altitude. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	12
10086	Bacterial Communities on the Surface of the Mineral Sandy Soil from the Desert of Maine (USA). <i>Current Microbiology</i> , 2020, 77, 1429-1437.	1.0	12
10087	Contrasting soil fungal communities at different habitats in a revegetated copper mine wasteland. <i>Soil Ecology Letters</i> , 2020, 2, 8-19.	2.4	7
10088	Gut Microbiota Alterations from Three-Strain Yogurt Formulation Treatments in Slow-Transit Constipation. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2020, 2020, 1-9.	0.7	10
10089	Characterization of the microbiome associated with in situ earthen materials. <i>Environmental Microbiomes</i> , 2020, 15, 4.	2.2	2
10090	Two Bariatric Surgical Procedures Differentially Alter the Intestinal Microbiota in Obesity Patients. <i>Obesity Surgery</i> , 2020, 30, 2345-2361.	1.1	19
10091	Small-scale spatial variation of meiofaunal communities in Lima estuary (NW Portugal) assessed through metabarcoding. <i>Estuarine, Coastal and Shelf Science</i> , 2020, 238, 106683.	0.9	20
10092	Growth and health status of Pacific white shrimp, <i>Litopenaeus vannamei</i> , exposed to chronic water born cobalt. <i>Fish and Shellfish Immunology</i> , 2020, 100, 137-145.	1.6	30
10093	Performance of a Geosynthetic-Clay-Liner Cover System at a Cu/Zn Mine Tailings Impoundment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	6
10094	Invasive <i>Spartina anglica</i> Greatly Alters the Rates and Pathways of Organic Carbon Oxidation and Associated Microbial Communities in an Intertidal Wetland of the Han River Estuary, Yellow Sea. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	13
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10096	Effect of selective logging on soil microbial communities in a <i>Pinus yunnanensis</i> forest. <i>Land Degradation and Development</i> , 2020, 31, 2268-2280.	1.8	14
10097	Microbial diversity in soils from antimony mining sites: geochemical control promotes species enrichment. <i>Environmental Chemistry Letters</i> , 2020, 18, 911-922.	8.3	20
10098	Propionic Acid Shapes the Multiple Sclerosis Disease Course by an Immunomodulatory Mechanism. <i>Cell</i> , 2020, 180, 1067-1080.e16.	13.5	367
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10101	Effects of sulfide on mixotrophic denitrification by <i>Thauera</i> -dominated denitrifying sludge. <i>Environmental Science: Water Research and Technology</i> , 2020, 6, 1186-1195.	1.2	23
10102	Compound probiotics alleviating aflatoxin B1 and zearalenone toxic effects on broiler production performance and gut microbiota. <i>Ecotoxicology and Environmental Safety</i> , 2020, 194, 110420.	2.9	50
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10548	A Sample-to-Report Solution for Taxonomic Identification of Cultured Bacteria in the Clinical Setting Based on Nanopore Sequencing. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	15
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10551	Wildfire effects on diversity and composition in soil bacterial communities. <i>Science of the Total Environment</i> , 2020, 726, 138636.	3.9	52
10552	Elucidation of the rhizosphere microbiome linked to <i>Spartina alterniflora</i> phenotype in a salt marsh on Skidaway Island, Georgia, USA. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	21
10553	Revegetation of urban green space rewilds soil microbiotas with implications for human health and urban design. <i>Restoration Ecology</i> , 2020, 28, S322.	1.4	43
10554	Gastric microbes associated with gastric inflammation, atrophy and intestinal metaplasia 1 year after <i>Helicobacter pylori</i> eradication. <i>Gut</i> , 2020, 69, 1572-1581.	6.1	145
10555	Characterization of Gut Microbiota Composition in Hemodialysis Patients With Normal Weight Obesity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 2006-2014.	1.8	8
10556	(My Microbiome) Would Walk 10,000 Miles: Maintenance and Turnover of Microbial Communities in Introduced Dung Beetles. <i>Microbial Ecology</i> , 2020, 80, 435-446.	1.4	27
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10558	Application of ²²² Rn and microbial diversity to characterize groundwater/surface-water interactions in a riverside area (South Korea). <i>Hydrogeology Journal</i> , 2020, 28, 1173-1189.	0.9	7
10559	Phylogeny and distribution of arbuscular mycorrhizal fungi associated with <i>Vachellia tortilis</i> ssp. <i>raddiana</i> in relation to soil properties under arid ecosystems of Tunisia. <i>Mycological Progress</i> , 2020, 19, 495-504.	0.5	5
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10565	Phylogenetic analysis of intestinal microbiota reveals novel <i>Mycoplasma</i> phylotypes in salmonid species. <i>Microbial Pathogenesis</i> , 2020, 145, 104210.	1.3	9
10566	Biogeography and emerging significance of Actinobacteria in Australia and Northern Antarctica soils. <i>Soil Biology and Biochemistry</i> , 2020, 146, 107805.	4.2	54
10567	Environmentally clean access to Antarctic subglacial aquatic environments. <i>Antarctic Science</i> , 2020, 32, 329-340.	0.5	13

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10577	Structural and Functional Changes in Prokaryotic Communities in Artificial Pit Mud during Chinese Baijiu Production. <i>MSystems</i> , 2020, 5, .	1.7	36
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10579	Gut leakage enhances sepsis susceptibility in iron-overloaded Î²-thalassemia mice through macrophage hyperinflammatory responses. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 318, G966-G979.	1.6	44
10580	Profiling of Oral Bacterial Communities. <i>Journal of Dental Research</i> , 2020, 99, 621-629.	2.5	45
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10582	The effect of acupuncture on tumor growth and gut microbiota in mice inoculated with osteosarcoma cells. <i>Chinese Medicine</i> , 2020, 15, 33.	1.6	16
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10585	The penile microbiota of Black South African men: relationship with human papillomavirus and HIV infection. <i>BMC Microbiology</i> , 2020, 20, 78.	1.3	27

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10590	Comparison of Soil Bacterial Communities from Juvenile Maize Plants of a Long-Term Monoculture and a Natural Grassland. <i>Agronomy</i> , 2020, 10, 341.	1.3	6
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10592	Biochar and Rhizobacteria Amendments Improve Several Soil Properties and Bacterial Diversity. <i>Microorganisms</i> , 2020, 8, 502.	1.6	55
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10594	Mobility and potential bioavailability of antimony in contaminated soils: Short-term impact on microbial community and soil biochemical functioning. <i>Ecotoxicology and Environmental Safety</i> , 2020, 196, 110576.	2.9	29
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10597	Variations in soil bacterial communities and putative functions in a sugarcane soil following five years of chemical fertilization. <i>Archives of Agronomy and Soil Science</i> , 2021, 67, 727-738.	1.3	5
10598	Association of subjective global assessment of nutritional status with gut microbiota in hemodialysis patients: a case-control study. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, 1104-1111.	0.4	15
10599	The microbiome of pediatric patients with chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2021, 11, 31-39.	1.5	18
10600	Real-time, MinION-based, amplicon sequencing for lineage typing of infectious bronchitis virus from upper respiratory samples. <i>Journal of Veterinary Diagnostic Investigation</i> , 2021, 33, 179-190.	0.5	7
10601	The RNA-binding protein tristetraprolin regulates RALDH2 expression by intestinal dendritic cells and controls local Treg homeostasis. <i>Mucosal Immunology</i> , 2021, 14, 80-91.	2.7	4
10602	A novel deep learning method for predictive modeling of microbiome data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
10603	Next Generation Sequencing Methods: Pushing the Boundaries. , 2021, , 19-46.		0

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10605	Underpinning unique genes in <i>Ca. Brocadia</i> sp. and its interspecies association potentials in a partial nitrification/anammox system with low-strength wastewater. <i>Chemical Engineering Journal</i> , 2021, 405, 125904.	6.6	13
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10607	Change of soil physicochemical properties, bacterial community and aggregation during desertification of grasslands in the Tibetan Plateau. <i>European Journal of Soil Science</i> , 2021, 72, 274-288.	1.8	14
10608	Patterns of fungal community succession triggered by C/N ratios during composting. <i>Journal of Hazardous Materials</i> , 2021, 401, 123344.	6.5	66
10609	Characterizing Microbial Signatures on Sculptures and Paintings of Similar Provenance. <i>Microbial Ecology</i> , 2021, 81, 1098-1105.	1.4	6
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10613	Evaluation of commercially available DNA extraction kits for the analysis of the broiler chicken cecal microbiota. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	6
10614	A single intravesical instillation of <i>Lactobacillus rhamnosus</i> GG is safe in children and adults with neuropathic bladder: A phase Ia clinical trial. <i>Journal of Spinal Cord Medicine</i> , 2021, 44, 62-69.	0.7	15
10615	Seasonal variation in the gut microbiota of rhesus macaques inhabiting limestone forests of southwest Guangxi, China. <i>Archives of Microbiology</i> , 2021, 203, 787-798.	1.0	7
10616	Unlocking the phylogenetic diversity, primary habitats, and abundances of free-living Symbiodiniaceae on a coral reef. <i>Molecular Ecology</i> , 2021, 30, 343-360.	2.0	33
10617	Unexpected high production of biohydrogen from the endogenous fermentation of grape must deposits. <i>Bioresource Technology</i> , 2021, 320, 124334.	4.8	14
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10620	Responses to chronic corticosterone on brain glucocorticoid receptors, adrenal gland, and gut microbiota in mice lacking neuronal serotonin. <i>Brain Research</i> , 2021, 1751, 147190.	1.1	8
10621	Associations between human bacterial pathogens and ARGs are magnified in leachates as landfill ages. <i>Chemosphere</i> , 2021, 264, 128446.	4.2	16

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10623	Impact of sulfate and iron oxide on bacterial community dynamics in paddy soil under alternate watering conditions. <i>Journal of Hazardous Materials</i> , 2021, 408, 124417.	6.5	23
10624	Biogeography and co-occurrence patterns of bacterial generalists and specialists in three subtropical marine bays. <i>Limnology and Oceanography</i> , 2021, 66, 793-806.	1.6	36
10625	Assessment of the bacterial diversity of agave sap concentrate, resistance to in vitro gastrointestinal conditions and short-chain fatty acids production. <i>Food Research International</i> , 2021, 140, 109862.	2.9	3
10626	Contribution of archaea and bacteria in sustaining climate change by oxidizing ammonia and sulfur in an Arctic fjord. <i>Genomics</i> , 2021, 113, 1272-1276.	1.3	9
10627	Low root functional dispersion enhances functionality of plant growth by influencing bacterial activities in European forest soils. <i>Environmental Microbiology</i> , 2021, 23, 1889-1906.	1.8	16
10628	Profiling microbial community structures and functions in bioremediation strategies for treating 1,4-dioxane-contaminated groundwater. <i>Journal of Hazardous Materials</i> , 2021, 408, 124457.	6.5	21
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10633	Insights on the microbial communities developed during the anaerobic fermentation of raw and pretreated microalgae biomass. <i>Chemosphere</i> , 2021, 263, 127942.	4.2	20
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10635	Regression Models for Compositional Data: General Log-Contrast Formulations, Proximal Optimization, and Microbiome Data Applications. <i>Statistics in Biosciences</i> , 2021, 13, 217-242.	0.6	15
10636	Electrochemical biofilm control by reconstructing microbial community in agricultural water distribution systems. <i>Journal of Hazardous Materials</i> , 2021, 403, 123616.	6.5	20
10637	Rare Feature Selection in High Dimensions. <i>Journal of the American Statistical Association</i> , 2021, 116, 887-900.	1.8	19
10638	The intestinal microbiome of an Indo-Pacific humpback dolphin (<i>Sousa chinensis</i>) stranded near the Pearl River Estuary, China. <i>Integrative Zoology</i> , 2021, 16, 287-299.	1.3	12
10639	Modulation of rumen fermentation and microbial community through increasing dietary cation-anion difference in Chinese Holstein dairy cows under heat stress conditions. <i>Journal of Applied Microbiology</i> , 2021, 130, 722-735.	1.4	8

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10641	Simultaneous leaching of multiple heavy metals from a soil column by extracellular polymeric substances of <i>Aspergillus tubingensis</i> F12. <i>Chemosphere</i> , 2021, 263, 127883.	4.2	17
10642	Rearing environment affects the genetic architecture and plasticity of DNA methylation in Chinook salmon. <i>Heredity</i> , 2021, 126, 38-49.	1.2	27
10643	The GLP-1R agonist liraglutide limits hepatic lipotoxicity and inflammatory response in mice fed a methionine-choline deficient diet. <i>Translational Research</i> , 2021, 227, 75-88.	2.2	61
10644	A drop in the ocean: Monitoring fish communities in spawning areas using environmental DNA. <i>Environmental DNA</i> , 2021, 3, 43-54.	3.1	19
10645	Heat waves intensify the effects of drought on bacterial diversity but not community composition in <i>Solanum lycopersicum</i> soil. <i>Journal of Soils and Sediments</i> , 2021, 21, 355-363.	1.5	6
10646	Evaluation of anaerobic membrane bioreactor (AnMBR) treating confectionery wastewater at long-term operation under different organic loading rates: Performance and membrane fouling. <i>Chemical Engineering Journal</i> , 2021, 404, 126261.	6.6	47
10647	Plant diversity and litter accumulation mediate the loss of foliar endophyte fungal richness following nutrient addition. <i>Ecology</i> , 2021, 102, e03210.	1.5	10
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10651	NextGen molecular barcoding of larval grouper diet in an extensive green-water pond system. <i>Aquaculture</i> , 2021, 531, 735971.	1.7	2
10652	Large-scale biogeographical patterns of antibiotic resistome in the forest soils across China. <i>Journal of Hazardous Materials</i> , 2021, 403, 123990.	6.5	27
10653	Elevated CO ₂ concentration modifies the effects of organic fertilizer substitution on rice yield and soil ARGs. <i>Science of the Total Environment</i> , 2021, 754, 141898.	3.9	12
10654	Understanding the microbial trends in a nitrification reactor fed with primary settled municipal wastewater. <i>Separation and Purification Technology</i> , 2021, 256, 117828.	3.9	5
10655	Bacterial contaminants and their antibiotic susceptibility patterns in ready-to-eat foods vended in Ogun state, Nigeria. <i>Letters in Applied Microbiology</i> , 2021, 72, 187-195.	1.0	8
10656	Microbial community assembly in a multi-layer dendritic metacommunity. <i>Oecologia</i> , 2021, 195, 13-24.	0.9	16
10657	Microbial diversity accumulates in a downstream direction in the Three Gorges Reservoir. <i>Journal of Environmental Sciences</i> , 2021, 101, 156-167.	3.2	20

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10658	Succession of bacterial community composition in coastal agricultural soils along a 1000-year reclamation chronosequence in Hangzhou Bay, China. <i>Ecological Indicators</i> , 2021, 121, 106972.	2.6	14
10659	Effect of Korea red ginseng on nonalcoholic fatty liver disease: an association of gut microbiota with liver function. <i>Journal of Ginseng Research</i> , 2021, 45, 316-324.	3.0	25
10660	Evaluation of plant microbial fuel cells for urban green roofs in a subtropical metropolis. <i>Science of the Total Environment</i> , 2021, 765, 142786.	3.9	20
10661	Air pollution could drive global dissemination of antibiotic resistance genes. <i>ISME Journal</i> , 2021, 15, 270-281.	4.4	95
10662	Diversity and Abundance of Denitrifying Bacteria in the Sediment of a Eutrophic Estuary. <i>Geomicrobiology Journal</i> , 2021, 38, 199-209.	1.0	9
10663	Habitat and seasonal variations in bacterial community structure and diversity in sediments of a Shallow lake. <i>Ecological Indicators</i> , 2021, 120, 106959.	2.6	46
10664	Colistin and amoxicillin combinatorial exposure alters the human intestinal microbiota and antibiotic resistome in the simulated human intestinal microbiota. <i>Science of the Total Environment</i> , 2021, 750, 141415.	3.9	14
10665	New insights into the vertical distribution and microbial degradation of microplastics in urban river sediments. <i>Water Research</i> , 2021, 188, 116449.	5.3	140
10666	Characterization of staphylococcal communities on healthy and allergic feline skin. <i>Veterinary Dermatology</i> , 2021, 32, 61.	0.4	3
10667	Diversity and community structure of ammonia-oxidizing archaea in rhizosphere soil of four plant groups in Ebinur Lake wetland. <i>Canadian Journal of Microbiology</i> , 2021, 67, 271-280.	0.8	6
10668	Fifteen-year no tillage of a Mollisol with residue retention indirectly affects topsoil bacterial community by altering soil properties. <i>Soil and Tillage Research</i> , 2021, 205, 104804.	2.6	28
10669	Acidobacteria are active and abundant members of diverse atmospheric H ₂ -oxidizing communities detected in temperate soils. <i>ISME Journal</i> , 2021, 15, 363-376.	4.4	23
10670	Temporal and spatial dynamics in the apple flower microbiome in the presence of the phytopathogen <i>Erwinia amylovora</i> . <i>ISME Journal</i> , 2021, 15, 318-329.	4.4	49
10671	Responses of microbial community and antibiotic resistance genes to the selection pressures of ampicillin, cephalixin and chloramphenicol in activated sludge reactors. <i>Science of the Total Environment</i> , 2021, 755, 142632.	3.9	45
10672	Phylogenetic diversity and prevalence of mycoflora in ready-to-eat supermarket and roadside-vended peanuts. <i>Mycologia</i> , 2021, 113, 1-11.	0.8	7
10673	Culturable bacteria from an Alpine coniferous forest site: biodegradation potential of organic polymers and pollutants. <i>Folia Microbiologica</i> , 2021, 66, 87-98.	1.1	9
10674	Sourdough cultures as reservoirs of maltose-negative yeasts for low-alcohol beer brewing. <i>Food Microbiology</i> , 2021, 94, 103629.	2.1	27
10675	Chemotaxis-selective colonization of mangrove rhizosphere microbes on nine different microplastics. <i>Science of the Total Environment</i> , 2021, 752, 142223.	3.9	69

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10677	Host specificity of microbiome assembly and its fitness effects in phytoplankton. <i>ISME Journal</i> , 2021, 15, 774-788.	4.4	48
10678	Survey of Bacterial Phylogenetic Diversity During the Glacier Melting Season in an Arctic Fjord. <i>Microbial Ecology</i> , 2021, 81, 579-591.	1.4	9
10679	Both artificial root exudates and natural <i>Koelreuteria paniculata</i> exudates modify bacterial community structure and enhance phenanthrene biodegradation in contaminated soils. <i>Chemosphere</i> , 2021, 263, 128041.	4.2	11
10680	Contrasting seasonal variations of geochemistry and microbial community in two adjacent acid mine drainage lakes in Anhui Province, China. <i>Environmental Pollution</i> , 2021, 268, 115826.	3.7	24
10681	Comparative decay of culturable faecal indicator bacteria, microbial source tracking marker genes, and enteric pathogens in laboratory microcosms that mimic a sub-tropical environment. <i>Science of the Total Environment</i> , 2021, 751, 141475.	3.9	21
10682	Microbial diversity reveals the partial denitrification-anammox process serves as a new pathway in the first mainstream anammox plant. <i>Science of the Total Environment</i> , 2021, 764, 142917.	3.9	31
10683	Comparative diversity analysis of halophiles at two polar saltern systems in Indramayu, West Java, Indonesia. <i>Letters in Applied Microbiology</i> , 2021, 72, 157-166.	1.0	1
10684	Dynamics of ammonia oxidizers in response to different fertilization inputs in intensively managed agricultural soils. <i>Applied Soil Ecology</i> , 2021, 157, 103729.	2.1	9
10685	Microbial physiology and interactions in anammox systems with the intermittent addition of organic carbons. <i>Bioresource Technology</i> , 2021, 319, 124226.	4.8	29
10686	Bacterial communities as indicators of environmental pollution by POPs in marine sediments. <i>Environmental Pollution</i> , 2021, 268, 115690.	3.7	31
10687	The stronger impact of inorganic nitrogen fertilization on soil bacterial community than organic fertilization in short-term condition. <i>Geoderma</i> , 2021, 382, 114752.	2.3	61
10688	Metagenomic exploration of antibiotic resistome in treated wastewater effluents and their receiving water. <i>Science of the Total Environment</i> , 2021, 765, 142755.	3.9	33
10689	Long-run bacteria-phage coexistence dynamics under natural habitat conditions in an environmental biotechnology system. <i>ISME Journal</i> , 2021, 15, 636-648.	4.4	12
10690	Experimental drought re-ordered assemblages of root-associated fungi across North American grasslands. <i>Journal of Ecology</i> , 2021, 109, 776-792.	1.9	17
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10692	Efficient removal of norfloxacin by biological aerated filters: Effect of zeolite modification and analysis of microbial communities. <i>Journal of Water Process Engineering</i> , 2021, 40, 101799.	2.6	7
10693	Rearing water microbiomes in white leg shrimp (<i>Litopenaeus vannamei</i>) larviculture assemble stochastically and are influenced by the microbiomes of live feed products. <i>Environmental Microbiology</i> , 2021, 23, 281-298.	1.8	17

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10798	Effect of rice bran fermented with <i>Bacillus</i> and <i>Lysinibacillus</i> species on dynamic microbial activity of Pacific white shrimp (<i>Penaeus vannamei</i>). <i>Aquaculture</i> , 2021, 531, 735958.	1.7	17
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10824	Comparison of DNA sequencing and morphological identification techniques to characterize environmental fungal communities. <i>Scientific Reports</i> , 2021, 11, 2633.	1.6	21
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10965	Application of computational approaches to analyze metagenomic data. <i>Journal of Microbiology</i> , 2021, 59, 233-241.	1.3	9
10966	Size fractionation of bioaerosol emissions from green-waste composting. <i>Environment International</i> , 2021, 147, 106327.	4.8	22
10967	Effect of consortium bioaugmentation and biostimulation on remediation efficiency and bacterial diversity of diesel-contaminated aged soil. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 46.	1.7	10
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10973	Symbiont shuffling across environmental gradients aligns with changes in carbon uptake and translocation in the reef-building coral <i>Pocillopora acuta</i> . <i>Coral Reefs</i> , 2021, 40, 595-607.	0.9	29
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10991	Lower endoscopic delivery of freeze-dried intestinal microbiota results in more rapid and efficient engraftment than oral administration. <i>Scientific Reports</i> , 2021, 11, 4519.	1.6	5
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10997	Differences in the Soil Bacterial Communities Under Organic Farming and Conventional Farming Modes Revealed by 16S rDNA Sequencing. <i>Journal of Biobased Materials and Bioenergy</i> , 2021, 15, 10-19.	0.1	2
10998	Antidepressants fluoxetine and amitriptyline induce alterations in intestinal microbiota and gut microbiome function in rats exposed to chronic unpredictable mild stress. <i>Translational Psychiatry</i> , 2021, 11, 131.	2.4	73
10999	Identification and Metabolism of Naturally Prevailing Microorganisms in Zinc and Copper Mineral Processing. <i>Minerals (Basel, Switzerland)</i> , 2021, 11, 156.	0.8	10
11000	High Plasticity of the Gut Microbiome and Muscle Metabolome of Chinese Mitten Crab (<i>Eriocheir tjingensis</i>) in Response to Overlock 10 Tf	0.9	10
11001	Rhizoplane and Rhizosphere Fungal Communities of Geographically Isolated Korean Bellflower (<i>Campanula takesimana</i> Nakai). <i>Biology</i> , 2021, 10, 138.	1.3	2
11002	Balance between geographic, soil, and host tree parameters to shape soil microbiomes associated to clonal oak varies across soil zones along a European North-South transect. <i>Environmental Microbiology</i> , 2021, 23, 2274-2292.	1.8	3
11003	Rubidium chloride modulated the fecal microbiota community in mice. <i>BMC Microbiology</i> , 2021, 21, 46.	1.3	7
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11007	User-friendly bioinformatics pipeline gDAT (graphical downstream analysis tool) for analysing rDNA sequences. <i>Molecular Ecology Resources</i> , 2021, 21, 1380-1392.	2.2	27
11008	The amphibian microbiome exhibits poor resilience following pathogen-induced disturbance. <i>ISME Journal</i> , 2021, 15, 1628-1640.	4.4	38
11009	Genomic evidence for sulfur intermediates as new biogeochemical hubs in a model aquatic microbial ecosystem. <i>Microbiome</i> , 2021, 9, 46.	4.9	32
11010	The impact of the varying nutrient concentrations on the enhanced biological phosphorus removal performance and functional phosphorus-accumulating and denitrifying genes in an anaerobic-aerobic-anoxic sequencing batch reactor. <i>Environmental Technology and Innovation</i> , 2021, 21, 101256.	3.0	10
11011	Alteration of Gut Microbiota in Carbapenem-Resistant Enterobacteriaceae Carriers during Fecal Microbiota Transplantation According to Decolonization Periods. <i>Microorganisms</i> , 2021, 9, 352.	1.6	11
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11014	Pelleting of a Total Mixed Ration Affects Growth Performance of Fattening Lambs. <i>Frontiers in Veterinary Science</i> , 2021, 8, 629016.	0.9	14

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11016	Local Geomorphological Gradients and Land Use Patterns Play Key Role on the Soil Bacterial Community Diversity and Dynamics in the Highly Endemic Indigenous Afrotropical Coastal Scarp Forest Biome. <i>Frontiers in Microbiology</i> , 2021, 12, 592725.	1.5	16
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11019	Targeting the Active Rhizosphere Microbiome of <i>Trifolium pratense</i> in Grassland Evidences a Stronger-Than-Expected Belowground Biodiversity-Ecosystem Functioning Link. <i>Frontiers in Microbiology</i> , 2021, 12, 629169.	1.5	18
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11021	Relationships of gut microbiota, short-chain fatty acids, inflammation, and the gut barrier in Parkinson's disease. <i>Molecular Neurodegeneration</i> , 2021, 16, 6.	4.4	197
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11024	Assembly Patterns of the Rhizosphere Microbiome Along the Longitudinal Root Axis of Maize (<i>Zea mays</i>) Tj ETQq1 1 0.784314rgBT /Ov	1.5	57
11025	16S rRNA Amplicon Sequencing of Microbial Biofilms from Marsberg Copper Mine, Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
11026	Effects of Substitution of Corn with Ground Brown Rice on Growth Performance, Nutrient Digestibility, and Gut Microbiota of Growing-Finishing Pigs. <i>Animals</i> , 2021, 11, 375.	1.0	8
11027	Development of a robust protocol for the characterization of the pulmonary microbiota. <i>Communications Biology</i> , 2021, 4, 164.	2.0	7
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11029	Dynamic Alterations of Oral Microbiota Related to Halitosis in Preschool Children. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 599467.	1.8	11
11030	Root exposure to apple replant disease soil triggers local defense response and rhizoplane microbiome dysbiosis. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	26
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11034	Dietary purslane (<i>Portulaca oleracea</i> L.) promotes the growth performance of broilers by modulation of gut microbiota. <i>AMB Express</i> , 2021, 11, 31.	1.4	11
11035	Microbial composition of a hydropower cooling water system reveals thermophilic bacteria with a possible role in primary biofilm formation. <i>Biofouling</i> , 2021, 37, 246-256.	0.8	4
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11037	Anaerobically fermented spent mushroom substrates improve nitrogen removal and lead (II) adsorption. <i>Water Science and Technology</i> , 2021, 83, 1691-1702.	1.2	2
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11044	Noninvasive imaging and quantification of bile salt hydrolase activity: From bacteria to humans. <i>Science Advances</i> , 2021, 7, .	4.7	25
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11046	The influence of intraspecific sequence variation during DNA metabarcoding: A case study of eleven fungal species. <i>Molecular Ecology Resources</i> , 2021, 21, 1141-1148.	2.2	39
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11058	Japanese quail (<i>Coturnix japonica</i>) as a novel model to study the relationship between the avian microbiome and microbial endocrinology-based host-microbe interactions. <i>Microbiome</i> , 2021, 9, 38.	4.9	11
11059	Estrogen induces shift in abundances of specific groups of the coral microbiome. <i>Scientific Reports</i> , 2021, 11, 2767.	1.6	9
11060	Comparative evaluation of <i>Vibrio</i> delineation methodologies in post-genomic era. <i>Environmental Microbiology Reports</i> , 2021, 13, 209-217.	1.0	0
11061	Exploration of the relationship between intestinal flora changes and gut acute graft-versus-host disease after hematopoietic stem cell transplantation. <i>Translational Pediatrics</i> , 2021, 10, 283-295.	0.5	4
11062	Distinctive distributions of halophilic Archaea across hypersaline environments within the Qaidam Basin of China. <i>Archives of Microbiology</i> , 2021, 203, 2029-2042.	1.0	3
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11069	Distinct rhizomicrobiota assemblages and plant performance in lettuce grown in soils with different agricultural management histories. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
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11071	Diversity and structure of phenanthrene degrading bacterial communities associated with fungal bioremediation in petroleum contaminated soil. <i>Journal of Hazardous Materials</i> , 2021, 403, 123895.	6.5	40
11072	Burkholderiaceae Are Key Acetate Assimilators During Complete Denitrification in Acidic Cryoturbated Peat Circles of the Arctic Tundra. <i>Frontiers in Microbiology</i> , 2021, 12, 628269.	1.5	26

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11075	Seasonal Variation in Fungal Community Composition Associated with <i>Tamarix chinensis</i> Roots in the Coastal Saline Soil of Bohai Bay, China. <i>Microbial Ecology</i> , 2021, 82, 652-665.	1.4	3
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11078	Effects of Xylo-Oligosaccharides on Growth and Gut Microbiota as Potential Replacements for Antibiotic in Weaning Piglets. <i>Frontiers in Microbiology</i> , 2021, 12, 641172.	1.5	33
11079	Comparison of Fecal Microbiota of Horses Suffering from Atypical Myopathy and Healthy Co-Grazers. <i>Animals</i> , 2021, 11, 506.	1.0	4
11080	Effects of maize (<i>Zea mays</i>) genotypes and microbial sources in shaping fall armyworm (<i>Spodoptera</i>) Tj ETQq0 0 0 rrgBT /Overlock 10 Tf	1.6	22
11081	Tumor-Associated Microbiota in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 641270.	1.8	28
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11087	Effects of Tobacco Stem-Derived Biochar on Soil Properties and Bacterial Community Structure under Continuous Cropping of <i>Bletilla striata</i> . <i>Journal of Soil Science and Plant Nutrition</i> , 2021, 21, 1318-1328.	1.7	11
11088	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	0.8	1
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11091	Gut Microbiomes of Freshwater Mussels (<i>Unionidae</i>) Are Taxonomically and Phylogenetically Variable across Years but Remain Functionally Stable. <i>Microorganisms</i> , 2021, 9, 411.	1.6	14
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11095	The Seagrass Holobiont: What We Know and What We Still Need to Disclose for Its Possible Use as an Ecological Indicator. <i>Water (Switzerland)</i> , 2021, 13, 406.	1.2	24
11096	Shifts in the Abundance and Community Composition of Particle-Associated and Free-Living <i>Nitrospira</i> Across Physicochemical Gradients in the Pearl River Estuary. <i>Estuaries and Coasts</i> , 2021, 44, 1931-1945.	1.0	10
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11100	R/G Value—A Numeric Index of Individual Periodontal Health and Oral Microbiome Dynamics. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 602643.	1.8	9
11101	Acenaphthene biodegradation and structural and functional metagenomics of the microbial community of an acenaphthene-enriched animal charcoal polluted soil. <i>Biocatalysis and Agricultural Biotechnology</i> , 2021, 32, 101951.	1.5	6
11102	Impact of Ambient Temperature Sample Storage on the Equine Fecal Microbiota. <i>Animals</i> , 2021, 11, 819.	1.0	11
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11105	Microbial Community Composition Correlates with Metal Sorption in an Ombrotrophic Boreal Bog: Implications for Radionuclide Retention. <i>Soil Systems</i> , 2021, 5, 19.	1.0	7
11107	Gut dysbiosis and mortality in hemodialysis patients. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 20.	2.9	26
11108	Alkylphenols and Chlorophenols Remediation in Vertical Flow Constructed Wetlands: Removal Efficiency and Microbial Community Response. <i>Water (Switzerland)</i> , 2021, 13, 715.	1.2	5
11109	Shifts in bacterial community in response to conservation management practices within a soybean production system. <i>Biology and Fertility of Soils</i> , 2021, 57, 575-586.	2.3	5
11110	Effective low-cost preservation of human stools in field-based studies for helminth and microbiota analysis. <i>International Journal for Parasitology</i> , 2021, 51, 741-748.	1.3	5
11111	Fermentation of African nightshade leaves with lactic acid bacterial starter cultures. <i>International Journal of Food Microbiology</i> , 2021, 342, 109056.	2.1	16
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11114	The endophytic microbiota of <i>Citrus limon</i> is transmitted from seed to shoot highlighting differences of bacterial and fungal community structures. <i>Scientific Reports</i> , 2021, 11, 7078.	1.6	22
11115	Bacterial and Archaeal Taxonomic Diversity of Mud Volcanoes (Beciu, Romania) via Metagenomic Approach. <i>Geomicrobiology Journal</i> , 2021, 38, 532-539.	1.0	6
11116	Abundance and Functional Importance of Complete Ammonia Oxidizers and Other Nitrifiers in a Riparian Ecosystem. <i>Environmental Science & Technology</i> , 2021, 55, 4573-4584.	4.6	38
11117	High-throughput sequencing reveals the spatial distribution variability of microbial community in coastal waters in Shenzhen. <i>Ecotoxicology</i> , 2021, 30, 1429-1436.	1.1	5
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11129	The Fecal Bacterial Microbiota in Horses with Equine Recurrent Uveitis. <i>Animals</i> , 2021, 11, 745.	1.0	6
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11133	Structural and Functional Shift in Soil Bacterial Community in Response to Long-Term Compost Amendment in Paddy Field. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 2183.	1.3	12
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11136	The Banana Root Endophytome: Differences between Mother Plants and Suckers and Evaluation of Selected Bacteria to Control <i>Fusarium oxysporum</i> f.sp. <i>cubense</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 194.	1.5	26
11137	Bacterial Communities Associated With <i>Penaeus vannamei</i> Boone, 1931 Surface and Its Rearing Water in Biofloc Culture System. <i>Asian Fisheries Science</i> , 2021, 34, .	0.1	1
11138	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021, 19, 41.	1.7	19
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11140	Comparison of Methods for Picking the Operational Taxonomic Units From Amplicon Sequences. <i>Frontiers in Microbiology</i> , 2021, 12, 644012.	1.5	21
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11145	Much ado about nothing? Off-target amplification can lead to false-positive bacterial brain microbiome detection in healthy and Parkinson's disease individuals. <i>Microbiome</i> , 2021, 9, 75.	4.9	31
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11149	<i>Lactobacillus acidophilus</i> LA5 improves saturated fat-induced obesity mouse model through the enhanced intestinal <i>Akkermansia muciniphila</i> . <i>Scientific Reports</i> , 2021, 11, 6367.	1.6	49
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11309	Exploring the capacity of aquatic biofilms to act as environmental DNA samplers: Test on macroinvertebrate communities in rivers. <i>Science of the Total Environment</i> , 2021, 763, 144208.	3.9	17
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11321	Differences in microbiota between acute and chronic perianal eczema. <i>Medicine (United States)</i> , 2021, 100, e25623.	0.4	4
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11333	Resistance, Resilience, and Recovery of Dryland Soil Bacterial Communities Across Multiple Disturbances. <i>Frontiers in Microbiology</i> , 2021, 12, 648455.	1.5	13
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11335	Effects of environmental factors on release amount of heavy metal and structure of microbial community in sediments. <i>International Journal of Environmental Science and Technology</i> , 2022, 19, 4007-4018.	1.8	6
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11348	Fungal succession in decomposing woody debris across a tropical forest disturbance gradient. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108142.	4.2	13

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11375	Effects of mancozeb on citrus rhizosphere bacterial community. <i>Microbial Pathogenesis</i> , 2021, 154, 104845.	1.3	12
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11380	Arbuscular mycorrhizal fungal communities of forbs and C3 grasses respond differently to cultivation and elevated nutrients. <i>Mycorrhiza</i> , 2021, 31, 455-470.	1.3	3
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11382	A Seed Mucilage-Degrading Fungus From the Rhizosphere Strengthens the Plant-Soil-Microbe Continuum and Potentially Regulates Root Nutrients of a Cold Desert Shrub. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 538-546.	1.4	1
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11385	Population differences in Chinook salmon (<i>Oncorhynchus tshawytscha</i>) DNA methylation: Genetic drift and environmental factors. <i>Ecology and Evolution</i> , 2021, 11, 6846-6861.	0.8	7
11386	Assessment of the Impact of Temperature on Biofilm Composition with a Laboratory Heat Exchanger Module. <i>Microorganisms</i> , 2021, 9, 1185.	1.6	9

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11399	Bacterial and Archaeal Communities in Polymetallic Nodules, Sediments, and Bottom Waters of the Abyssal Clarion-Clipperton Zone: Emerging Patterns and Future Monitoring Considerations. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	6
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11401	Treatment of petroleum hydrocarbon-polluted groundwater with innovative in situ sulfate-releasing biobarrier. <i>Journal of Cleaner Production</i> , 2021, 295, 126424.	4.6	14
11402	Eukaryotic Biodiversity and Spatial Patterns in the Clarion-Clipperton Zone and Other Abyssal Regions: Insights From Sediment DNA and RNA Metabarcoding. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	33
11403	Alteration of vaginal microbiota in patients with recurrent miscarriage. <i>Journal of Obstetrics and Gynaecology</i> , 2022, 42, 248-255.	0.4	12
11406	Refinement of 16S rRNA gene analysis for low biomass biospecimens. <i>Scientific Reports</i> , 2021, 11, 10741.	1.6	11
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11409	Cyanobiont genetic diversity and host specificity of cyanobiont-bearing dinoflagellate <i>Ornithocercus</i> in temperate coastal waters. <i>Scientific Reports</i> , 2021, 11, 9458.	1.6	6
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11413	Effects of a Bioprocessed Soybean Meal Ingredient on the Intestinal Microbiota of Hybrid Striped Bass, <i>Morone chrysops</i> x <i>M. saxatilis</i> . <i>Microorganisms</i> , 2021, 9, 1032.	1.6	8
11414	<i>Candida</i> Administration in Bilateral Nephrectomy Mice Elevates Serum (1â†’3)-Î²-D-glucan That Enhances Systemic Inflammation Through Energy Augmentation in Macrophages. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5031.	1.8	24
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11419	Endozoicomonadaceae symbiont in gills of <i>Acesta</i> clam encodes genes for essential nutrients and polysaccharide degradation. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
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11421	Mixed plantations of <i>Metasequoia glyptostroboides</i> and <i>Bischofia polycarpa</i> change soil fungal and archaeal communities and enhance soil phosphorus availability in Shanghai, China. <i>Ecology and Evolution</i> , 2021, 11, 7239-7249.	0.8	8
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11423	Potential of fecal microbiota for detection and postoperative surveillance of colorectal cancer. <i>BMC Microbiology</i> , 2021, 21, 156.	1.3	10
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11429	General Unified Microbiome Profiling Pipeline (GUMPP) for Large Scale, Streamlined and Reproducible Analysis of Bacterial 16S rRNA Data to Predicted Microbial Metagenomes, Enzymatic Reactions and Metabolic Pathways. <i>Metabolites</i> , 2021, 11, 336.	1.3	1
11430	HCK and ABAA: A Newly Designed Pipeline to Improve Fungi Metabarcoding Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 640693.	1.5	0
11431	Microbiota identified from preserved Anopheles. <i>Malaria Journal</i> , 2021, 20, 230.	0.8	10
11432	Bacterial Diversity Profiling of the New Zealand Parasitic Blowfly <i>Lucilia sericata</i> Based on 16S rRNA Gene Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
11433	Association of Gut Microbiota during Early Pregnancy with Risk of Incident Gestational Diabetes Mellitus. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e4128-e4141.	1.8	21
11434	DUOX2 variants associate with preclinical disturbances in microbiota-immune homeostasis and increased inflammatory bowel disease risk. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	35
11435	Clearance of <i>Clostridioides difficile</i> Colonization Is Associated with Antibiotic-Specific Bacterial Changes. <i>MSphere</i> , 2021, 6, .	1.3	15
11436	Intestinal microbial diversity is higher in Pacific abalone (<i>Haliotis discus hannai</i>) with slower growth rates. <i>Aquaculture</i> , 2021, 537, 736500.	1.7	19
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11442	Epiphytic Diatom-Based Biomonitoring in Mediterranean Ponds: Traditional Microscopy versus Metabarcoding Approaches. <i>Water (Switzerland)</i> , 2021, 13, 1351.	1.2	13
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11446	Bacterial community dynamics during a harmful algal bloom of <i>Heterosigma akashiwo</i> . <i>Aquatic Microbial Ecology</i> , 2021, 86, 153-167.	0.9	13
11447	Consistent patterns of fungal communities within ant-plants across a large geographic range strongly suggest a multipartite mutualism. <i>Mycological Progress</i> , 2021, 20, 681-699.	0.5	5
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11450	CONSTAX2: improved taxonomic classification of environmental DNA markers. <i>Bioinformatics</i> , 2021, 37, 3941-3943.	1.8	17
11451	Dadaist2: A Toolkit to Automate and Simplify Statistical Analysis and Plotting of Metabarcoding Experiments. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5309.	1.8	12
11453	Gut Microbiome Alterations and Functional Prediction in Chronic Spontaneous Urticaria Patients. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 747-755.	0.9	17
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11864	The plant secondary compound swainsonine reshapes gut microbiota in plateau pikas (<i>Ochotona</i>) Tj ETQq0 0 0 rgBT./Overlock 10 Tf 50	1.7	8
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11902	Microbiota of Breast Tissue and Its Potential Association with Regional Recurrence of Breast Cancer in Korean Women. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 1643-1655.	0.9	8
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11907	The effect of combined pollution by PAHs and heavy metals on the topsoil microbial communities of Spolic Technosols of the lake Atamanskoe, Southern Russia. <i>Environmental Geochemistry and Health</i> , 2022, 44, 1299-1315.	1.8	15
11908	Succession and potential role of bacterial communities during <i>Pleurotus ostreatus</i> production. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6

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11910	Endophytic <i>Serratia</i> sp. PW7 shifts bacterial endophytes in wheat (<i>Triticum aestivum</i> L.) to reduce pyrene contamination. <i>Bioremediation Journal</i> , 2022, 26, 292-304.	1.0	1
11911	Effects of Î²-glucan, probiotics, and synbiotics on obesity-associated colitis and hepatic manifestations in C57BL/6 mice. <i>European Journal of Nutrition</i> , 2022, 61, 793-807.	1.8	19
11912	Direct Evidence for Deterministic Assembly of Bacterial Communities in Full-Scale Municipal Wastewater Treatment Facilities. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0108621.	1.4	5
11913	DNA metabarcoding reveals the significant influence of anthropogenic effects on microeukaryotic communities in urban waterbodies. <i>Environmental Pollution</i> , 2021, 285, 117336.	3.7	8
11914	Emerging Pathogenic Gammaproteobacteria <i>Wohlfahrtiimonas chitiniclastica</i> and <i>Ignatzschineria</i> Species in a Turkey Vulture (<i>Cathartes aura</i>). , 2021, 35, 280-289.		1
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11917	The temporal shift of peri-implant microbiota during the biofilm formation and maturation in a canine model. <i>Microbial Pathogenesis</i> , 2021, 158, 105100.	1.3	7
11918	Soil Bacterial Community Composition Following Cover Crops and Corn N Management. <i>Soil Science Society of America Journal</i> , 0, , .	1.2	3
11920	16S rRNA gene diversity and gut microbial composition of the Indian white shrimp (<i>Penaeus indicus</i>). <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 2019-2031.	0.7	9
11921	Exploring the Role of Fungal Endophytes in the Sudden Death Syndrome of the Invasive Shrub <i>Chrysanthemoides monilifera</i> subsp. <i>rotundata</i> in Australia. <i>Phytobiomes Journal</i> , 2022, 6, 13-25.	1.4	1
11922	Human Fecal Contamination Corresponds to Changes in the Freshwater Bacterial Communities of a Large River Basin. <i>Microbiology Spectrum</i> , 2021, 9, e0120021.	1.2	4
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11924	Aquatic microbial community is partially functionally redundant: Insights from an in situ reciprocal transplant experiment. <i>Science of the Total Environment</i> , 2021, 786, 147433.	3.9	3
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11930	Species-Level Resolution of Female Bladder Microbiota from 16S rRNA Amplicon Sequencing. <i>MSystems</i> , 2021, 6, e0051821.	1.7	19
11931	A mesocosm study on bacteria-kelp interactions: Importance of nitrogen availability and kelp genetics. <i>Journal of Phycology</i> , 2021, 57, 1777-1791.	1.0	5
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11935	An Osmotic Laxative Renders Mice Susceptible to Prolonged <i>Clostridioides difficile</i> Colonization and Hinders Clearance. <i>MSphere</i> , 2021, 6, e0062921.	1.3	9
11936	Seasonal Dynamics of Epiphytic Microbial Communities on Marine Macrophyte Surfaces. <i>Frontiers in Microbiology</i> , 2021, 12, 671342.	1.5	11
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11938	Biomethane potential test reveals microbial adaptation and increased methane yield during anaerobic co-digestion. <i>Bioresource Technology Reports</i> , 2021, 15, 100754.	1.5	5
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11940	Colonization status and community structure of arbuscular mycorrhizal fungi in the coniferous tree, <i>Cryptomeria japonica</i> , with special reference to root orders. <i>Plant and Soil</i> , 2021, 468, 423-438.	1.8	15
11941	Is soil management system really important? comparison of microbial community diversity and structure in soils managed under organic and conventional regimes with some view on soil properties. <i>PLoS ONE</i> , 2021, 16, e0256969.	1.1	10
11943	Diversity and characteristics of raw milk microbiota from Korean dairy farms using metagenomic and culturomic analysis. <i>Food Control</i> , 2021, 127, 108160.	2.8	12
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11945	Evaluation of a commercial microbial enrichment kit used prior DNA extraction to improve the molecular detection of vector-borne pathogens from naturally infected dogs. <i>Journal of Microbiological Methods</i> , 2021, 188, 106163.	0.7	3
11946	Fish as a winter reservoir for <i>Vibrio</i> spp. in the southern Baltic Sea coast. <i>Journal of Marine Systems</i> , 2021, 221, 103574.	0.9	2
11947	Gut region induces gastrointestinal microbiota community shift in Ujimqin sheep (<sc><i>Ovis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.8	10

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11950	Diversity, abundance and expression of the antibiotic resistance genes in a Chinese landfill: Effect of deposit age. <i>Journal of Hazardous Materials</i> , 2021, 417, 126027.	6.5	14
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11952	Water diversion induces more changes in bacterial and archaeal communities of river sediments than seasonality. <i>Journal of Environmental Management</i> , 2021, 293, 112876.	3.8	14
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11956	The Leaf Bacterial Microbiota of Female and Male Kiwifruit Plants in Distinct Seasons: Assessing the Impact of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Phytobiomes Journal</i> , 2021, 5, 275-287.	1.4	11
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11962	Eucalyptus Plantation Age and Species Govern Soil Fungal Community Structure and Function Under a Tropical Monsoon Climate in China. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	0
11964	An investigation into the anaerobic spoilage microbiota of beef carcass and rump steak cuts using high-throughput sequencing. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	3
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11966	The network structure of intertidal meiofaunal communities from environmental DNA metabarcoding surveys in Northwest Iberia. <i>Aquatic Sciences</i> , 2021, 83, 1.	0.6	7
11967	Diversity of <i>Treponema denticola</i> and Other Oral Treponeme Lineages in Subjects with Periodontitis and Gingivitis. <i>Microbiology Spectrum</i> , 2021, 9, e0070121.	1.2	19

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11969	Community and single cell analyses reveal complex predatory interactions between bacteria in high diversity systems. <i>Nature Communications</i> , 2021, 12, 5481.	5.8	14
11970	Mycophagy of White-Tailed Deer (<i>Odocoileus virginianus</i> Zimmermann) in the Boreal Forest. <i>Forests</i> , 2021, 12, 1247.	0.9	0
11971	Microbial diversity associated with spontaneous coffee bean fermentation process and specialty coffee production in northern Colombia. <i>International Journal of Food Microbiology</i> , 2021, 354, 109282.	2.1	12
11972	Comparison of Periodontal Bacteria of Edo and Modern Periods Using Novel Diagnostic Approach for Periodontitis With Micro-CT. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 723821.	1.8	10
11973	A new landscape of rabbit gut microbiota shaped by the infection of precocious parasites of <i>Eimeria intestinalis</i> . <i>Veterinary Parasitology</i> , 2021, 300, 109579.	0.7	4
11974	Effects of addition of nitrogen-enriched biochar on bacteria and fungi community structure and C, N, P, and Fe stoichiometry in subtropical paddy soils. <i>European Journal of Soil Biology</i> , 2021, 106, 103351.	1.4	19
11975	Landscapes and bacterial signatures of mucosa-associated intestinal microbiota in Chilean and Spanish patients with inflammatory bowel disease. <i>Microbial Cell</i> , 2021, 8, 223-238.	1.4	11
11976	Early Life Fecal Microbiota Transplantation in Neonatal Dairy Calves Promotes Growth Performance and Alleviates Inflammation and Oxidative Stress during Weaning. <i>Animals</i> , 2021, 11, 2704.	1.0	16
11977	Exploring the mechanisms by which reindeer droppings induce fen peat methane production. <i>Soil Biology and Biochemistry</i> , 2021, 160, 108318.	4.2	3
11978	Biodegradation Potential and Putative Catabolic Genes of Culturable Bacteria from an Alpine Deciduous Forest Site. <i>Microorganisms</i> , 2021, 9, 1920.	1.6	6
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11981	The Variations of Bacterial Community Structures in Tailing Soils Suffering from Heavy Metal Contaminations. <i>Water, Air, and Soil Pollution</i> , 2021, 232, 1.	1.1	10
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11984	Transition and regulation mechanism of bacterial biota in Kishu saba-narezushi (mackerel narezushi) during its fermentation step. <i>Journal of Bioscience and Bioengineering</i> , 2021, 132, 606-612.	1.1	8
11985	Effects of Dietary Fishmeal Replacement by Poultry By-Product Meal and Hydrolyzed Feather Meal on Liver and Intestinal Histomorphology and on Intestinal Microbiota of Gilthead Seabream (<i>Sparus</i>)	1.0	10

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11987	Horizontal gene transfer-mediated bacterial strain variation affects host fitness in <i>Drosophila</i> . <i>BMC Biology</i> , 2021, 19, 187.	1.7	4
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11989	Pilot Study of Eco-Physiological Pepper Responses to Starfish-Based Organic Soil Amendments in Open-Field and Greenhouse Cultivations. <i>Horticulturae</i> , 2021, 7, 344.	1.2	2
11990	Determination of bacterial abundance and communities in the nipple drinking system of cascading cage layer houses. <i>Scientific Reports</i> , 2021, 11, 19169.	1.6	4
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11993	Lactoferrin impact on gut microbiota in preterm infants with late-onset sepsis or necrotising enterocolitis: the MAGPIE mechanisms of action study. <i>Efficacy and Mechanism Evaluation</i> , 2021, 8, 1-88.	0.9	6
11994	Tomato Domestication Affects Potential Functional Molecular Pathways of Root-Associated Soil Bacteria. <i>Plants</i> , 2021, 10, 1942.	1.6	10
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11997	Activity and structure of methanogenic microbial communities in sediments of cascade hydropower reservoirs, Southwest China. <i>Science of the Total Environment</i> , 2021, 786, 147515.	3.9	7
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11999	Gut and faecal bacterial community of the terrestrial isopod <i>Porcellionides pruinosus</i> : potential use for monitoring exposure scenarios. <i>Ecotoxicology</i> , 2021, 30, 2096-2108.	1.1	1
12000	Micropollutant transformation and taxonomic composition in hybrid MBBR – A comparison of carrier-attached biofilm and suspended sludge. <i>Water Research</i> , 2021, 202, 117441.	5.3	31
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12002	Temporal and geographical comparison of bulk tank milk and water microbiota composition in Brazilian dairy farms. <i>Food Microbiology</i> , 2021, 98, 103793.	2.1	2
12003	Longitudinal Fecal Microbiome Study of Total Body Irradiated Mice Treated With Radiation Mitigators Identifies Bacterial Associations With Survival. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 715396.	1.8	5

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12005	Diversity, seasonal succession and host specificity of bacteria associated with cyanobacterial aggregates in a freshwater lake. <i>Environmental Technology and Innovation</i> , 2021, 24, 101988.	3.0	6
12007	Structure and Long-Term Stability of the Microbiome in Diverse Diatom Cultures. <i>Microbiology Spectrum</i> , 2021, 9, e0026921.	1.2	8
12008	Distinguishing feature of gut microbiota in Tibetan highland coronary artery disease patients and its link with diet. <i>Scientific Reports</i> , 2021, 11, 18486.	1.6	16
12009	Methanotroph community structure and processes in an inland river affected by natural gas macro-seeps. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
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12016	Bioemulsification and Microbial Community Reconstruction in Thermally Processed Crude Oil. <i>Microorganisms</i> , 2021, 9, 2054.	1.6	2
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12019	Guadipyr, a new insecticide, induces microbiota dysbiosis and immune disorders in the midgut of silkworms (<i>Bombyx mori</i>). <i>Environmental Pollution</i> , 2021, 286, 117531.	3.7	11
12020	Both pH and salinity shape the microbial communities of the lakes in Badain Jaran Desert, NW China. <i>Science of the Total Environment</i> , 2021, 791, 148108.	3.9	29
12021	Evaluating Different Quantitative PCR Assays to Enumerate Specific Microbial Populations in Anaerobic Digesters Treating Municipal Wastewater Solids. <i>Journal of Environmental Engineering, ASCE</i> , 2021, 147, 04021035.	0.7	0
12022	Changes of soil bacterial and fungal community structure along a natural aridity gradient in desert grassland ecosystems, Inner Mongolia. <i>Catena</i> , 2021, 205, 105470.	2.2	25
12023	Pollutant removal, electricity generation and microbial community in an electrochemical membrane bioreactor during co-treatment of sewage and landfill leachate. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 106205.	3.3	25

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12025	Prospects for multi-omics in the microbial ecology of water engineering. <i>Water Research</i> , 2021, 205, 117608.	5.3	26
12026	Microbial interkingdom associations across soil depths reveal network connectivity and keystone taxa linked to soil fine-fraction carbon content. <i>Agriculture, Ecosystems and Environment</i> , 2021, 320, 107559.	2.5	21
12027	Nutrients available in the soil regulate the changes of soil microbial community alongside degradation of alpine meadows in the northeast of the Qinghai-Tibet Plateau. <i>Science of the Total Environment</i> , 2021, 792, 148363.	3.9	47
12028	Ammonia stress influences intestinal histomorphology, immune status and microbiota of Chinese striped-neck turtle (<i>Mauremys sinensis</i>). <i>Ecotoxicology and Environmental Safety</i> , 2021, 222, 112471.	2.9	22
12029	Resilience of soil fungal community to hurricane Patricia (category 4). <i>Forest Ecology and Management</i> , 2021, 498, 119550.	1.4	4
12030	Fermentation as a tool for increasing food security and nutritional quality of indigenous African leafy vegetables: the case of <i>Cucurbita</i> sp.. <i>Food Microbiology</i> , 2021, 99, 103820.	2.1	18
12031	Co-occurrence patterns and assembly processes of microeukaryotic communities in a semi-enclosed aquaculture bay. <i>Continental Shelf Research</i> , 2021, 228, 104550.	0.9	6
12032	Organic manure induced soil food web of microbes and nematodes drive soil organic matter under jackfruit planting. <i>Applied Soil Ecology</i> , 2021, 166, 103994.	2.1	19
12033	Management of biofloc concentrations as an ecological strategy for microbial control in intensive shrimp culture. <i>Aquaculture</i> , 2021, 543, 736969.	1.7	12
12034	Involvement of the metabolically active bacteria in the organic matter degradation during olive mill waste composting. <i>Science of the Total Environment</i> , 2021, 789, 147975.	3.9	18
12035	High-throughput sequencing of <i>Fasciola</i> spp. shows co-infection and intermediate forms in Balochistan, but only <i>Fasciola gigantica</i> in the Punjab province of Pakistan. <i>Infection, Genetics and Evolution</i> , 2021, 94, 105012.	1.0	7
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12037	Use of a packed-bed biofilm reactor to achieve rapid formation of anammox biofilms for high-rate nitrogen removal. <i>Journal of Cleaner Production</i> , 2021, 321, 128999.	4.6	24
12038	Toxic effects of ammonia on intestinal health and microbiota in red-eared slider (<i>Trachemys scripta</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	4.2	17
12039	Effects of heavy metals and organic matter fractions on the fungal communities in mangrove sediments from Techeng Isle, South China. <i>Ecotoxicology and Environmental Safety</i> , 2021, 222, 112545.	2.9	12
12040	Shotgun metagenomic analysis reveals the prevalence of antibiotic resistance genes and mobile genetic elements in full scale hospital wastewater treatment plants. <i>Journal of Environmental Management</i> , 2021, 296, 113270.	3.8	29
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12042	Microbiome reduction prevents lipid accumulation during early diapause in the northern house mosquito, <i>Culex pipiens pipiens</i> . <i>Journal of Insect Physiology</i> , 2021, 134, 104295.	0.9	12
12043	Enhancing the retention of phosphorus through bacterial oxidation of iron or sulfide in the eutrophic sediments of Lake Taihu. <i>Science of the Total Environment</i> , 2021, 791, 148039.	3.9	10
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12045	Survival of a commercial AM fungal inoculant and its impact on indigenous AM fungal communities in field soils. <i>Applied Soil Ecology</i> , 2021, 166, 103979.	2.1	15
12046	Integrated analysis reveals an association between the rhizosphere microbiome and root rot of arecanut palm. <i>Pedosphere</i> , 2021, 31, 725-735.	2.1	7
12047	Variations in nitrogen removal rates and microbial communities over sediment depth in Daya Bay, China. <i>Environmental Pollution</i> , 2021, 286, 117267.	3.7	27
12048	Exogenous Fecal Microbial Transplantation Alters Fearfulness, Intestinal Morphology, and Gut Microbiota in Broilers. <i>Frontiers in Veterinary Science</i> , 2021, 8, 706987.	0.9	14
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12050	Examination of host-taxon, environment, and distance effects on leaf fungal endophytes in the dominant woody genus, <i>Metrosideros</i> , on O'ahu. <i>Fungal Ecology</i> , 2021, 53, 101093.	0.7	0
12051	Substrate type and plant phenolics influence epiphytic bacterial assembly during short-term succession. <i>Science of the Total Environment</i> , 2021, 792, 148410.	3.9	12
12052	Urbanization reduces overall cyanobacterial abundance but favors heterocystous forms. <i>Applied Soil Ecology</i> , 2021, 167, 104059.	2.1	2
12053	Rapid pathogen discovery in diseased turbot (<i>Scophthalmus maximus</i>) using 16S rRNA high throughput sequencing. <i>Aquaculture Reports</i> , 2021, 21, 100835.	0.7	3
12054	Significant association between soil dissolved organic matter and soil microbial communities following vegetation restoration in the Loess Plateau. <i>Ecological Engineering</i> , 2021, 169, 106305.	1.6	24
12055	Geochemical stability of zero-valent iron modified raw wheat straw innovatively applied to in situ permeable reactive barrier: N ₂ selectivity and long-term denitrification. <i>Ecotoxicology and Environmental Safety</i> , 2021, 224, 112649.	2.9	8
12056	Evaluation of infections in orthopedic patients using next-generation sequencing. <i>Journal of Infection and Chemotherapy</i> , 2021, 27, 1626-1633.	0.8	2
12057	Variations of tongue coating microbiota in children with Henoch-Schönlein purpura nephritis. <i>Microbial Pathogenesis</i> , 2021, 160, 105192.	1.3	0
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12063	Microbial carbon use and associated changes in microbial community structure in high-Arctic tundra soils under elevated temperature. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108419.	4.2	12
12064	Microbial colonizers of microplastics in an Arctic freshwater lake. <i>Science of the Total Environment</i> , 2021, 795, 148640.	3.9	35
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12074	Reduction in VOC emissions by intermittent aeration in bioreactor landfills with gas-water joint regulation. <i>Environmental Pollution</i> , 2021, 290, 118059.	3.7	10
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12081	Humic acids enrich the plant microbiota with bacterial candidates for the suppression of pathogens. <i>Applied Soil Ecology</i> , 2021, 168, 104146.	2.1	13
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12086	Microbial community analysis of biopiles in Antarctica provides evidence of successful hydrocarbon biodegradation and initial soil ecosystem recovery. <i>Environmental Pollution</i> , 2021, 290, 117977.	3.7	5
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12106	Microbial sludge formation in Brazilian marine diesel oil (B0) and soybean methylic biodiesel blends (B10 and B20) during simulated storage. <i>Fuel</i> , 2022, 308, 121905.	3.4	5
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12583	A 454 Survey Reveals the Community Composition and Core Microbiome of the Common Bed Bug (<i>Cimex</i>) Tj ETQq _{1,1} 0.784314 rgBT (C	1.1	47
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12642	The Contribution of DNA Metabarcoding to Fungal Conservation: Diversity Assessment, Habitat Partitioning and Mapping Red-Listed Fungi in Protected Coastal <i>Salix repens</i> Communities in the Netherlands. PLoS ONE, 2014, 9, e99852.	1.1	66
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12667	Relative Abundance of and Composition within Fungal Orders Differ between Cheatgrass (<i>Bromus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	31
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14137	Effects of Four Cropping Patterns of <i>Lilium brownii</i> on Rhizosphere Microbiome Structure and Replant Disease. <i>Plants</i> , 2022, 11, 824.	1.6	5
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14140	Effects of Lower Fishmeal With Hydrolyzed Fish Protein Powder on the Growth Performance and Intestinal Development of Juvenile Pearl Gentian Grouper (<i>Epinephelus fuscoguttatus</i> and <i>Epinephelus</i>) <i>Tj ETQn 0 0 rg BT /Overlock</i>	1.0	3
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14142	How does familiarity in rhizobial interactions impact the performance of invasive and native legumes?. <i>NeoBiota</i> , 0, 72, 129-156.	1.0	4
14143	Unique bacterial communities associated with components of an artificial aquarium ecosystem and their possible contributions to nutrient cycling in this microecosystem. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 72.	1.7	2
14144	Assessment of Microbial Community Composition Changes in the Presence of Phytoplankton-Derived Exudates in Two Contrasting Areas from Chilean Patagonia. <i>Diversity</i> , 2022, 14, 195.	0.7	5
14145	Biodiversity and Biogeography of Abundant and Rare Microbial Assemblages in the Western Subtropical Pacific Ocean. <i>Frontiers in Microbiology</i> , 2022, 13, 839562.	1.5	6
14146	Compatibility of Diatom Valve Records With Sedimentary Ancient DNA Amplicon Data: A Case Study in a Brackish, Alkaline Tibetan Lake. <i>Frontiers in Earth Science</i> , 2022, 10, .	0.8	8
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14151	Biogeochemical Characteristics of Earth's Volcanic Permafrost: An Analog of Extraterrestrial Environments. <i>Astrobiology</i> , 2022, 22, 812-828.	1.5	2
14152	Nitrogen use efficiency, rhizosphere bacterial community, and root metabolome reprogramming due to maize seed treatment with microbial biostimulants. <i>Physiologia Plantarum</i> , 2022, 174, e13679.	2.6	13
14153	Ammonia-Oxidizing Bacterial Communities in Tilapia Pond Systems and the Influencing Factors. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 3438.	1.3	3
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14155	The Effect of Feedstock Concentration on the Microbial Community Dynamics During Textile Waste Composting. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	7
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14158	Intestinal microbiota score could predict survival following allogeneic hematopoietic stem cell transplantation. <i>Annals of Hematology</i> , 2022, 101, 1283-1294.	0.8	3
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14161	Feeding Strategy of the Wild Korean Seahorse (<i>Hippocampus haema</i>). <i>Journal of Marine Science and Engineering</i> , 2022, 10, 357.	1.2	2
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14173	Effects of Dietary Lipid Sources on Alleviating the Negative Impacts Induced by the Fishmeal Replacement With <i>Clostridium autoethanogenum</i> Protein in the Diet of Pacific White Shrimp (<i>Litopenaeus vannamei</i>). <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	9
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14179	Stimulants and donors promote megaplasmid pND6-2 horizontal gene transfer in activated sludge. <i>Journal of Environmental Sciences</i> , 2023, 126, 742-753.	3.2	1
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14182	Human Milk Oligosaccharides and Bacterial Profile Modulate Infant Body Composition during Exclusive Breastfeeding. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2865.	1.8	16
14183	Dynamics of phoD- and gcd-Harboring Microbial Communities Across an Age Sequence of Biological Soil Crusts Under Sand-Fixation Plantation. <i>Frontiers in Microbiology</i> , 2022, 13, 831888.	1.5	1

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14198	Community Structure and Ecological Network's Changes of Vaginal Microbiome in Women Right After Delivery. <i>Frontiers in Pediatrics</i> , 2022, 10, 750860.	0.9	4
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14210	Assessing the effects of experimental bacterial challenge with <i>Pasteurella multocida</i> and ampicillin on the respiratory microbiota of pre-weaned Holstein calves. <i>Veterinary Microbiology</i> , 2022, 269, 109428.	0.8	0
14211	Variation in Bacterial Community Structure Under Long-Term Fertilization, Tillage, and Cover Cropping in Continuous Cotton Production. <i>Frontiers in Microbiology</i> , 2022, 13, 847005.	1.5	10
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14218	The relationship between dietary trophic level, parasites and the microbiome of Pacific walrus (<i>Odobenus rosmarus</i>). <i>Frontiers in Microbiology</i> , 2022, 13, 82513.	1.2	3
14219	Occurrence of hepatitis E virus (HEV) in Calabrian wild boars. <i>International Journal of Food Microbiology</i> , 2022, 371, 109671.	2.1	8
14220	Temporal dynamics of <i>Campylobacter</i> and <i>Arcobacter</i> in a freshwater lake that receives fecal inputs from migratory geese. <i>Water Research</i> , 2022, 217, 118397.	5.3	7
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14224	Effect of dietary honeysuckle (<i>Lonicera caerulea</i> L.) supplementation on lipid metabolism, immunity and intestinal microbiota in grass carp (<i>Ctenopharyngodon idellus</i>). <i>Aquaculture Reports</i> , 2022, 23, 101063.	0.7	8
14225	Gut Microbiome Signatures Are Predictive of Cognitive Impairment in Hypertension Patientsâ€™A Cohort Study. <i>Frontiers in Microbiology</i> , 2022, 13, 841614.	1.5	8
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14241	Screening for suitable mixed microbial consortia from anaerobic sludge and animal dungs for biodegradation of brewery spent grain. <i>Biomass and Bioenergy</i> , 2022, 159, 106396.	2.9	4
14242	Harnessing Cu@Fe ₃ O ₄ core shell nanostructure for biogas production from sewage sludge: Experimental study and microbial community shift. <i>Renewable Energy</i> , 2022, 188, 1059-1071.	4.3	20

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14244	An optimized approach for processing of frozen lung and lavage samples for microbiome studies. <i>PLoS ONE</i> , 2022, 17, e0265891.	1.1	2
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14246	Shifts in benthic bacterial communities associated with farming stages and a microbiological proxy for assessing sulfidic sediment conditions at fish farms. <i>Marine Pollution Bulletin</i> , 2022, 178, 113603.	2.3	7
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14256	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.	1.5	1
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14259	Effects of slag and biochar amendments on microorganisms and fractions of soil organic carbon during flooding in a paddy field after two years in southeastern China. <i>Science of the Total Environment</i> , 2022, 824, 153783.	3.9	12
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14262	Data on metagenomic profiles of bacterial endophyte communities associated with <i>Dicoma anomala</i> . <i>Data in Brief</i> , 2022, 42, 108112.	0.5	1
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14264	Gut microbiome and daytime function in Chinese patients with major depressive disorder. <i>Journal of Psychosomatic Research</i> , 2022, 157, 110787.	1.2	7
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16201	The effect of oxytetracycline treatment on the gut microbiome community dynamics in rainbow trout (<i>Oncorhynchus mykiss</i>) over time. <i>Aquaculture</i> , 2022, 560, 738559.	1.7	11
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16204	An Engineered λ Phage Enables Enhanced and Strain-Specific Killing of Enterohemorrhagic <i>Escherichia coli</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	8
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16293	Gut microbiota-derived metabolites confer protection against SARS-CoV-2 infection. <i>Gut Microbes</i> , 2022, 14, .	4.3	26
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16300	Microbial Profiling of Potato-Associated Rhizosphere Bacteria under Bacteriophage Therapy. <i>Antibiotics</i> , 2022, 11, 1117.	1.5	4
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16310	Dietary ellagic acid supplementation attenuates intestinal damage and oxidative stress by regulating gut microbiota in weanling piglets. <i>Animal Nutrition</i> , 2022, 11, 322-333.	2.1	16
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16313	Precise Monitoring of Lettuce Functional Responses to Minimal Nutrient Supplementation Identifies Aquaponic System's Nutrient Limitations and Their Time-Course. <i>Agriculture (Switzerland)</i> , 2022, 12, 1278.	1.4	9
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16331	The association between fecal microbiota, age and endoparasitism in adult alpacas. <i>PLoS ONE</i> , 2022, 17, e0272556.	1.1	2
16332	Multi-omic analyses identify mucosa bacteria and fecal metabolites associated with weight loss after fecal microbiota transplantation. <i>Innovation(China)</i> , 2022, 3, 100304.	5.2	2
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#	ARTICLE	IF	CITATIONS
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16969	Effects of direct-fed <i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i> on production performance and milk fatty acid profile in dairy cows. <i>Journal of Dairy Science</i> , 2023, 106, 1815-1825.	1.4	5
16970	Microbial biotechnology for wastewater treatment into circular economy. , 2023, , 333-354.		0
16971	Influence of neo-adjuvant radiotherapy on the intestinal microbiota of rectal cancer patients. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 6085-6096.	1.2	0
16972	Gastrointestinal microbiome: Evaluation of testing technologies. , 2023, , 147-161.		0
16973	Habitat type and host grazing regimen influence the soil microbial diversity and communities within potential biting midge larval habitats. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	3
16974	Adding a polyphenol-rich fiber bundle to food impacts the gastrointestinal microbiome and metabolome in dogs. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
16975	Effect of different straw retention techniques on soil microbial community structure in wheatâ€“maize rotation system. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
16976	Bacterial Contamination of the Surgical Site at the Time of Elective Caesarean Section in Belgian Blue Cowsâ€”Part 2: Identified by 16Sr DNA Amplicon Sequencing. <i>Veterinary Sciences</i> , 2023, 10, 94.	0.6	0
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16980	Characteristics of key microorganisms and metabolites in irradiated marbled beef. <i>Meat Science</i> , 2023, 199, 109121.	2.7	3
16981	Comparison of methods for biological sequence clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, , 1-24.	1.9	0
16982	Evaluating the Optimal Oil Concentrations in the Startup Performance of a Membrane Bioreactor Treating Oily Noodle-soup Wastewater. <i>Journal of Oleo Science</i> , 2023, 72, 357-367.	0.6	0
16983	Effects of Italian ryegrass silage-based total mixed ration on rumen fermentation, growth performance, blood metabolites, and bacterial communities of growing Hanwoo heifers. <i>Journal of Animal Science and Technology</i> , 2023, 65, 951-970.	0.8	1
16984	Best practice for wildlife gut microbiome research: A comprehensive review of methodology for 16S rRNA gene investigations. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
16985	Nitrifying Microorganisms Linked to Biotransformation of Perfluoroalkyl Sulfonamido Precursors from Legacy Aqueous Film-Forming Foams. <i>Environmental Science & Technology</i> , 2023, 57, 5592-5602.	4.6	5
16986	<i>Moringa oleifera</i> Leaf Powder as New Source of Protein-Based Feedstuff Improves Growth Performance and Cecal Microbial Diversity of Broiler Chicken. <i>Animals</i> , 2023, 13, 1104.	1.0	2
16988	Earthworms Exposed to Polyethylene and Biodegradable Microplastics in Soil: Microplastic Characterization and Microbial Community Analysis. <i>ACS Agricultural Science and Technology</i> , 2023, 3, 340-349.	1.0	9

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16990	The effect of C/N ratio and its frequent addition on commensal and pathogenic bacterial abundances in shrimp <i>Litopenaeus vannamei</i> gut in a biofloc system: Ratio and frequent addition interaction matters. <i>PLoS ONE</i> , 2023, 18, e0283841.	1.1	0
16991	Amylopectin Partially Substituted by Cellulose in the Hindgut Was Beneficial to Short-Chain Fatty Acid Production and Probiotic Colonization. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
16992	<scp>eDNA</scp> metabarcoding from aquatic biofilms allows studying spatial and temporal fluctuations of fish communities from Lake Geneva. <i>Environmental DNA</i> , 2023, 5, 570-581.	3.1	3
16993	Insights into the Gut Microbiota of the Freshwater Crab <i>Sinopotamon planum</i> across Three Seasons and Its Associations with the Surrounding Aquatic Microbiota. <i>Diversity</i> , 2023, 15, 519.	0.7	2
16994	Mycorrhizae Enhance Soybean Plant Growth and Aluminum Stress Tolerance by Shaping the Microbiome Assembly in an Acidic Soil. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
16995	Acute temperature stresses trigger liver transcriptome and microbial community remodeling in largemouth bass (<i>Micropterus salmoides</i>). <i>Aquaculture</i> , 2023, 573, 739573.	1.7	7
16996	B Lymphocyte Development in the Bursa of Fabricius of Young Broilers is Influenced by the Gut Microbiota. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
16997	Effect of Enrofloxacin on the Microbiome, Metabolome, and Abundance of Antibiotic Resistance Genes in the Chicken Cecum. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
16998	Evaluation of a Red Grape Marc Extract as a Natural Nitrification Inhibitor and its Effect on Soil Bacterial Community. <i>Journal of Soil Science and Plant Nutrition</i> , 0, .	1.7	0
17000	Effects of Phage Cocktail, Probiotics, and Their Combination on Growth Performance and Gut Microbiota of Broiler Chickens. <i>Animals</i> , 2023, 13, 1328.	1.0	5
17001	Responses of root architecture and the rhizosphere microbiome assembly of maize (<i>Zea mays</i> L.) to a soil texture gradient. <i>Soil Biology and Biochemistry</i> , 2023, 181, 109026.	4.2	3
17002	Effects of phenyl acids on different degradation phases during thermophilic anaerobic digestion. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
17003	Combined impacts of algae-induced variations in water soluble organic matter and heavy metals on bacterial community structure in sediment from Chaohu Lake, a eutrophic shallow lake. <i>Science of the Total Environment</i> , 2023, 874, 162481.	3.9	4
17004	Discrepancies in rhizobacterial assembly caused by glyphosate application and herbicide-tolerant soybean Co-expressing GAT and EPSPS. <i>Journal of Hazardous Materials</i> , 2023, 450, 131053.	6.5	2
17005	Hydrogen inhalation ameliorates hepatic inflammation and modulates gut microbiota in rats with high-fat diet-induced non-alcoholic fatty liver disease. <i>European Journal of Pharmacology</i> , 2023, 947, 175698.	1.7	3
17006	Graphene oxide addition to anaerobic digestion of waste activated sludge: Impact on methane production and removal of emerging contaminants. <i>Environmental Pollution</i> , 2023, 324, 121343.	3.7	5
17007	Characterization of the eukaryotic microbial communities in the chicken ileum in cage-free and conventional commercial housing systems. <i>Poultry Science</i> , 2023, 102, 102621.	1.5	0

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17010	The effects of long-term hexabromocyclododecanes contamination on microbial communities in the microcosms. <i>Chemosphere</i> , 2023, 325, 138412.	4.2	3
17011	Structure, stability, and potential function of groundwater microbial community responses to permafrost degradation on varying permafrost of the Qinghai-Tibet Plateau. <i>Science of the Total Environment</i> , 2023, 875, 162693.	3.9	2
17012	Community structures and biodeterioration processes of epilithic biofilms imply the significance of micro-environments. <i>Science of the Total Environment</i> , 2023, 876, 162665.	3.9	4
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17014	A bacterial signature-based method for the identification of seven forensically relevant human body fluids. <i>Forensic Science International: Genetics</i> , 2023, 65, 102865.	1.6	2
17015	Micro-topography dominated microhabitat significantly influences colonization and development of incubated-cyanobacteria biocrusts in a harsh sandy desert environment. <i>Applied Soil Ecology</i> , 2023, 188, 104874.	2.1	1
17016	Fungal-bacterial associations in urban allotment garden soils. <i>Applied Soil Ecology</i> , 2023, 188, 104896.	2.1	1
17017	The impact of metallic nanoparticles on gut fermentation processes: An integrated metabolomics and metagenomics approach following an in vitro digestion and fecal fermentation model. <i>Journal of Hazardous Materials</i> , 2023, 453, 131331.	6.5	1
17018	Shifts of soil archaeal nitrification and methanogenesis with elevation in water level fluctuation zone of the three Gorges Reservoir, China. <i>Journal of Environmental Management</i> , 2023, 339, 117871.	3.8	3
17020	Simultaneous removal of nitrate and pesticides from contaminated groundwater using aerobic granular biomass technology. <i>Journal of Environmental Chemical Engineering</i> , 2023, 11, 109527.	3.3	7
17021	Soil bacterial communities of paddy are dependent on root compartment niches but independent of growth stages from Mollisols of Northeast China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
17022	From the shallow to the mesophotic: a characterization of Symbiodiniaceae diversity in the Red Sea NEOM region. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	3
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17025	Climate and geochemistry at different altitudes influence soil fungal community aggregation patterns in alpine grasslands. <i>Science of the Total Environment</i> , 2023, 881, 163375.	3.9	2
17026	Biofilm colonization of stone materials from an Australian outdoor sculpture: Importance of geometry and exposure. <i>Journal of Environmental Management</i> , 2023, 339, 117948.	3.8	2

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17057	Microbiological quality and safety of vacuum-packaged white-tailed deer meat stored at 4°C. <i>International Journal of Food Microbiology</i> , 2023, 390, 110110.	2.1	2
17058	Overview of microbial profiles in human hepatocellular carcinoma and adjacent nontumor tissues. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	10
17059	Beta Diversity of Arbuscular Mycorrhizal Communities Increases in Time after Crop Establishment of Peruvian Sacha Inchi (<i>Plukenetia volubilis</i>). <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 194.	1.5	1
17060	Ambient oxygen levels regulate intestinal dysbiosis and GVHD severity after allogeneic stem cell transplantation. <i>Immunity</i> , 2023, 56, 353-368.e6.	6.6	9
17061	MicrobiotaProcess: A comprehensive R package for deep mining microbiome. <i>Innovation(China)</i> , 2023, 4, 100388.	5.2	22
17062	Altered Gut Microbiota Composition and Its Potential Association in Patients with Advanced Hepatocellular Carcinoma. <i>Current Oncology</i> , 2023, 30, 1818-1830.	0.9	9
17063	The temperature dependence of microbial community respiration is amplified by changes in species interactions. <i>Nature Microbiology</i> , 2023, 8, 272-283.	5.9	11
17064	Rhizobiome Signature and Its Alteration Due to Watering in the Wild Plant <i>Moringa oleifera</i> . <i>Sustainability</i> , 2023, 15, 2745.	1.6	0
17065	Anaerobic membrane bioreactor-based treatment of poultry slaughterhouse wastewater: Microbial community adaptation and antibiotic resistance gene profiles. <i>Biochemical Engineering Journal</i> , 2023, 192, 108847.	1.8	6
17067	Antarctic Ardley Island terrace – An ideal place to study the marine to terrestrial succession of microbial communities. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
17068	Additive fungal interactions drive biocontrol of <i>Fusarium</i> wilt disease. <i>New Phytologist</i> , 2023, 238, 1198-1214.	3.5	12
17069	Nitrifier Assemblages and Dynamics in Secondary Water Supply Systems: Predominance of <i>Comammox Nitrospira</i> in Tank Biofilm and Sediment. <i>ACS ES&T Water</i> , 2023, 3, 1007-1018.	2.3	2
17070	Untangling the Effects of Plant Genotype and Soil Conditions on the Assembly of Bacterial and Fungal Communities in the Rhizosphere of the Wild Andean Blueberry (<i>Vaccinium floribundum</i> Kunth). <i>Microorganisms</i> , 2023, 11, 399.	1.6	1
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17073	Carbon amendment rather than nitrate fertilization dominated the reassembly of the total, denitrifying, and DNRA bacterial community in the anaerobic subsoil. <i>Journal of Soils and Sediments</i> , 2023, 23, 1913-1926.	1.5	0
17074	Metabolomic signatures of corals thriving across extreme reef habitats reveal strategies of heat stress tolerance. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	1.2	6
17075	Combined Omics Approach Reveals Key Differences between Aerobic and Microaerobic Xylene-Degrading Enrichment Bacterial Communities: <i>Rhodoferrax</i> – A Hitherto Unknown Player Emerges from the Microbial Dark Matter. <i>Environmental Science & Technology</i> , 2023, 57, 2846-2855.	4.6	5

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17077	Dietary supplementation of solubles from shredded, steam-exploded pine particles modulates cecal microbiome composition in broiler chickens. <i>Journal of Animal Science and Technology</i> , 0, , .	0.8	1
17078	Analysis of Dynamics and Diversity of Microbial Community during Production of Germinated Brown Rice. <i>Foods</i> , 2023, 12, 755.	1.9	2
17079	How anaerobic sludge microbiome respond to different concentrations of nitrite, nitrate, and ammonium ions: a comparative analysis. <i>Environmental Science and Pollution Research</i> , 2023, 30, 49026-49037.	2.7	3
17080	Dynamic Analysis of the Bacterial Community and Determination of Antioxidant Capacity during the Fermentation of Sour Tea. <i>Fermentation</i> , 2023, 9, 161.	1.4	0
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17084	Genomic microbiome analyses of surface sand samples from the Kyzyl-Kum Desert (Uzbekistan): characterization and comparative study. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	0
17085	Environmental Selection and Biogeography Shape the Microbiome of Subsurface Petroleum Reservoirs. <i>MSystems</i> , 2023, 8, .	1.7	1
17086	Effects of β -glucan on <i>Salmonella enterica</i> serovar Typhimurium swine colonization and microbiota alterations. <i>Porcine Health Management</i> , 2023, 9, .	0.9	4
17088	Competitive Reactions during Ethanol Chain Elongation Were Temporarily Suppressed by Increasing Hydrogen Partial Pressure through Methanogenesis Inhibition. <i>Environmental Science & Technology</i> , 2023, 57, 3369-3379.	4.6	8
17089	Metabolic turnover rate, digestive enzyme activities, and bacterial communities in the white shrimp <i>Litopenaeus vannamei</i> under compensatory growth. <i>PeerJ</i> , 0, 11, e14747.	0.9	3
17090	Plant colonization mediates the microbial community dynamics in glacier forelands of the Tibetan Plateau. , 2023, 2, .		5
17091	Immobilization of metribuzin-degrading bacteria on biochar: Enhanced soil remediation and bacterial community restoration. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
17093	Reliability of species detection in 16S microbiome analysis: Comparison of five widely used pipelines and recommendations for a more standardized approach. <i>PLoS ONE</i> , 2023, 18, e0280870.	1.1	6
17094	Evaluation of efficacy and mechanism of <i>Bacillus velezensis</i> CB13 for controlling peanut stem rot caused by <i>Sclerotium rolfsii</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
17095	High-Throughput Sequencing of Oral Microbiota in Candida Carriage Sjögren's Syndrome Patients: A Pilot Cross-Sectional Study. <i>Journal of Clinical Medicine</i> , 2023, 12, 1559.	1.0	3
17096	Disrupted diurnal oscillations of the gut microbiota in patients with alcohol dependence. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	2

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17098	Correlations among Antibiotic Resistance Genes, Mobile Genetic Elements and Microbial Communities in Municipal Sewage Treatment Plants Revealed by High-Throughput Sequencing. <i>International Journal of Environmental Research and Public Health</i> , 2023, 20, 3593.	1.2	2
17099	Bacterial Communities in a Gradient of Abiotic Factors Near a Sulfide Thermal Spring in Northern Baikal. <i>Diversity</i> , 2023, 15, 298.	0.7	2
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17101	Best practices for generating and analyzing 16S rRNA amplicon data to track coral microbiome dynamics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
17102	Subgingival microbiome at different levels of cognition. <i>Journal of Oral Microbiology</i> , 2023, 15, .	1.2	1
17103	Full-Length 16S rRNA Gene Analysis Using Long-Read Nanopore Sequencing for Rapid Identification of Bacteria from Clinical Specimens. <i>Methods in Molecular Biology</i> , 2023, , 193-213.	0.4	4
17104	Changes of In Situ Prokaryotic and Eukaryotic Communities in the Upper Sanya River to the Sea over a Nine-Hour Period. <i>Microorganisms</i> , 2023, 11, 536.	1.6	1
17105	Nutritional additives dominance in driving the bacterial communities succession and bioremediation of hydrocarbon and heavy metal contaminated soil microcosms. <i>Microbiological Research</i> , 2023, 270, 127343.	2.5	4
17106	Skin, gut, and sand metagenomic data on placebo-controlled sandbox biodiversity intervention study. <i>Data in Brief</i> , 2023, 47, 109003.	0.5	0
17107	Characterizing Free-Living and Particle-Attached Bacterial Communities of a Shallow Lake on the Inner Mongolia-Xinjiang Plateau, China. <i>Water (Switzerland)</i> , 2023, 15, 836.	1.2	0
17109	Key Soil Physicochemical Properties Regulating Microbial Community Structure under Vegetation Restoration in a Karst Region of China. <i>Ecosystem Health and Sustainability</i> , 2023, 9, .	0.0	1
17110	Variations of arbuscular mycorrhizal fungi following succession stages in a tropical lowland rainforest ecosystem of South China. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	1
17111	Effect of tillage state of paddy soils with heavy metal pollution on the <i>nosZ</i> gene of N ₂ O reductase. <i>Journal of Environmental Sciences</i> , 2024, 137, 469-477.	3.2	0
17112	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N ₂ O cycling. <i>Communications Biology</i> , 2023, 6, .	2.0	0
17113	Metabolic and inflammatory linkage of the chicken cecal microbiome to growth performance. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
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17115	Infant Fecal Fermentations with Galacto-Oligosaccharides and 2- ² -Fucosyllactose Show Differential <i>Bifidobacterium longum</i> Stimulation at Subspecies Level. <i>Children</i> , 2023, 10, 430.	0.6	1

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17117	Dark microbiome and extremely low organics in Atacama fossil delta unveil Mars life detection limits. <i>Nature Communications</i> , 2023, 14, .	5.8	11
17118	Significant enhancement by casamino acids of caproate production via chain elongation. <i>Biochemical Engineering Journal</i> , 2023, 193, 108879.	1.8	3
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17120	Bamboo Plant Part Preference Affects the Nutrients Digestibility and Intestinal Microbiota of Geriatric Giant Pandas. <i>Animals</i> , 2023, 13, 844.	1.0	1
17123	Hierarchical Effects of Lactic Fermentation and Grain Germination on the Microbial and Metabolomic Profile of Rye Doughs. <i>Foods</i> , 2023, 12, 998.	1.9	0
17124	Particle Size Matters: Distribution, Source, and Seasonality Characteristics of Airborne and Pathogenic Bacteria in Wastewater Treatment Plants. <i>Atmosphere</i> , 2023, 14, 465.	1.0	1
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17126	<tt>SCRAPT:</tt>an iterative algorithm for clustering large 16S rRNA gene data sets. <i>Nucleic Acids Research</i> , 0, , .	6.5	0
17127	Disturbed rhythmicity of intestinal hydrogen peroxide alters gut microbial oscillations in BMAL1-deficient monkeys. <i>Cell Reports</i> , 2023, 42, 112183.	2.9	2
17128	Disentangling the mixed effects of soil management on microbial diversity and soil functions: A case study in vineyards. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
17129	Soil Bacterial Community Response to Fire Varies with Slope Aspect at Zhenshan Mountain, East China. <i>Eurasian Soil Science</i> , 2023, 56, 599-610.	0.5	1
17130	Fluorescence activated cell sorting and fermentation analysis to study rumen microbiome responses to administered live microbials and yeast cell wall derived prebiotics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
17131	<i>Polygonatum sibiricum</i> polysaccharides improve cognitive function in D-galactose-induced aging mice by regulating the microbiota-gut-brain axis. <i>Journal of Functional Foods</i> , 2023, 103, 105476.	1.6	8
17132	Glucose oxidase as an alternative to antibiotic growth promoters improves the immunity function, antioxidative status, and cecal microbiota environment in white-feathered broilers. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
17133	Experimentally Induced Dieback Conditions Limit <i>Phragmites australis</i> Growth. <i>Microorganisms</i> , 2023, 11, 639.	1.6	0
17134	CNN_FunBar: Advanced Learning Technique for Fungi ITS Region Classification. <i>Genes</i> , 2023, 14, 634.	1.0	2
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17138	Mycobiome structure does not affect field litter decomposition in Eucalyptus and Acacia plantations. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
17139	Metagenomics-Based Analysis of Candidate Lactate Utilizers from the Rumen of Beef Cattle. <i>Microorganisms</i> , 2023, 11, 658.	1.6	2
17141	The Metagenomic Composition and Effects of Fecal-Microbe-Derived Extracellular Vesicles on Intestinal Permeability Depend on the Patient's Disease. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4971.	1.8	3
17142	Gut Microbial Profile Changes in Patients with Gallbladder Stones after UDCA/CDCA Treatment. <i>Biomedicines</i> , 2023, 11, 777.	1.4	2
17143	Spatiotemporal Shift of T4-Like Phage Community Structure in the Three Largest Estuaries of China. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
17145	Distinct response of total and active fungal communities and functions to seasonal changes in a semi-enclosed bay with mariculture (<sc>Dongshan Bay</sc>, Southern <sc>China</sc>). <i>Limnology and Oceanography</i> , 2023, 68, 1048-1063.	1.6	1
17146	The abundance of the potential pathogen <i>Staphylococcus hominis</i> in the air microbiome in a dental clinic and its susceptibility to far-UV light. <i>MicrobiologyOpen</i> , 2023, 12, .	1.2	0
17147	An active microbiome in Old Faithful geyser. , 2023, 2, .		2
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17149	Effects of metal contamination with physicochemical properties on the sediment microbial communities in a tropical eutrophic-hypereutrophic urban reservoir in Brazil. <i>Environmental Science and Pollution Research</i> , 2023, 30, 54961-54978.	2.7	0
17150	Effects of topical fluoride application on oral microbiota in young children with severe dental caries. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
17152	Effect of Different Host Plants on the Diversity of Gut Bacterial Communities of Spodoptera frugiperda (J. E. Smith, 1797). <i>Insects</i> , 2023, 14, 264.	1.0	0
17153	Effects of synthetic and environmentally friendly fungicides on powdery mildew management and the phyllosphere microbiome of cucumber. <i>PLoS ONE</i> , 2023, 18, e0282809.	1.1	5
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