

Naïve Bayesian Classifier for Rapid Assignment of rRNA Taxonomy

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Citation Report

#	ARTICLE	IF	CITATIONS
25	A Nonextensive Entropy Approach to Solar Wind Intermittency. <i>Astrophysical Journal</i> , 2005, 618, 547-555.	1.6	116
26	Electricity generation by thermophilic microorganisms from marine sediment. <i>Applied Microbiology and Biotechnology</i> , 2008, 78, 147-155.	1.7	117
27	Changes in Bacterial Communities Accompanied by Aggregation in a Fed-Batch Composting Reactor. <i>Current Microbiology</i> , 2008, 56, 458-467.	1.0	24
28	Antibiotic susceptibility of faecal bacteria in Antarctic penguins. <i>Polar Biology</i> , 2008, 31, 759-763.	0.5	27
29	Prokaryotic microbiota of recycled paper mills with low or zero effluent. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2008, 35, 1165-1173.	1.4	21
30	The effect of long-term nitrate treatment on SRB activity, corrosion rate and bacterial community composition in offshore water injection systems. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2008, 35, 1625-1636.	1.4	85
31	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	1.9	202
32	New tools for discovering and characterizing microbial diversity. <i>Current Opinion in Biotechnology</i> , 2008, 19, 544-549.	3.3	146
33	Antimicrobial potential of sponge associated marine actinomycetes. <i>Journal De Mycologie Medicale</i> , 2008, 18, 16-22.	0.7	66
34	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	6.0	3,171
35	Metabonomic and Microbiological Analysis of the Dynamic Effect of Vancomycin-Induced Gut Microbiota Modification in the Mouse. <i>Journal of Proteome Research</i> , 2008, 7, 3718-3728.	1.8	202
36	Novelty and Uniqueness Patterns of Rare Members of the Soil Biosphere. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5422-5428.	1.4	189
37	Bacterial diversity of <i>Taxus</i> rhizosphere: culture-independent and culture-dependent approaches. <i>FEMS Microbiology Letters</i> , 2008, 284, 204-212.	0.7	35
38	Members of the phylum <i>Acidobacteria</i> are dominant and metabolically active in rhizosphere soil. <i>FEMS Microbiology Letters</i> , 2008, 285, 263-269.	0.7	165
39	Metagenomic analysis of a freshwater toxic cyanobacteria bloom. <i>FEMS Microbiology Ecology</i> , 2008, 64, 9-27.	1.3	64
40	Spatial and temporal variability in epilithic biofilm bacterial communities along an upland river gradient. <i>FEMS Microbiology Ecology</i> , 2008, 64, 407-418.	1.3	47
41	Characterization of Fe(II) oxidizing bacterial activities and communities at two acidic Appalachian coalmine drainage-impacted sites. <i>ISME Journal</i> , 2008, 2, 1134-1145.	4.4	59
42	Innate immunity and intestinal microbiota in the development of Type 1 diabetes. <i>Nature</i> , 2008, 455, 1109-1113.	13.7	1,745

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44	Elevated atmospheric CO ₂ affects soil microbial diversity associated with trembling aspen. <i>Environmental Microbiology</i> , 2008, 10, 926-941.	1.8	235
45	Marine methylotrophs revealed by stable isotope probing, multiple displacement amplification and metagenomics. <i>Environmental Microbiology</i> , 2008, 10, 1526-1535.	1.8	110
46	Gradients of coastal fish farm effluents and their effect on coral reef microbes. <i>Environmental Microbiology</i> , 2008, 10, 2299-2312.	1.8	55
47	Phylogenetic analyses of ribosomal DNA-containing bacterioplankton genome fragments from a 4000m vertical profile in the North Pacific Subtropical Gyre. <i>Environmental Microbiology</i> , 2008, 10, 2313-2330.	1.8	104
48	The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. <i>Environmental Microbiology</i> , 2008, 10, 3275-3283.	1.8	135
49	Use of pyrosequencing and DNA barcodes to monitor variations in Firmicutes and Bacteroidetes communities in the gut microbiota of obese humans. <i>BMC Genomics</i> , 2008, 9, 576.	1.2	72
50	Comparative Analysis of Human Gut Microbiota by Barcoded Pyrosequencing. <i>PLoS ONE</i> , 2008, 3, e2836.	1.1	901
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52	The Pervasive Effects of an Antibiotic on the Human Gut Microbiota, as Revealed by Deep 16S rRNA Sequencing. <i>PLoS Biology</i> , 2008, 6, e280.	2.6	2,013
53	Concentration dependency of nonequilibrium thermal dissociation curves in complex target samples. <i>Journal of Microbiological Methods</i> , 2008, 74, 82-88.	0.7	8
54	In vitro antagonism of an actinobacterial <i>Kitasatospora</i> isolate against the plant pathogen <i>Phytophthora citricola</i> as elucidated with ultrahigh resolution mass spectrometry. <i>Journal of Microbiological Methods</i> , 2008, 75, 188-195.	0.7	17
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56	Characterization of a Bacterial Community in an Abandoned Semiarid Lead-Zinc Mine Tailing Site. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3899-3907.	1.4	162
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59	Attached Bacterial Populations Shared by Four Species of Aquatic Angiosperms. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5948-5957.	1.4	120
60	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. <i>PLoS ONE</i> , 2008, 3, e2527.	1.1	667

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62	Characterization of the Community Structure of a Dechlorinating Mixed Culture and Comparisons of Gene Expression in Planktonic and Biofloc-Associated <i>Dehalococcoides</i> and <i>Methanospirillum</i> Species. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6709-6719.	1.4	52
63	Accumulation of <i>trans</i> -C _{18:1} Fatty Acids in the Rumen after Dietary Algal Supplementation Is Associated with Changes in the <i>Butyrivibrio</i> Community. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6923-6930.	1.4	121
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71	Archaeal Diversity of Upland Rice Field Soils Assessed by the Terminal Restriction Fragment Length Polymorphism Method Combined with Real Time Quantitative-PCR and a Clone Library Analysis. <i>Microbes and Environments</i> , 2008, 23, 237-243.	0.7	23
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74	Metagenome Fragment Classification Using -Mer Frequency Profiles. <i>Advances in Bioinformatics</i> , 2008, 2008, 1-12.	5.7	85
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80	Bacterial Microbiota Profiling in Gastritis without <i>Helicobacter pylori</i> Infection or Non-Steroidal Anti-Inflammatory Drug Use. PLoS ONE, 2009, 4, e7985.	1.1	204
81	ENDOPHYTIC BACTERIA FROM SEEDS OF <i>NICOTIANA TABACUM</i> CAN REDUCE CADMIUM PHYTOTOXICITY. International Journal of Phytoremediation, 2009, 11, 251-267.	1.7	240
82	Effects of Experimental Choices and Analysis Noise on Surveys of the "Rare Biosphere". Applied and Environmental Microbiology, 2009, 75, 3263-3270.	1.4	43
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101	<i>Blochmannia</i> endosymbionts improve colony growth and immune defence in the ant <i>Camponotus fellah</i> . <i>BMC Microbiology</i> , 2009, 9, 29.	1.3	64
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134	Analysis of bacterial activity, biomass and diversity during windrow composting. <i>Waste Management</i> , 2009, 29, 598-605.	3.7	36
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144	Metagenomic study of the oral microbiota by Illumina high-throughput sequencing. <i>Journal of Microbiological Methods</i> , 2009, 79, 266-271.	0.7	289
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159	Assessment of Bias Associated with Incomplete Extraction of Microbial DNA from Soil. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5428-5433.	1.4	253
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1091	Fecal Microbiota Composition Differs Between Children With β -Cell Autoimmunity and Those Without. <i>Diabetes</i> , 2013, 62, 1238-1244.	0.3	498
1092	Diet-Induced Alterations of Host Cholesterol Metabolism Are Likely To Affect the Gut Microbiota Composition in Hamsters. <i>Applied and Environmental Microbiology</i> , 2013, 79, 516-524.	1.4	180
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1096	Prevalence and diversity of <i>Synergistetes</i> taxa in periodontal health and disease. <i>Journal of Periodontal Research</i> , 2013, 48, 159-168.	1.4	37
1097	Gut microbiome composition is linked to whole grain-induced immunological improvements. <i>ISME Journal</i> , 2013, 7, 269-280.	4.4	462
1098	Anaerobic biodegradation of crude oil under sulphate-reducing conditions leads to only modest enrichment of recognized sulphate-reducing taxa. <i>International Biodeterioration and Biodegradation</i> , 2013, 81, 105-113.	1.9	112
1099	Comparing Metabolic Functionalities, Community Structures, and Dynamics of Herbicide-Degrading Communities Cultivated with Different Substrate Concentrations. <i>Applied and Environmental Microbiology</i> , 2013, 79, 367-375.	1.4	33
1100	Barcoded pyrosequencing analysis of the microbial community in a simulator of the human gastrointestinal tract showed a colon region-specific microbiota modulation for two plant-derived polysaccharide blends. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 409-420.	0.7	19
1101	Removal of alachlor in anoxic soil slurries and related alteration of the active communities. <i>Environmental Science and Pollution Research</i> , 2013, 20, 1089-1105.	2.7	16
1102	Cell sorting analysis of geographically separated hypersaline environments. <i>Extremophiles</i> , 2013, 17, 265-275.	0.9	46
1103	Small core communities and high variability in bacteria associated with the introduced ascidian <i>Styela plicata</i> . <i>Symbiosis</i> , 2013, 59, 35-46.	1.2	24
1104	The role of biogeography in shaping diversity of the intestinal microbiota in house mice. <i>Molecular Ecology</i> , 2013, 22, 1904-1916.	2.0	171
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1108	Use of cassette-electrode microbial fuel cell for wastewater treatment. <i>Journal of Bioscience and Bioengineering</i> , 2013, 115, 176-181.	1.1	61
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1110	Richness and composition of sediment bacterial assemblages in an Atlantic port environment. <i>Science of the Total Environment</i> , 2013, 452-453, 172-180.	3.9	16
1111	Redox effects on the microbial degradation of refractory organic matter in marine sediments. <i>Geochimica Et Cosmochimica Acta</i> , 2013, 121, 582-598.	1.6	49
1112	Screening and selection of growth-promoting bacteria for <i>Dunaliella</i> cultures. <i>Algal Research</i> , 2013, 2, 212-222.	2.4	111

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1114	Diversity of chlorobiphenyl-metabolizing bacteria and their biphenyl dioxygenases in contaminated sediment. <i>Chemosphere</i> , 2013, 93, 1548-1555.	4.2	28
1115	Bacterial DGGE fingerprints of biofilms on electrodes of membraneless microbial fuel cells. <i>International Biodeterioration and Biodegradation</i> , 2013, 84, 211-219.	1.9	55
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1125	Effects of red pepper powder on microbial communities and metabolites during kimchi fermentation. <i>International Journal of Food Microbiology</i> , 2013, 160, 252-259.	2.1	108
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1128	CO ₂ -induced shift in microbial activity affects carbon trapping and water quality in anoxic bioreactors. <i>Geochimica Et Cosmochimica Acta</i> , 2013, 122, 198-208.	1.6	28
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1134	Vertical distribution of bacterioplankton in Lake Averno in relation to water chemistry. <i>FEMS Microbiology Ecology</i> , 2013, 84, 176-188.	1.3	14
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1137	General and rare bacterial taxa demonstrating different temporal dynamic patterns in an activated sludge bioreactor. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1755-1765.	1.7	96
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1150	Bacterial succession in Antarctic soils of two glacier forefields on Larsemann Hills, East Antarctica. <i>FEMS Microbiology Ecology</i> , 2013, 85, 128-142.	1.3	113
1151	Rapid identification of bacterial isolates from wheat roots by high resolution whole cell MALDI-TOF MS analysis. <i>Journal of Biotechnology</i> , 2013, 165, 167-174.	1.9	36
1152	Comparison among different algorithms in classifying explosives using OFETs. <i>Sensors and Actuators B: Chemical</i> , 2013, 176, 46-51.	4.0	13
1153	Effect of Stacked Insecticidal Cry Proteins from Maize Pollen on Nurse Bees (<i>Apis mellifera carnica</i>) and Their Gut Bacteria. <i>PLoS ONE</i> , 2013, 8, e59589.	1.1	39
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1163	<i>Gramella aestuarii</i> sp. nov., isolated from a tidal flat, and emended description of <i>Gramella echinicola</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2872-2878.	0.8	20
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1544	Biomethane by Psychrophilic Methanogenic Community Isolated from Sediment of Crane Lake in Zhalong Wetland, Northeast China. <i>Advanced Materials Research</i> , 2014, 878, 138-146.	0.3	0
1545	Comparative Metagenomic Analysis of Human Gut Microbiome Composition Using Two Different Bioinformatic Pipelines. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	68
1546	Capacity of Aromatic Compound Degradation by Bacteria from Amazon Dark Earth. <i>Diversity</i> , 2014, 6, 339-353.	0.7	20
1547	Oligotyping reveals differences between gut microbiomes of free-ranging sympatric Namibian carnivores (<i>Acinonyx jubatus</i> , <i>Canis mesomelas</i>) on a bacterial species-like level. <i>Frontiers in Microbiology</i> , 2014, 5, 526.	1.5	43
1548	Depth-dependent geochemical and microbiological gradients in Fe(III) deposits resulting from coal mine-derived acid mine drainage. <i>Frontiers in Microbiology</i> , 2014, 5, 215.	1.5	41
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1552	Effects of bacterial inoculants on the indigenous microbiome and secondary metabolites of chamomile plants. <i>Frontiers in Microbiology</i> , 2014, 5, 64.	1.5	123
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1558	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. <i>BMC Microbiology</i> , 2014, 14, 189.	1.3	292
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1563	Rich bacterial assemblages from Maritime Antarctica (Potter Cove, South Shetlands) reveal several kinds of endemic and undescribed phylotypes. <i>Revista Argentina De Microbiologia</i> , 2014, 46, 218-230.	0.4	5
1564	Strand. , 2014, , .		7
1565	Multiple Omics Uncover Host-Gut Microbial Mutualism During Prebiotic Fructooligosaccharide Supplementation. <i>DNA Research</i> , 2014, 21, 469-480.	1.5	101
1566	Metagenomic Sequencing of Two Salton Sea Microbiomes. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
1567	Hive-stored pollen of honey bees: many lines of evidence are consistent with pollen preservation, not nutrient conversion. <i>Molecular Ecology</i> , 2014, 23, 5904-5917.	2.0	170
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1570	<i>Photobacterium aestuarii</i> sp. nov., a marine bacterium isolated from a tidal flat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 625-630.	0.8	21
1571	Contrasting primary successional trajectories of fungi and bacteria in retreating glacier soils. <i>Molecular Ecology</i> , 2014, 23, 481-497.	2.0	208
1572	Nasopharyngeal colonization by potentially pathogenic bacteria found in healthy semi-captive wild-born chimpanzees in Uganda. <i>American Journal of Primatology</i> , 2014, 76, 103-110.	0.8	10
1573	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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1576	Shotgun microbial profiling of fossil remains. <i>Molecular Ecology</i> , 2014, 23, 1780-1798.	2.0	55
1577	Molecular Characterization of Prokaryotic Communities Associated with Lonar Crater Basalts. <i>Geomicrobiology Journal</i> , 2014, 31, 519-528.	1.0	20
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1582	Environmental bacteria produce abundant and diverse antibiofilm compounds. <i>Journal of Applied Microbiology</i> , 2014, 117, 1663-1673.	1.4	10
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1586	Host-specific microbial communities in three sympatric North Sea sponges. <i>FEMS Microbiology Ecology</i> , 2014, 90, n/a-n/a.	1.3	42

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1590	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
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1622	Characterization and comparison of bacterial communities in benign vocal fold lesions. <i>Microbiome</i> , 2014, 2, 43.	4.9	30
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1696	The bacteriological composition of biomass recovered by flushing an operational drinking water distribution system. <i>Water Research</i> , 2014, 54, 100-114.	5.3	95
1697	Impacts of naturally elevated soil CO ₂ concentrations on communities of soil archaea and bacteria. <i>Soil Biology and Biochemistry</i> , 2014, 68, 348-356.	4.2	53
1698	Analysis of the Gull Fecal Microbial Community Reveals the Dominance of <i>Catellibacterium marimammalium</i> in Relation to Culturable Enterococci. <i>Applied and Environmental Microbiology</i> , 2014, 80, 757-765.	1.4	30

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1700	Diversity and novelty of actinobacteria in Arctic marine sediments. <i>Antonie Van Leeuwenhoek</i> , 2014, 105, 743-754.	0.7	38
1701	Phylogenetic and Functional Analysis of Gut Microbiota of a Fungus-Growing Higher Termite: Bacteroidetes from Higher Termites Are a Rich Source of β -Glucosidase Genes. <i>Microbial Ecology</i> , 2014, 68, 416-425.	1.4	46
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1704	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
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1708	Survival of prokaryotes in a polluted waste dump during remediation by alkaline hydrolysis. <i>Ecotoxicology</i> , 2014, 23, 404-418.	1.1	9
1709	VAMPS: a website for visualization and analysis of microbial population structures. <i>BMC Bioinformatics</i> , 2014, 15, 41.	1.2	189
1710	Stability of the Maternal Gut Microbiota During Late Pregnancy and Early Lactation. <i>Current Microbiology</i> , 2014, 68, 419-427.	1.0	126
1711	Effects of organochlorines on microbial diversity and community structure in <i>Phragmites australis</i> rhizosphere. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4257-4266.	1.7	17
1712	A systematic search for discriminating sites in the 16S ribosomal RNA gene. <i>Microbial Informatics and Experimentation</i> , 2014, 4, 2.	7.6	17
1713	Characterization of Bacterial Communities in Sediments Receiving Various Wastewater Effluents with High-Throughput Sequencing Analysis. <i>Microbial Ecology</i> , 2014, 67, 612-623.	1.4	63
1714	Changes in bacterial and archaeal community assemblages along an ombrotrophic peat bog profile. <i>Biology and Fertility of Soils</i> , 2014, 50, 815-826.	2.3	14
1715	Composition of bacterial communities in sand dunes of subtropical coastal forests. <i>Biology and Fertility of Soils</i> , 2014, 50, 809-814.	2.3	18
1716	Association of dietary type with fecal microbiota in vegetarians and omnivores in Slovenia. <i>European Journal of Nutrition</i> , 2014, 53, 1051-1064.	1.8	155

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1719	Predicting the responsiveness of soil biodiversity to deforestation: a cross-biome study. <i>Global Change Biology</i> , 2014, 20, 2983-2994.	4.2	101
1720	Mutualistic ants as an indirect defence against leaf pathogens. <i>New Phytologist</i> , 2014, 202, 640-650.	3.5	42
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1722	Salivary Microbiota and Metabolome Associated with Celiac Disease. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3416-3425.	1.4	93
1723	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
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1725	Fate of malathion and a phosphonic acid in activated sludge with varying solids retention times. <i>Water Research</i> , 2014, 57, 127-139.	5.3	21
1726	The complete genome sequence for putative <i>H₂S</i> -oxidizer <i>Candidatus Sulfuricum sp.</i> , assembled <i>de novo</i> from an aquifer-derived metagenome. <i>Environmental Microbiology</i> , 2014, 16, 3443-3462.	1.8	69
1727	Pyrosequencing reveals higher impact of silver nanoparticles than Ag ⁺ on the microbial community structure of activated sludge. <i>Water Research</i> , 2014, 48, 317-325.	5.3	155
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1731	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
1732	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
1733	Bacterial community composition of divergent soil habitats in a polar desert. <i>FEMS Microbiology Ecology</i> , 2014, 89, 490-494.	1.3	44
1734	Why are some microbes more ubiquitous than others? Predicting the habitat breadth of soil bacteria. <i>Ecology Letters</i> , 2014, 17, 794-802.	3.0	243

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1736	Aerobic biodegradation of bisphenol A in river sediment and associated bacterial community change. <i>Science of the Total Environment</i> , 2014, 470-471, 1184-1188.	3.9	66
1737	Peatland succession induces a shift in the community composition of <i>Sphagnum</i> -associated active methanotrophs. <i>FEMS Microbiology Ecology</i> , 2014, 88, 596-611.	1.3	50
1738	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
1739	Altered Fecal Microbiota Composition Associated with Food Allergy in Infants. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2546-2554.	1.4	295
1740	Dynamics and functions of bacterial communities in bark, charcoal and sand filters treating greywater. <i>Water Research</i> , 2014, 54, 21-32.	5.3	40
1741	Mosquitoes rely on their gut microbiota for development. <i>Molecular Ecology</i> , 2014, 23, 2727-2739.	2.0	429
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1743	Structure and function of bacterial communities in ageing soils: Insights from the Mendocino ecological staircase. <i>Soil Biology and Biochemistry</i> , 2014, 69, 265-274.	4.2	46
1744	Pyrosequencing survey of intestinal microbiota diversity in cultured sea bass (<i>Dicentrarchus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 1.3 119	1.3	119
1745	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
1746	Global biogeography of <i>Streptomyces</i> antibiotic inhibition, resistance, and resource use. <i>FEMS Microbiology Ecology</i> , 2014, 88, 386-397.	1.3	47
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1752	Dynamics of bacterial and fungal communities associated with eggshells during incubation. <i>Ecology and Evolution</i> , 2014, 4, 1140-1157.	0.8	43

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1756	A glimpse of Escherichia coli O157:H7 survival in soils from eastern China. Science of the Total Environment, 2014, 476-477, 49-56.	3.9	25
1757	Biodegradation of nonylphenol by two alphaproteobacterial strains in liquid culture and sediment microcosm. International Biodeterioration and Biodegradation, 2014, 92, 1-5.	1.9	25
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1759	Diversity and structure of bacterial communities associated with <i>Panerochaete chrysosporium</i> during wood decay. Environmental Microbiology, 2014, 16, 2238-2252.	1.8	51
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1761	An assessment of microbial communities associated with surface mining-disturbed overburden. Environmental Monitoring and Assessment, 2014, 186, 1917-1929.	1.3	29
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1767	Metaproteomics Analysis Reveals the Adaptation Process for the Chicken Gut Microbiota. Applied and Environmental Microbiology, 2014, 80, 478-485.	1.4	65
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1774	Rhizosphere microbiome assemblage is affected by plant development. <i>ISME Journal</i> , 2014, 8, 790-803.	4.4	1,128
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1779	<i>Flaviumibacter solisilvae</i> sp. nov., isolated from forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2897-2901.	0.8	30
1780	High-fat maternal diet during pregnancy persistently alters the offspring microbiome in a primate model. <i>Nature Communications</i> , 2014, 5, 3889.	5.8	361
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1786	SEK: sparsity exploiting k-mer-based estimation of bacterial community composition. <i>Bioinformatics</i> , 2014, 30, 2423-2431.	1.8	11
1787	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
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1794	Response of phyllosphere bacterial communities to elevated CO ₂ during rice growing season. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9459-9471.	1.7	59
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1798	Bacterial profiling in brine samples of the Emalaheni Water Reclamation Plant, South Africa, using 454-pyrosequencing method. <i>FEMS Microbiology Letters</i> , 2014, 359, 55-63.	0.7	11
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1803	Recovery of the Gut Microbiome following Fecal Microbiota Transplantation. <i>MBio</i> , 2014, 5, e00893-14.	1.8	267
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1820	Investigation of bacterial and fungal diversity in tarag using high-throughput sequencing. Journal of Dairy Science, 2014, 97, 6085-6096.	1.4	61
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1827	Application of Qualitative and Quantitative Real-Time PCR, Direct Sequencing, and Terminal Restriction Fragment Length Polymorphism Analysis for Detection and Identification of Polymicrobial 16S rRNA Genes in Ascites. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1754-1757.	1.8	14
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1829	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. <i>Nature</i> , 2014, 514, 508-512.	13.7	366
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1831	Temporal Dynamics of the Cecal Gut Microbiota of Juvenile Arctic Ground Squirrels: a Strong Litter Effect across the First Active Season. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4260-4268.	1.4	15
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1833	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
1834	Endospore-enriched sequencing approach reveals unprecedented diversity of <i>irmicutes</i> in sediments. <i>Environmental Microbiology Reports</i> , 2014, 6, 631-639.	1.0	43
1835	Animal Rennets as Sources of Dairy Lactic Acid Bacteria. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2050-2061.	1.4	42
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1837	Contrasting Response Patterns of Rice Phyllosphere Bacterial Taxa to Elevated CO ₂ . <i>Pedosphere</i> , 2014, 24, 544-552.	2.1	8
1838	Human Mitochondrial DNA and Endogenous Bacterial Surrogates for Risk Assessment of Graywater Reuse. <i>Environmental Science & Technology</i> , 2014, 48, 7993-8002.	4.6	20
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1844	Computational integration of genomic traits into 16S rDNA microbiota sequencing studies. <i>Gene</i> , 2014, 549, 186-191.	1.0	19
1845	Improved resolution of bacteria by high throughput sequence analysis of the rRNA internal transcribed spacer. <i>Journal of Microbiological Methods</i> , 2014, 105, 82-87.	0.7	30
1846	Ethyl tert-butyl ether (ETBE)-degrading microbial communities in enrichments from polluted environments. <i>Journal of Hazardous Materials</i> , 2014, 279, 502-510.	6.5	6
1847	The Human Gut Microbiome as a Screening Tool for Colorectal Cancer. <i>Cancer Prevention Research</i> , 2014, 7, 1112-1121.	0.7	463
1848	Contrasting diversity of epibiotic bacteria and surrounding bacterioplankton of a common submerged macrophyte, <i>Potamogeton crispus</i> , in freshwater lakes. <i>FEMS Microbiology Ecology</i> , 2014, 90, 551-562.	1.3	53
1849	Rhizosphere effect and salinity competing to shape microbial communities in <i>Phragmites australis</i> (Cav.) Trin. ex-Steud. <i>FEMS Microbiology Letters</i> , 2014, 359, 193-200.	0.7	41
1850	Interactions among soil, plants, and microorganisms drive secondary succession in a dry environment. <i>Soil Biology and Biochemistry</i> , 2014, 78, 298-306.	4.2	152
1851	Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. <i>Nature Communications</i> , 2014, 5, 4724.	5.8	302
1852	TRIF Signaling Drives Homeostatic Intestinal Epithelial Antimicrobial Peptide Expression. <i>Journal of Immunology</i> , 2014, 193, 4223-4234.	0.4	29
1854	Gamma proteobacterial Methanotrophs Dominate Cold Methane Seeps in Floodplains of West Siberian Rivers. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5944-5954.	1.4	27
1855	How substrate influences nitrogen transformations in tidal flow constructed wetlands treating high ammonium wastewater?. <i>Ecological Engineering</i> , 2014, 73, 478-486.	1.6	74
1856	Gastrointestinal microbiota of wild and inbred individuals of two house mouse subspecies assessed using high-throughput parallel pyrosequencing. <i>Molecular Ecology</i> , 2014, 23, 5048-5060.	2.0	66
1857	Functional diversification within bacterial lineages promotes wide functional overlapping between taxonomic groups in a Mediterranean forest soil. <i>FEMS Microbiology Ecology</i> , 2014, 90, 54-67.	1.3	18
1858	“Rare biosphere” bacteria as key phenanthrene degraders in coastal seawaters. <i>Environmental Pollution</i> , 2014, 194, 246-253.	3.7	74
1860	MT-Toolbox: improved amplicon sequencing using molecule tags. <i>BMC Bioinformatics</i> , 2014, 15, 284.	1.2	22
1861	Exercise induction of gut microbiota modifications in obese, non-obese and hypertensive rats. <i>BMC Genomics</i> , 2014, 15, 511.	1.2	244
1862	Conservation of streptococcal CRISPRs on human skin and saliva. <i>BMC Microbiology</i> , 2014, 14, 146.	1.3	44
1863	Midichlorians - the biomeme hypothesis: is there a microbial component to religious rituals?. <i>Biology Direct</i> , 2014, 9, 14.	1.9	8

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1864	Salivary glands harbor more diverse microbial communities than gut in <i>Anopheles culicifacies</i> . <i>Parasites and Vectors</i> , 2014, 7, 235.	1.0	101
1865	Comparative assessment of the bacterial communities associated with <i>Aedes aegypti</i> larvae and water from domestic water storage containers. <i>Parasites and Vectors</i> , 2014, 7, 391.	1.0	71
1866	Co-occurrence of driver and passenger bacteria in human colorectal cancer. <i>Gut Pathogens</i> , 2014, 6, 26.	1.6	100
1867	Structure of the gut microbiome following colonization with human feces determines colonic tumor burden. <i>Microbiome</i> , 2014, 2, 20.	4.9	268
1868	Characterization of the nasopharyngeal microbiota in health and during rhinovirus challenge. <i>Microbiome</i> , 2014, 2, 22.	4.9	107
1869	The dynamics of a family's gut microbiota reveal variations on a theme. <i>Microbiome</i> , 2014, 2, 25.	4.9	85
1870	Isolation and enzyme bioprospection of endophytic bacteria associated with plants of Brazilian mangrove ecosystem. <i>SpringerPlus</i> , 2014, 3, 382.	1.2	87
1871	Human oral viruses are personal, persistent and gender-consistent. <i>ISME Journal</i> , 2014, 8, 1753-1767.	4.4	159
1872	Association between BVAB1 and high Nugent scores among women with bacterial vaginosis. <i>Diagnostic Microbiology and Infectious Disease</i> , 2014, 80, 321-323.	0.8	17
1873	Immunoglobulin A Coating Identifies Colitogenic Bacteria in Inflammatory Bowel Disease. <i>Cell</i> , 2014, 158, 1000-1010.	13.5	982
1874	A Hidden Pitfall in the Preparation of Agar Media Undermines Microorganism Cultivability. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7659-7666.	1.4	192
1875	Rate-specific responses of prokaryotic diversity and structure to nitrogen deposition in the <i>Leymus chinensis</i> steppe. <i>Soil Biology and Biochemistry</i> , 2014, 79, 81-90.	4.2	175
1876	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. <i>ISME Journal</i> , 2014, 8, 2431-2444.	4.4	149
1877	Soil type-dependent effects of a potential biocontrol inoculant on indigenous bacterial communities in the rhizosphere of field-grown lettuce. <i>FEMS Microbiology Ecology</i> , 2014, 90, 718-730.	1.3	52
1878	Diversity of bacterioplankton in coastal seawaters of Fildes Peninsula, King George Island, Antarctica. <i>Archives of Microbiology</i> , 2014, 196, 137-147.	1.0	27
1879	Pyrosequencing Reveals the Microbial Communities in the Red Sea Sponge <i>Carteriospongia foliascens</i> and Their Impressive Shifts in Abnormal Tissues. <i>Microbial Ecology</i> , 2014, 68, 621-632.	1.4	37
1880	Pioneer Microbial Communities of the Fimmvörðuháls Lava Flow, Eyjafjallajökull, Iceland. <i>Microbial Ecology</i> , 2014, 68, 504-518.	1.4	48
1881	Bacterial Community Assemblages Associated with the Phyllosphere, Dermosphere, and Rhizosphere of Tree Species of the Atlantic Forest are Host Taxon Dependent. <i>Microbial Ecology</i> , 2014, 68, 567-574.	1.4	92

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1882	Metabolic Characteristics of a Glycogen-Accumulating Organism in <i>DeFluviicoccus</i> Cluster II Revealed by Comparative Genomics. <i>Microbial Ecology</i> , 2014, 68, 716-728.	1.4	22
1883	Tracking human sewage microbiome in a municipal wastewater treatment plant. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3317-3326.	1.7	126
1884	Native soil fungi associated with compostable plastics in three contrasting agricultural settings. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6467-6485.	1.7	39
1885	Diversity, abundance, and spatial distribution of riverine microbial communities response to effluents from swine farm versus farmhouse restaurant. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7597-7608.	1.7	6
1886	Effect of Haylage and Monensin Supplementation on Ruminant Bacterial Communities of Feedlot Cattle. <i>Current Microbiology</i> , 2014, 69, 169-175.	1.0	13
1887	Diversity of Prokaryotic Community at a Shallow Marine Hydrothermal Site Elucidated by Illumina Sequencing Technology. <i>Current Microbiology</i> , 2014, 69, 457-466.	1.0	52
1888	Bacterial Community Survey of <i>Solenopsis invicta</i> Buren (Red imported fire Ant) Colonies in the Presence and Absence of <i>Solenopsis invicta</i> Virus (SINV). <i>Current Microbiology</i> , 2014, 69, 580-585.	1.0	10
1889	Changes in weathering effectiveness and community of culturable mineral-weathering bacteria along a soil profile. <i>Biology and Fertility of Soils</i> , 2014, 50, 1025-1034.	2.3	10
1890	Bacterial colonization of a fumigated alkaline saline soil. <i>Extremophiles</i> , 2014, 18, 733-743.	0.9	4
1891	Geochemistry and microbial ecology in alkaline hot springs of Ambitle Island, Papua New Guinea. <i>Extremophiles</i> , 2014, 18, 763-778.	0.9	25
1892	Bacterial diversity in snow on North Pole ice floes. <i>Extremophiles</i> , 2014, 18, 945-951.	0.9	26
1893	Aspirated bile: a major host trigger modulating respiratory pathogen colonisation in cystic fibrosis patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2014, 33, 1763-1771.	1.3	31
1894	Spatial distribution of bacterial communities in high-altitude freshwater wetland sediment. <i>Limnology</i> , 2014, 15, 249-256.	0.8	38
1895	Gastro-intestinal microbiota of two migratory shorebird species during spring migration staging in Delaware Bay, USA. <i>Journal of Ornithology</i> , 2014, 155, 969-977.	0.5	42
1896	Lysis of Antarctic algal strains by bacterial pathogen. <i>Antonie Van Leeuwenhoek</i> , 2014, 105, 997-1005.	0.7	7
1897	<i>Bartonella</i> -like bacteria carried by domestic mite species. <i>Experimental and Applied Acarology</i> , 2014, 64, 21-32.	0.7	33
1898	Niche partitioning of bacterial communities in biological crusts and soils under grasses, shrubs and trees in the Kalahari. <i>Biodiversity and Conservation</i> , 2014, 23, 1709-1733.	1.2	47
1899	Analyses of dryland biological soil crusts highlight lichens as an important regulator of microbial communities. <i>Biodiversity and Conservation</i> , 2014, 23, 1735-1755.	1.2	72

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1900	Heavy oil exposure increases viral production in natural marine bacterial populations. <i>Journal of Oceanography</i> , 2014, 70, 115-122.	0.7	4
1901	Soil bacterial communities of different natural forest types in Northeast China. <i>Plant and Soil</i> , 2014, 383, 203-216.	1.8	82
1902	Diversity of Bacterial Communities in a Profile of a Winter Wheat Field: Known and Unknown Members. <i>Microbial Ecology</i> , 2014, 68, 822-833.	1.4	31
1903	An improved dual-indexing approach for multiplexed 16S rRNA gene sequencing on the Illumina MiSeq platform. <i>Microbiome</i> , 2014, 2, 6.	4.9	1,454
1904	Comparison of soil bacterial communities in a natural hardwood forest and coniferous plantations in perhumid subtropical low mountains. , 2014, 55, 50.		20
1905	Bacterial community structure in fumigated soil. <i>Soil Biology and Biochemistry</i> , 2014, 73, 122-129.	4.2	26
1906	Implementing sponge physiological and genomic information to enhance the diversity of its culturable associated bacteria. <i>FEMS Microbiology Ecology</i> , 2014, 87, 486-502.	1.3	37
1907	Strong functional stability of soil microbial communities under semiarid Mediterranean conditions and subjected to long-term shifts in baseline precipitation. <i>Soil Biology and Biochemistry</i> , 2014, 69, 223-233.	4.2	121
1908	Long-term changes in soil microbial communities during primary succession. <i>Soil Biology and Biochemistry</i> , 2014, 69, 359-370.	4.2	71
1909	Bacterial composition of soils in ponderosa pine and mixed conifer forests exposed to different wildfire burn severity. <i>Soil Biology and Biochemistry</i> , 2014, 69, 242-250.	4.2	62
1910	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
1911	Recovering glycoside hydrolase genes from active tundra cellulolytic bacteria. <i>Canadian Journal of Microbiology</i> , 2014, 60, 469-476.	0.8	29
1912	Stable Sulfur and Oxygen Isotope Fractionation of Anoxic Sulfide Oxidation by Two Different Enzymatic Pathways. <i>Environmental Science & Technology</i> , 2014, 48, 9094-9102.	4.6	57
1913	Effects of Season and Host Physiological State on the Diversity, Density, and Activity of the Arctic Ground Squirrel Cecal Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5611-5622.	1.4	87
1914	DegePrime, a Program for Degenerate Primer Design for Broad-Taxonomic-Range PCR in Microbial Ecology Studies. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5116-5123.	1.4	355
1915	Biosequestration of lead using <i>Bacillus</i> strains isolated from seleniferous soils and sediments of Punjab. <i>Environmental Science and Pollution Research</i> , 2014, 21, 10186-10193.	2.7	11
1916	Population Analysis of Mesophilic Microbial Fuel Cells Fed with Carbon Monoxide. <i>Applied Biochemistry and Biotechnology</i> , 2014, 172, 713-726.	1.4	19
1917	Identifying airborne fungi in Seoul, Korea using metagenomics. <i>Journal of Microbiology</i> , 2014, 52, 465-472.	1.3	42

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1918	A genomic perspective on a new bacterial genus and species from the Alcaligenaceae family, <i>Basilea psittacipulmonis</i> . BMC Genomics, 2014, 15, 169.	1.2	10
1919	The intestinal microbiome of fish under starvation. BMC Genomics, 2014, 15, 266.	1.2	242
1920	Comparison of methods for fecal microbiome biospecimen collection. BMC Microbiology, 2014, 14, 103.	1.3	150
1921	Polymicrobial airway bacterial communities in adult bronchiectasis patients. BMC Microbiology, 2014, 14, 130.	1.3	50
1922	Natural rice rhizospheric microbes suppress rice blast infections. BMC Plant Biology, 2014, 14, 130.	1.6	188
1923	Amphibian skin may select for rare environmental microbes. ISME Journal, 2014, 8, 2207-2217.	4.4	255
1924	Microbial Successions Are Associated with Changes in Chemical Profiles of a Model Refrigerated Fresh Pork Sausage during an 80-Day Shelf Life Study. Applied and Environmental Microbiology, 2014, 80, 5178-5194.	1.4	69
1925	Indigenous Bacteria and Fungi Drive Traditional Kimoto Sake Fermentations. Applied and Environmental Microbiology, 2014, 80, 5522-5529.	1.4	86
1926	Diversity and Community Structure of Primary Wood-Inhabiting Bacteria in Boreal Forest. Geomicrobiology Journal, 2014, 31, 315-324.	1.0	37
1927	Intestinal Microbiota and Species Diversity of <i>Campylobacter</i> and <i>Helicobacter</i> spp. in Migrating Shorebirds in Delaware Bay. Applied and Environmental Microbiology, 2014, 80, 1838-1847.	1.4	58
1928	<i>Bifidobacterium longum</i> subsp. <i>infantis</i> in experimental necrotizing enterocolitis: alterations in inflammation, innate immune response, and the microbiota. Pediatric Research, 2014, 76, 326-333.	1.1	95
1929	Microbiota in the Throat and Risk Factors for Laryngeal Carcinoma. Applied and Environmental Microbiology, 2014, 80, 7356-7363.	1.4	57
1930	Neotropical Andes hot springs harbor diverse and distinct planktonic microbial communities. FEMS Microbiology Ecology, 2014, 89, 56-66.	1.3	21
1931	Microbial community dynamics during fermentation of doenjang-meju, traditional Korean fermented soybean. International Journal of Food Microbiology, 2014, 185, 112-120.	2.1	123
1932	Aging of fullerene C60 nanoparticle suspensions in the presence of microbes. Water Research, 2014, 65, 282-289.	5.3	26
1933	Differences in vaginal microbiome in African American women versus women of European ancestry. Microbiology (United Kingdom), 2014, 160, 2272-2282.	0.7	390
1934	Response of Different <i>Nitrospira</i> Species To Anoxic Periods Depends on Operational DO. Environmental Science & Technology, 2014, 48, 2934-2941.	4.6	139
1935	To pool or not to pool? Impact of the use of individual and pooled fecal samples for in vitro fermentation studies. Journal of Microbiological Methods, 2014, 107, 1-7.	0.7	89

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1936	Bacterial community variations in an alfalfa-rice rotation system revealed by 16S rRNA gene 454-pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2014, 87, 650-663.	1.3	72
1937	Response of Soil-Associated Microbial Communities to Intrusion of Coal Mine-Derived Acid Mine Drainage. <i>Environmental Science & Technology</i> , 2014, 48, 8556-8563.	4.6	51
1938	Description of <i>Chishuiella changwenlii</i> gen. nov., sp. nov., isolated from freshwater, and transfer of <i>Wautersiella falsenii</i> to the genus <i>Empedobacter</i> as <i>Empedobacter falsenii</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2723-2728.	0.8	45
1939	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
1940	Abiotic stress tolerance and competition-related traits underlie phylogenetic clustering in soil bacterial communities. <i>Ecology Letters</i> , 2014, 17, 1191-1201.	3.0	98
1941	Effects of polycyclic aromatic hydrocarbons on microbial community structure and PAH ring hydroxylating dioxygenase gene abundance in soil. <i>Biodegradation</i> , 2014, 25, 835-847.	1.5	75
1942	Enhanced nucleic acid amplification with blood in situ by wire-guided droplet manipulation (WDM). <i>Biosensors and Bioelectronics</i> , 2014, 53, 167-174.	5.3	23
1943	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
1944	Biogeochemical Processes Governing Natural Pyrite Oxidation and Release of Acid Metalliferous Drainage. <i>Environmental Science & Technology</i> , 2014, 48, 5537-5545.	4.6	84
1945	Aeration remediation of a polluted waterway increases near-surface coarse and culturable microbial aerosols. <i>Science of the Total Environment</i> , 2014, 478, 184-189.	3.9	21
1946	<i>Artemisia</i> supplementation differentially affects the mucosal and luminal ileal microbiota of diet-induced obese mice. <i>Nutrition</i> , 2014, 30, S26-S30.	1.1	9
1947	Use of pyrosequencing to explore the benthic bacterial community structure in a river impacted by wastewater treatment plant discharges. <i>Research in Microbiology</i> , 2014, 165, 468-471.	1.0	30
1948	Comparative assessment of a biofilter, a biotrickling filter and a hollow fiber membrane bioreactor for odor treatment in wastewater treatment plants. <i>Water Research</i> , 2014, 49, 339-350.	5.3	84
1949	Long-term batch brewing accumulates adaptive microbes, which comprehensively produce more flavorful Chinese liquors. <i>Food Research International</i> , 2014, 62, 894-901.	2.9	45
1950	Managing the interactions between sulfate- and perchlorate-reducing bacteria when using hydrogen-fed biofilms to treat a groundwater with a high perchlorate concentration. <i>Water Research</i> , 2014, 55, 215-224.	5.3	57
1951	The source of inoculum plays a defining role in the development of MEC microbial consortia fed with acetic and propionic acid mixtures. <i>Journal of Biotechnology</i> , 2014, 182-183, 11-18.	1.9	52
1952	Bacterial and methanogenic archaeal communities during the single-stage anaerobic digestion of high-strength food wastewater. <i>Bioresource Technology</i> , 2014, 165, 174-182.	4.8	140
1953	Predominance of cluster I <i>Clostridium</i> in hydrogen fermentation of galactose seeded with various heat-treated anaerobic sludges. <i>Bioresource Technology</i> , 2014, 157, 98-106.	4.8	56

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1954	Spatial variability of winter bacterioplankton community composition in the Gulf of Finland (the Tj ETQq0 0 0 rgBT/Qoverlock 10 Tf 50 7	0.9	15
1955	Characterization of the intestinal microbiome of Hirschsprungâ€™s disease with and without enterocolitis. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 269-274.	1.0	50
1956	The headspace of microaerobic reactors: Sulphide-oxidising population and the impact of cleaning on the efficiency of biogas desulphurisation. <i>Bioresource Technology</i> , 2014, 158, 63-73.	4.8	30
1957	A large column analog experiment of stable isotope variations during reactive transport: II. Carbon mass balance, microbial community structure and predation. <i>Geochimica Et Cosmochimica Acta</i> , 2014, 124, 394-409.	1.6	17
1958	Distributions and assemblages of microbial communities along a sediment core retrieved from a potential hydrate-bearing region offshore southwestern Taiwan. <i>Journal of Asian Earth Sciences</i> , 2014, 92, 276-292.	1.0	18
1959	Variations in 16S rRNA-based microbiome profiling between pyrosequencing runs and between pyrosequencing facilities. <i>Journal of Microbiology</i> , 2014, 52, 355-365.	1.3	33
1960	Microbial diversities (16S and 18S rRNA gene pyrosequencing) and environmental pathogens within drinking water biofilms grown on the common premise plumbing materials unplasticized polyvinylchloride and copper. <i>FEMS Microbiology Ecology</i> , 2014, 88, 280-295.	1.3	67
1961	Can marine bacteria be recruited from freshwater sources and the air?. <i>ISME Journal</i> , 2014, 8, 2423-2430.	4.4	55
1962	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. <i>ISME Journal</i> , 2014, 8, 1989-2001.	4.4	221
1963	Human milk oligosaccharides shorten rotavirus-induced diarrhea and modulate piglet mucosal immunity and colonic microbiota. <i>ISME Journal</i> , 2014, 8, 1609-1620.	4.4	129
1964	Is bacterial moisture niche a good predictor of shifts in community composition under longâ€™term drought?. <i>Ecology</i> , 2014, 95, 110-122.	1.5	97
1965	Species matter: the role of competition in the assembly of congeneric bacteria. <i>ISME Journal</i> , 2014, 8, 531-540.	4.4	38
1966	Seasonal changes in dominant bacterial taxa from acidic peatlands of the Atlantic Rain Forest. <i>Research in Microbiology</i> , 2014, 165, 517-525.	1.0	11
1967	Assessing effects of the fungicide tebuconazole to heterotrophic microbes in aquatic microcosms. <i>Science of the Total Environment</i> , 2014, 490, 1002-1011.	3.9	55
1968	Methane abatement in a gas-recycling biotrickling filter: Evaluating innovative operational strategies to overcome mass transfer limitations. <i>Chemical Engineering Journal</i> , 2014, 253, 385-393.	6.6	69
1969	Active and diverse rainwater bacteria collected at an inland site in spring and summer 2011. <i>Atmospheric Environment</i> , 2014, 94, 409-416.	1.9	29
1970	Performance and bacterial enrichment of bioelectrochemical systems during methane and acetate production. <i>International Journal of Hydrogen Energy</i> , 2014, 39, 21864-21875.	3.8	78
1971	rRNA-based monitoring of the microbiota involved in Fontina PDO cheese production in relation to different stages of cow lactation. <i>International Journal of Food Microbiology</i> , 2014, 185, 127-135.	2.1	46

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1972	Soil properties and tree species drive α -diversity of soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2014, 76, 201-209.	4.2	92
1973	Comparison of root-associated communities of native and non-native ectomycorrhizal hosts in an urban landscape. <i>Mycorrhiza</i> , 2014, 24, 267-280.	1.3	21
1974	Enrichment of anodic biofilm inoculated with anaerobic or aerobic sludge in single chambered air-cathode microbial fuel cells. <i>Bioresource Technology</i> , 2014, 167, 124-132.	4.8	120
1975	Chronic impact of sulfamethoxazole on acetate utilization kinetics and population dynamics of fast growing microbial culture. <i>Bioresource Technology</i> , 2014, 166, 219-228.	4.8	15
1976	Structure, inter-annual recurrence, and global-scale connectivity of airborne microbial communities. <i>Science of the Total Environment</i> , 2014, 487, 187-195.	3.9	89
1977	Evaluation of three activated carbons for combined adsorption and biodegradation of PCBs in aquatic sediment. <i>Water Research</i> , 2014, 59, 304-315.	5.3	41
1978	Commensal Bacterial Endocytosis in Epithelial Cells Is Dependent on Myosin Light Chain Kinase-Activated Brush Border Fanning by Interferon- γ . <i>American Journal of Pathology</i> , 2014, 184, 2260-2274.	1.9	45
1979	Conversion of activated-sludge reactors to microbial fuel cells for wastewater treatment coupled to electricity generation. <i>Journal of Bioscience and Bioengineering</i> , 2014, 118, 533-539.	1.1	55
1980	The responses of the taxa composition of particle-attached bacterial community to the decomposition of <i>Microcystis</i> blooms. <i>Science of the Total Environment</i> , 2014, 488-489, 236-242.	3.9	67
1981	Monitoring of the microbiota profile in nukadoko, a naturally fermented rice bran bed for pickling vegetables. <i>Journal of Bioscience and Bioengineering</i> , 2014, 118, 520-525.	1.1	27
1982	Surface soil fungal and bacterial communities in aspen stands are resilient to eleven years of elevated CO ₂ and O ₃ . <i>Soil Biology and Biochemistry</i> , 2014, 76, 227-234.	4.2	29
1983	Dynamic processes of indigenous microorganisms from a low-temperature petroleum reservoir during nutrient stimulation. <i>Journal of Bioscience and Bioengineering</i> , 2014, 117, 215-221.	1.1	25
1984	Impacts of carbon sources on simazine biodegradation by <i>Arthrobacter</i> strain SD3-25 in liquid culture and soil microcosm. <i>International Biodeterioration and Biodegradation</i> , 2014, 89, 1-6.	1.9	28
1985	Effects of enhanced denitrification on hydrodynamics and microbial community structure in a soil column system. <i>Chemosphere</i> , 2014, 111, 112-119.	4.2	38
1986	Effects of Elevated Carbon Dioxide, Elevated Temperature, and Rice Growth Stage on the Community Structure of Rice Root-Associated Bacteria. <i>Microbes and Environments</i> , 2014, 29, 184-190.	0.7	41
1987	Metatranscriptomics reveals overall active bacterial composition in caries lesions. <i>Journal of Oral Microbiology</i> , 2014, 6, 25443.	1.2	125
1988	Integrative workflows for metagenomic analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 70.	1.8	32
1989	Roles of thermophilic thiosulfate-reducing bacteria and methanogenic archaea in the biocorrosion of oil pipelines. <i>Frontiers in Microbiology</i> , 2014, 5, 89.	1.5	57

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1991	Genetically identical co-housed pigs as models for dietary studies of gut microbiomes. Microbiome Science and Medicine, 2014, 1, .	0.3	3
1992	Localized electron transfer rates and microelectrode-based enrichment of microbial communities within a phototrophic microbial mat. Frontiers in Microbiology, 2014, 5, 11.	1.5	31
1993	BOTUX: Bayesian-like operational taxonomic unit examiner. International Journal of Computational Biology and Drug Design, 2014, 7, 130.	0.3	1
1994	Pyrosequencing Analysis Reveals High Population Dynamics of the Soil Microcosm Degrading Octachlorodibenzofuran. Microbes and Environments, 2014, 29, 393-400.	0.7	20
1995	The Bacterial Community Structure of Hydrocarbon-Polluted Marine Environments as the Basis for the Definition of an Ecological Index of Hydrocarbon Exposure. Microbes and Environments, 2014, 29, 269-276.	0.7	32
1996	Time-Resolved DNA Stable Isotope Probing Links <i>Desulfobacteriales</i> - and <i>Coriobacteriaceae</i> -Related Bacteria to Anaerobic Degradation of Benzene under Methanogenic Conditions. Microbes and Environments, 2014, 29, 191-199.	0.7	40
1997	Characterization of Early Microbial Communities on Volcanic Deposits along a Vegetation Gradient on the Island of Miyake, Japan. Microbes and Environments, 2014, 29, 38-49.	0.7	26
1998	A Fine-Scale Phylogenetic Analysis of Free-Living <i>Burkholderia</i> Species in Sugarcane Field Soil. Microbes and Environments, 2014, 29, 434-437.	0.7	24
1999	The effects of intestinal tract bacterial diversity on mortality following allogeneic hematopoietic stem cell transplantation. Blood, 2014, 124, 1174-1182.	0.6	711
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2009	Biodiversity hot spot on a hot spot: novel extremophile diversity in Hawaiian fumaroles. <i>MicrobiologyOpen</i> , 2015, 4, 267-281.	1.2	16
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2012	The stool microbiota of insulin resistant women with recent gestational diabetes, a high risk group for type 2 diabetes. <i>Scientific Reports</i> , 2015, 5, 13212.	1.6	105
2013	Community Analysis of Root- and Tuber-Associated Bacteria in Field-Grown Potato Plants Harboring Different Resistance Levels against Common Scab. <i>Microbes and Environments</i> , 2015, 30, 301-309.	0.7	34
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2043	Aboveground-belowground biodiversity linkages differ in early and late successional temperate forests. <i>Scientific Reports</i> , 2015, 5, 12234.	1.6	20

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2045	Abundance and Diversity of Bacterial Nitrifiers and Denitrifiers and Their Functional Genes in Tannery Wastewater Treatment Plants Revealed by High-Throughput Sequencing. , 2015, , 101-123.		1
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2052	Back to Basics – The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. <i>PLoS ONE</i> , 2015, 10, e0132783.	1.1	437
2053	Evidence of bacterioplankton community adaptation in response to long-term mariculture disturbance. <i>Scientific Reports</i> , 2015, 5, 15274.	1.6	45
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2059	Source Tracking and Succession of Kimchi Lactic Acid Bacteria during Fermentation. <i>Journal of Food Science</i> , 2015, 80, M1871-7.	1.5	77
2060	<sc>metaxa</sc>2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. <i>Molecular Ecology Resources</i> , 2015, 15, 1403-1414.	2.2	426
2061	Freshwater ice as habitat: partitioning of phytoplankton and bacteria between ice and water in central <sc>E</sc>uropean reservoirs. <i>Environmental Microbiology Reports</i> , 2015, 7, 887-898.	1.0	10

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2070	Development of gut inflammation in mice colonized with mucosa-associated bacteria from patients with ulcerative colitis. <i>Gut Pathogens</i> , 2015, 7, 32.	1.6	43
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2072	Strong spurious transcription likely contributes to DNA insert bias in typical metagenomic clone libraries. <i>Microbiome</i> , 2015, 3, 22.	4.9	25
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2081	High diversity of viable bacteria isolated from lymph nodes of slaughter pigs and its possible impacts for food safety. <i>Journal of Applied Microbiology</i> , 2015, 119, 1420-1432.	1.4	20
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2091	Terrestrial origin of bacterial communities in complex boreal freshwater networks. <i>Ecology Letters</i> , 2015, 18, 1198-1206.	3.0	227
2092	Characterisation of the faecal metabolome and microbiome of Thoroughbred racehorses. <i>Equine Veterinary Journal</i> , 2015, 47, 580-586.	0.9	51
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2095	The effect of antibiotics on the microbiome in acute exacerbations of chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2015, 5, 884-893.	1.5	38
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2105	Microbial diversity in shallow water hydrothermal sediments of Kueishan Island, Taiwan as revealed by pyrosequencing. <i>Journal of Basic Microbiology</i> , 2015, 55, 1308-1318.	1.8	34
2106	Temporal dynamics of plant-soil feedback and root-associated fungal communities over 100 years of invasion by a non-native plant. <i>Journal of Ecology</i> , 2015, 103, 1557-1569.	1.9	25
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2122	Archaeal Communities in a Heterogeneous Hypersaline-Alkaline Soil. <i>Archaea</i> , 2015, 2015, 1-11.	2.3	24
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2132	riboFrame: An Improved Method for Microbial Taxonomy Profiling from Non-Targeted Metagenomics. <i>Frontiers in Genetics</i> , 2015, 6, 329.	1.1	15
2133	The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. <i>Frontiers in Genetics</i> , 2015, 6, 348.	1.1	252

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2136	Single cell genomics indicates horizontal gene transfer and viral infections in a deep subsurface Firmicutes population. <i>Frontiers in Microbiology</i> , 2015, 6, 349.	1.5	61
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2138	Benthic microbial communities of coastal terrestrial and ice shelf Antarctic meltwater ponds. <i>Frontiers in Microbiology</i> , 2015, 6, 485.	1.5	28
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2151	Rhizosphere bacterial communities of dominant steppe plants shift in response to a gradient of simulated nitrogen deposition. <i>Frontiers in Microbiology</i> , 2015, 6, 789.	1.5	20

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2153	Response of leaf endophytic bacterial community to elevated CO ₂ at different growth stages of rice plant. <i>Frontiers in Microbiology</i> , 2015, 6, 855.	1.5	26
2154	Microbial mineral colonization across a subsurface redox transition zone. <i>Frontiers in Microbiology</i> , 2015, 6, 858.	1.5	20
2155	The effect of D123 wheat as a companion crop on soil enzyme activities, microbial biomass and microbial communities in the rhizosphere of watermelon. <i>Frontiers in Microbiology</i> , 2015, 6, 899.	1.5	30
2156	Co-occurrence of <i>Methanosarcina mazei</i> and Geobacteraceae in an iron (III)-reducing enrichment culture. <i>Frontiers in Microbiology</i> , 2015, 6, 941.	1.5	43
2157	French invasive Asian tiger mosquito populations harbor reduced bacterial microbiota and genetic diversity compared to Vietnamese autochthonous relatives. <i>Frontiers in Microbiology</i> , 2015, 6, 970.	1.5	86
2158	Metabolomic and high-throughput sequencing analysis—modern approach for the assessment of biodeterioration of materials from historic buildings. <i>Frontiers in Microbiology</i> , 2015, 6, 979.	1.5	86
2159	Bacterial endophyte communities in the foliage of coast redwood and giant sequoia. <i>Frontiers in Microbiology</i> , 2015, 6, 1008.	1.5	49
2160	An abundance of Epsilonproteobacteria revealed in the gut microbiome of the laboratory cultured sea urchin, <i>Lytechinus variegatus</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1047.	1.5	82
2161	Variation in fungal microbiome (mycobiome) and aflatoxin in stored in-shell peanuts at four different areas of China. <i>Frontiers in Microbiology</i> , 2015, 6, 1055.	1.5	37
2162	Rumen microbial communities influence metabolic phenotypes in lambs. <i>Frontiers in Microbiology</i> , 2015, 6, 1060.	1.5	98
2163	Metagenomic analysis of the rumen microbial community following inhibition of methane formation by a halogenated methane analog. <i>Frontiers in Microbiology</i> , 2015, 6, 1087.	1.5	97
2164	Pyrosequencing of the bacteria associated with <i>Platygyra carnosus</i> corals with skeletal growth anomalies reveals differences in bacterial community composition in apparently healthy and diseased tissues. <i>Frontiers in Microbiology</i> , 2015, 6, 1142.	1.5	35
2165	Panamanian frog species host unique skin bacterial communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1171.	1.5	144
2166	Microbiome composition and geochemical characteristics of deep subsurface high-pressure environment, Pyhäsalmi mine Finland. <i>Frontiers in Microbiology</i> , 2015, 6, 1203.	1.5	53
2167	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
2168	Survival of free-living <i>Acholeplasma</i> in aerated pig manure slurry revealed by ¹³ C-labeled bacterial biomass probing. <i>Frontiers in Microbiology</i> , 2015, 6, 1206.	1.5	15
2169	Substrate Type and Free Ammonia Determine Bacterial Community Structure in Full-Scale Mesophilic Anaerobic Digesters Treating Cattle or Swine Manure. <i>Frontiers in Microbiology</i> , 2015, 6, 1337.	1.5	80

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2171	Bacterial Exchange in Household Washing Machines. <i>Frontiers in Microbiology</i> , 2015, 6, 1381.	1.5	64
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2173	Comparative Gut Microbiota of 59 Neotropical Bird Species. <i>Frontiers in Microbiology</i> , 2015, 6, 1403.	1.5	216
2174	Intestinal Microbiota Signatures Associated with Inflammation History in Mice Experiencing Recurring Colitis. <i>Frontiers in Microbiology</i> , 2015, 6, 1408.	1.5	106
2175	Transplanting Soil Microbiomes Leads to Lasting Effects on Willow Growth, but not on the Rhizosphere Microbiome. <i>Frontiers in Microbiology</i> , 2015, 6, 1436.	1.5	98
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2178	Functional Characterization of Bacteria Isolated from Ancient Arctic Soil Exposes Diverse Resistance Mechanisms to Modern Antibiotics. <i>PLoS ONE</i> , 2015, 10, e0069533.	1.1	202
2179	Prokaryotic Diversity in the Rhizosphere of Organic, Intensive, and Transitional Coffee Farms in Brazil. <i>PLoS ONE</i> , 2015, 10, e0106355.	1.1	45
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2182	Endosymbiont Dominated Bacterial Communities in a Dwarf Spider. <i>PLoS ONE</i> , 2015, 10, e0117297.	1.1	52
2183	Biotic Stress Shifted Structure and Abundance of Enterobacteriaceae in the Lettuce Microbiome. <i>PLoS ONE</i> , 2015, 10, e0118068.	1.1	51
2184	Transient Changes in Bacterioplankton Communities Induced by the Submarine Volcanic Eruption of El Hierro (Canary Islands). <i>PLoS ONE</i> , 2015, 10, e0118136.	1.1	22
2185	Deep Sequencing and Ecological Characterization of Gut Microbial Communities of Diverse Bumble Bee Species. <i>PLoS ONE</i> , 2015, 10, e0118566.	1.1	22
2186	The Unique Chemistry of Eastern Mediterranean Water Masses Selects for Distinct Microbial Communities by Depth. <i>PLoS ONE</i> , 2015, 10, e0120605.	1.1	65
2187	Redox-Specialized Bacterioplankton Metacommunity in a Temperate Estuary. <i>PLoS ONE</i> , 2015, 10, e0122304.	1.1	11

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2189	Comprehensive Analysis of a <i>Vibrio parahaemolyticus</i> Strain Extracellular Serine Protease VpSP37. <i>PLoS ONE</i> , 2015, 10, e0126349.	1.1	17
2190	Biochemical Association of Metabolic Profile and Microbiome in Chronic Pressure Ulcer Wounds. <i>PLoS ONE</i> , 2015, 10, e0126735.	1.1	45
2191	<i>Bifidobacterium pseudocatenulatum</i> CECT 7765 Reduces Obesity-Associated Inflammation by Restoring the Lymphocyte-Macrophage Balance and Gut Microbiota Structure in High-Fat Diet-Fed Mice. <i>PLoS ONE</i> , 2015, 10, e0126976.	1.1	179
2192	Microbiome Profiles in Periodontitis in Relation to Host and Disease Characteristics. <i>PLoS ONE</i> , 2015, 10, e0127077.	1.1	99
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2195	Intercropped Silviculture Systems, a Key to Achieving Soil Fungal Community Management in Eucalyptus Plantations. <i>PLoS ONE</i> , 2015, 10, e0118515.	1.1	38
2196	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003929.	1.3	62
2197	Effects of Vaccination with 10-Valent Pneumococcal Non-Typeable <i>Haemophilus influenzae</i> Protein D Conjugate Vaccine (PHiD-CV) on the Nasopharyngeal Microbiome of Kenyan Toddlers. <i>PLoS ONE</i> , 2015, 10, e0128064.	1.1	26
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2199	Esophageal Microbiome in Eosinophilic Esophagitis. <i>PLoS ONE</i> , 2015, 10, e0128346.	1.1	134
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2202	Insights into Diversity and Imputed Metabolic Potential of Bacterial Communities in the Continental Shelf of Agatti Island. <i>PLoS ONE</i> , 2015, 10, e0129864.	1.1	26
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2204	Cultivation-Based and Molecular Assessment of Bacterial Diversity in the Rhizosphere of Wheat under Different Crop Rotations. <i>PLoS ONE</i> , 2015, 10, e0130030.	1.1	47
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2207	Seasonal Dynamics of Marine Microbial Community in the South Sea of Korea. <i>PLoS ONE</i> , 2015, 10, e0131633.	1.1	67
2208	Deep Characterization of the Microbiomes of <i>Calophya</i> spp. (Hemiptera: Calophyidae) Gall-Inducing Psyllids Reveals the Absence of Plant Pathogenic Bacteria and Three Dominant Endosymbionts. <i>PLoS ONE</i> , 2015, 10, e0132248.	1.1	22
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2211	Illumina MiSeq Phylogenetic Amplicon Sequencing Shows a Large Reduction of an Uncharacterised <i>Succinivibrionaceae</i> and an Increase of the <i>Methanobrevibacter gottschalkii</i> Clade in Feed Restricted Cattle. <i>PLoS ONE</i> , 2015, 10, e0133234.	1.1	86
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2215	Cleanroom Maintenance Significantly Reduces Abundance but Not Diversity of Indoor Microbiomes. <i>PLoS ONE</i> , 2015, 10, e0134848.	1.1	56
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2222	Does Dietary Mitigation of Enteric Methane Production Affect Rumen Function and Animal Productivity in Dairy Cows?. <i>PLoS ONE</i> , 2015, 10, e0140282.	1.1	83
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2226	The Characterization of Novel Tissue Microbiota Using an Optimized 16S Metagenomic Sequencing Pipeline. PLoS ONE, 2015, 10, e0142334.	1.1	155
2227	Spatial Homogeneity of Bacterial Communities Associated with the Surface Mucus Layer of the Reef-Building Coral <i>Acropora palmata</i> . PLoS ONE, 2015, 10, e0143790.	1.1	20
2228	Antibiotic Treatment Affects Intestinal Permeability and Gut Microbial Composition in Wistar Rats Dependent on Antibiotic Class. PLoS ONE, 2015, 10, e0144854.	1.1	175
2229	Comparative Analysis of Prokaryotic Communities Associated with Organic and Conventional Farming Systems. PLoS ONE, 2015, 10, e0145072.	1.1	83
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2231	Comparative Metagenomic Profiling of Symbiotic Bacterial Communities Associated with <i>Ixodes persulcatus</i> , <i>Ixodes pavlovskyi</i> and <i>Dermacentor reticulatus</i> Ticks. PLoS ONE, 2015, 10, e0131413.	1.1	41
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2237	Bacterial Diversity Associated with the Coccolithophorid Algae <i>Emiliana huxleyi</i> and <i>Coccolithus pelagicus</i> f. <i>braarudii</i> . <i>BioMed Research International</i> , 2015, 2015, 1-15.	0.9	66
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2239	The effect of polydextrose and probiotic lactobacilli in a <i>Clostridium difficile</i> infected human colonic model. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 27988.	3.8	16
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2245	Characterization of the human gut microbiome during travelers' diarrhea. <i>Gut Microbes</i> , 2015, 6, 110-119.	4.3	111
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2256	Big data analytics and business analytics. <i>Journal of Management Analytics</i> , 2015, 2, 1-21.	1.6	116
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2258	Baiting of rhizosphere bacteria with hyphae of common soil fungi reveals a diverse group of potentially mycophagous secondary consumers. <i>Soil Biology and Biochemistry</i> , 2015, 88, 73-82.	4.2	58
2259	Analyses of soil microbial community compositions and functional genes reveal potential consequences of natural forest succession. <i>Scientific Reports</i> , 2015, 5, 10007.	1.6	162
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2264	Bio-electrochemical characterization of air-cathode microbial fuel cells with microporous polyethylene/silica membrane as separator. <i>Bioelectrochemistry</i> , 2015, 106, 115-124.	2.4	18
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2266	High diversity of skin-associated bacterial communities of marine fishes is promoted by their high variability among body parts, individuals and species. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv061.	1.3	90
2267	Abiotic autumnal organic matter deposition and grazing disturbance effects on epilithic biofilm succession. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv060.	1.3	26
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2269	Microbial community composition of a household sand filter used for arsenic, iron, and manganese removal from groundwater in Vietnam. <i>Chemosphere</i> , 2015, 138, 47-59.	4.2	84
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2274	Analysis of microbial community structure and composition in leachates from a young landfill by 454 pyrosequencing. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5657-5668.	1.7	75
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2276	Targeted disruption of CD1d prevents NKT cell development in pigs. <i>Mammalian Genome</i> , 2015, 26, 264-270.	1.0	20
2277	Microbial communities inhabiting oil-contaminated soils from two major oilfields in Northern China: Implications for active petroleum-degrading capacity. <i>Journal of Microbiology</i> , 2015, 53, 371-378.	1.3	53
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2281	The truth about metagenomics: quantifying and counteracting bias in 16S rRNA studies. <i>BMC Microbiology</i> , 2015, 15, 66.	1.3	388
2282	Comparative metagenomics of biogas-producing microbial communities from production-scale biogas plants operating under wet or dry fermentation conditions. <i>Biotechnology for Biofuels</i> , 2015, 8, 14.	6.2	159
2283	Accelerated methanogenesis from effluents of hydrogen-producing stage in anaerobic digestion by mixed cultures enriched with acetate and nano-sized magnetite particles. <i>Bioresource Technology</i> , 2015, 190, 132-139.	4.8	49
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2294	An Improved K-Means Algorithm for DNA Sequence Clustering. , 2015, , .		6
2295	Modelling content lifespan in online social networks using data mining. <i>International Journal of Web Based Communities</i> , 2015, 11, 234.	0.2	0
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2443	Microbial community composition and diversity in Caspian Sea sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	1.3	70
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2447	Bacterial community structure in treated sewage sludge with mesophilic and thermophilic anaerobic digestion. <i>Folia Microbiologica</i> , 2015, 60, 531-539.	1.1	18
2448	High-throughput assessment of bacterial ecology in hog, cow and ovine casings used in sausages production. <i>International Journal of Food Microbiology</i> , 2015, 212, 49-59.	2.1	26
2449	<i>Lactobacillus rhamnosus</i> lowers zebrafish lipid content by changing gut microbiota and host transcription of genes involved in lipid metabolism. <i>Scientific Reports</i> , 2015, 5, 9336.	1.6	194
2450	Phylogenetic diversity analyses reveal disparity between fungal and bacterial communities during microbial primary succession. <i>Soil Biology and Biochemistry</i> , 2015, 89, 52-60.	4.2	49
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2452	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycoKeys</i> , 0, 10, 1-43.	0.8	409
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2456	Archaeal abundance in post-mortem ruminal digesta may help predict methane emissions from beef cattle. <i>Scientific Reports</i> , 2014, 4, 5892.	1.6	88
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2581	Two decades of warming increases diversity of a potentially lignolytic bacterial community. <i>Frontiers in Microbiology</i> , 2015, 6, 480.	1.5	73
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2583	Composition of bacterial and archaeal communities during landfill refuse decomposition processes. <i>Microbiological Research</i> , 2015, 181, 105-111.	2.5	64
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2588	The Perinatal Microbiome and Pregnancy: Moving Beyond the Vaginal Microbiome. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a023051-a023051.	2.9	101
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2590	Collagen degradation and MMP9 activation by <i>Enterococcus faecalis</i> contribute to intestinal anastomotic leak. <i>Science Translational Medicine</i> , 2015, 7, 286ra68.	5.8	287
2591	Quantitative detection of syntrophic fatty acid-degrading bacterial communities in methanogenic environments. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1189-1197.	0.7	23
2592	The Soil Microbiome Influences Grapevine-Associated Microbiota. <i>MBio</i> , 2015, 6, .	1.8	747
2593	Effect of preservation method on spider monkey (<i>Ateles geoffroyi</i>) fecal microbiota over 8 weeks. <i>Journal of Microbiological Methods</i> , 2015, 113, 16-26.	0.7	118
2594	Composition and activity of endophytic bacterial communities in field-grown maize plants inoculated with <i>Azospirillum brasilense</i> . <i>Annals of Microbiology</i> , 2015, 65, 2187-2200.	1.1	26
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2597	Declining diversity of egg-associated bacteria during development of naturally spawned whitefish embryos (<i>Coregonus</i> spp.). <i>Aquatic Sciences</i> , 2015, 77, 481-497.	0.6	17
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2879	Populations of Stored Product Mite Tyrophagus putrescentiae Differ in Their Bacterial Communities. <i>Frontiers in Microbiology</i> , 2016, 7, 1046.	1.5	43
2880	Biogeographic Distribution Patterns of Bacteria in Typical Chinese Forest Soils. <i>Frontiers in Microbiology</i> , 2016, 7, 1106.	1.5	90
2881	Diet Diversity Is Associated with Beta but not Alpha Diversity of Pika Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 1169.	1.5	117
2882	Diversity and Composition of Bacterial Community in Soils and Lake Sediments from an Arctic Lake Area. <i>Frontiers in Microbiology</i> , 2016, 7, 1170.	1.5	59
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2897	Phytoplankton-Associated Bacterial Community Composition and Succession during Toxic Diatom Bloom and Non-Bloom Events. <i>Frontiers in Microbiology</i> , 2016, 7, 1433.	1.5	60
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3060	Amphibian gut microbiota shifts differentially in community structure but converges on habitat-specific predicted functions. <i>Nature Communications</i> , 2016, 7, 13699.	5.8	145
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3118	Formation of oxygenated polycyclic aromatic hydrocarbons from polycyclic aromatic hydrocarbons during aerobic activated sludge treatment and their removal process. <i>Chemical Engineering Journal</i> , 2016, 302, 50-57.	6.6	28
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3129	Multiple paths of electron flow to current in microbial electrolysis cells fed with low and high concentrations of propionate. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 5999-6011.	1.7	56
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3145	Probiotic Administration in Infants With Gastroschisis. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 62, 852-857.	0.9	17
3146	Independent Benthic Microbial Fuel Cells Powering Sensors and Acoustic Communications with the MARS Underwater Observatory. <i>Journal of Atmospheric and Oceanic Technology</i> , 2016, 33, 607-617.	0.5	28
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3148	Unique microbial-derived volatile organic compounds in portal venous circulation in murine non-alcoholic fatty liver disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1337-1344.	1.8	20
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3155	The Identification of Discriminating Patterns from 16S rRNA Gene to Generate Signature for Bacillus Genus. <i>Journal of Computational Biology</i> , 2016, 23, 651-661.	0.8	8
3156	pH affects bacterial community composition in soils across the Huashan Watershed, China. <i>Canadian Journal of Microbiology</i> , 2016, 62, 726-734.	0.8	6
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3159	Plants of the fynbos biome harbour host species-specific bacterial communities. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw122.	0.7	16
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3457	A watering manipulation in a semiarid grassland induced changes in fungal but not bacterial community composition. <i>Pedobiologia</i> , 2016, 59, 121-127.	0.5	24
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3461	Overcoming organic and nitrogen overload in thermophilic anaerobic digestion of pig slurry by coupling a microbial electrolysis cell. <i>Bioresource Technology</i> , 2016, 216, 362-372.	4.8	66
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3463	Antibiotic-Induced Alterations of the Gut Microbiota Alter Secondary Bile Acid Production and Allow for <i>Clostridium difficile</i> Spore Germination and Outgrowth in the Large Intestine. <i>MSphere</i> , 2016, 1, .	1.3	349
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3612	Identification of bacterial pathogens and races of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> from dry bean fields in Western Canada. <i>Canadian Journal of Plant Pathology</i> , 2016, 38, 41-54.	0.8	6
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3616	Comparison of biogas sludge and raw crop material as source of hydrolytic cultures for anaerobic digestion. <i>Bioresource Technology</i> , 2016, 207, 244-251.	4.8	27
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3688	The change of microbial community from chlorinated solvent-contaminated groundwater after biostimulation using the metagenome analysis. <i>Journal of Hazardous Materials</i> , 2016, 302, 144-150.	6.5	80
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3699	Bacterial diversity indicates dietary overlap among bats of different feeding habits. <i>Microbiological Research</i> , 2016, 182, 99-108.	2.5	42
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3724	Evaluation of organic matter removal and electricity generation by using integrated microbial fuel cells for wastewater treatment. <i>Environmental Technology (United Kingdom)</i> , 2016, 37, 228-236.	1.2	7
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3738	Enhanced summer warming reduces fungal decomposer diversity and litter mass loss more strongly in dry than in wet tundra. <i>Global Change Biology</i> , 2017, 23, 406-420.	4.2	71
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3740	Bacterial community structure in intertidal sediments of Fildes Peninsula, maritime Antarctica. <i>Polar Biology</i> , 2017, 40, 339-349.	0.5	28
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3742	Identification by MALDI-TOF Mass Spectrometry of Mercury-resistant Bacteria Associated with the Rhizosphere of an Apple Orchard. <i>Geomicrobiology Journal</i> , 2017, 34, 176-182.	1.0	7
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3747	Identification of oral bacteria on titanium implant surfaces by 16S rDNA sequencing. <i>Clinical Oral Implants Research</i> , 2017, 28, 697-703.	1.9	22
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3756	Evolution of gut microbiota composition from birth to 24 weeks in the INFANTMET Cohort. <i>Microbiome</i> , 2017, 5, 4.	4.9	390
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3866	Geographic and environmental sources of variation in bacterial community composition in a large-scale municipal landfill site in China. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 761-769.	1.7	30
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3876	Unique Bacteria Community Composition and Co-occurrence in the Milk of Different Ruminants. <i>Scientific Reports</i> , 2017, 7, 40950.	1.6	32
3877	The gut microbiome of hooded cranes (<i>Grus monacha</i>) wintering at Shengjin Lake, China. <i>MicrobiologyOpen</i> , 2017, 6, e00447.	1.2	34
3878	Structural dynamics of microbial communities in polycyclic aromatic hydrocarbon-contaminated tropical estuarine sediments undergoing simulated aerobic biotreatment. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4299-4314.	1.7	20
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3882	Ovarian cycling and reproductive state shape the vaginal microbiota in wild baboons. <i>Microbiome</i> , 2017, 5, 8.	4.9	41
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3891	Safety of <i>Bifidobacterium animalis</i> Subsp. <i>Lactis</i> (<i>B. lactis</i>) Strain BBâ€™12â€™ Supplemented Yogurt in Healthy Children. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2017, 64, 302-309.	0.9	15
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4029	A pea (<i>Pisum sativum</i> L.) seed albumin extract prevents colonic DSS induced dysbiosis in mice. <i>Journal of Functional Foods</i> , 2017, 35, 279-294.	1.6	14
4030	Performance and microbial community dynamics of electricity-assisted sequencing batch reactor (SBR) for treatment of saline petrochemical wastewater. <i>Environmental Science and Pollution Research</i> , 2017, 24, 17556-17565.	2.7	20
4031	Molecular characterization of antibiotic resistance in cultivable multidrug-resistant bacteria from livestock manure. <i>Environmental Pollution</i> , 2017, 229, 188-198.	3.7	66
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4034	Characterisation of lactic acid bacteria in spontaneously fermented camel milk and selection of strains for fermentation of camel milk. <i>International Dairy Journal</i> , 2017, 73, 19-24.	1.5	38
4035	Impacts of diet on hindgut microbiota and short-chain fatty acids in grass carp (<i>Ctenopharyngodon idellus</i>). <i>Aquaculture Research</i> , 2017, 48, 5595-5605.	0.9	60
4036	CD44 deletion leading to attenuation of experimental autoimmune encephalomyelitis results from alterations in gut microbiome in mice. <i>European Journal of Immunology</i> , 2017, 47, 1188-1199.	1.6	40
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4038	PipeCraft: Flexible open-source toolkit for bioinformatics analysis of custom high-throughput amplicon sequencing data. <i>Molecular Ecology Resources</i> , 2017, 17, e234-e240.	2.2	116
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4126	Impacts of cerium oxide nanoparticles on bacterial community in activated sludge. <i>AMB Express</i> , 2017, 7, 63.	1.4	20
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4128	The presence of aggressive ants is associated with fewer insect visits to and altered microbe communities in coffee flowers. <i>Basic and Applied Ecology</i> , 2017, 20, 62-74.	1.2	12
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4136	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
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4143	Duodenal endoluminal barrier sleeve alters gut microbiota of ZDF rats. <i>International Journal of Obesity</i> , 2017, 41, 381-389.	1.6	17
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4155	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
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4164	Agricultural soil denitrifiers possess extensive nitrite reductase gene diversity. <i>Environmental Microbiology</i> , 2017, 19, 1189-1208.	1.8	61
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4168	Depth-resolved microbial community analyses in two contrasting soil cores contaminated by antimony and arsenic. <i>Environmental Pollution</i> , 2017, 221, 244-255.	3.7	60
4169	Determination of the fungal community of pit mud in fermentation cellars for Chinese strong-flavor liquor, using DGGE and Illumina MiSeq sequencing. <i>Food Research International</i> , 2017, 91, 80-87.	2.9	60
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4461	The effects of ibuprofen on activated sludge: Shift in bacterial community structure and resistance to ciprofloxacin. <i>Journal of Hazardous Materials</i> , 2017, 340, 291-299.	6.5	37
4462	<i>Streptococcus</i> sp. in neonatal endotracheal tube biofilms is associated with ventilator-associated pneumonia and enhanced biofilm formation of <i>Pseudomonas aeruginosa</i> PAO1. <i>Scientific Reports</i> , 2017, 7, 3423.	1.6	5

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4475	Responses of earthworms and microbial communities in their guts to Triclosan. <i>Chemosphere</i> , 2017, 168, 1194-1202.	4.2	63
4476	Membrane vesicles in sea water: heterogeneous DNA content and implications for viral abundance estimates. <i>ISME Journal</i> , 2017, 11, 394-404.	4.4	96
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4478	Microbial communities of biomethanization digesters fed with raw and heat pre-treated microalgae biomasses. <i>Chemosphere</i> , 2017, 168, 1013-1021.	4.2	41
4479	Human Oral Buccal Microbiomes Are Associated with Farmworker Status and Azinphos-Methyl Agricultural Pesticide Exposure. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	33
4480	Microbial community analysis of pH 4 thermal springs in Yellowstone National Park. <i>Extremophiles</i> , 2017, 21, 135-152.	0.9	30

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4481	Enrichment of Cryoconite Hole Anaerobes: Implications for the Subglacial Microbiome. <i>Microbial Ecology</i> , 2017, 73, 532-538.	1.4	23
4482	Amplicon-based profiling of bacteria in raw and secondary treated wastewater from treatment plants across Australia. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1253-1266.	1.7	34
4483	Size-related bacterial diversity and tetracycline resistance gene abundance in the air of concentrated poultry feeding operations. <i>Environmental Pollution</i> , 2017, 220, 1342-1348.	3.7	63
4484	Elevated CO ₂ levels modify TiO ₂ nanoparticle effects on rice and soil microbial communities. <i>Science of the Total Environment</i> , 2017, 578, 408-416.	3.9	58
4485	Rational application of treated sewage sludge with urea increases GHG mitigation opportunities in Mediterranean soils. <i>Agriculture, Ecosystems and Environment</i> , 2017, 238, 114-127.	2.5	15
4486	Prevotella and Klebsiella proportions in fecal microbial communities are potential characteristic parameters for patients with major depressive disorder. <i>Journal of Affective Disorders</i> , 2017, 207, 300-304.	2.0	209
4487	Methodology for a vaginal and urinary microbiome study in women with mixed urinary incontinence. <i>International Urogynecology Journal</i> , 2017, 28, 711-720.	0.7	17
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4489	Exploring the diversity of the root-associated microbiome of <i>Ilex paraguariensis</i> St. Hil. (Yerba Mate). <i>Applied Soil Ecology</i> , 2017, 109, 23-31.	2.1	21
4490	Intensified nitrate and phosphorus removal in an electrolysis -integrated horizontal subsurface-flow constructed wetland. <i>Water Research</i> , 2017, 108, 39-45.	5.3	83
4491	Microbial legacies alter decomposition in response to simulated global change. <i>ISME Journal</i> , 2017, 11, 490-499.	4.4	112
4492	High temporal variability in airborne bacterial diversity and abundance inside single-family residences. <i>Indoor Air</i> , 2017, 27, 576-586.	2.0	24
4493	Fungal diversity associated with pulses and its influence on the subsequent wheat crop in the Canadian prairies. <i>Plant and Soil</i> , 2017, 414, 13-31.	1.8	66
4494	Characterizing and contrasting the microbial ecology of laboratory and full-scale EBPR systems cultured on synthetic and real wastewaters. <i>Water Research</i> , 2017, 108, 124-136.	5.3	62
4495	Environmental spread of microbes impacts the development of metabolic phenotypes in mice transplanted with microbial communities from humans. <i>ISME Journal</i> , 2017, 11, 676-690.	4.4	63
4496	Metagenomic Evaluation of Bacteria from Voles. <i>Vector-Borne and Zoonotic Diseases</i> , 2017, 17, 123-133.	0.6	9
4497	Diversity study of microbial community in bacon using metagenomic analysis. <i>Journal of Food Safety</i> , 2017, 37, e12334.	1.1	12
4498	Phyllosphere Metaproteomes of Trees from the Brazilian Atlantic Forest Show High Levels of Functional Redundancy. <i>Microbial Ecology</i> , 2017, 73, 123-134.	1.4	49

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4500	Microbial Nursery Production of High-Quality Biological Soil Crust Biomass for Restoration of Degraded Dryland Soils. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	55
4501	Microbiome analysis shows enrichment for specific bacteria in separate anatomical regions of the deep-sea carnivorous sponge <i>Chondrocladia grandis</i> . <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw214.	1.3	22
4502	An introduction to microbiome analysis for human biology applications. <i>American Journal of Human Biology</i> , 2017, 29, e22931.	0.8	22
4503	Spatial Microbial Composition Along the Gastrointestinal Tract of Captive Attwater's Prairie Chicken. <i>Microbial Ecology</i> , 2017, 73, 966-977.	1.4	21
4504	An in situ inventory of fungi and their associated migrating bacteria in forest soils using fungal highway columns. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw217.	1.3	29
4505	Fe- and S-Metabolizing Microbial Communities Dominate an AMD-Contaminated River Ecosystem and Play Important Roles in Fe and S Cycling. <i>Geomicrobiology Journal</i> , 2017, 34, 695-705.	1.0	24
4506	Impacts of detrital nano- and micro-scale particles (dNP) on contaminant dynamics in a coal mine AMD treatment system. <i>Science of the Total Environment</i> , 2017, 575, 941-955.	3.9	12
4507	Inducing the rhizosphere microbiome by biofertilizer application to suppress banana Fusarium wilt disease. <i>Soil Biology and Biochemistry</i> , 2017, 104, 39-48.	4.2	241
4508	Diversity and oceanic distribution of prasinophytes clade VII, the dominant group of green algae in oceanic waters. <i>ISME Journal</i> , 2017, 11, 512-528.	4.4	70
4509	Combination of zero-valent iron and anaerobic microorganisms immobilized in luffa sponge for degrading 1,1,1-trichloroethane and the relevant microbial community analysis. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 783-796.	1.7	15
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4511	Investigation of different configurations of microbial fuel cells for the treatment of oilfield produced water. <i>Applied Energy</i> , 2017, 192, 457-465.	5.1	67
4512	The dynamic changes and interactional networks of prokaryotic community between co-digestion and mono-digestions of corn stalk and pig manure. <i>Bioresource Technology</i> , 2017, 225, 23-33.	4.8	44
4513	Discordant Temporal Turnovers of Sediment Bacterial and Eukaryotic Communities in Response to Dredging: Nonresilience and Functional Changes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	24
4514	Amplicon-based taxonomic characterization of bacteria in urban and peri-urban roof-harvested rainwater stored in tanks. <i>Science of the Total Environment</i> , 2017, 576, 326-334.	3.9	46
4515	Genome reduction in an abundant and ubiquitous soil bacterium <i>Candidatus Udaeobacter copiosus</i> . <i>Nature Microbiology</i> , 2017, 2, 16198.	5.9	168
4516	Nutrients, heavy metals and microbial communities co-driven distribution of antibiotic resistance genes in adjacent environment of Aquaculture. <i>Environmental Pollution</i> , 2017, 220, 909-918.	3.7	137

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4518	Mannan- and xylooligosaccharides modulate caecal microbiota and expression of inflammatory-related cytokines and reduce caecal <i>Salmonella</i> Enteritidis colonisation in young chickens. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw226.	1.3	50
4519	Preserved Gut Microbial Diversity Accompanies Upregulation of TGR5 and Hepatobiliary Transporters in Bile Acid-Treated Animals Receiving Parenteral Nutrition. <i>Journal of Parenteral and Enteral Nutrition</i> , 2017, 41, 198-207.	1.3	22
4520	Microbial Factors Associated with Postoperative Crohn's Disease Recurrence. <i>Journal of Crohn's and Colitis</i> , 2017, 11, 191-203.	0.6	86
4521	Metal stressors consistently modulate bacterial conjugal plasmid uptake potential in a phylogenetically conserved manner. <i>ISME Journal</i> , 2017, 11, 152-165.	4.4	114
4522	454-Pyrosequencing analysis of highly adapted azo dye-degrading microbial communities in a two-stage anaerobic-aerobic bioreactor treating textile effluent. <i>Environmental Technology (United Kingdom)</i> , 2017, 38, 687-693.	1.2	22
4523	Probiotics, gut microbiota, and their influence on host health and disease. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1600240.	1.5	678
4524	Evaluation of the urinary microbiota of women with uncomplicated stress urinary incontinence. <i>American Journal of Obstetrics and Gynecology</i> , 2017, 216, 55.e1-55.e16.	0.7	133
4525	Anode macrostructures influence electricity generation in microbial fuel cells for wastewater treatment. <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 91-95.	1.1	14
4526	Pyrene biodegradation enhancement potential of lipopeptide biosurfactant produced by <i>Paenibacillus dendritiformis</i> CN5 strain. <i>Journal of Hazardous Materials</i> , 2017, 321, 218-227.	6.5	71
4527	Endolithic microbial diversity in sandstone and granite from the McMurdo Dry Valleys, Antarctica. <i>Polar Biology</i> , 2017, 40, 997-1006.	0.5	99
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4529	Efficacy and safety of electrochemotherapy combined with peritumoral IL-12 gene electrotransfer of canine mast cell tumours. <i>Veterinary and Comparative Oncology</i> , 2017, 15, 641-654.	0.8	66
4530	Long-Term Recovery of Microbial Communities in the Boreal Bryosphere Following Fire Disturbance. <i>Microbial Ecology</i> , 2017, 73, 75-90.	1.4	28
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4533	The Bacterial Community Structure and Dynamics of Carbon and Nitrogen when Maize (<i>Zea mays</i> L.) and Its Neutral Detergent Fibre Were Added to Soil from Zimbabwe with Contrasting Management Practices. <i>Microbial Ecology</i> , 2017, 73, 135-152.	1.4	36
4534	Temperature sensitivity of soil respiration: Synthetic effects of nitrogen and phosphorus fertilization on Chinese Loess Plateau. <i>Science of the Total Environment</i> , 2017, 574, 1665-1673.	3.9	29

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4536	Diversity and temporal patterns of planktonic protist assemblages at a Mediterranean Long Term Ecological Research site. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw200.	1.3	173
4537	Seasonal variation in an acid mine drainage microbial community. <i>Canadian Journal of Microbiology</i> , 2017, 63, 137-152.	0.8	16
4538	D-tryptophan from probiotic bacteria influences the gut microbiome and allergic airway disease. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1525-1535.	1.5	119
4539	Effects of polysaccharide from mycelia of <i>Ganoderma lucidum</i> on intestinal barrier functions of rats. <i>International Journal of Biological Macromolecules</i> , 2017, 94, 1-9.	3.6	102
4540	Significant relationship between soil bacterial community structure and incidence of bacterial wilt disease under continuous cropping system. <i>Archives of Microbiology</i> , 2017, 199, 267-275.	1.0	111
4541	Microenvironmental heterogeneity of gut compartments drives bacterial community structure in wood- and humus-feeding higher termites. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw210.	1.3	59
4542	Bacterial community succession and metabolite changes during doubanjiang-meju fermentation, a Chinese traditional fermented broad bean (<i>Vicia faba</i> L.) paste. <i>Food Chemistry</i> , 2017, 218, 534-542.	4.2	118
4543	Bacteria in drinking water sources of a First Nation reserve in Canada. <i>Science of the Total Environment</i> , 2017, 575, 813-819.	3.9	32
4544	Groundwater shapes sediment biogeochemistry and microbial diversity in a submerged Great Lake sinkhole. <i>Geobiology</i> , 2017, 15, 225-239.	1.1	26
4545	Cutaneous Bacterial Communities of a Poisonous Salamander: a Perspective from Life Stages, Body Parts and Environmental Conditions. <i>Microbial Ecology</i> , 2017, 73, 455-465.	1.4	29
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4548	Culture-independent study of bacterial communities in tropical river sediment. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 200-209.	0.6	8
4549	Biochar increases arsenic release from an anaerobic paddy soil due to enhanced microbial reduction of iron and arsenic. <i>Environmental Pollution</i> , 2017, 220, 514-522.	3.7	143
4550	Environmental and physiological factors shape the gut microbiota of Atlantic salmon parr (<i>Salmo</i>) Tj ETQq1 1 0.784314 rgBT/Overlode	1.7	354
4551	A Window to the Subsurface: Microbial Diversity in Hot Springs of a Sulfidic Cave (Kaklik, Turkey). <i>Geomicrobiology Journal</i> , 2017, 34, 374-384.	1.0	12
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4554	Removal of nitrogen and phosphorus by heterotrophic nitrification-aerobic denitrification of a denitrifying phosphorus-accumulating bacterium <i>Enterobacter cloacae</i> HW-15. <i>Ecological Engineering</i> , 2017, 99, 199-208.	1.6	94
4555	Eye of the Finch: characterization of the ocular microbiome of house finches in relation to mycoplasmal conjunctivitis. <i>Environmental Microbiology</i> , 2017, 19, 1439-1449.	1.8	17
4556	Dual-specificity phosphatase 6 deficiency regulates gut microbiome and transcriptome response against diet-induced obesity in mice. <i>Nature Microbiology</i> , 2017, 2, 16220.	5.9	47
4557	Microbial community structure of surface sediments from a tropical estuarine environment using next generation sequencing. <i>Ecological Indicators</i> , 2017, 74, 172-181.	2.6	30
4558	Root isoflavonoids and hairy root transformation influence key bacterial taxa in the soybean rhizosphere. <i>Environmental Microbiology</i> , 2017, 19, 1391-1406.	1.8	42
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4561	Long-term effects of nickel oxide nanoparticles on performance, microbial enzymatic activity, and microbial community of a sequencing batch reactor. <i>Chemosphere</i> , 2017, 169, 387-395.	4.2	23
4562	Coastal marine habitats harbor novel early-diverging fungal diversity. <i>Fungal Ecology</i> , 2017, 25, 1-13.	0.7	116
4563	Diversity of free-living nitrogen fixing <i>Streptomyces</i> in soils of the badlands of South Dakota. <i>Microbiological Research</i> , 2017, 195, 31-39.	2.5	98
4564	Evidence of microbiota dysbiosis in chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2017, 7, 230-239.	1.5	143
4565	Monitoring the mycobiota during Greco di Tufo and Aglianico wine fermentation by 18S rRNA gene sequencing. <i>Food Microbiology</i> , 2017, 63, 117-122.	2.1	35
4566	Contribution of different dispersal sources to the metabolic response of lake bacterioplankton following a salinity change. <i>Environmental Microbiology</i> , 2017, 19, 251-260.	1.8	19
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4568	High-throughput Sequencing of Viable Microbial Communities in Raw Pork Subjected to a Fast Cooling Process. <i>Journal of Food Science</i> , 2017, 82, 145-153.	1.5	14
4569	The role of microbiota in compensatory growth of protein-restricted rats. <i>Microbial Biotechnology</i> , 2017, 10, 480-491.	2.0	16
4570	Plant domestication and the assembly of bacterial and fungal communities associated with strains of the common sunflower, <i>Helianthus annuus</i> . <i>New Phytologist</i> , 2017, 214, 412-423.	3.5	185

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4572	Diversity, abundance, and possible sources of fecal bacteria in the Yangtze River. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2143-2152.	1.7	28
4573	Role of Lactic Acid Bacteria in the Eating Qualities of Fermented Rice Noodles. <i>Cereal Chemistry</i> , 2017, 94, 349-356.	1.1	19
4574	Disruption of plant-soil microbial relationships influences plant growth. <i>Journal of Ecology</i> , 2017, 105, 816-827.	1.9	26
4575	Honey bee gut microbial communities are robust to the fungicide Pristine® consumed in pollen. <i>Apidologie</i> , 2017, 48, 340-352.	0.9	21
4576	Experimental metagenomics and ribosomal profiling of the human skin microbiome. <i>Experimental Dermatology</i> , 2017, 26, 211-219.	1.4	34
4577	Fucosylation Deficiency in Mice Leads to Colitis and Adenocarcinoma. <i>Gastroenterology</i> , 2017, 152, 193-205.e10.	0.6	48
4578	Changes in the bacterial microbiome of patients with chronic rhinosinusitis after endoscopic sinus surgery. <i>International Forum of Allergy and Rhinology</i> , 2017, 7, 7-15.	1.5	39
4579	Microbial responses to various process disturbances in a continuous hydrogen reactor fed with galactose. <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 216-222.	1.1	17
4580	Based on BP Neural Network Classification of Medical History of Traditional Chinese Medicine Literature Research. , 2017, , .		1
4581	Comparison of the gut microbiota composition between wild and captive sika deer (<i>Cervus nippon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.4	102
4582	Recruitment and establishment of the gut microbiome in arctic shorebirds. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	64
4583	Intraruminal infusion of oligofructose alters ruminal microbiota and induces acute laminitis in sheep. <i>Journal of Animal Science</i> , 2017, 95, 5407-5419.	0.2	5
4584	High-throughput sequencing revealed novel Dehalococcoidia in dechlorinating microbial enrichments from PCB-contaminated marine sediments. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	21
4585	Assessment of bacterial communities of black soybean grown in fields. <i>Communicative and Integrative Biology</i> , 2017, 10, e1378290.	0.6	5
4586	Comparison of Thaumarchaeotal populations from four deep sea basins. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	15
4587	Eikelboom filamentous morphotypes 0675 and 0041 embrace members of the Chloroflexi: resolving their phylogeny, and design of fluorescence in situ hybridisation probes for their identification. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	17
4588	Gut region influences the diversity and interactions of bacterial communities in pikas (<i>Ochotona</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.3	28

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4590	Plant-plant competition outcomes are modulated by plant effects on the soil bacterial community. <i>Scientific Reports</i> , 2017, 7, 17756.	1.6	66
4591	Possible role of the gut microbiotaâ€œbrain axis in the antidepressant effects of (R)-ketamine in a social defeat stress model. <i>Translational Psychiatry</i> , 2017, 7, 1294.	2.4	173
4592	Ground <i>Juniperus pinchotii</i> and urea in supplements fed to Rambouillet ewe lambs Part 2: Ewe lamb rumen microbial communities1. <i>Journal of Animal Science</i> , 2017, 95, 4587-4599.	0.2	15
4593	A switch of chlorinated substrate causes emergence of a previously undetected native <i>Dehalobacter</i> population in an established <i>Dehalococcoides</i> -dominated chloroethene-dechlorinating enrichment culture. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	10
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4595	Reconciliation between operational taxonomic units and species boundaries. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	71
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4597	Unravelling vaginal microbial genetic diversity and abundance between Holstein and Fleckvieh cattle. <i>RSC Advances</i> , 2017, 7, 56137-56143.	1.7	9
4598	The modularity of microbial interaction network in healthy human saliva: Stability and specificity. , 2017, , .		3
4599	Variations in airborne bacterial communities at high altitudes over the Noto Peninsula (Japan) in response to Asian dust events. <i>Atmospheric Chemistry and Physics</i> , 2017, 17, 11877-11897.	1.9	58
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4601	Upper and lower respiratory tract microbiota in horses: bacterial communities associated with health and mild asthma (inflammatory airway disease) and effects of dexamethasone. <i>BMC Microbiology</i> , 2017, 17, 184.	1.3	49
4602	<i>Faecalibacterium</i> Gut Colonization Is Accelerated by Presence of Older Siblings. <i>MSphere</i> , 2017, 2, .	1.3	37
4603	IL-17 signalling restructures the nasal microbiome and drives dynamic changes following <i>Streptococcus pneumoniae</i> colonization. <i>BMC Genomics</i> , 2017, 18, 807.	1.2	12
4604	A phylogeny-free microbiome dysbiosis detection pipeline for non-invasive disease diagnosis. , 2017, , .		0
4605	Impact of hypoxia on gene expression patterns by the human pathogen, <i>Vibrio vulnificus</i> , and bacterial community composition in a North Carolina estuary. <i>GeoHealth</i> , 2017, 1, 37-50.	1.9	7
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4608	An approach for detecting groundwater runoff connectivity using cluster analysis. , 2017, , .		0
4609	Bacterial Communities Associated With the Pine Wilt Disease Vector <i>Monoctonus alternatus</i> (Coleoptera: Cerambycidae) During Different Larval Instars. <i>Journal of Insect Science</i> , 2017, 17, .	0.6	7
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4614	Natural history and conservation of the rediscovered Hula painted frog, <i>Latonia nigriventer</i> . <i>Contributions To Zoology</i> , 2017, 86, 11-37.	0.2	16
4615	You Are What You Eat: A Genomic Analysis of the Gut Microbiome of Captive and Wild <i>Octopus vulgaris</i> Paralarvae and Their Zooplankton Prey. <i>Frontiers in Physiology</i> , 2017, 8, 362.	1.3	27
4616	Variation of Soil Bacterial Communities in a Chronosequence of Rubber Tree (<i>Hevea brasiliensis</i>) Plantations. <i>Frontiers in Plant Science</i> , 2017, 8, 849.	1.7	68
4617	The Influence of Land Use Intensity on the Plant-Associated Microbiome of <i>Dactylis glomerata</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 930.	1.7	57
4618	Dominant Groups of Potentially Active Bacteria Shared by Barley Seeds become Less Abundant in Root Associated Microbiome. <i>Frontiers in Plant Science</i> , 2017, 8, 1005.	1.7	70
4619	Template Preparation Affects 16S rRNA High-Throughput Sequencing Analysis of Phyllosphere Microbial Communities. <i>Frontiers in Plant Science</i> , 2017, 8, 1623.	1.7	14
4620	Individual Signatures Define Canine Skin Microbiota Composition and Variability. <i>Frontiers in Veterinary Science</i> , 2017, 4, 6.	0.9	26
4621	Aislamiento de microorganismos electrogÃ©nicos con potencial para reducir cromo hexavalente. <i>Acta Biologica Colombiana</i> , 2017, 22, 27.	0.1	1
4622	Starter feeding altered ruminal epithelial bacterial communities and some key immune-related genes' expression before weaning in lambs. <i>Journal of Animal Science</i> , 2017, 95, 910-921.	0.2	21
4623	Gut Microbiota Analysis Results Are Highly Dependent on the 16S rRNA Gene Target Region, Whereas the Impact of DNA Extraction Is Minor. <i>Journal of Biomolecular Techniques</i> , 2017, 28, 19-30.	0.8	130
4624	A Place to Call Home: An Analysis of the Bacterial Communities in Two <i>Tethya rubra</i> Samaai and Gibbons 2005 Populations in Algoa Bay, South Africa. <i>Marine Drugs</i> , 2017, 15, 95.	2.2	11

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4628	Chlorogenic Acid Ameliorates Experimental Colitis by Promoting Growth of <i>Akkermansia</i> in Mice. <i>Nutrients</i> , 2017, 9, 677.	1.7	116
4629	Deep Learning in Medical Imaging: General Overview. <i>Korean Journal of Radiology</i> , 2017, 18, 570.	1.5	834
4630	Assessment of <i>Bifidobacterium</i> Species Using <i>groEL</i> Gene on the Basis of Illumina MiSeq High-Throughput Sequencing. <i>Genes</i> , 2017, 8, 336.	1.0	38
4631	Analysis of Bacterial Community Composition of Corroded Steel Immersed in Sanya and Xiamen Seawaters in China via Method of Illumina MiSeq Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 1737.	1.5	43
4632	Microbial Succession and the Dynamics of Chemical Compounds during the Solid-State Fermentation of Pu-erh Tea. <i>Applied Sciences (Switzerland)</i> , 2017, 7, 166.	1.3	29
4633	Onshore Wind Speed Modulates Microbial Aerosols along an Urban Waterfront. <i>Atmosphere</i> , 2017, 8, 215.	1.0	16
4634	Dietary Milk Sphingomyelin Reduces Systemic Inflammation in Diet-Induced Obese Mice and Inhibits LPS Activity in Macrophages. <i>Beverages</i> , 2017, 3, 37.	1.3	30
4635	Bayesian Inference of Ecological Interactions from Spatial Data. <i>Entropy</i> , 2017, 19, 547.	1.1	14
4636	Fault Diagnosis of Rolling Bearings Based on EWT and KDEC. <i>Entropy</i> , 2017, 19, 633.	1.1	15
4637	Differences in the Bacteriome of Smokeless Tobacco Products with Different Oral Carcinogenicity: Compositional and Predicted Functional Analysis. <i>Genes</i> , 2017, 8, 106.	1.0	47
4638	Effects of Short-Term Set-Aside Management Practices on Soil Microorganism and Enzyme Activity in China. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 913.	1.2	7
4639	The Cause of Death of a Child in the 18th Century Solved by Bone Microbiome Typing Using Laser Microdissection and Next Generation Sequencing. <i>International Journal of Molecular Sciences</i> , 2017, 18, 109.	1.8	10
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4641	The Intestinal Eukaryotic and Bacterial Biome of Spotted Hyenas: The Impact of Social Status and Age on Diversity and Composition. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 262.	1.8	34
4642	Urinary Microbiome and Psychological Factors in Women with Overactive Bladder. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 488.	1.8	79

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4645	Microbial Community Structure and Interannual Change in the Last Epishelf Lake Ecosystem in the North Polar Region. <i>Frontiers in Marine Science</i> , 2017, 3, .	1.2	21
4646	Metabarcoding Reveals Seasonal and Temperature-Dependent Succession of Zooplankton Communities in the Red Sea. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	23
4647	Cryptic Zooplankton Diversity Revealed by a Metagenetic Approach to Monitoring Metazoan Communities in the Coastal Waters of the Okhotsk Sea, Northeastern Hokkaido. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	33
4648	Acidification Enhances Hybrid N ₂ O Production Associated with Aquatic Ammonia-Oxidizing Microorganisms. <i>Frontiers in Microbiology</i> , 2016, 7, 2104.	1.5	45
4649	Nutritional Models of Experimentally-Induced Subacute Ruminant Acidosis (SARA) Differ in Their Impact on Rumen and Hindgut Bacterial Communities in Dairy Cows. <i>Frontiers in Microbiology</i> , 2016, 7, 2128.	1.5	97
4650	Sampling Modification Effects in the Subgingival Microbiome Profile of Healthy Children. <i>Frontiers in Microbiology</i> , 2017, 7, 2142.	1.5	13
4651	Linking Periparturient Dynamics of Ruminant Microbiota to Dietary Changes and Production Parameters. <i>Frontiers in Microbiology</i> , 2017, 7, 2143.	1.5	58
4652	Human Catestatin Alters Gut Microbiota Composition in Mice. <i>Frontiers in Microbiology</i> , 2016, 7, 2151.	1.5	37
4653	A New Approach to Modify Plant Microbiomes and Traits by Introducing Beneficial Bacteria at Flowering into Progeny Seeds. <i>Frontiers in Microbiology</i> , 2017, 8, 11.	1.5	313
4654	Temporal Stability and the Effect of Transgenerational Transfer on Fecal Microbiota Structure in a Long Distance Migratory Bird. <i>Frontiers in Microbiology</i> , 2017, 8, 50.	1.5	70
4655	Geological and Geochemical Controls on Subsurface Microbial Life in the Samail Ophiolite, Oman. <i>Frontiers in Microbiology</i> , 2017, 8, 56.	1.5	126
4656	Home-Made Cost Effective Preservation Buffer Is a Better Alternative to Commercial Preservation Methods for Microbiome Research. <i>Frontiers in Microbiology</i> , 2017, 8, 102.	1.5	73
4657	High Prevalence of Gammaproteobacteria in the Sediments of Admiralty Bay and North Bransfield Basin, Northwestern Antarctic Peninsula. <i>Frontiers in Microbiology</i> , 2017, 08, 153.	1.5	40
4658	Critical Issues in Mycobiota Analysis. <i>Frontiers in Microbiology</i> , 2017, 8, 180.	1.5	83
4659	Methane Production in Dairy Cows Correlates with Rumen Methanogenic and Bacterial Community Structure. <i>Frontiers in Microbiology</i> , 2017, 8, 226.	1.5	218
4660	Fungal ITS1 Deep-Sequencing Strategies to Reconstruct the Composition of a 26-Species Community and Evaluation of the Gut Mycobiota of Healthy Japanese Individuals. <i>Frontiers in Microbiology</i> , 2017, 8, 238.	1.5	79

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4662	Bacterial Community and PHB-Accumulating Bacteria Associated with the Wall and Specialized Niches of the Hindgut of the Forest Cockchafer (<i>Melolontha hippocastani</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 291.	1.5	24
4663	Compositional Stability of the Bacterial Community in a Climate-Sensitive Sub-Arctic Peatland. <i>Frontiers in Microbiology</i> , 2017, 8, 317.	1.5	20
4664	Effects of Copper Addition on Copper Resistance, Antibiotic Resistance Genes, and intl1 during Swine Manure Composting. <i>Frontiers in Microbiology</i> , 2017, 8, 344.	1.5	107
4665	Short-Term Exposure of Paddy Soil Microbial Communities to Salt Stress Triggers Different Transcriptional Responses of Key Taxonomic Groups. <i>Frontiers in Microbiology</i> , 2017, 8, 400.	1.5	19
4666	Members of the Oral Microbiota Are Associated with IL-8 Release by Gingival Epithelial Cells in Healthy Individuals. <i>Frontiers in Microbiology</i> , 2017, 08, 416.	1.5	17
4667	Starter Feeding Supplementation Alters Colonic Mucosal Bacterial Communities and Modulates Mucosal Immune Homeostasis in Newborn Lambs. <i>Frontiers in Microbiology</i> , 2017, 8, 429.	1.5	60
4668	Reactivation of Deep Subsurface Microbial Community in Response to Methane or Methanol Amendment. <i>Frontiers in Microbiology</i> , 2017, 08, 431.	1.5	28
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4670	Structure and Function of the Fecal Microbiota in Diarrheic Neonatal Piglets. <i>Frontiers in Microbiology</i> , 2017, 8, 502.	1.5	103
4671	Mosquito Microbiome Dynamics, a Background for Prevalence and Seasonality of West Nile Virus. <i>Frontiers in Microbiology</i> , 2017, 8, 526.	1.5	114
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4673	Biochar Addition Increases the Rates of Dissimilatory Iron Reduction and Methanogenesis in Ferrihydrite Enrichments. <i>Frontiers in Microbiology</i> , 2017, 8, 589.	1.5	31
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4675	Bioreactor Scalability: Laboratory-Scale Bioreactor Design Influences Performance, Ecology, and Community Physiology in Expanded Granular Sludge Bed Bioreactors. <i>Frontiers in Microbiology</i> , 2017, 8, 664.	1.5	36
4676	Arbuscular and Ectomycorrhizal Fungi Associated with the Invasive Brazilian Pepper Tree (<i>Schinus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	1.5	18
4677	Guar Gum Stimulates Biogenic Sulfide Production at Elevated Pressures: Implications for Shale Gas Extraction. <i>Frontiers in Microbiology</i> , 2017, 8, 679.	1.5	14
4678	A Critical Assessment of the Microorganisms Proposed to be Important to Enhanced Biological Phosphorus Removal in Full-Scale Wastewater Treatment Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 718.	1.5	212

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4680	Biogeographic Comparison of Lophelia-Associated Bacterial Communities in the Western Atlantic Reveals Conserved Core Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 796.	1.5	50
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4682	Global Diversity of Desert Hypolithic Cyanobacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 867.	1.5	61
4683	Evaluating the Detection of Hydrocarbon-Degrading Bacteria in 16S rRNA Gene Sequencing Surveys. <i>Frontiers in Microbiology</i> , 2017, 8, 896.	1.5	25
4684	Modulation of the Gut Microbiota by Krill Oil in Mice Fed a High-Sugar High-Fat Diet. <i>Frontiers in Microbiology</i> , 2017, 8, 905.	1.5	54
4685	Impact of Ferrous Iron on Microbial Community of the Biofilm in Microbial Fuel Cells. <i>Frontiers in Microbiology</i> , 2017, 8, 920.	1.5	19
4686	Methanogenic Community Was Stable in Two Contrasting Freshwater Marshes Exposed to Elevated Atmospheric CO ₂ . <i>Frontiers in Microbiology</i> , 2017, 8, 932.	1.5	10
4687	Cable Bacteria and the Bioelectrochemical Snorkel: The Natural and Engineered Facets Playing a Role in Hydrocarbons Degradation in Marine Sediments. <i>Frontiers in Microbiology</i> , 2017, 8, 952.	1.5	48
4688	Multigenerational Influences of the Fut2 Gene on the Dynamics of the Gut Microbiota in Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 991.	1.5	20
4689	Long-Term Survey Is Necessary to Reveal Various Shifts of Microbial Composition in Corals. <i>Frontiers in Microbiology</i> , 2017, 8, 1094.	1.5	38
4690	Monensin and Nisin Affect Rumen Fermentation and Microbiota Differently In Vitro. <i>Frontiers in Microbiology</i> , 2017, 8, 1111.	1.5	63
4691	Temporal Dynamics of Soil Microbial Communities below the Seedbed under Two Contrasting Tillage Regimes. <i>Frontiers in Microbiology</i> , 2017, 8, 1127.	1.5	124
4692	Oropharyngeal and Sputum Microbiomes Are Similar Following Exacerbation of Chronic Obstructive Pulmonary Disease. <i>Frontiers in Microbiology</i> , 2017, 8, 1163.	1.5	26
4693	Cyanobacterial Diversity in Microbial Mats from the Hypersaline Lagoon System of Araruama, Brazil: An In-depth Polyphasic Study. <i>Frontiers in Microbiology</i> , 2017, 8, 1233.	1.5	38
4694	Nutrient and Rainfall Additions Shift Phylogenetically Estimated Traits of Soil Microbial Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 1271.	1.5	25
4695	Fertilization Shapes Bacterial Community Structure by Alteration of Soil pH. <i>Frontiers in Microbiology</i> , 2017, 8, 1325.	1.5	183
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4698	Temporal Microbial Community Dynamics in Microbial Electrolysis Cells – Influence of Acetate and Propionate Concentration. <i>Frontiers in Microbiology</i> , 2017, 8, 1371.	1.5	27
4699	Cutaneous Microbial Community Variation across Populations of Eastern Hellbenders (<i>Cryptobranchus alleganiensis alleganiensis</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 1379.	1.5	39
4700	The Cyanobacteria-Dominated Sponge <i>Dactylospongia elegans</i> in the South China Sea: Prokaryotic Community and Metagenomic Insights. <i>Frontiers in Microbiology</i> , 2017, 8, 1387.	1.5	15
4701	Watershed Urbanization Linked to Differences in Stream Bacterial Community Composition. <i>Frontiers in Microbiology</i> , 2017, 8, 1452.	1.5	94
4702	Crop Establishment Practices Are a Driver of the Plant Microbiota in Winter Oilseed Rape (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.5	34
4703	Changes in the Total Fecal Bacterial Population in Individual Horses Maintained on a Restricted Diet Over 6 Weeks. <i>Frontiers in Microbiology</i> , 2017, 8, 1502.	1.5	37
4704	The Rhizosphere Bacterial Microbiota of <i>Vitis vinifera</i> cv. Pinot Noir in an Integrated Pest Management Vineyard. <i>Frontiers in Microbiology</i> , 2017, 8, 1528.	1.5	76
4705	Host Ecology Rather Than Host Phylogeny Drives Amphibian Skin Microbial Community Structure in the Biodiversity Hotspot of Madagascar. <i>Frontiers in Microbiology</i> , 2017, 8, 1530.	1.5	116
4706	Unraveling the Fecal Microbiota and Metagenomic Functional Capacity Associated with Feed Efficiency in Pigs. <i>Frontiers in Microbiology</i> , 2017, 8, 1555.	1.5	171
4707	Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. <i>Frontiers in Microbiology</i> , 2017, 8, 1561.	1.5	265
4708	Culture Media and Individual Hosts Affect the Recovery of Culturable Bacterial Diversity from Amphibian Skin. <i>Frontiers in Microbiology</i> , 2017, 8, 1574.	1.5	35
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4710	Succession and Fermentation Products of Grass Carp (<i>Ctenopharyngodon idellus</i>) Hindgut Microbiota in Response to an Extreme Dietary Shift. <i>Frontiers in Microbiology</i> , 2017, 8, 1585.	1.5	77
4711	High-Resolution Microbiome Profiling for Detection and Tracking of <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1587.	1.5	31
4712	A Structural and Functional Elucidation of the Rumen Microbiome Influenced by Various Diets and Microenvironments. <i>Frontiers in Microbiology</i> , 2017, 8, 1605.	1.5	207
4713	Prophylactic Supplementation of <i>Bifidobacterium longum</i> 51A Protects Mice from Ovariectomy-Induced Exacerbated Allergic Airway Inflammation and Airway Hyperresponsiveness. <i>Frontiers in Microbiology</i> , 2017, 8, 1732.	1.5	27
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4716	A Review on the Applications of Next Generation Sequencing Technologies as Applied to Food-Related Microbiome Studies. <i>Frontiers in Microbiology</i> , 2017, 8, 1829.	1.5	245
4717	Isolation and Characterization of <i>Pseudomonas</i> spp. Strains That Efficiently Decompose Sodium Dodecyl Sulfate. <i>Frontiers in Microbiology</i> , 2017, 8, 1872.	1.5	28
4718	Adaptation of Methanogenic Inocula to Anaerobic Digestion of Maize Silage. <i>Frontiers in Microbiology</i> , 2017, 8, 1881.	1.5	45
4719	<i>Myriophyllum aquaticum</i> Constructed Wetland Effectively Removes Nitrogen in Swine Wastewater. <i>Frontiers in Microbiology</i> , 2017, 8, 1932.	1.5	44
4720	In Vivo Isotopic Labeling of Symbiotic Bacteria Involved in Cellulose Degradation and Nitrogen Recycling within the Gut of the Forest Cockchafer (<i>Melolontha hippocastani</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 1970.	1.5	28
4721	Diet, Environments, and Gut Microbiota. A Preliminary Investigation in Children Living in Rural and Urban Burkina Faso and Italy. <i>Frontiers in Microbiology</i> , 2017, 8, 1979.	1.5	222
4722	The Low-Diversity Fecal Microbiota of the Critically Endangered <i>Kākāpō</i> Is Robust to Anthropogenic Dietary and Geographic Influences. <i>Frontiers in Microbiology</i> , 2017, 8, 2033.	1.5	15
4723	Characterization of Bacterial and Fungal Community Dynamics by High-Throughput Sequencing (HTS) Metabarcoding during Flax Dew-Retting. <i>Frontiers in Microbiology</i> , 2017, 8, 2052.	1.5	32
4724	Microbial Taxa Distribution Is Associated with Ecological Trophic Cascades along an Elevation Gradient. <i>Frontiers in Microbiology</i> , 2017, 8, 2071.	1.5	144
4725	Diets Alter the Gut Microbiome of Crocodile Lizards. <i>Frontiers in Microbiology</i> , 2017, 8, 2073.	1.5	73
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4727	In Silico Analysis of Putrefaction Pathways in Bacteria and Its Implication in Colorectal Cancer. <i>Frontiers in Microbiology</i> , 2017, 8, 2166.	1.5	75
4728	Low-Molecular-Weight Chitosan Supplementation Increases the Population of <i>Prevotella</i> in the Cecal Contents of Weanling Pigs. <i>Frontiers in Microbiology</i> , 2017, 8, 2182.	1.5	31
4729	Illumina-Based Analysis of Endophytic and Rhizosphere Bacterial Diversity of the Coastal Halophyte <i>Messerschmidia sibirica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2288.	1.5	84
4730	The Gut Entomotype of Red Palm Weevil <i>Rhynchophorus ferrugineus</i> Olivier (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2291.	1.5	96
4731	Environmental Factors Shape Water Microbial Community Structure and Function in Shrimp Cultural Enclosure Ecosystems. <i>Frontiers in Microbiology</i> , 2017, 8, 2359.	1.5	137
4732	Balanced Fertilization Decreases Environmental Filtering on Soil Bacterial Community Assemblage in North China. <i>Frontiers in Microbiology</i> , 2017, 8, 2376.	1.5	44

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4733	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
4734	Natural Selection in Synthetic Communities Highlights the Roles of Methylococcaceae and Methylophilaceae and Suggests Differential Roles for Alternative Methanol Dehydrogenases in Methane Consumption. <i>Frontiers in Microbiology</i> , 2017, 8, 2392.	1.5	51
4735	EPSP of <i>L. casei</i> BL23 Protected against the Infection Caused by <i>Aeromonas veronii</i> via Enhancement of Immune Response in Zebrafish. <i>Frontiers in Microbiology</i> , 2017, 8, 2406.	1.5	28
4736	Enhancing the Resolution of Rumen Microbial Classification from Metatranscriptomic Data Using Kraken and Mothur. <i>Frontiers in Microbiology</i> , 2017, 8, 2445.	1.5	47
4737	Exploring the Cultivable Ectocarpus Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 2456.	1.5	48
4738	Seasonal Changes in a Maize-Based Polyculture of Central Mexico Reshape the Co-occurrence Networks of Soil Bacterial Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 2478.	1.5	36
4739	Prokaryotic Community Composition in Arctic Kongsfjorden and Sub-Arctic Northern Bering Sea Sediments As Revealed by 454 Pyrosequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2498.	1.5	22
4740	Glyphosate Shapes a Dinoflagellate-Associated Bacterial Community While Supporting Algal Growth as Sole Phosphorus Source. <i>Frontiers in Microbiology</i> , 2017, 8, 2530.	1.5	42
4741	Temporal Variation of the Skin Bacterial Community and <i>Batrachochytrium dendrobatidis</i> Infection in the Terrestrial Cryptic Frog <i>Philoria loveridgei</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2535.	1.5	33
4742	<i>Bacillus amyloliquefaciens</i> L-S60 Reforms the Rhizosphere Bacterial Community and Improves Growth Conditions in Cucumber Plug Seedling. <i>Frontiers in Microbiology</i> , 2017, 8, 2620.	1.5	39
4743	Community and Proteomic Analysis of Anaerobic Consortia Converting Tetramethylammonium to Methane. <i>Archaea</i> , 2017, 2017, 1-14.	2.3	4
4744	Metabolic Differences between Dogs of Different Body Sizes. <i>Journal of Nutrition and Metabolism</i> , 2017, 2017, 1-11.	0.7	29
4745	L-Glutamine Supplementation Alleviates Constipation during Late Gestation of Mini Sows by Modifying the Microbiota Composition in Feces. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	28
4746	Metagenome of the Siberian Underground Water Reservoir. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
4747	Review of Molecular Techniques for the Identification of Bacterial Communities in Biological Effluent Treatment Facilities at Pulp and Paper Mills. <i>BioResources</i> , 2017, 12, .	0.5	11
4748	<i>Bradyrhizobium elkanii</i> nod regulon: insights through genomic analysis. <i>Genetics and Molecular Biology</i> , 2017, 40, 703-716.	0.6	5
4749	Effect of Plant Antimicrobial Agents Containing Marinades on Storage Stability and Microbiological Quality of Broiler Chicken Cuts Packed with Modified Atmosphere Packaging. <i>Journal of Food Protection</i> , 2017, 80, 1689-1696.	0.8	11
4750	Primary and heterotrophic productivity relate to multikingdom diversity in a hypersaline mat. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	7

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4753	The US National Mall Microbiome: A Census of Rhizosphere Bacteria Inhabiting Landscape Turf. <i>Crop Science</i> , 2017, 57, S-341.	0.8	15
4754	Rett Syndrome: A Focus on Gut Microbiota. <i>International Journal of Molecular Sciences</i> , 2017, 18, 344.	1.8	63
4755	Nasopharyngeal Microbiome Diversity Changes over Time in Children with Asthma. <i>PLoS ONE</i> , 2017, 12, e0170543.	1.1	55
4756	Inoculum composition determines microbial community and function in an anaerobic sequential batch reactor. <i>PLoS ONE</i> , 2017, 12, e0171369.	1.1	23
4757	Effects of dietary nutrient levels on microbial community composition and diversity in the ileal contents of pregnant Huanjiang mini-pigs. <i>PLoS ONE</i> , 2017, 12, e0172086.	1.1	28
4758	The distinct features of microbial "dysbiosis"™ of Crohn's™ disease do not occur to the same extent in their unaffected, genetically-linked kindred. <i>PLoS ONE</i> , 2017, 12, e0172605.	1.1	33
4759	Characterization of bacterial community associated with phytoplankton bloom in a eutrophic lake in South Norway using 16S rRNA gene amplicon sequence analysis. <i>PLoS ONE</i> , 2017, 12, e0173408.	1.1	85
4760	Olive oil bioactives protect pigs against experimentally-induced chronic inflammation independently of alterations in gut microbiota. <i>PLoS ONE</i> , 2017, 12, e0174239.	1.1	35
4761	Assessing biosynthetic potential of agricultural groundwater through metagenomic sequencing: A diverse anammox community dominates nitrate-rich groundwater. <i>PLoS ONE</i> , 2017, 12, e0174930.	1.1	26
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4763	Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716.	1.1	107
4764	The feline skin microbiota: The bacteria inhabiting the skin of healthy and allergic cats. <i>PLoS ONE</i> , 2017, 12, e0178555.	1.1	41
4765	Variation between the oral and faecal microbiota in a free-living passerine bird, the great tit (<i>Parus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	24
4766	Natural and artificial feeding management before weaning promote different rumen microbial colonization but not differences in gene expression levels at the rumen epithelium of newborn goats. <i>PLoS ONE</i> , 2017, 12, e0182235.	1.1	39
4767	Association between statin use, the vaginal microbiome, and <i>Gardnerella vaginalis</i> vaginolysin-mediated cytotoxicity. <i>PLoS ONE</i> , 2017, 12, e0183765.	1.1	21
4768	Methanobrevibacter attenuation via probiotic intervention reduces flatulence in adult human: A non-randomised paired-design clinical trial of efficacy. <i>PLoS ONE</i> , 2017, 12, e0184547.	1.1	20
4769	Bacterial and diazotrophic diversities of endophytes in <i>Dendrobium catenatum</i> determined through barcoded pyrosequencing. <i>PLoS ONE</i> , 2017, 12, e0184717.	1.1	36

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4904	Diversity of herbaceous plants and bacterial communities regulates soil resistome across forest biomes. <i>Environmental Microbiology</i> , 2018, 20, 3186-3200.	1.8	55
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4913	Restoration of short chain fatty acid and bile acid metabolism following fecal microbiota transplantation in patients with recurrent <i>Clostridium difficile</i> infection. <i>Anaerobe</i> , 2018, 53, 64-73.	1.0	144
4914	Diversity and community composition of pico- and nanoplanktonic protists in the Vistula River estuary (Gulf of Gdansk, Baltic Sea). <i>Estuarine, Coastal and Shelf Science</i> , 2018, 207, 242-249.	0.9	22
4915	In situ microbiota distinguished primary anthropogenic stressor in freshwater sediments. <i>Environmental Pollution</i> , 2018, 239, 189-197.	3.7	19
4916	Tuna Oil Alleviates <i>d</i> -Galactose Induced Aging in Mice Accompanied by Modulating Gut Microbiota and Brain Protein Expression. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 5510-5520.	2.4	23
4917	Comparative biogeography of the gut microbiome between Jinhua and Landrace pigs. <i>Scientific Reports</i> , 2018, 8, 5985.	1.6	101

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4918	Dynamic changes in morphology, gene expression and microbiome in the jejunum of compensatoryâ€growth rats induced by protein restriction. <i>Microbial Biotechnology</i> , 2018, 11, 734-746.	2.0	13
4919	Nitrogen enrichment suppresses other environmental drivers and homogenizes salt marsh leaf microbiome. <i>Ecology</i> , 2018, 99, 1411-1418.	1.5	13
4920	Transport of crude oil and associated microbial populations by washover events on coastal headland beaches. <i>Marine Pollution Bulletin</i> , 2018, 130, 229-239.	2.3	9
4921	The ecology and diversity of microbial eukaryotes in geothermal springs. <i>ISME Journal</i> , 2018, 12, 1918-1928.	4.4	42
4922	The interplay between oral microbiome, lifestyle factors and genetic polymorphisms in the risk of oral squamous cell carcinoma. <i>Carcinogenesis</i> , 2018, 39, 778-787.	1.3	100
4923	River Flow Impacts Bacterial and Archaeal Community Structure in Surface Sediments in the Northern Gulf of Mexico. <i>Microbial Ecology</i> , 2018, 76, 941-953.	1.4	4
4924	Changes in intestinal microbiota across an altitudinal gradient in the lizard <i>Phrynocephalus vlangalii</i> . <i>Ecology and Evolution</i> , 2018, 8, 4695-4703.	0.8	51
4925	Comparative analyses of the gut microbiota among three different wild geese species in the genus <i>Anser</i> . <i>Journal of Basic Microbiology</i> , 2018, 58, 543-553.	1.8	10
4926	The Endotoxemia Marker Lipopolysaccharideâ€Binding Protein is Reduced in Overweightâ€Obese Subjects Consuming Pomegranate Extract by Modulating the Gut Microbiota: A Randomized Clinical Trial. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1800160.	1.5	97
4927	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
4928	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
4929	Investigation of the core microbiome in main soil types from the East European plain. <i>Science of the Total Environment</i> , 2018, 631-632, 1421-1430.	3.9	43
4930	HIV-exposure, early life feeding practices and delivery mode impacts on faecal bacterial profiles in a South African birth cohort. <i>Scientific Reports</i> , 2018, 8, 5078.	1.6	28
4931	Nematodeâ€associated microbial taxa do not correlate with host phylogeny, geographic region or feeding morphology in marine sediment habitats. <i>Molecular Ecology</i> , 2018, 27, 1930-1951.	2.0	49
4932	Effects of Lactogen 13, a New Probiotic Preparation, on Gut Microbiota and Endocrine Signals Controlling Growth and Appetite of <i>Oreochromis niloticus</i> Juveniles. <i>Microbial Ecology</i> , 2018, 76, 1063-1074.	1.4	23
4933	Mechanisms by which organic fertilizer and effective microbes mitigate peanut continuous cropping yield constraints in a red soil of south China. <i>Applied Soil Ecology</i> , 2018, 128, 23-34.	2.1	80
4934	Rumen bacterial community structure impacts feed efficiency in beef cattle. <i>Journal of Animal Science</i> , 2018, 96, 1045-1058.	0.2	71
4935	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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4936	High diversity and variability in the bacterial microbiota of the coffee berry borer (<i>Coleoptera</i>) Tj ETQq0 0 0 14 /Overlock 10 Tf	1.4	15
4937	Responses in the rumen microbiome of <i>Bos taurus</i> and <i>indicus</i> steers fed a low-quality rice straw diet and supplemented protein. <i>Journal of Animal Science</i> , 2018, 96, 1032-1044.	0.2	18
4938	Soil abiotic variables are more important than <i>Salicaceae</i> phylogeny or habitat specialization in determining soil microbial community structure. <i>Molecular Ecology</i> , 2018, 27, 2007-2024.	2.0	44
4939	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
4940	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
4941	eDNA-based bioassessment of coastal sediments impacted by an oil spill. <i>Environmental Pollution</i> , 2018, 238, 739-748.	3.7	47
4942	Bacterial diversity and community structure in the rhizosphere of four <i>Ferula</i> species. <i>Scientific Reports</i> , 2018, 8, 5345.	1.6	33
4943	Feeding-Related Gut Microbial Composition Associates With Peripheral T-Cell Activation and Mucosal Gene Expression in African Infants. <i>Clinical Infectious Diseases</i> , 2018, 67, 1237-1246.	2.9	31
4944	Gut-dependent microbial translocation induces inflammation and cardiovascular events after ST-elevation myocardial infarction. <i>Microbiome</i> , 2018, 6, 66.	4.9	185
4945	Nitrogen removal performance and microbial community of an enhanced multistage A/O biofilm reactor treating low-strength domestic wastewater. <i>Biodegradation</i> , 2018, 29, 285-299.	1.5	27
4946	Tidal Stage Changes in Structure and Diversity of Intertidal Benthic Diatom Assemblages: a Case Study from Two Contrasting Charleston Harbor Flats. <i>Estuaries and Coasts</i> , 2018, 41, 772-783.	1.0	10
4947	Instability diagnosis and syntrophic acetate oxidation during thermophilic digestion of vegetable waste. <i>Water Research</i> , 2018, 139, 263-271.	5.3	57
4948	Responses of soil bacterial community and enzyme activity to experimental warming of an alpine meadow. <i>European Journal of Soil Science</i> , 2018, 69, 429-438.	1.8	47
4949	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
4950	Characterization of the ruminal fermentation and microbiome in lambs supplemented with hydrolysable and condensed tannins. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	28
4951	Spatial Variation of the Native Colon Microbiota in Healthy Adults. <i>Cancer Prevention Research</i> , 2018, 11, 393-402.	0.7	49
4952	Temperature sensitivity of soil respiration to nitrogen and phosphorous fertilization: Does soil initial fertility matter?. <i>Geoderma</i> , 2018, 325, 172-182.	2.3	26
4953	Responses of bacterial community to dibutyl phthalate pollution in a soil-vegetable ecosystem. <i>Journal of Hazardous Materials</i> , 2018, 353, 142-150.	6.5	104

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4954	A large-scale survey of the postmortem human microbiome, and its potential to provide insight into the living health condition. <i>Scientific Reports</i> , 2018, 8, 5724.	1.6	102
4955	Dietary supplementation with flaxseed meal and oat hulls modulates intestinal histomorphometric characteristics, digesta- and mucosa-associated microbiota in pigs. <i>Scientific Reports</i> , 2018, 8, 5880.	1.6	30
4956	Fecal Microbiota Composition Drives Immune Activation in HIV-infected Individuals. <i>EBioMedicine</i> , 2018, 30, 192-202.	2.7	78
4957	Long-term fertilisation form, level and duration affect the diversity, structure and functioning of soil microbial communities in the field. <i>Soil Biology and Biochemistry</i> , 2018, 122, 91-103.	4.2	134
4958	No Significant Association Between the Fecal Microbiome and the Presence of Irritable Bowel Syndrome-type Symptoms in Patients with Quiescent Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 1597-1605.	0.9	20
4959	Obtaining high-quality draft genomes from uncultured microbes by cleaning and co-assembly of single-cell amplified genomes. <i>Scientific Reports</i> , 2018, 8, 2059.	1.6	48
4960	Variation in Raw Milk Microbiota Throughout 12 Months and the Impact of Weather Conditions. <i>Scientific Reports</i> , 2018, 8, 2371.	1.6	90
4961	Effects of water flow on submerged macrophyte-biofilm systems in constructed wetlands. <i>Scientific Reports</i> , 2018, 8, 2650.	1.6	25
4962	Amphibian chytridiomycosis outbreak dynamics are linked with host skin bacterial community structure. <i>Nature Communications</i> , 2018, 9, 693.	5.8	126
4963	Bacterial Community Shift and Coexisting/Coexcluding Patterns Revealed by Network Analysis in a Uranium-Contaminated Site after Bioreduction Followed by Reoxidation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	37
4964	Response of goose intestinal microflora to the source and level of dietary fiber. <i>Poultry Science</i> , 2018, 97, 2086-2094.	1.5	11
4965	Biogeographical Differences in the Influence of Maternal Microbial Sources on the Early Successional Development of the Bovine Neonatal Gastrointestinal tract. <i>Scientific Reports</i> , 2018, 8, 3197.	1.6	133
4966	Taxonomic structure and function of seed-inhabiting bacterial microbiota from common reed (<i>Phragmites australis</i>) and narrowleaf cattail (<i>Typha angustifolia</i> L.). <i>Archives of Microbiology</i> , 2018, 200, 869-876.	1.0	11
4967	Pretreatment with probiotic Bifico ameliorates colitis-associated cancer in mice: Transcriptome and gut flora profiling. <i>Cancer Science</i> , 2018, 109, 666-677.	1.7	87
4968	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
4969	Impact of temperature and substrate concentration on degradation rates of acetate, propionate and hydrogen and their links to microbial community structure. <i>Bioresource Technology</i> , 2018, 256, 44-52.	4.8	41
4970	What lies beneath? Fungal diversity at the bottom of Lake Michigan and Lake Superior. <i>Journal of Great Lakes Research</i> , 2018, 44, 263-270.	0.8	29
4971	Biogeography and ecological processes affecting root-associated bacterial communities in soybean fields across China. <i>Science of the Total Environment</i> , 2018, 627, 20-27.	3.9	53

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4973	Characterization of soil bacterial, archaeal and fungal communities inhabiting archaeological human-impacted layers at Monte Iato settlement (Sicily, Italy). <i>Scientific Reports</i> , 2018, 8, 1903.	1.6	33
4974	A missing link in the estuarine nitrogen cycle?: Coupled nitrification-denitrification mediated by suspended particulate matter. <i>Scientific Reports</i> , 2018, 8, 2282.	1.6	30
4975	A fungal mock community control for amplicon sequencing experiments. <i>Molecular Ecology Resources</i> , 2018, 18, 541-556.	2.2	69
4976	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
4977	Longitudinal Effects of Supplemental Forage on the Honey Bee (<i>Apis mellifera</i>) Microbiota and Inter- and Intra-Colony Variability. <i>Microbial Ecology</i> , 2018, 76, 814-824.	1.4	36
4978	Biodegradation of n-alkanes on oil-seawater interfaces at different temperatures and microbial communities associated with the degradation. <i>Biodegradation</i> , 2018, 29, 141-157.	1.5	39
4979	Potential of dissimilatory nitrate reduction pathways in polycyclic aromatic hydrocarbon degradation. <i>Chemosphere</i> , 2018, 199, 54-67.	4.2	46
4980	The effect of temperature on the microbial communities of peak biogas production in batch biogas reactors. <i>Renewable Energy</i> , 2018, 123, 15-25.	4.3	56
4981	Distribution of thermophilic endospores in a temperate estuary indicate that dispersal history structures sediment microbial communities. <i>Environmental Microbiology</i> , 2018, 20, 1134-1147.	1.8	25
4982	Fecal Microbiome and Food Allergy in Pediatric Atopic Dermatitis: A Cross-Sectional Pilot Study. <i>International Archives of Allergy and Immunology</i> , 2018, 175, 77-84.	0.9	58
4983	Free-living bacteria and potential bacterial pathogens in sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2455-2464.	1.7	47
4984	Detection of 16S rRNA and KPC Genes from Complex Matrix Utilizing a Molecular Inversion Probe Assay for Next-Generation Sequencing. <i>Scientific Reports</i> , 2018, 8, 2028.	1.6	9
4985	Microbial diversity and community structure in agricultural soils suffering from 4 years of Pb contamination. <i>Canadian Journal of Microbiology</i> , 2018, 64, 305-316.	0.8	15
4986	Community structure explains antibiotic resistance gene dynamics over a temperature gradient in soil. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	40
4987	In children, the microbiota of the nasopharynx and bronchoalveolar lavage fluid are both similar and different. <i>Pediatric Pulmonology</i> , 2018, 53, 475-482.	1.0	31
4988	Climate change favours specific fungal communities in boreal peatlands. <i>Soil Biology and Biochemistry</i> , 2018, 120, 28-36.	4.2	43
4989	Antibiotic resistome in landfill leachate from different cities of China deciphered by metagenomic analysis. <i>Water Research</i> , 2018, 134, 126-139.	5.3	138

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4991	Metabolomics-based chemotaxonomy of root endophytic fungi for natural products discovery. <i>Environmental Microbiology</i> , 2018, 20, 1253-1270.	1.8	24
4992	Microbial rRNA Synthesis and Growth Compared through Quantitative Stable Isotope Probing with H ₂ ¹⁸ O. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	27
4993	Airborne microbial communities in the atmospheric environment of urban hospitals in China. <i>Journal of Hazardous Materials</i> , 2018, 349, 10-17.	6.5	73
4994	Bioaugmentation of sidestream nitrifying-denitrifying phosphorus-accumulating granules in a low-SRT activated sludge system at low temperature. <i>Water Research</i> , 2018, 135, 241-250.	5.3	46
4995	Initial evenness determines diversity and cell density dynamics in synthetic microbial ecosystems. <i>Scientific Reports</i> , 2018, 8, 340.	1.6	12
4996	Influence of immunogenetics, sex and body condition on the cutaneous microbial communities of two giant salamanders. <i>Molecular Ecology</i> , 2018, 27, 1915-1929.	2.0	21
4997	Lipopolysaccharide-induced maternal inflammation induces direct placental injury without alteration in placental blood flow and induces a secondary fetal intestinal injury that persists into adulthood. <i>American Journal of Reproductive Immunology</i> , 2018, 79, e12816.	1.2	55
4998	Specific plasmid patterns and high rates of bacterial co-occurrence within the coral holobiont. <i>Ecology and Evolution</i> , 2018, 8, 1818-1832.	0.8	27
4999	Anaerobic degradation of 1-methylnaphthalene by a member of the Thermoanaerobacteraceae contained in an iron-reducing enrichment culture. <i>Biodegradation</i> , 2018, 29, 23-39.	1.5	35
5000	Root-Associated Bacterial and Fungal Community Profiles of <i>Arabidopsis thaliana</i> Are Robust Across Contrasting Soil P Levels. <i>Phytobiomes Journal</i> , 2018, 2, 24-34.	1.4	37
5001	Exploration of the Fecal Microbiota and Biomarker Discovery in Equine Grass Sickness. <i>Journal of Proteome Research</i> , 2018, 17, 1120-1128.	1.8	18
5002	CD1d-mediated lipid presentation by CD11c ⁺ cells regulates intestinal homeostasis. <i>EMBO Journal</i> , 2018, 37, .	3.5	44
5003	Mosquito vector-associated microbiota: Metabarcoding bacteria and eukaryotic symbionts across habitat types in Thailand endemic for dengue and other arthropod-borne diseases. <i>Ecology and Evolution</i> , 2018, 8, 1352-1368.	0.8	99
5004	Selection of <i>Leuconostoc</i> strains isolated from artisanal Serrano Catarinense cheese for use as adjuncts in cheese manufacture. <i>Journal of the Science of Food and Agriculture</i> , 2018, 98, 3899-3906.	1.7	5
5005	Grass and maize vegetation systems restore saline-sodic soils in the Songnen Plain of northeast China. <i>Land Degradation and Development</i> , 2018, 29, 1107-1119.	1.8	48
5006	Effects of biochar on Cd and Pb mobility and microbial community composition in a calcareous soil planted with tobacco. <i>Biology and Fertility of Soils</i> , 2018, 54, 373-383.	2.3	56
5007	Short-Term Overfeeding with Dairy Cream Does Not Modify Gut Permeability, the Fecal Microbiota, or Glucose Metabolism in Young Healthy Men. <i>Journal of Nutrition</i> , 2018, 148, 77-85.	1.3	10

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5008	Temperature and nutrients as drivers of microbially mediated arsenic oxidation and removal from acid mine drainage. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2413-2424.	1.7	17
5009	Taxonomy of anaerobic digestion microbiome reveals biases associated with the applied high throughput sequencing strategies. <i>Scientific Reports</i> , 2018, 8, 1926.	1.6	70
5010	Reversal of visceral hypersensitivity in rat by Menthacarin [®] , a proprietary combination of essential oils from peppermint and caraway, coincides with mycobiome modulation. <i>Neurogastroenterology and Motility</i> , 2018, 30, e13299.	1.6	25
5011	Identification of possible nutritional and stress risk factors in the development of marmoset wasting syndrome. <i>Zoo Biology</i> , 2018, 37, 98-106.	0.5	23
5012	Analysis of the succession of structure of the bacteria community in soil from long-term continuous cotton cropping in Xinjiang using high-throughput sequencing. <i>Archives of Microbiology</i> , 2018, 200, 653-662.	1.0	53
5013	Effects of a galacto-oligosaccharide-rich diet on fecal microbiota and metabolite profiles in mice. <i>Food and Function</i> , 2018, 9, 1612-1620.	2.1	70
5014	Experimental insights into the importance of ecologically dissimilar bacteria to community assembly along a salinity gradient. <i>Environmental Microbiology</i> , 2018, 20, 1170-1184.	1.8	32
5015	Incomplete Co-cladogenesis Between <i>Zootermopsis</i> Termites and Their Associated Protists. <i>Environmental Entomology</i> , 2018, 47, 184-195.	0.7	19
5016	Clinical Relevance of Gastrointestinal Microbiota During Pregnancy: A Primer for Nurses. <i>Biological Research for Nursing</i> , 2018, 20, 84-102.	1.0	9
5017	Sex dependent effects of silver nanoparticles on the zebrafish gut microbiota. <i>Environmental Science: Nano</i> , 2018, 5, 740-751.	2.2	55
5018	Tick saliva microbiomes isolated from engorged and partially fed adults of <i>Haemaphysalis flava</i> tick females. <i>Journal of Applied Entomology</i> , 2018, 142, 173-180.	0.8	8
5019	Comparative analysis of microbial diversity and bacterial seedling disease-suppressive activity in organic-farmed and standardized commercial conventional soils for rice nursery cultivation. <i>Journal of Phytopathology</i> , 2018, 166, 249-264.	0.5	10
5020	Effect of snowpack on the soil bacteria of alpine meadows in the Qinghai-Tibetan Plateau of China. <i>Catena</i> , 2018, 164, 13-22.	2.2	33
5021	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. <i>Cell Systems</i> , 2018, 6, 157-170.e8.	2.9	183
5022	Oral microbiota of periodontal health and disease and their changes after nonsurgical periodontal therapy. <i>ISME Journal</i> , 2018, 12, 1210-1224.	4.4	188
5023	High resolution time series reveals cohesive but short-lived communities in coastal plankton. <i>Nature Communications</i> , 2018, 9, 266.	5.8	122
5024	Identification of active denitrifiers by DNA-stable isotope probing and amplicon sequencing reveals Betaproteobacteria as responsible for attenuation of nitrate contamination in a low impacted aquifer. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	24
5025	Restoration of real sewage partial nitrification-anammox process from nitrate accumulation using free nitrous acid treatment. <i>Bioresource Technology</i> , 2018, 251, 341-349.	4.8	50

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5027	Modulation of gut microbiota by dietary supplementation with tuna oil and algae oil alleviates the effects of D-galactose-induced ageing. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2791-2801.	1.7	21
5028	Response of soil microbial communities to red mud-based stabilizer remediation of cadmium-contaminated farmland. <i>Environmental Science and Pollution Research</i> , 2018, 25, 11661-11669.	2.7	16
5029	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
5030	Rampant Host Switching Shaped the Termite Gut Microbiome. <i>Current Biology</i> , 2018, 28, 649-654.e2.	1.8	101
5031	Succession sequence of lactic acid bacteria driven by environmental factors and substrates throughout the brewing process of Shanxi aged vinegar. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2645-2658.	1.7	26
5032	Performance, granule conductivity and microbial community analysis of upflow anaerobic sludge blanket (UASB) reactors from mesophilic to thermophilic operation. <i>Biochemical Engineering Journal</i> , 2018, 133, 59-65.	1.8	14
5033	Diet affects gut microbiota and modulates hospitalization risk differentially in an international cirrhosis cohort. <i>Hepatology</i> , 2018, 68, 234-247.	3.6	92
5034	The mycobiota of the sand fly <i>Phlebotomus perniciosus</i> : Involvement of yeast symbionts in uric acid metabolism. <i>Environmental Microbiology</i> , 2018, 20, 1064-1077.	1.8	14
5035	Microbial community assembly in wild populations of the fruit fly <i>Drosophila melanogaster</i> . <i>ISME Journal</i> , 2018, 12, 959-972.	4.4	129
5036	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
5037	<i>Lactobacillus kunkeei</i> strains decreased the infection by honey bee pathogens <i>Paenibacillus larvae</i> and <i>Nosema ceranae</i> . <i>Beneficial Microbes</i> , 2018, 9, 279-290.	1.0	83
5038	Assembly and ecological function of the root microbiome across angiosperm plant species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1157-E1165.	3.3	739
5039	Addition of graphene sheets enhances reductive dissolution of arsenic and iron from arsenic contaminated soil. <i>Land Degradation and Development</i> , 2018, 29, 572-584.	1.8	18
5040	Succession of microbial communities and changes of incremental oil in a post-polymer flooded reservoir with nutrient stimulation. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2007-2017.	1.7	22
5041	The effect of an isoflavonid-rich liquorice extract on fermentation, methanogenesis and the microbiome in the rumen simulation technique. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	31
5042	Dominant plant species shape soil bacterial community in semiarid sandy land of northern China. <i>Ecology and Evolution</i> , 2018, 8, 1693-1704.	0.8	31
5043	Co-occurring Mangroves and Salt Marshes Differ in Microbial Community Composition. <i>Wetlands</i> , 2018, 38, 497-508.	0.7	36

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5044	Biofilm community structure and the associated drag penalties of a groomed fouling release ship hull coating. <i>Biofouling</i> , 2018, 34, 162-172.	0.8	33
5045	Long-term and legacy effects of manure application on soil microbial community composition. <i>Biology and Fertility of Soils</i> , 2018, 54, 269-283.	2.3	82
5046	Red mud-modified biochar reduces soil arsenic availability and changes bacterial composition. <i>Environmental Chemistry Letters</i> , 2018, 16, 615-622.	8.3	60
5047	Soil microbial beta-diversity is linked with compositional variation in aboveground plant biomass in a semi-arid grassland. <i>Plant and Soil</i> , 2018, 423, 465-480.	1.8	33
5048	The Coal Seam Microbiome (CSMB) reference set, a lingua franca for the microbial coal-to-methane community. <i>International Journal of Coal Geology</i> , 2018, 186, 41-50.	1.9	46
5049	Metagenomic survey of bacterial diversity in the atmosphere of Mexico City using different sampling methods. <i>Environmental Pollution</i> , 2018, 235, 20-29.	3.7	33
5050	Degradation of Deepwater Horizon oil buried in a Florida beach influenced by tidal pumping. <i>Marine Pollution Bulletin</i> , 2018, 126, 488-500.	2.3	40
5051	Dysbiosis Signatures of Gut Microbiota Along the Sequence from Healthy, Young Patients to Those with Overweight and Obesity. <i>Obesity</i> , 2018, 26, 351-361.	1.5	155
5052	Bacterial rather than fungal community composition is associated with microbial activities and nutrient-use efficiencies in a paddy soil with short-term organic amendments. <i>Plant and Soil</i> , 2018, 424, 335-349.	1.8	88
5053	Comparative Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1704, 243-260.	0.4	2
5054	Short-term particulate matter exposure influences nasal microbiota in a population of healthy subjects. <i>Environmental Research</i> , 2018, 162, 119-126.	3.7	56
5055	Antibiotic Treatment Leads to Fecal <i>Escherichia coli</i> and Coliphage Expansion in Severely Malnourished Diarrhea Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 5, 458-460.e6.	2.3	15
5056	Correlation between system performance and bacterial composition under varied mixing intensity in thermophilic anaerobic digestion of food waste. <i>Journal of Environmental Management</i> , 2018, 206, 472-481.	3.8	22
5057	Oral administration of liquid iron preparation containing excess iron induces intestine and liver injury, impairs intestinal barrier function and alters the gut microbiota in rats. <i>Journal of Trace Elements in Medicine and Biology</i> , 2018, 47, 12-20.	1.5	52
5058	Vitamin B12 effects on chlorinated methanes-degrading microcosms: Dual isotope and metabolically active microbial populations assessment. <i>Science of the Total Environment</i> , 2018, 621, 1615-1625.	3.9	16
5059	Responses of the soil microbial community to nitrogen fertilizer regimes and historical exposure to extreme weather events: Flooding or prolonged-drought. <i>Soil Biology and Biochemistry</i> , 2018, 118, 227-236.	4.2	68
5060	Responses of bulk and rhizosphere soil microbial communities to thermoclimatic changes in a Mediterranean ecosystem. <i>Soil Biology and Biochemistry</i> , 2018, 118, 130-144.	4.2	23
5061	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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5063	The sinonasal microbiota, neural signaling, and depression in chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2018, 8, 394-405.	1.5	18
5064	Long-term fertilization changes bacterial diversity and bacterial communities in the maize rhizosphere of Chinese Mollisols. <i>Applied Soil Ecology</i> , 2018, 125, 88-96.	2.1	94
5065	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
5066	An <i>in vitro</i> study to assess the impact of tetracycline on the human intestinal microbiome. <i>Anaerobe</i> , 2018, 49, 85-94.	1.0	32
5067	Microbial community structure and function in sediments from e-waste contaminated rivers at Guiyu area of China. <i>Environmental Pollution</i> , 2018, 235, 171-179.	3.7	119
5068	Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis. <i>Molecular Ecology</i> , 2018, 27, 313-338.	2.0	248
5069	Abundance of antibiotic resistance genes and bacterial community composition in wild freshwater fish species. <i>Chemosphere</i> , 2018, 196, 115-119.	4.2	59
5070	Long-term warming rather than grazing significantly changed total and active soil prokaryotic community structures. <i>Geoderma</i> , 2018, 316, 1-10.	2.3	55
5071	Significant improvement of intestinal microbiota of gibel carp (<i>Carassius auratus gibelio</i>) after traditional Chinese medicine feeding. <i>Journal of Applied Microbiology</i> , 2018, 124, 829-841.	1.4	51
5072	Deciphering the core fouling-causing microbiota in a membrane bioreactor: Low abundance but important roles. <i>Chemosphere</i> , 2018, 195, 108-118.	4.2	54
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5074	Variations of bacteria and fungi in PM2.5 in Beijing, China. <i>Atmospheric Environment</i> , 2018, 172, 55-64.	1.9	83
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5076	Zebrafish Axenic Larvae Colonization with Human Intestinal Microbiota. <i>Zebrafish</i> , 2018, 15, 96-106.	0.5	10
5077	Field study reveals core plant microbiota and relative importance of their drivers. <i>Environmental Microbiology</i> , 2018, 20, 124-140.	1.8	255
5078	Ammonium nitrogen content is a dominant predictor of bacterial community composition in an acidic forest soil with exogenous nitrogen enrichment. <i>Science of the Total Environment</i> , 2018, 624, 407-415.	3.9	128
5079	Antimony Redox Biotransformation in the Subsurface: Effect of Indigenous Sb(V) Respiring Microbiota. <i>Environmental Science & Technology</i> , 2018, 52, 1200-1207.	4.6	48

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5082	Intraspecies variation in a widely distributed tree species regulates the responses of soil microbiome to different temperature regimes. <i>Environmental Microbiology Reports</i> , 2018, 10, 167-178.	1.0	8
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5084	Distribution and diversity of magnetotactic bacteria in sediments of the Yellow Sea continental shelf. <i>Journal of Soils and Sediments</i> , 2018, 18, 2634-2646.	1.5	15
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5086	Low amounts of dietary fibre increase in vitro production of short-chain fatty acids without changing human colonic microbiota structure. <i>Scientific Reports</i> , 2018, 8, 435.	1.6	75
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5094	Increased Variance in Oral and Gastric Microbiome Correlates With Esophagectomy Anastomotic Leak. <i>Annals of Thoracic Surgery</i> , 2018, 105, 865-870.	0.7	29
5095	Habitual dietary fibre intake influences gut microbiota response to an inulin-type fructan prebiotic: a randomised, double-blind, placebo-controlled, cross-over, human intervention study. <i>British Journal of Nutrition</i> , 2018, 119, 176-189.	1.2	163
5096	FROGS: Find, Rapidly, OTUs with Galaxy Solution. <i>Bioinformatics</i> , 2018, 34, 1287-1294.	1.8	660
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5099	Fingerprint of Exhaust Gases and Database of Microbial Diversity During Silkworm Excrement Composting. <i>Compost Science and Utilization</i> , 2018, 26, 40-51.	1.2	2
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5104	Spatiotemporal changes in bacterial community and microbial activity in a full-scale drinking water treatment plant. <i>Science of the Total Environment</i> , 2018, 625, 449-459.	3.9	79
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5107	Probiotic/prebiotic correction for adverse effects of iron fortification on intestinal resistance to <i>Salmonella</i> infection in weaning mice. <i>Food and Function</i> , 2018, 9, 1070-1078.	2.1	22
5108	Biofilms in Full-Scale Drinking Water Ozone Contactors Contribute Viable Bacteria to Ozonated Water. <i>Environmental Science & Technology</i> , 2018, 52, 2618-2628.	4.6	26
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5117	<i>Bacillus subtilis</i> spore with surface display of paramyosin from <i>Clonorchis sinensis</i> potentializes a promising oral vaccine candidate. <i>Parasites and Vectors</i> , 2018, 11, 156.	1.0	36
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5119	Upflow anaerobic-microaerobic fixed biofilm reactor integrating methanogenesis with partial nitrification. <i>Chemical Engineering Journal</i> , 2018, 348, 281-291.	6.6	14
5120	Tributyltin exposure induces gut microbiome dysbiosis with increased body weight gain and dyslipidemia in mice. <i>Environmental Toxicology and Pharmacology</i> , 2018, 60, 202-208.	2.0	29
5121	Enhancement of volatile fatty acid production and biogas yield from food waste following sonication pretreatment. <i>Journal of Environmental Management</i> , 2018, 217, 797-804.	3.8	30
5122	A genetically and functionally diverse group of non-diazotrophic <i>Bradyrhizobium</i> spp. colonizes the root endophytic compartment of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2018, 18, 61.	1.6	26
5123	Seasonal and algal diet-driven patterns of the digestive microbiota of the European abalone <i>Haliotis tuberculata</i> , a generalist marine herbivore. <i>Microbiome</i> , 2018, 6, 60.	4.9	50
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5125	Core gut microbiota in Jinhua pigs and its correlation with strain, farm and weaning age. <i>Journal of Microbiology</i> , 2018, 56, 346-355.	1.3	50
5126	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
5127	Microbial ecological succession during municipal solid waste decomposition. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5731-5740.	1.7	23
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5129	Differences in weathering pattern, stress resistance and community structure of culturable rock-weathering bacteria between altered rocks and soils. <i>RSC Advances</i> , 2018, 8, 14201-14211.	1.7	8
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5147	Diversity, structure and sources of bacterial communities in earthworm cocoons. <i>Scientific Reports</i> , 2018, 8, 6632.	1.6	20
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5155	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
5156	Fertilizer N application rate impacts plant-soil feedback in a sanqi production system. <i>Science of the Total Environment</i> , 2018, 633, 796-807.	3.9	113
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5166	Host range of antibiotic resistance genes in wastewater treatment plant influent and effluent. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	148
5167	Tapering Courses of Oral Vancomycin Induce Persistent Disruption of the Microbiota That Provide Colonization Resistance to <i>Clostridium difficile</i> and Vancomycin-Resistant Enterococci in Mice. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	23
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5171	Microbial community and metagenome dynamics during biodegradation of dispersed oil reveals potential key-players in cold Norwegian seawater. <i>Marine Pollution Bulletin</i> , 2018, 129, 370-378.	2.3	91
5172	Fecal Microbiota Transplantation in Gestating Sows and Neonatal Offspring Alters Lifetime Intestinal Microbiota and Growth in Offspring. <i>MSystems</i> , 2018, 3, .	1.7	57
5173	High salt diet exacerbates colitis in mice by decreasing <i>Lactobacillus</i> levels and butyrate production. <i>Microbiome</i> , 2018, 6, 57.	4.9	176
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5178	Changes in Larval Mosquito Microbiota Reveal Non-target Effects of Insecticide Treatments in Hurricane-Created Habitats. <i>Microbial Ecology</i> , 2018, 76, 719-728.	1.4	13
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5189	Relationship between rhizosphere soil properties and blossom-end rot of tomatoes in coastal saline-alkali land. <i>Applied Soil Ecology</i> , 2018, 127, 96-101.	2.1	20
5190	Dietary butyrate glycerides modulate intestinal microbiota composition and serum metabolites in broilers. <i>Scientific Reports</i> , 2018, 8, 4940.	1.6	32
5191	An Aberrant Microbiota is not Strongly Associated with Incidental Colonic Diverticulosis. <i>Scientific Reports</i> , 2018, 8, 4951.	1.6	29
5192	Vanillic acid changed cucumber (<i>Cucumis sativus</i> L.) seedling rhizosphere total bacterial, <i>Pseudomonas</i> and <i>Bacillus</i> spp. communities. <i>Scientific Reports</i> , 2018, 8, 4929.	1.6	31
5193	A Distinctive Urinary Metabolomic Fingerprint Is Linked With Endoscopic Postoperative Disease Recurrence in Crohn's Disease Patients. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 861-870.	0.9	24
5194	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
5195	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
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5197	Optimization of simultaneous production of volatile fatty acids and bio-hydrogen from food waste using response surface methodology. <i>RSC Advances</i> , 2018, 8, 10457-10464.	1.7	34
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5201	A Novel <i>Glaesserella</i> sp. Isolated from Pigs with Severe Respiratory Infections Has a Mosaic Genome with Virulence Factors Putatively Acquired by Horizontal Transfer. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
5202	A global comparison of the microbiome compositions of three gut locations in commercial pigs with extreme feed conversion ratios. <i>Scientific Reports</i> , 2018, 8, 4536.	1.6	121
5203	Spatial scale affects the relative role of stochasticity versus determinism in soil bacterial communities in wheat fields across the North China Plain. <i>Microbiome</i> , 2018, 6, 27.	4.9	286
5204	Chemical regulation of body feather microbiota in a wild bird. <i>Molecular Ecology</i> , 2018, 27, 1727-1738.	2.0	25
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5207	Iron limitation effects on nitrogen-fixing organisms with possible implications for cyanobacterial blooms. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	25
5208	Role of microbial activity in Fe(III) hydroxysulfate mineral transformations in an acid mine drainage-impacted site from the Dabaoshan Mine. <i>Science of the Total Environment</i> , 2018, 616-617, 647-657.	3.9	80
5209	Systemic Homeostasis in Metabolome, Ionome, and Microbiome of Wild Yellowfin Goby in Estuarine Ecosystem. <i>Scientific Reports</i> , 2018, 8, 3478.	1.6	23
5210	Opportunistic pathogens are abundant in the gut of cultured giant spiny frog (<i>Paa spinosa</i>). <i>Aquaculture Research</i> , 2018, 49, 2033-2041.	0.9	51
5211	World's Largest Mass Bathing Event Influences the Bacterial Communities of Godavari, a Holy River of India. <i>Microbial Ecology</i> , 2018, 76, 706-718.	1.4	39
5212	Integrated network analysis reveals the importance of microbial interactions for maize growth. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3805-3818.	1.7	94
5213	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
5214	Comparative Analysis of the Gut Bacterial Community of Four <i>Anastrepha</i> Fruit Flies (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422	1.0	59
5215	Oyster microbial communities and implications for chalky deposit formation. <i>Hydrobiologia</i> , 2018, 816, 121-135.	1.0	22
5216	The significance of the diversity and composition of the cecal microbiota of the Tibetan swine. <i>Annals of Microbiology</i> , 2018, 68, 185-194.	1.1	15
5217	Detailed ecological associations of triatomines revealed by metabarcoding and next-generation sequencing: implications for triatomine behavior and <i>Trypanosoma cruzi</i> transmission cycles. <i>Scientific Reports</i> , 2018, 8, 4140.	1.6	106
5218	Automated high throughput animal CO1 metabarcoding classification. <i>Scientific Reports</i> , 2018, 8, 4226.	1.6	112
5219	Physiological Regulation of Drug Metabolism and Transport: Pregnancy, Microbiome, Inflammation, Infection, and Fasting. <i>Drug Metabolism and Disposition</i> , 2018, 46, 503-513.	1.7	40
5220	Tissue Localization and Variation of Major Symbionts in <i>Haemaphysalis longicornis</i> , <i>Rhipicephalus haemaphysaloides</i> , and <i>Dermacentor silvarum</i> in China. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	28
5221	The Impact of Pasture Systems on Soil Microbial Biomass and Community-level Physiological Profiles. <i>Land Degradation and Development</i> , 2018, 29, 284-291.	1.8	23
5222	A different gut microbial community between larvae and adults of a wild bumblebee nest (<i>Bombus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.5	23
5223	Comparative analyses of the bacterial community of hydrothermal deposits and seafloor sediments across Okinawa Trough. <i>Journal of Marine Systems</i> , 2018, 180, 162-172.	0.9	18

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5225	Bacterial community profile of contaminated soils in a typical antimony mining site. <i>Environmental Science and Pollution Research</i> , 2018, 25, 141-152.	2.7	41
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5227	Characteristics of microbial community involved in early biofilms formation under the influence of wastewater treatment plant effluent. <i>Journal of Environmental Sciences</i> , 2018, 66, 113-124.	3.2	33
5228	The Cucurbita pepo seed microbiome: genotype-specific composition and implications for breeding. <i>Plant and Soil</i> , 2018, 422, 35-49.	1.8	131
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5236	Neutrophil extracellular traps are associated with disease severity and microbiota diversity in patients with chronic obstructive pulmonary disease. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 117-127.	1.5	207
5237	Intestinal microbiota in patients with chronic hepatitis C with and without cirrhosis compared with healthy controls. <i>Liver International</i> , 2018, 38, 50-58.	1.9	72
5238	Opportunities and challenges in metabarcoding approaches for helminth community identification in wild mammals. <i>Parasitology</i> , 2018, 145, 608-621.	0.7	28
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5243	Effect of post-fermentation and packing stages on the volatile composition of Spanish-style green table olives. <i>Food Chemistry</i> , 2018, 239, 343-353.	4.2	25
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5250	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
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5258	TREM-1 Inhibition Restores Impaired Autophagy Activity and Reduces Colitis in Mice. <i>Journal of Crohn's and Colitis</i> , 2018, 12, 230-244.	0.6	55
5259	MATAM: reconstruction of phylogenetic marker genes from short sequencing reads in metagenomes. <i>Bioinformatics</i> , 2018, 34, 585-591.	1.8	50

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5261	Evaluation of different 16S rRNA gene V regions for exploring bacterial diversity in a eutrophic freshwater lake. <i>Science of the Total Environment</i> , 2018, 618, 1254-1267.	3.9	115
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5263	CORK Study in Cystic Fibrosis. <i>Chest</i> , 2018, 153, 395-403.	0.4	74
5264	Prokaryotic community profiling of local algae wastewaters using advanced 16S rRNA gene sequencing. <i>Environmental Science and Pollution Research</i> , 2018, 25, 704-711.	2.7	10
5265	Quantitative losses vs. qualitative stability of ectomycorrhizal community responses to 3 years of experimental summer drought in a beech-spruce forest. <i>Global Change Biology</i> , 2018, 24, e560-e576.	4.2	39
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5268	Fate of antibiotic resistance genes and metal resistance genes during thermophilic aerobic digestion of sewage sludge. <i>Bioresource Technology</i> , 2018, 249, 635-643.	4.8	48
5269	Cloacal microbiota of barn swallows from Northern Italy. <i>Ethology Ecology and Evolution</i> , 2018, 30, 362-372.	0.6	7
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5273	Potential testing of reprocessing procedures by real-time polymerase chain reaction: A multicenter study of colonoscopy devices. <i>American Journal of Infection Control</i> , 2018, 46, 159-164.	1.1	22
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5283	Assessment of microbial diversity in the rhizosphere of <i>Pinus roxburghii</i> (Sarg.) and bioinoculant potential of selected pine bacterial isolates for wheat varieties based on culture-independent and culture-dependent techniques. <i>Plant Biology</i> , 2018, 20, 143-150.	1.8	3
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5285	Occurrence and diversity of antibiotic resistance in untreated hospital wastewater. <i>Science of the Total Environment</i> , 2018, 621, 990-999.	3.9	189
5286	Growth performance of piglets during the first two weeks of lactation affects the development of the intestinal microbiota. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2018, 102, 525-532.	1.0	24
5287	Of mammals and bacteria in a rainforest: Temporal dynamics of soil bacteria in response to simulated N pulse from mammalian urine. <i>Functional Ecology</i> , 2018, 32, 773-784.	1.7	15
5288	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
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5292	Metabarcoding of lake benthic diatoms: from structure assemblages to ecological assessment. <i>Hydrobiologia</i> , 2018, 807, 37-51.	1.0	90
5293	Phosphorus dissolution from dewatered anaerobic sludge: Effect of pHs, microorganisms, and sequential extraction. <i>Bioresource Technology</i> , 2018, 249, 464-472.	4.8	39
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5301	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
5302	Do different probing depths exhibit striking differences in microbial profiles?. <i>Journal of Clinical Periodontology</i> , 2018, 45, 26-37.	2.3	49
5303	The intestinal microbiota determines the colitis-inducing potential of β -deficient Th cells in mice. <i>European Journal of Immunology</i> , 2018, 48, 161-167.	1.6	11
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5305	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
5306	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
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5309	Microbial Lineages in Sarcoidosis. A Metagenomic Analysis Tailored for Low-Microbial Content Samples. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 225-234.	2.5	59
5310	Engineering doc2vec for automatic classification of product descriptions on O2O applications. <i>Electronic Commerce Research</i> , 2018, 18, 433-456.	3.0	16
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5312	The Influence of Oyster Farming on Sediment Bacterial Communities. <i>Estuaries and Coasts</i> , 2018, 41, 800-814.	1.0	15
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5317	Intestinal Microbiota in Large Yellow Croaker, <i>Larimichthys crocea</i> , at Different Ages. <i>Journal of the World Aquaculture Society</i> , 2018, 49, 256-267.	1.2	11
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5322	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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5331	The Intestinal Microbiome in Nonalcoholic Fatty Liver Disease. <i>Clinics in Liver Disease</i> , 2018, 22, 121-132.	1.0	25
5332	Distribution and Diversity of Ocular Microbial Communities in Diabetic Patients Compared with Healthy Subjects. <i>Current Eye Research</i> , 2018, 43, 314-324.	0.7	49

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5337	The microbiome in PTEN hamartoma tumor syndrome. <i>Endocrine-Related Cancer</i> , 2018, 25, 233-243.	1.6	5
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5353	Natural lymphatic (atypical) actinobacillosis in cattle caused by <i>Actinobacillus lignieresii</i> . <i>Journal of Veterinary Diagnostic Investigation</i> , 2018, 30, 218-225.	0.5	13
5354	Gut microbiota composition is associated with environmental landscape in honey bees. <i>Ecology and Evolution</i> , 2018, 8, 441-451.	0.8	106
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5358	Retrieved 16S rRNA and nifH sequences reveal co-dominance of <i>Bradyrhizobium</i> and <i>Ensifer</i> (<i>Sinorhizobium</i>) strains in field-collected root nodules of the promiscuous host <i>Vigna radiata</i> (L.) R. Wilczek. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 485-497.	1.7	23
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5364	Ennoblement, corrosion, and biofouling in brackish seawater: Comparison between six stainless steel grades. <i>Bioelectrochemistry</i> , 2018, 120, 27-42.	2.4	24
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5497	Treating wheat seeds with neonicotinoid insecticides does not harm the rhizosphere microbial community. <i>PLoS ONE</i> , 2018, 13, e0205200.	1.1	21
5498	Gut microbiota signatures in cystic fibrosis: Loss of host CFTR function drives the microbiota enterophenotype. <i>PLoS ONE</i> , 2018, 13, e0208171.	1.1	107
5499	Zoonotic multidrug-resistant microorganisms among small companion animals in Germany. <i>PLoS ONE</i> , 2018, 13, e0208364.	1.1	49
5500	Fungal diversity regulates plant-soil feedbacks in temperate grassland. <i>Science Advances</i> , 2018, 4, eaau4578.	4.7	161
5501	Great differences in performance and outcome of high-throughput sequencing data analysis platforms for fungal metabarcoding. <i>MycKeys</i> , 2018, 39, 29-40.	0.8	52
5502	Comparative analysis of the gut microbiota in distinct statin response patients in East China. <i>Journal of Microbiology</i> , 2018, 56, 886-892.	1.3	22
5503	Gut Microbiota Is a Major Contributor to Adiposity in Pigs. <i>Frontiers in Microbiology</i> , 2018, 9, 3045.	1.5	63
5504	<i>Lactobacillus reuteri</i> HCM2 protects mice against Enterotoxigenic <i>Escherichia coli</i> through modulation of gut microbiota. <i>Scientific Reports</i> , 2018, 8, 17485.	1.6	38
5505	Gut Microbiome and Plasma Microbiome-Related Metabolites in Patients With Decompensated and Compensated Heart Failure. <i>Circulation Journal</i> , 2018, 83, 182-192.	0.7	81
5506	Gene mutation associated with <i>esl</i> mediates shifts on fungal community composition in rhizosphere soil of rice at grain-filling stage. <i>Scientific Reports</i> , 2018, 8, 17521.	1.6	2
5507	Effect of calcium salt of long-chain fatty acids and alfalfa supplementation on performance of Holstein bulls. <i>Oncotarget</i> , 2018, 9, 3029-3042.	0.8	16
5508	The Equine Gastrointestinal Microbiome: Impacts of Age and Obesity. <i>Frontiers in Microbiology</i> , 2018, 9, 3017.	1.5	46
5509	Rhizobacterial communities of five co-occurring desert halophytes. <i>PeerJ</i> , 2018, 6, e5508.	0.9	16
5510	Co-existence of multiple bacterivorous clevelandellid ciliate species in hindgut of wood-feeding cockroaches in light of their prokaryotic consortium. <i>Scientific Reports</i> , 2018, 8, 17749.	1.6	15
5511	The effects of dietary astaxanthin on intestinal health of juvenile tiger puffer <i>Takifugu rubripes</i> in terms of antioxidative status, inflammatory response and microbiota. <i>Aquaculture Nutrition</i> , 2018, 25, 466.	1.1	2
5512	Extracellular polymeric substances (EPS) producing and oil degrading bacteria isolated from the northern Gulf of Mexico. <i>PLoS ONE</i> , 2018, 13, e0208406.	1.1	53
5513	Concentration Pulse Method for the Investigation of Transformation Pathways in a Glycerol-Fed Bioelectrochemical System. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	8
5514	Enantioselectivity in degradation and ecological risk of the chiral pesticide ethiprole. <i>Land Degradation and Development</i> , 2018, 29, 4242-4251.	1.8	25

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5515	Characterization of gut bacterial community associated with worker and soldier castes of <i>Globitermes sulphureus</i> Haviland (Blattodea: Termitidae) using 16S rRNA metagenomic. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 1268-1274.	0.4	7
5516	Diversity of bacteria associated with corn roots inoculated with Canadian woodland soils, and description of <i>Pseudomonas aylmerense</i> sp. nov.. <i>Heliyon</i> , 2018, 4, e00761.	1.4	13
5517	A multi-amplicon 16S rRNA sequencing and analysis method for improved taxonomic profiling of bacterial communities. <i>Journal of Microbiological Methods</i> , 2018, 154, 6-13.	0.7	44
5518	Inhibiting Growth of <i>Clostridioides difficile</i> by Restoring Valerate, Produced by the Intestinal Microbiota. <i>Gastroenterology</i> , 2018, 155, 1495-1507.e15.	0.6	127
5519	Electrode Colonization by the Feammox Bacterium <i>Acidimicrobiaceae</i> sp. Strain A6. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	38
5520	A Method for Collecting Atmospheric Microbial Samples From Set Altitudes for Use With Next-Generation Sequencing Techniques to Characterize Communities. <i>Air, Soil and Water Research</i> , 2018, 11, 117862211878887.	1.2	8
5521	Loss of murine Paneth cell function alters the immature intestinal microbiome and mimics changes seen in neonatal necrotizing enterocolitis. <i>PLoS ONE</i> , 2018, 13, e0204967.	1.1	53
5522	Long-Term Biogas Production from Glycolate by Diverse and Highly Dynamic Communities. <i>Microorganisms</i> , 2018, 6, 103.	1.6	12
5523	Biodegradation of sulfamethoxazole by a bacterial consortium of <i>Achromobacter denitrificans</i> PR1 and <i>Leucobacter</i> sp. GP. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10299-10314.	1.7	36
5524	Characterization of the vaginal microbiota of Japanese women. <i>Anaerobe</i> , 2018, 54, 172-177.	1.0	20
5525	Prokaryotic communities of Indo-Pacific giant barrel sponges are more strongly influenced by geography than host phylogeny. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	26
5526	Rhizosphere Microbial Response to Multiple Metal(loid)s in Different Contaminated Arable Soils Indicates Crop-Specific Metal-Microbe Interactions. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
5527	Microbial community dynamics in an ANAMMOX reactor for piggery wastewater treatment with startup, raising nitrogen load, and stable performance. <i>AMB Express</i> , 2018, 8, 156.	1.4	17
5528	Methods and Strategies to Examine the Human Breastmilk Microbiome. <i>Methods in Molecular Biology</i> , 2018, 1849, 63-86.	0.4	15
5529	Contrasting dynamics of polychlorinated biphenyl dissipation and fungal community composition in low and high organic carbon soils with biochar amendment. <i>Environmental Science and Pollution Research</i> , 2018, 25, 33432-33442.	2.7	12
5530	The fungal ecology of seabird nesting sites in the Falkland Islands indicates a niche for mycoparasites. <i>Fungal Ecology</i> , 2018, 36, 99-108.	0.7	3
5531	Subversion of Systemic Glucose Metabolism as a Mechanism to Support the Growth of Leukemia Cells. <i>Cancer Cell</i> , 2018, 34, 659-673.e6.	7.7	90
5532	Chinese Black Truffle (<i>Tuber indicum</i>) Alters the Ectomycorrhizosphere and Endoectomycosphere Microbiome and Metabolic Profiles of the Host Tree <i>Quercus aliena</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2202.	1.5	38

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5534	Extending the dynamic range of biochemical oxygen demand sensing with multi-stage microbial fuel cells. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 2029-2040.	1.2	31
5535	The impact of epidermal growth factor supernatant on pig performance and ileal microbiota. <i>Translational Animal Science</i> , 2018, 2, 184-194.	0.4	7
5536	Pathogenic functions of host microbiota. <i>Microbiome</i> , 2018, 6, 174.	4.9	70
5537	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
5538	Altered Gut Microbiota and Compositional Changes in Firmicutes and Proteobacteria in Mexican Undernourished and Obese Children. <i>Frontiers in Microbiology</i> , 2018, 9, 2494.	1.5	99
5539	Review: The application of omics to rumen microbiota function. <i>Animal</i> , 2018, 12, s233-s245.	1.3	31
5540	Green microalgae in marine coastal waters: The Ocean Sampling Day (OSD) dataset. <i>Scientific Reports</i> , 2018, 8, 14020.	1.6	75
5541	Natural Secretory Immunoglobulins Promote Enteric Viral Infections. <i>Journal of Virology</i> , 2018, 92, .	1.5	18
5542	Identification of Halophilic Microbes in Lung Fibrotic Tissue by Oligotyping. <i>Frontiers in Microbiology</i> , 2018, 9, 1892.	1.5	15
5543	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
5544	Foliar application of Fe resonates to the belowground rhizosphere microbiome in Andean landrace potatoes. <i>Applied Soil Ecology</i> , 2018, 131, 89-98.	2.1	8
5545	The gut of the finch: uniqueness of the gut microbiome of the Galápagos vampire finch. <i>Microbiome</i> , 2018, 6, 167.	4.9	63
5546	Possible aplanochytrid (<i>Labyrinthulea</i>) 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
5547	Microbiome profiling in extremely acidic soils affected by hydrothermal fluids: the case of the Solfatara Crater (Campi Flegrei, southern Italy). <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	19
5548	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
5549	<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
5550	Molecular Alteration Analysis of Human Gut Microbial Composition in Graves' disease Patients. <i>International Journal of Biological Sciences</i> , 2018, 14, 1558-1570.	2.6	74

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5552	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
5553	Association of metformin administration with gut microbiome dysbiosis in healthy volunteers. <i>PLoS ONE</i> , 2018, 13, e0204317.	1.1	96
5554	Binning enables efficient host genome reconstruction in cnidarian holobionts. <i>GigaScience</i> , 2018, 7, .	3.3	16
5555	Variation of bacterial community associated with <i>Phaeodactylum tricornutum</i> in response to different inorganic nitrogen concentrations. <i>Acta Oceanologica Sinica</i> , 2018, 37, 118-128.	0.4	4
5556	Effects of host species, environmental filtering and forest age on community assembly of ectomycorrhizal fungi in fragmented forests. <i>Fungal Ecology</i> , 2018, 36, 89-98.	0.7	30
5557	Tong-Xie-Yao-Fang Regulates 5-HT Level in Diarrhea Predominant Irritable Bowel Syndrome Through Gut Microbiota Modulation. <i>Frontiers in Pharmacology</i> , 2018, 9, 1110.	1.6	41
5558	Local confinement of disease-related microbiome facilitates recovery of gorgonian sea fans from necrotic-patch disease. <i>Scientific Reports</i> , 2018, 8, 14636.	1.6	17
5559	Rabbit Microbiota Changes Throughout the Intestinal Tract. <i>Frontiers in Microbiology</i> , 2018, 9, 2144.	1.5	50
5560	The impacts of deglaciation and human activity on the taxonomic structure of prokaryotic communities in Antarctic soils on King George Island. <i>Antarctic Science</i> , 2018, 30, 278-288.	0.5	7
5561	Pediatric asthma comprises different phenotypic clusters with unique nasal microbiotas. <i>Microbiome</i> , 2018, 6, 179.	4.9	45
5562	An assessment of the microbial community in an urban fringing tidal marsh with an emphasis on petroleum hydrocarbon degradative genes. <i>Marine Pollution Bulletin</i> , 2018, 136, 351-364.	2.3	4
5563	Highly cited papers in Microbiology: identification and conceptual analysis. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	16
5564	Using pseudoalignment and base quality to accurately quantify microbial community composition. <i>PLoS Computational Biology</i> , 2018, 14, e1006096.	1.5	20
5565	Microbial micropatches within microbial hotspots. <i>PLoS ONE</i> , 2018, 13, e0197224.	1.1	6
5566	Biases in Prokaryotic Community Amplicon Sequencing Affected by DNA Extraction Methods in Both Saline and Non-saline Soil. <i>Frontiers in Microbiology</i> , 2018, 9, 1796.	1.5	12
5567	Intermittent fasting for microbes: how discontinuous feeding increases functional stability in anaerobic digestion. <i>Biotechnology for Biofuels</i> , 2018, 11, 274.	6.2	30
5568	Reduced Chlorine in Drinking Water Distribution Systems Impacts Bacterial Biodiversity in Biofilms. <i>Frontiers in Microbiology</i> , 2018, 9, 2520.	1.5	73

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5570	Laboratory examination of greenhouse gaseous and microbial dynamics during thawing of frozen soil core collected from a black spruce forest in Interior Alaska. <i>Soil Science and Plant Nutrition</i> , 2018, 64, 793-802.	0.8	4
5571	Intestinal toxicity of deoxynivalenol is limited by supplementation with <i>Lactobacillus plantarum</i> JM113 and consequentially altered gut microbiota in broiler chickens. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 74.	2.1	65
5572	Soil acidification amendments change the rhizosphere bacterial community of tobacco in a bacterial wilt affected field. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9781-9791.	1.7	83
5573	High-throughput sequencing analysis of the microbial community in coastal intensive mariculture systems. <i>Aquacultural Engineering</i> , 2018, 83, 93-102.	1.4	19
5574	Diversity of foliar endophytic ascomycetes in the endemic Corsican pine forests. <i>Fungal Ecology</i> , 2018, 36, 128-140.	0.7	14
5575	Greco-Roman mineral (litho)therapeutics and their relationship to their microbiome: The case of the red pigment milto. <i>Journal of Archaeological Science: Reports</i> , 2018, 22, 179-192.	0.2	7
5576	Ultrastructural Organization of a Novel Halotolerant Strain <i>Kocuria</i> sp. ICIS A2.2 (Actinobacteria) after a Change of Carbon Source. <i>Inland Water Biology</i> , 2018, 11, 129-135.	0.2	0
5577	Microbiome composition within a sympatric species complex of intertidal isopods (<i>Jaera albifrons</i>). <i>PLoS ONE</i> , 2018, 13, e0202212.	1.1	12
5578	Protective Effect of <i>Pediococcus pentosaceus</i> LI05 Against <i>Clostridium difficile</i> Infection in a Mouse Model. <i>Frontiers in Microbiology</i> , 2018, 9, 2396.	1.5	26
5579	Foliar fungal endophyte communities are structured by environment but not host ecotype in <i>Panicum virgatum</i> (switchgrass). <i>Ecology</i> , 2018, 99, 2703-2711.	1.5	59
5580	Low variation in arbuscular mycorrhizal fungal associations and effects on biomass among switchgrass cultivars. <i>Biomass and Bioenergy</i> , 2018, 119, 503-508.	2.9	21
5581	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
5582	Neonatal gut and respiratory microbiota: coordinated development through time and space. <i>Microbiome</i> , 2018, 6, 193.	4.9	68
5583	Association between the vaginal microbiota, menopause status, and signs of vulvovaginal atrophy. <i>Menopause</i> , 2018, 25, 1321-1330.	0.8	63
5584	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. <i>Genome Medicine</i> , 2018, 10, 78.	3.6	107
5585	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
5586	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

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5588	Dosing Regimen of Enrofloxacin Impacts Intestinal Pharmacokinetics and the Fecal Microbiota in Steers. <i>Frontiers in Microbiology</i> , 2018, 9, 2190.	1.5	14
5589	Plant Nutrient Resource Use Strategies Shape Active Rhizosphere Microbiota Through Root Exudation. <i>Frontiers in Plant Science</i> , 2018, 9, 1662.	1.7	67
5590	Legitimate visitors and nectar robbers of <i>Aquilegia formosa</i> have different effects on nectar bacterial communities. <i>Ecosphere</i> , 2018, 9, e02459.	1.0	16
5591	Orally administered gold nanoparticles protect against colitis by attenuating Toll-like receptor 4- and reactive oxygen/nitrogen species-mediated inflammatory responses but could induce gut dysbiosis in mice. <i>Journal of Nanobiotechnology</i> , 2018, 16, 86.	4.2	48
5592	Assessing Pathogen Presence in an Intensively Tile Drained, Agricultural Watershed. <i>Journal of Environmental Quality</i> , 2018, 47, 1033-1042.	1.0	14
5593	Bacterial Communities in Tissues and Surficial Mucus of the Cold-Water Coral <i>Paragorgia arborea</i> . <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	35
5594	Fungal Endophytic Communities of Two Wild <i>Rosa</i> Varieties With Different Powdery Mildew Susceptibilities. <i>Frontiers in Microbiology</i> , 2018, 9, 2462.	1.5	18
5595	Genotype-Environment Interaction Shapes the Microbial Assemblage in Grapevine's Phyllosphere and Carposphere: An NGS Approach. <i>Microorganisms</i> , 2018, 6, 96.	1.6	54
5596	Microbial communities in different regions of the gastrointestinal tract in East Asian finless porpoises (<i>Neophocaena asiaeorientalis sunameri</i>). <i>Scientific Reports</i> , 2018, 8, 14142.	1.6	19
5597	16S rRNA amplicon sequencing reveals a polymicrobial nature of complicated claw horn disruption lesions and interdigital phlegmon in dairy cattle. <i>Scientific Reports</i> , 2018, 8, 15529.	1.6	26
5598	Community profiling of the urinary microbiota: considerations for low-biomass samples. <i>Nature Reviews Urology</i> , 2018, 15, 735-749.	1.9	87
5599	Gut microbiome can be restored without adverse events after <i>Helicobacter pylori</i> eradication therapy in teenagers. <i>Helicobacter</i> , 2018, 23, e12541.	1.6	41
5600	Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows. <i>PLoS Genetics</i> , 2018, 14, e1007580.	1.5	198
5601	Simulated reactive zone with emulsified vegetable oil for the long-term remediation of Cr(VI)-contaminated aquifer: dynamic evolution of geological parameters and groundwater microbial community. <i>Environmental Science and Pollution Research</i> , 2018, 25, 34392-34402.	2.7	12
5602	Precise Fecal Microbiome of the Herbivorous Tibetan Antelope Inhabiting High-Altitude Alpine Plateau. <i>Frontiers in Microbiology</i> , 2018, 9, 2321.	1.5	33
5603	Experimental evaluation of the importance of colonization history in early-life gut microbiota assembly. <i>ELife</i> , 2018, 7, .	2.8	140
5604	Upgrading lignocellulosic ethanol for caproate production via chain elongation fermentation. <i>International Biodeterioration and Biodegradation</i> , 2018, 135, 103-109.	1.9	28

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5606	Reindeer grazing alter soil fungal community structure and litter decomposition related enzyme activities in boreal coniferous forests in Finnish Lapland. Applied Soil Ecology, 2018, 132, 74-82.	2.1	20
5607	Fast object detection based on binary deep convolution neural networks. CAAI Transactions on Intelligence Technology, 2018, 3, 191-197.	3.4	30
5608	Response of bentonite microbial communities to stresses relevant to geodisposal of radioactive waste. Chemical Geology, 2018, 501, 58-67.	1.4	22
5609	An Interleukin-23-Interleukin-22 Axis Regulates Intestinal Microbial Homeostasis to Protect from Diet-Induced Atherosclerosis. Immunity, 2018, 49, 943-957.e9.	6.6	118
5610	Prey Range and Genome Evolution of Halobacteriovorax marinus Predatory Bacteria from an Estuary. MSphere, 2018, 3, .	1.3	10
5611	Milk microbiome diversity and bacterial group prevalence in a comparison between healthy Holstein Friesian and Rendena cows. PLoS ONE, 2018, 13, e0205054.	1.1	70
5612	Contribution of Host Genetics to the Variation of Microbial Composition of Cecum Lumen and Feces in Pigs. Frontiers in Microbiology, 2018, 9, 2626.	1.5	44
5613	Dietary supplement with a mixture of fish oil and krill oil has sex-dependent effects on obese mice gut microbiota. Journal of Functional Foods, 2018, 51, 47-54.	1.6	8
5614	Deciphering the bacterial composition in the rhizosphere of Baphicacanthus cusia (Nees) Bremek. Scientific Reports, 2018, 8, 15831.	1.6	15
5615	Ecological Analyses of Mycobacteria in Showerhead Biofilms and Their Relevance to Human Health. MBio, 2018, 9, .	1.8	90
5616	Over 2.5 million COI sequences in GenBank and growing. PLoS ONE, 2018, 13, e0200177.	1.1	125
5617	Bleaching-Associated Changes in the Microbiome of Large Benthic Foraminifera of the Great Barrier Reef, Australia. Frontiers in Microbiology, 2018, 9, 2404.	1.5	12
5618	Phylogenetic trait conservatism predicts patterns of plant-soil feedback. Ecosphere, 2018, 9, e02409.	1.0	7
5619	Microbial Interkingdom Interactions in Roots Promote Arabidopsis Survival. Cell, 2018, 175, 973-983.e14.	13.5	707
5620	Temperature-controlled thermophilic bacterial communities in hot springs of western Sichuan, China. BMC Microbiology, 2018, 18, 134.	1.3	45
5621	The severity of human peri-implantitis lesions correlates with the level of submucosal microbial dysbiosis. Journal of Clinical Periodontology, 2018, 45, 1498-1509.	2.3	60
5622	TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution. MSphere, 2018, 3, .	1.3	60

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5623	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
5624	Bacterial diversity in snow from mid-latitude mountain areas: Alps, Eastern Anatolia, Karakoram and Himalaya. <i>Annals of Glaciology</i> , 2018, 59, 10-20.	2.8	16
5625	Spatiotemporal variations in microbial diversity across the three domains of life in a tropical thalassohaline lake (Dziani Dzaha, Mayotte Island). <i>Molecular Ecology</i> , 2018, 27, 4775-4786.	2.0	27
5626	16S rRNA Gene Primer Validation for Bacterial Diversity Analysis of Vegetable Products. <i>Journal of Food Protection</i> , 2018, 81, 848-859.	0.8	5
5627	Characterization of bacterial and microbial eukaryotic communities associated with an ephemeral hypoxia event in Taihu Lake, a shallow eutrophic Chinese lake. <i>Environmental Science and Pollution Research</i> , 2018, 25, 31543-31557.	2.7	20
5628	Effects of endogenous inhibitors on the evolution of antibiotic resistance genes during high solid anaerobic digestion of swine manure. <i>Bioresource Technology</i> , 2018, 270, 328-336.	4.8	30
5629	The gastric mucosal-associated microbiome in patients with gastric polyposis. <i>Scientific Reports</i> , 2018, 8, 13817.	1.6	30
5630	Poisoning with Soman, an Organophosphorus Nerve Agent, Alters Fecal Bacterial Biota and Urine Metabolites: a Case for Novel Signatures for Asymptomatic Nerve Agent Exposure. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	6
5631	Biodegradability of polar compounds formed from weathered diesel. <i>Biodegradation</i> , 2018, 29, 443-461.	1.5	10
5632	Biochar does not attenuate triclosan's impact on soil bacterial communities. <i>Chemosphere</i> , 2018, 213, 215-225.	4.2	17
5633	One Health Relationships Between Human, Animal, and Environmental Microbiomes: A Mini-Review. <i>Frontiers in Public Health</i> , 2018, 6, 235.	1.3	122
5634	Broad Bean (<i>Vicia faba</i> L.) Induces Intestinal Inflammation in Grass Carp (<i>Ctenopharyngodon idellus</i> C.) Tj ETQq1 1 0.784314 rgBT /Over in <i>Microbiology</i> , 2018, 9, 1913.	1.5	17
5635	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
5636	Emerging investigator series: inhibition and recovery of anaerobic granular sludge performance in response to short-term polystyrene nanoparticle exposure. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 1902-1911.	1.2	24
5637	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
5638	Improved Glucose and Lipid Metabolism in the Early Life of Female Offspring by Maternal Dietary Genistein Is Associated With Alterations in the Gut Microbiota. <i>Frontiers in Endocrinology</i> , 2018, 9, 516.	1.5	73
5639	Effects of Reforestation on the Structure and Diversity of Bacterial Communities in Subtropical Low Mountain Forest Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 1968.	1.5	10
5640	Comparisons of gut microbiota profiles in wild-type and gelatinase B/matrix metalloproteinase-9-deficient mice in acute DSS-induced colitis. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 18.	2.9	10

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5642	Endophytic fungal community of <i>Dysphania ambrosioides</i> from two heavy metal-contaminated sites: evaluated by culture-dependent and culture-independent approaches. <i>Microbial Biotechnology</i> , 2018, 11, 1170-1183.	2.0	18
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5790	Theoretical and Applied Aspects of Systems Biology. <i>Computational Biology</i> , 2018, , .	0.1	3
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5793	Aflatoxin B1 (AFB1) induced dysregulation of intestinal microbiota and damage of antioxidant system in pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2018, 495, 940-947.	1.7	62
5794	Evaluating in situ biodegradation of 13C-labelled naphthenic acids in groundwater near oil sands tailings ponds. <i>Science of the Total Environment</i> , 2018, 643, 392-399.	3.9	24
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5808	Influence of gender and menopausal status on gut microbiota. <i>Maturitas</i> , 2018, 116, 43-53.	1.0	153
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5852	Greater Microbial Translocation and Vulnerability to Metabolic Disease in Healthy Aged Female Monkeys. <i>Scientific Reports</i> , 2018, 8, 11373.	1.6	36
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5895	Environmental and Host Effects on Skin Bacterial Community Composition in Panamanian Frogs. <i>Frontiers in Microbiology</i> , 2018, 9, 298.	1.5	49
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5897	Amplicon Sequencing Reveals Microbiological Signatures in Spent Nuclear Fuel Storage Basins. <i>Frontiers in Microbiology</i> , 2018, 9, 377.	1.5	13
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5929	Relationships Between Gastrointestinal Parasite Infections and the Fecal Microbiome in Free-Ranging Western Lowland Gorillas. <i>Frontiers in Microbiology</i> , 2018, 9, 1202.	1.5	21

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5930	Microbial Interactions With Dissolved Organic Matter Drive Carbon Dynamics and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 1234.	1.5	107
5931	Gut Bacterial Communities of <i>Dendroctonus valens</i> and Monoterpenes and Carbohydrates of <i>Pinus tabuliformis</i> at Different Attack Densities to Host Pines. <i>Frontiers in Microbiology</i> , 2018, 9, 1251.	1.5	7
5932	Plasmids of Psychrotolerant <i>Polaromonas</i> spp. Isolated From Arctic and Antarctic Glaciers – Diversity and Role in Adaptation to Polar Environments. <i>Frontiers in Microbiology</i> , 2018, 9, 1285.	1.5	38
5933	Whole-Cell MALDI-TOF MS Versus 16S rRNA Gene Analysis for Identification and Dereplication of Recurrent Bacterial Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 1294.	1.5	76
5934	Exposure to Arsenic Alters the Microbiome of Larval Zebrafish. <i>Frontiers in Microbiology</i> , 2018, 9, 1323.	1.5	42
5935	Persistence of Cellulolytic Bacteria <i>Fibrobacter</i> and <i>Treponema</i> After Short-Term Corn Stover-Based Dietary Intervention Reveals the Potential to Improve Rumen Fibrolytic Function. <i>Frontiers in Microbiology</i> , 2018, 9, 1363.	1.5	92
5936	Evaluating Established Methods for Rumen 16S rRNA Amplicon Sequencing With Mock Microbial Populations. <i>Frontiers in Microbiology</i> , 2018, 9, 1365.	1.5	44
5937	Sex-Based Differences in Gut Microbiota Composition in Response to Tuna Oil and Algae Oil Supplementation in a D-galactose-Induced Aging Mouse Model. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 187.	1.7	22
5938	Gut Microbiome Composition in Non-human Primates Consuming a Western or Mediterranean Diet. <i>Frontiers in Nutrition</i> , 2018, 5, 28.	1.6	125
5939	Resistant ammonia-oxidizing archaea endure, but adapting ammonia-oxidizing bacteria thrive in boreal lake sediments receiving nutrient-rich effluents. <i>Environmental Microbiology</i> , 2018, 20, 3616-3628.	1.8	12
5940	Spatial Distribution and Diverse Metabolic Functions of Lignocellulose-Degrading Uncultured Bacteria as Revealed by Genome-Centric Metagenomics. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	72
5941	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	4.9	109
5942	Modulation of the honey bee queen microbiota: Effects of early social contact. <i>PLoS ONE</i> , 2018, 13, e0200527.	1.1	43
5943	A Novel Fault Diagnosis Method of Rolling Bearings Based on AFEWT-KDEMI. <i>Entropy</i> , 2018, 20, 455.	1.1	8
5944	Massive Sequencing: A New Tool for the Control of Alcoholic Fermentation in Wine?. <i>Fermentation</i> , 2018, 4, 7.	1.4	10
5945	Correlation between microbiota and flavours in fermentation of Chinese Sichuan Paocai. <i>Food Research International</i> , 2018, 114, 123-132.	2.9	172
5946	Analysis of the Gut Microbiome of Rural and Urban Healthy Indians Living in Sea Level and High Altitude Areas. <i>Scientific Reports</i> , 2018, 8, 10104.	1.6	104
5947	Spatial distribution of microbial community composition along a steep slope plot of the Loess Plateau. <i>Applied Soil Ecology</i> , 2018, 130, 226-236.	2.1	22

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5949	Effects of mercury addition on microbial community composition and nitrate removal inside permeable reactive barriers. <i>Environmental Pollution</i> , 2018, 242, 797-806.	3.7	6
5950	Genomic evidence for the degradation of terrestrial organic matter by pelagic Arctic Ocean Chloroflexi bacteria. <i>Communications Biology</i> , 2018, 1, 90.	2.0	81
5951	A common garden experiment with <i>Porphyr</i> a <i>umbilicalis</i> (Rhodophyta) evaluates methods to study spatial differences in the macroalgal microbiome. <i>Journal of Phycology</i> , 2018, 54, 653-664.	1.0	25
5952	Glycation of fish protein impacts its fermentation metabolites and gut microbiota during in vitro human colonic fermentation. <i>Food Research International</i> , 2018, 113, 189-196.	2.9	29
5953	Manipulation of microbial community in the rhizosphere alleviates the replanting issues in Panax ginseng. <i>Soil Biology and Biochemistry</i> , 2018, 125, 64-74.	4.2	64
5954	A Lytic Bacteriophage for Controlling <i>Pseudomonas lactis</i> in Raw Cow's Milk. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	26
5955	A Long-Standing Complex Tropical Dipole Shapes Marine Microbial Biogeography. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	6
5956	Pasture Feeding Changes the Bovine Rumen and Milk Metabolome. <i>Metabolites</i> , 2018, 8, 27.	1.3	70
5957	Isolation of β -1,3-Glucanase-Producing Microorganisms from <i>Poria cocos</i> Cultivation Soil via Molecular Biology. <i>Molecules</i> , 2018, 23, 1555.	1.7	30
5958	UAV-Assisted Dynamic Clustering of Wireless Sensor Networks for Crop Health Monitoring. <i>Sensors</i> , 2018, 18, 555.	2.1	63
5959	A Novel Early Warning System Based on a Sediment Microbial Fuel Cell for In Situ and Real Time Hexavalent Chromium Detection in Industrial Wastewater. <i>Sensors</i> , 2018, 18, 642.	2.1	39
5960	Microbial Diversity and Toxin Risk in Tropical Freshwater Reservoirs of Cape Verde. <i>Toxins</i> , 2018, 10, 186.	1.5	8
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5962	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
5963	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	4.9	3,159
5964	Daily variation in the prokaryotic community during a spring bloom in shelf waters of the East China Sea. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	11
5965	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

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5967	Gestational diabetes is associated with change in the gut microbiota composition in third trimester of pregnancy and postpartum. <i>Microbiome</i> , 2018, 6, 89.	4.9	286
5968	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
5969	Effect of Dietary Fructooligosaccharide (FOS) Supplementation on Ileal Microbiota in Broiler Chickens. <i>Poultry Science</i> , 2018, 97, 3622-3634.	1.5	48
5970	Post operation inactivation of acidophilic bioleaching microorganisms using natural chloride-rich mine water. <i>Hydrometallurgy</i> , 2018, 180, 236-245.	1.8	10
5971	16S rRNA sequencing reveals likely beneficial core microbes within faecal samples of the EU protected slug <i>Geomalacus maculosus</i> . <i>Scientific Reports</i> , 2018, 8, 10402.	1.6	10
5972	16S metagenomics for diagnosis of bloodstream infections: opportunities and pitfalls. <i>Expert Review of Molecular Diagnostics</i> , 2018, 18, 749-759.	1.5	46
5973	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
5974	Developing climate-smart restoration: Can plant microbiomes be hardened against heat waves?. <i>Ecological Applications</i> , 2018, 28, 1594-1605.	1.8	8
5975	A microbial community snapshot of windrows from a commercial composting facility. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8069-8077.	1.7	14
5976	Dietary non-fermentable fiber prevents autoimmune neurological disease by changing gut metabolic and immune status. <i>Scientific Reports</i> , 2018, 8, 10431.	1.6	63
5977	The short-term impact of probiotic consumption on the oral cavity microbiome. <i>Scientific Reports</i> , 2018, 8, 10476.	1.6	36
5978	Metabolic Biosynthesis Pathways Identified from Fecal Microbiome Associated with Prostate Cancer. <i>European Urology</i> , 2018, 74, 575-582.	0.9	117
5979	The impact of spatial isolation and local habitat conditions on colonization of recent forest stands by ectomycorrhizal fungi. <i>Forest Ecology and Management</i> , 2018, 429, 84-92.	1.4	26
5980	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
5981	Dietary values of macroalgae <i>Porphyra haitanensis</i> in <i>Litopenaeus vannamei</i> under normal rearing and WSSV challenge conditions: Effect on growth, immune response and intestinal microbiota. <i>Fish and Shellfish Immunology</i> , 2018, 81, 135-149.	1.6	35
5982	Thermal processing of food reduces gut microbiota diversity of the host and triggers adaptation of the microbiota: evidence from two vertebrates. <i>Microbiome</i> , 2018, 6, 99.	4.9	42
5983	Oral microbiota in youth with perinatally acquired HIV infection. <i>Microbiome</i> , 2018, 6, 100.	4.9	24

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5985	Evolutionary Perspectives of Genotype-Phenotype Factors in <i>Leishmania</i> Metabolism. <i>Journal of Molecular Evolution</i> , 2018, 86, 443-456.	0.8	0
5986	Diversity of key genes for carbon and nitrogen fixation in soils from the Sør Rondane Mountains, East Antarctica. <i>Polar Biology</i> , 2018, 41, 2181-2198.	0.5	14
5987	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
5988	Attachment between heterotrophic bacteria and microalgae influences symbiotic microscale interactions. <i>Environmental Microbiology</i> , 2018, 20, 4385-4400.	1.8	55
5989	Isolation of Previously Uncultured Slow-Growing Bacteria by Using a Simple Modification in the Preparation of Agar Media. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	68
5990	The Development of Microbiota and Metabolome in Small Intestine of Sika Deer (<i>Cervus nippon</i>) from Birth to Weaning. <i>Frontiers in Microbiology</i> , 2018, 9, 4.	1.5	41
5991	Resource Availability Drives Responses of Soil Microbial Communities to Short-term Precipitation and Nitrogen Addition in a Desert Shrubland. <i>Frontiers in Microbiology</i> , 2018, 9, 186.	1.5	82
5992	Body Mass Index and Sex Affect Diverse Microbial Niches within the Gut. <i>Frontiers in Microbiology</i> , 2018, 9, 213.	1.5	87
5993	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
5994	VITCOMIC2: visualization tool for the phylogenetic composition of microbial communities based on 16S rRNA gene amplicons and metagenomic shotgun sequencing. <i>BMC Systems Biology</i> , 2018, 12, 30.	3.0	23
5995	High phosphorus intake and gut-related parameters – results of a randomized placebo-controlled human intervention study. <i>Nutrition Journal</i> , 2018, 17, 23.	1.5	31
5996	High-Fat Diet Consumption Induces Microbiota Dysbiosis and Intestinal Inflammation in Zebrafish. <i>Microbial Ecology</i> , 2018, 76, 1089-1101.	1.4	68
5997	Physicochemical differences between malanga (<i>Xanthosoma sagittifolium</i>) and potato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overload Functional Foods, 2018, 45, 268-276.	1.6	11
5998	Analysis of microbial abundance and community composition in esophagus and intestinal tract of wild veined rapa whelk (<i>Rapana venosa</i>) by 16S rRNA gene sequencing. <i>Journal of General and Applied Microbiology</i> , 2018, 64, 158-166.	0.4	18
5999	Vaginal dysbiosis increases risk of preterm fetal membrane rupture, neonatal sepsis and is exacerbated by erythromycin. <i>BMC Medicine</i> , 2018, 16, 9.	2.3	202
6000	Outlier detection in BLAST hits. <i>Algorithms for Molecular Biology</i> , 2018, 13, 7.	0.3	14
6001	Lignolytic-consortium omics analyses reveal novel genomes and pathways involved in lignin modification and valorization. <i>Biotechnology for Biofuels</i> , 2018, 11, 75.	6.2	65

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6003	Microbial community response reveals underlying mechanism of industrial-scale manganese sand biofilters used for the simultaneous removal of iron, manganese and ammonia from groundwater. <i>AMB Express</i> , 2018, 8, 2.	1.4	17
6004	Influenza A virus infection impacts systemic microbiota dynamics and causes quantitative enteric dysbiosis. <i>Microbiome</i> , 2018, 6, 9.	4.9	194
6005	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. <i>Microbiome</i> , 2018, 6, 16.	4.9	208
6006	Haemophilus is overrepresented in the nasopharynx of infants hospitalized with RSV infection and associated with increased viral load and enhanced mucosal CXCL8 responses. <i>Microbiome</i> , 2018, 6, 10.	4.9	49
6007	Crawling-induced floor dust resuspension affects the microbiota of the infant breathing zone. <i>Microbiome</i> , 2018, 6, 25.	4.9	40
6008	Filter forensics: microbiota recovery from residential HVAC filters. <i>Microbiome</i> , 2018, 6, 22.	4.9	35
6009	Microbial effects of part-stream low-frequency ultrasonic pretreatment on sludge anaerobic digestion as revealed by high-throughput sequencing-based metagenomics and metatranscriptomics. <i>Biotechnology for Biofuels</i> , 2018, 11, 47.	6.2	26
6010	Effect of heat shock on hot water plumbing microbiota and Legionella pneumophila control. <i>Microbiome</i> , 2018, 6, 30.	4.9	20
6011	The active microbial community more accurately reflects the anaerobic digestion process: 16S rRNA (gene) sequencing as a predictive tool. <i>Microbiome</i> , 2018, 6, 63.	4.9	138
6012	DNA-SIP Reveals the Diversity of Chemolithoautotrophic Bacteria Inhabiting Three Different Soil Types in Typical Karst Rocky Desertification Ecosystems in Southwest China. <i>Microbial Ecology</i> , 2018, 76, 976-990.	1.4	16
6013	A novel approach for toluene gas treatment using a downflow hanging sponge reactor. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5625-5634.	1.7	9
6014	Insight into heavy metal resistome of soil psychrotolerant bacteria originating from King George Island (Antarctica). <i>Polar Biology</i> , 2018, 41, 1319-1333.	0.5	78
6015	Oilseed rape cultivation increases the microbial richness and diversity in soils contaminated with cadmium. <i>Journal of Soils and Sediments</i> , 2018, 18, 2451-2462.	1.5	6
6016	Feminizing Wolbachia influence microbiota composition in the terrestrial isopod Armadillidium vulgare. <i>Scientific Reports</i> , 2018, 8, 6998.	1.6	45
6017	Tracking antibiotic resistome during wastewater treatment using high throughput quantitative PCR. <i>Environment International</i> , 2018, 117, 146-153.	4.8	152
6018	The microbiome of Haemaphysalis lemuris (Acari: Ixodidae), a possible vector of pathogens of endangered lemur species in Madagascar. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1252-1260.	1.1	15
6019	Soil bacterial community shifts driven by restoration time and steppe types in the degraded steppe of Inner Mongolia. <i>Catena</i> , 2018, 165, 228-236.	2.2	35

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6021	Microbial taxonomic and metabolic alterations during faecal microbiota transplantation to treat infection. <i>Journal of Infection</i> , 2018, 77, 107-118.	1.7	39
6022	Detection of Chlamydiaceae and Chlamydia-like organisms on the ocular surface of children and adults from a trachoma-endemic region. <i>Scientific Reports</i> , 2018, 8, 7432.	1.6	7
6023	Different rearing conditions alter gut microbiota composition and host physiology in Shaoxing ducks. <i>Scientific Reports</i> , 2018, 8, 7387.	1.6	38
6024	Analysis of endometrial microbiota by 16S ribosomal <i>scpA</i> gene sequencing among infertile patients: a single-center pilot study. <i>Reproductive Medicine and Biology</i> , 2018, 17, 297-306.	1.0	128
6025	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
6026	Unrevealing variation of microbial communities and correlation with environmental variables in a full culture-cycle of <i>Undaria pinnatifida</i> . <i>Marine Environmental Research</i> , 2018, 139, 46-56.	1.1	26
6027	Root diameter predicts the extramatrical hyphal exploration distance of the ectomycorrhizal fungal community. <i>Ecosphere</i> , 2018, 9, e02202.	1.0	15
6028	Microbial diversity and ecotoxicity of sediments 3 years after the Jiaozhou Bay oil spill. <i>AMB Express</i> , 2018, 8, 79.	1.4	19
6029	Near full-length 16S rRNA gene next-generation sequencing revealed <i>Asaia</i> as a common midgut bacterium of wild and domesticated Queensland fruit fly larvae. <i>Microbiome</i> , 2018, 6, 85.	4.9	82
6030	Intestinal microbiota in growing pigs: effects of stocking density. <i>Food and Agricultural Immunology</i> , 2018, 29, 524-535.	0.7	2
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6033	Mycobiome analysis of asymptomatic and symptomatic Norway spruce trees naturally infected by the conifer pathogens <i>Heterobasidion</i> spp.. <i>Environmental Microbiology Reports</i> , 2018, 10, 532-541.	1.0	43
6034	Hybridization capture reveals microbial diversity missed using current profiling methods. <i>Microbiome</i> , 2018, 6, 61.	4.9	34
6035	Watermelon planting is capable to restructure the soil microbiome that regulated by reductive soil disinfection. <i>Applied Soil Ecology</i> , 2018, 129, 52-60.	2.1	48
6036	Gut microbiota profiling in Han Chinese with type 1 diabetes. <i>Diabetes Research and Clinical Practice</i> , 2018, 141, 256-263.	1.1	68
6037	Differences in gut microbiota between silkworms (<i>Bombyx mori</i>) reared on fresh mulberry (<i>Morus alba</i> var. <i>multicaulis</i>) leaves or an artificial diet. <i>RSC Advances</i> , 2018, 8, 26188-26200.	1.7	34

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6039	Interaction between ferruginous clay sediment and an iron-reducing hyperthermophilic <i>Pyrobaculum</i> sp. in a terrestrial hot spring. FEMS Microbiology Ecology, 2018, 94, .	1.3	2
6040	The relative abundance of alkane-degrading bacteria oscillated similarly to a sinusoidal curve in an artificial ecosystem model from oil-well products. Environmental Microbiology, 2018, 20, 3772-3783.	1.8	5
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6042	Bacterial Biomarkers of Marcellus Shale Activity in Pennsylvania. Frontiers in Microbiology, 2018, 9, 1697.	1.5	11
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6044	Eighteen-Year Farming Management Moderately Shapes the Soil Microbial Community Structure but Promotes Habitat-Specific Taxa. Frontiers in Microbiology, 2018, 9, 1776.	1.5	38
6045	Presence and distribution of heavy metal tolerant fungi in surface soils of a temperate pine forest. Applied Soil Ecology, 2018, 131, 66-74.	2.1	26
6046	Robust Domination of <i>Lactobacillus sakei</i> in Microbiota During Traditional Japanese Sake Starter Yamahai-Moto Fermentation and the Accompanying Changes in Metabolites. Current Microbiology, 2018, 75, 1498-1505.	1.0	36
6047	Periodontal therapy favorably modulates the oral-gut-hepatic axis in cirrhosis. American Journal of Physiology - Renal Physiology, 2018, 315, G824-G837.	1.6	61
6048	Neutrophilic Asthma Is Associated with Increased Airway Bacterial Burden and Disordered Community Composition. BioMed Research International, 2018, 2018, 1-11.	0.9	58
6049	Effects of Different Doses of Fructooligosaccharides (FOS) on the Composition of Mice Fecal Microbiota, Especially the Bifidobacterium Composition. Nutrients, 2018, 10, 1105.	1.7	69
6050	Chronic d-serine supplementation impairs insulin secretion. Molecular Metabolism, 2018, 16, 191-202.	3.0	29
6051	The Microbiome of the Gastrointestinal Tract of a Range-Shifting Marine Herbivorous Fish. Frontiers in Microbiology, 2018, 9, 2000.	1.5	67
6052	Responses of soil N-fixing bacterial communities to redroot pigweed (<i>Amaranthus retroflexus</i> L.) invasion under Cu and Cd heavy metal soil pollution. Agriculture, Ecosystems and Environment, 2018, 267, 15-22.	2.5	25
6053	Effects of transportation to and co-mingling at an auction market on nasopharyngeal and tracheal bacterial communities of recently weaned beef cattle. Veterinary Microbiology, 2018, 223, 126-133.	0.8	31
6054	Spatial Patterns and Drivers of Microbial Taxa in a Karst Broadleaf Forest. Frontiers in Microbiology, 2018, 9, 1691.	1.5	25
6055	Stationary and portable sequencing-based approaches for tracing wastewater contamination in urban stormwater systems. Scientific Reports, 2018, 8, 11907.	1.6	24

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6057	Diversity of Bacterial Communities in the Intestinal Tracts of Two Geographically Distant Populations of <i>Bactrocera dorsalis</i> (Diptera: Tephritidae). <i>Journal of Economic Entomology</i> , 2018, 111, 2861-2868.	0.8	20
6058	Gut microbiota alterations in moderate to severe acne vulgaris patients. <i>Journal of Dermatology</i> , 2018, 45, 1166-1171.	0.6	59
6059	Comparison of microbiomes of cold-water corals <i>Primnoa pacifica</i> and <i>Primnoa resedaeformis</i> , with possible link between microbiome composition and host genotype. <i>Scientific Reports</i> , 2018, 8, 12383.	1.6	25
6060	Rapid and complete dehalogenation of halonitromethanes in simulated gastrointestinal tract and its influence on toxicity. <i>Chemosphere</i> , 2018, 211, 1147-1155.	4.2	20
6061	Effects on survival and bacterial community composition of the aquaculture water and gastrointestinal tract of shrimp (<i>Litopenaeus vannamei</i>) exposed to probiotic treatments after an induced infection of acute hepatopancreatic necrosis disease. <i>Aquaculture Research</i> , 2018, 49, 3270-3288.	0.9	28
6062	High PAH degradation and activity of degrading bacteria during alfalfa growth where a contrasted active community developed in comparison to unplanted soil. <i>Environmental Science and Pollution Research</i> , 2018, 25, 29556-29571.	2.7	24
6063	Bacterial bioclusters relate to hydrochemistry in New Zealand groundwater. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	10
6064	Insect exclusion limits variation in bacterial microbiomes of tomato flowers and fruit. <i>Journal of Applied Microbiology</i> , 2018, 125, 1749-1760.	1.4	23
6065	Dynamics of compost microbiota during the cultivation of <i>Agaricus bisporus</i> in the presence of <i>Bacillus velezensis</i> QST713 as biocontrol agent against <i>Trichoderma aggressivum</i> . <i>Biological Control</i> , 2018, 127, 39-54.	1.4	18
6066	Differential biodiversity responses between kingdoms (plants, fungi, bacteria and metazoa) along an Alpine succession gradient. <i>Molecular Ecology</i> , 2018, 27, 3671-3685.	2.0	33
6067	A comparative analysis of metabarcoding and morphology-based identification of benthic communities across different regional seas. <i>Ecology and Evolution</i> , 2018, 8, 8908-8920.	0.8	57
6068	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. <i>Cell Reports</i> , 2018, 24, 1842-1851.	2.9	72
6069	Following the terrestrial tracks of <i>Caulobacter</i> - redefining the ecology of a reputed aquatic oligotroph. <i>ISME Journal</i> , 2018, 12, 3025-3037.	4.4	56
6070	Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818.	8.1	208
6071	The Role of Pulmonary and Systemic Immunosenescence in Acute Lung Injury. , 2018, 9, 553.		34
6072	A Freeloader? The Highly Eroded Yet Large Genome of the <i>Serratia symbiotica</i> Symbiont of <i>Cinara strobil</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2178-2189.	1.1	29
6073	Distributing regionally, distinguishing locally: examining the underlying effects of local land use on airborne bacterial biodiversity. <i>Environmental Microbiology</i> , 2018, 20, 3529-3542.	1.8	26

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6075	Yellow Canopy Syndrome in sugarcane is associated with shifts in the rhizosphere soil metagenome but not with overall soil microbial function. <i>Soil Biology and Biochemistry</i> , 2018, 125, 275-285.	4.2	9
6076	Stimulation of carbon nanomaterials on syntrophic oxidation of butyrate in sediment enrichments and a defined coculture. <i>Scientific Reports</i> , 2018, 8, 12185.	1.6	16
6077	Microbial Biogeography Along the Gastrointestinal Tract of a Red Panda. <i>Frontiers in Microbiology</i> , 2018, 9, 1411.	1.5	26
6078	Bacteria and Competing Herbivores Weaken Top-Down and Bottom-Up Aphid Suppression. <i>Frontiers in Plant Science</i> , 2018, 9, 1239.	1.7	16
6079	Linking microbial co-occurrences to soil ecological processes across a woodland-grassland ecotone. <i>Ecology and Evolution</i> , 2018, 8, 8217-8230.	0.8	38
6080	Substrate-Induced Response in Biogas Process Performance and Microbial Community Relates Back to Inoculum Source. <i>Microorganisms</i> , 2018, 6, 80.	1.6	21
6081	Petroleum hydrocarbon and microbial community structure successions in marine oil-related aggregates associated with diatoms relevant for Arctic conditions. <i>Marine Pollution Bulletin</i> , 2018, 135, 759-768.	2.3	13
6082	Postnatal colonization with human "infant-type" <i>Bifidobacterium</i> species alters behavior of adult gnotobiotic mice. <i>PLoS ONE</i> , 2018, 13, e0196510.	1.1	66
6083	Fecal microbiome of periparturient dairy cattle and associations with the onset of <i>Salmonella</i> shedding. <i>PLoS ONE</i> , 2018, 13, e0196171.	1.1	15
6084	Urinary symptoms are associated with certain urinary microbes in urogynecologic surgical patients. <i>International Urogynecology Journal</i> , 2018, 29, 1765-1771.	0.7	68
6085	Manure amendment reduced plant uptake and enhanced rhizodegradation of 2,2,4,4-tetrabrominated diphenyl ether in soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 807-817.	2.3	15
6086	Impact of soil salinity on the microbial structure of halophyte rhizosphere microbiome. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 136.	1.7	57
6087	Implications of co-contamination with aged heavy metals and total petroleum hydrocarbons on natural attenuation and ecotoxicity in Australian soils. <i>Environmental Pollution</i> , 2018, 243, 94-102.	3.7	49
6088	IDTAXA: a novel approach for accurate taxonomic classification of microbiome sequences. <i>Microbiome</i> , 2018, 6, 140.	4.9	336
6089	Soil Microbial Communities Reflect both Inherent Soil Properties and Management Practices in Wisconsin Potato Fields. <i>American Journal of Potato Research</i> , 2018, 95, 696-708.	0.5	21
6090	Anode potential selection for sulfide removal in contaminated marine sediments. <i>Journal of Hazardous Materials</i> , 2018, 360, 498-503.	6.5	8
6091	Introducing insoluble wheat bran as a gut microbiota niche in an <i>in vitro</i> dynamic gut model stimulates propionate and butyrate production and induces colon region specific shifts in the luminal and mucosal microbial community. <i>Environmental Microbiology</i> , 2018, 20, 3406-3426.	1.8	35

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6093	Sample size effects on the assessment of eukaryotic diversity and community structure in aquatic sediments using high-throughput sequencing. <i>Scientific Reports</i> , 2018, 8, 11737.	1.6	55
6094	Evaluation of performance and microbial community successional patterns in an integrated OCO reactor under ZnO nanoparticle stress. <i>RSC Advances</i> , 2018, 8, 26928-26933.	1.7	4
6095	Disruption of skin microbiota contributes to salamander disease. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180758.	1.2	45
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6097	Why the COI barcode should be the community <sc>DNA</sc> metabarcoding for the metazoa. <i>Molecular Ecology</i> , 2018, 27, 3968-3975.	2.0	131
6098	Biodegradation of Crude Oil and Corexit 9500 in Arctic Seawater. <i>Frontiers in Microbiology</i> , 2018, 9, 1788.	1.5	51
6099	Diet simplification selects for high gut microbial diversity and strong fermenting ability in high-altitude pikas. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 6739-6751.	1.7	75
6100	The effect of several activated biochars on Cd immobilization and microbial community composition during in-situ remediation of heavy metal contaminated sediment. <i>Chemosphere</i> , 2018, 208, 655-664.	4.2	113
6101	Time-resolved microbial guild responses to tidal cycling in a coastal acid-sulfate system. <i>Environmental Chemistry</i> , 2018, 15, 2.	0.7	5
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6106	Leveraging Existing 16S rRNA Gene Surveys To Identify Reproducible Biomarkers in Individuals with Colorectal Tumors. <i>MBio</i> , 2018, 9, .	1.8	46
6107	Trichoderma improves the growth of <i>Leymus chinensis</i> . <i>Biology and Fertility of Soils</i> , 2018, 54, 685-696.	2.3	32
6108	Composition and richness of the serum microbiome differ by age and link to systemic inflammation. <i>GeroScience</i> , 2018, 40, 257-268.	2.1	63
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6112	Phylogenetic-scale disparities in the soil microbial diversityâ€ecosystem functioning relationship. <i>ISME Journal</i> , 2018, 12, 2152-2162.	4.4	26
6113	Long-term in situ permafrost thaw effects on bacterial communities and potential aerobic respiration. <i>ISME Journal</i> , 2018, 12, 2129-2141.	4.4	73
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6116	Comprehensive skin microbiome analysis reveals the uniqueness of human skin and evidence for phyllosymbiosis within the class Mammalia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5786-E5795.	3.3	184
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6118	Season, age, and sex affect the fecal mycobiota of free-ranging Tibetan macaques (<i>Macaca</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	0.8	24
6119	16S rRNA-Based Taxonomy Profiling in the Metagenomics Era. , 2018, , 103-119.		12
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6121	Dynamics and interactions of highly resolved marine plankton via automated high-frequency sampling. <i>ISME Journal</i> , 2018, 12, 2417-2432.	4.4	66
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6129	Establishing a model for childhood obesity in adolescent pigs. <i>Obesity Science and Practice</i> , 2018, 4, 396-406.	1.0	2
6130	Does the biological treatment or membrane separation reduce the antibiotic resistance genes from swine wastewater through a sequencing-batch membrane bioreactor treatment process. <i>Environment International</i> , 2018, 118, 274-281.	4.8	39
6131	Cultivable anaerobic and aerobic bacterial communities in the fermentation chambers of <i>Holotrichia parallela</i> (coleoptera: scarabaeidae) larvae. <i>PLoS ONE</i> , 2018, 13, e0190663.	1.1	10
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6136	Biogeographic patterns of abundant and rare bacterioplankton in three subtropical bays resulting from selective and neutral processes. <i>ISME Journal</i> , 2018, 12, 2198-2210.	4.4	269
6137	Co-occurrence Network Reveals the Higher Fragmentation of the Bacterial Community in Kaidu River Than Its Tributaries in Northwestern China. <i>Microbes and Environments</i> , 2018, 33, 127-134.	0.7	22
6138	Culture-Independent Analysis of Pediatric Bronchoalveolar Lavage Specimens. <i>Annals of the American Thoracic Society</i> , 2018, 15, 1047-1056.	1.5	5
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6140	Microbial communities and natural fermentation of corn silages prepared with farm bunker-silo in Southwest China. <i>Bioresource Technology</i> , 2018, 265, 282-290.	4.8	180
6141	A case study for late Archean and Proterozoic biogeochemical iron and sulphur cycling in a modern habitat – the Arvadi Spring. <i>Geobiology</i> , 2018, 16, 353-368.	1.1	5
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6147	Vertical and horizontal biogeographic patterns and major factors affecting bacterial communities in the open South China Sea. <i>Scientific Reports</i> , 2018, 8, 8800.	1.6	27
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6153	Long-range-transported bioaerosols captured in snow cover on Mount Tateyama, Japan: impacts of Asian-dust events on airborne bacterial dynamics relating to ice-nucleation activities. <i>Atmospheric Chemistry and Physics</i> , 2018, 18, 8155-8171.	1.9	27
6154	The urinary microbiome in women with mixed urinary incontinence compared to similarly aged controls. <i>International Urogynecology Journal</i> , 2018, 29, 1785-1795.	0.7	58
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6166	Modulation of intestinal microbiota and immunometabolic parameters by caloric restriction and lactic acid bacteria. <i>Food Research International</i> , 2019, 124, 188-199.	2.9	16
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6170	Harnessing microfluidic streak plate technique to investigate the gut microbiome of <i>Reticulitermes chinensis</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00654.	1.2	16
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6185	Quantitative and qualitative assessment of pollen <scp>DNA</scp> metabarcoding using constructed species mixtures. <i>Molecular Ecology</i> , 2019, 28, 431-455.	2.0	114
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6188	Inhibition of anammox activity by phenol: Suppression effect, community analysis and mechanism simulation. <i>International Biodeterioration and Biodegradation</i> , 2019, 141, 30-38.	1.9	22
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6190	Initial description of the core ocular surface microbiome in dogs: Bacterial community diversity and composition in a defined canine population. <i>Veterinary Ophthalmology</i> , 2019, 22, 337-344.	0.6	29
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6198	In situ degradation, ruminal fermentation, and the rumen bacterial community of cattle fed corn stover fermented by lignocellulolytic microorganisms. <i>Animal Feed Science and Technology</i> , 2019, 248, 10-19.	1.1	14
6199	Metagenomic binning through low-density hashing. <i>Bioinformatics</i> , 2019, 35, 219-226.	1.8	21

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6201	Effects of moderate, voluntary ethanol consumption on the rat and human gut microbiome. <i>Addiction Biology</i> , 2019, 24, 617-630.	1.4	46
6202	Microbial Composition and Activity of Natural, Restored, and Reclaimed Wetland Soils: a Case Study of Poyang Lake Basin, China. <i>Wetlands</i> , 2019, 39, 113-123.	0.7	6
6203	MIMOSA: Algorithms for Microbial Profiling. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1-1.	1.9	1
6204	Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019, 3, 1298-1308.	3.4	34
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6206	Environmental filtering increases with elevation for the assembly of gut microbiota in wild pikas. <i>Microbial Biotechnology</i> , 2019, 12, 976-992.	2.0	55
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6211	Understanding soil biodiversity using two orthogonal 1000km transects across New South Wales, Australia. <i>Geoderma</i> , 2019, 354, 113860.	2.3	10
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6213	Electrode material properties for designing effective microbial electrosynthesis systems. <i>Journal of Materials Chemistry A</i> , 2019, 7, 24420-24436.	5.2	59
6214	Enhanced tomato plant growth in soil under reduced P supply through microbial inoculants and microbiome shifts. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	23
6215	Microbiota of newborn calves and their mothers reveals possible transfer routes for newborn calves' gastrointestinal microbiota. <i>PLoS ONE</i> , 2019, 14, e0220554.	1.1	61
6216	Evaluation of the Antimicrobial and Anti-inflammatory Properties of Bacillus-DFM (Norumâ„¢) in Broiler Chickens Infected With Salmonella Enteritidis. <i>Frontiers in Veterinary Science</i> , 2019, 6, 282.	0.9	28
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6219	Decrease in diversity and shift in composition of the soil bacterial community were closely related to high available phosphorus in agricultural Fluvisols of North China. <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 2019, 69, 618-630.	0.3	4
6220	<i>Porphyromonas gingivalis</i> in saliva associates with chronic and aggressive periodontitis. <i>Journal of Oral Microbiology</i> , 2019, 11, 1653123.	1.2	42
6221	Frequent fire reorganizes fungal communities and slows decomposition across a heterogeneous pine savanna landscape. <i>New Phytologist</i> , 2019, 224, 916-927.	3.5	49
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6223	Environmental pollution effects on plant microbiota: the case study of poplar bacterial-fungal response to silver nanoparticles. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 8215-8227.	1.7	21
6224	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
6225	The effect of C:N ratio on heterotrophic nitrification in acidic soils. <i>Soil Biology and Biochemistry</i> , 2019, 137, 107562.	4.2	32
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6227	Pretreatment With <i>Bacillus cereus</i> Preserves Against D-Galactosamine-Induced Liver Injury in a Rat Model. <i>Frontiers in Microbiology</i> , 2019, 10, 1751.	1.5	15
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6229	Gut-associated IgA+ immune cells regulate obesity-related insulin resistance. <i>Nature Communications</i> , 2019, 10, 3650.	5.8	131
6230	Oral vancomycin treatment does not alter markers of postprandial inflammation in lean and obese subjects. <i>Physiological Reports</i> , 2019, 7, e14199.	0.7	10
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6238	Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes. <i>Cell</i> , 2019, 178, 795-806.e12.	13.5	830
6239	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
6240	Age and Mothers: Potent Influences of Children's Skin Microbiota. <i>Journal of Investigative Dermatology</i> , 2019, 139, 2497-2505.e6.	0.3	46
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6361	Multienzymatic capacity of cultivable intestinal bacteria from captive <i>Litopenaeus vannamei</i> (Boone,) Tj ETQq1 1 0,784314 rgBT /Ove	1.1	9

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6654	Composition and Drivers of Gut Microbial Communities in Arctic-Breeding Shorebirds. <i>Frontiers in Microbiology</i> , 2019, 10, 2258.	1.5	49
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6656	Geochemical and Metagenomic Characterization of Jinata Onsen, a Proterozoic-Analog Hot Spring, Reveals Novel Microbial Diversity including Iron-Tolerant Phototrophs and Thermophilic Lithotrophs. <i>Microbes and Environments</i> , 2019, 34, 278-292.	0.7	48
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6659	Modification of wheat bran particle size and tissue composition affects colonisation and metabolism by human faecal microbiota. <i>Food and Function</i> , 2019, 10, 379-396.	2.1	22
6660	Evolution of microbial community and drug resistance during enrichment of tetracycline-degrading bacteria. <i>Ecotoxicology and Environmental Safety</i> , 2019, 171, 746-752.	2.9	62
6661	Organic matter from Arctic sea-ice loss alters bacterial community structure and function. <i>Nature Climate Change</i> , 2019, 9, 170-176.	8.1	48
6662	Plant-microbe interactions before drought influence plant physiological responses to subsequent severe drought. <i>Scientific Reports</i> , 2019, 9, 249.	1.6	39
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6740	Aerobic cometabolism of tetrabromobisphenol A by marine bacterial consortia. <i>Environmental Science and Pollution Research</i> , 2019, 26, 23832-23841.	2.7	17
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6747	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019, 10, 2719.	5.8	428
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6766	Diversity of tetracycline- and erythromycin-resistant bacteria in aerosols and manures from four types of animal farms in China. <i>Environmental Science and Pollution Research</i> , 2019, 26, 24213-24222.	2.7	20
6767	Effects of struvite-humic acid loaded biochar/bentonite composite amendment on Zn(II) and antibiotic resistance genes in manure-soil. <i>Chemical Engineering Journal</i> , 2019, 375, 122013.	6.6	41
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6772	Changes in endophytic bacterial communities during different growth stages of cucumber (<i>Cucumis Tj ETQq1 1 0.784314 rgBT /Ove</i>	1.7	12
6773	Role of Polysaccharides in Diatom <i>Thalassiosira pseudonana</i> and its Associated Bacteria in Hydrocarbon Presence. <i>Plant Physiology</i> , 2019, 180, 1898-1911.	2.3	40
6774	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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6776	Changing how we think about infectious diseases. , 2019, , 321-365.		3
6777	Sequential biowashing-biopile processes for remediation of crude oil contaminated soil in Kuwait. <i>Journal of Hazardous Materials</i> , 2019, 378, 120710.	6.5	11
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6780	Chronic obstructive pulmonary disease upper airway microbiota alpha diversity is associated with exacerbation phenotype: a case-control observational study. <i>Respiratory Research</i> , 2019, 20, 114.	1.4	32
6781	Interaction among soil physicochemical properties, bacterial community structure, and arsenic contamination: Clay-induced change in long-term arsenic contaminated soils. <i>Journal of Hazardous Materials</i> , 2019, 378, 120729.	6.5	23
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6789	Effects of a Lactulose-Rich Diet on Fecal Microbiome and Metabolome in Pregnant Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 7674-7683.	2.4	19
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6791	Effect of gastrointestinal microbiome and its diversity on the expression of tumor-infiltrating lymphocytes in breast cancer. <i>Oncology Letters</i> , 2019, 17, 5050-5056.	0.8	13
6792	In Vitro Digestion and Fermentation of Three Polysaccharide Fractions from <i>Laminaria japonica</i> and Their Impact on Lipid Metabolism-Associated Human Gut Microbiota. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 7496-7505.	2.4	52
6793	Bacterial Community 16S rRNA Gene Sequencing Characterizes Riverine Microbial Impact on Lake Michigan. <i>Frontiers in Microbiology</i> , 2019, 10, 996.	1.5	30
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6796	Modification of the Gastric Mucosal Microbiota by a Strain-Specific <i>Helicobacter pylori</i> Oncoprotein and Carcinogenic Histologic Phenotype. <i>MBio</i> , 2019, 10, .	1.8	36

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6806	Effects of soil properties, heavy metals, and PBDEs on microbial community of e-waste contaminated soil. <i>Ecotoxicology and Environmental Safety</i> , 2019, 180, 705-714.	2.9	47
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6928	Skin Microbiome Differences in Atopic Dermatitis and Healthy Controls in Egyptian Children and Adults, and Association with Serum Immunoglobulin E. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 247-260.	1.0	16
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6936	Composts of poultry litter or dairy manure differentially affect survival of enteric bacteria in fields with spinach. <i>Journal of Applied Microbiology</i> , 2019, 126, 1910-1922.	1.4	23
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6952	Thermal disruption of soil bacterial assemblages decreases diversity and assemblage similarity. <i>Ecosphere</i> , 2019, 10, e02598.	1.0	2
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7031	Mycobiome Profiles in Breast Milk from Healthy Women Depend on Mode of Delivery, Geographic Location, and Interaction with Bacteria. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	76
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7084	Variations in early gut microbiome are associated with childhood eczema. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	16
7085	16S rRNA Amplicon Profiling of Cranberry (<i>Vaccinium macrocarpon</i> Ait.) Flower and Berry Surfaces. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	9
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7089	Microbial Ecology of Snow Reveals Taxa-Specific Biogeographical Structure. <i>Microbial Ecology</i> , 2019, 77, 946-958.	1.4	28
7090	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	2.9	17
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7092	Host NLRP6 exacerbates graft-versus-host disease independent of gut microbial composition. <i>Nature Microbiology</i> , 2019, 4, 800-812.	5.9	36
7093	Prospective observational study of vaginal microbiota pre- and post-rescue cervical cerclage. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2019, 126, 916-925.	1.1	47
7094	Lime and ammonium carbonate fumigation coupled with bio-organic fertilizer application steered banana rhizosphere to assemble a unique microbiome against Panama disease. <i>Microbial Biotechnology</i> , 2019, 12, 515-527.	2.0	23
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7096	Draft Genome Sequence of the Marine Bacterium <i>Alteromonas</i> sp. Strain KS69. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
7097	Prokaryotic Community Structure of Long-Term Fertilization Field Andisols in Central Japan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
7098	16S rRNA sequence embeddings: Meaningful numeric feature representations of nucleotide sequences that are convenient for downstream analyses. <i>PLoS Computational Biology</i> , 2019, 15, e1006721.	1.5	27
7099	Nitrogen- and phosphorus-starved <i>Triticum aestivum</i> show distinct belowground microbiome profiles. <i>PLoS ONE</i> , 2019, 14, e0210538.	1.1	26
7100	The fecal, oral, and skin microbiota of children with Chagas disease treated with benznidazole. <i>PLoS ONE</i> , 2019, 14, e0212593.	1.1	21
7101	The nasal and oropharyngeal microbiomes of healthy livestock workers. <i>PLoS ONE</i> , 2019, 14, e0212949.	1.1	18
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7107	Analysis of rhizosphere bacterial and fungal communities associated with rusty root disease of Panax ginseng. <i>Applied Soil Ecology</i> , 2019, 138, 245-252.	2.1	31
7108	Spatial Heterogeneity of <i>Vibrio</i> spp. in Sediments of Chinese Marginal Seas. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	18
7109	Effect of Dietary Carbohydrate-to-Protein Ratio on Gut Microbiota in Atlantic Salmon (<i>Salmo salar</i>). <i>Animals</i> , 2019, 9, 89.	1.0	31
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7117	Rhizosphere microbiota compositional changes reflect potato blackleg disease. <i>Applied Soil Ecology</i> , 2019, 140, 11-17.	2.1	9
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7120	Recovery of Benthic Microalgal Biomass and Community Structure Following Beach Renourishment at Folly Beach, South Carolina. <i>Estuaries and Coasts</i> , 2019, 42, 157-172.	1.0	12
7121	The drivers of bacterial community underlying biogeographical pattern in Mollisol area of China. <i>Ecotoxicology and Environmental Safety</i> , 2019, 177, 93-99.	2.9	14
7122	Associations of Gut Microbiota With Heat Stress-Induced Changes of Growth, Fat Deposition, Intestinal Morphology, and Antioxidant Capacity in Ducks. <i>Frontiers in Microbiology</i> , 2019, 10, 903.	1.5	59

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7126	Impact of Saskatoon berry powder on insulin resistance and relationship with intestinal microbiota in high fat–high sucrose diet-induced obese mice. <i>Journal of Nutritional Biochemistry</i> , 2019, 69, 130-138.	1.9	25
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7128	Denitrifying Bacteria Active in Woodchip Bioreactors at Low-Temperature Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 635.	1.5	33
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7142	Anaerobic membrane bioreactor for biogas production from concentrated sewage produced during sewer mining. <i>Science of the Total Environment</i> , 2019, 670, 993-1000.	3.9	26
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7155	Vertical stratification of peatland microbial communities follows a gradient of functional types across hummock-hollow microtopographies. <i>Ecoscience</i> , 2019, 26, 249-258.	0.6	17
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7174	The Growth Rate, Immune Status, Duodenal Development, and Cecal Microbial Diversity of 24-Day-Old Offspring of SD Rats Received <i>Bacillus subtilis</i> -Cu or CuSO ₄ During Pregnancy and Lactation Periods. <i>Biological Trace Element Research</i> , 2019, 191, 435-442.	1.9	4
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7179	Bioaugmentation with <i>Thermoanaerobacterium thermosaccharolyticum</i> W16 to enhance thermophilic hydrogen production using corn stover hydrolysate. <i>International Journal of Hydrogen Energy</i> , 2019, 44, 5821-5829.	3.8	34
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7183	Draft Genome Sequence of <i>Halomonas</i> sp. Strain SL1, a Putative Polyhydroxyalkanoate-Producing Halophile. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
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7198	Nasal and skin microbiomes are associated with disease severity in paediatric atopic dermatitis. <i>British Journal of Dermatology</i> , 2019, 181, 796-804.	1.4	30
7199	Differences in Systemic IgA Reactivity and Circulating Th Subsets in Healthy Volunteers With Specific Microbiota Enterotypes. <i>Frontiers in Immunology</i> , 2019, 10, 341.	2.2	15
7200	SqueezeMeta, A Highly Portable, Fully Automatic Metagenomic Analysis Pipeline. <i>Frontiers in Microbiology</i> , 2018, 9, 3349.	1.5	214
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7206	Metabarcoding free-living marine nematodes using curated 18S and CO1 reference sequence databases for species-level taxonomic assignments. <i>Ecology and Evolution</i> , 2019, 9, 1211-1226.	0.8	66
7207	Microbiomes of China's Space Station During Assembly, Integration, and Test Operations. <i>Microbial Ecology</i> , 2019, 78, 631-650.	1.4	13
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7218	Host plant and population source drive diversity of microbial gut communities in two polyphagous insects. <i>Scientific Reports</i> , 2019, 9, 2792.	1.6	97
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7221	The Ovotransferrin-Derived Peptide IRW Attenuates Lipopolysaccharide-Induced Inflammatory Responses. <i>BioMed Research International</i> , 2019, 2019, 1-7.	0.9	22
7222	Soil Physicochemical Properties and the Rhizosphere Soil Fungal Community in a Mulberry (<i>Morus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	0.9	35
7223	<i>Amnimonas aquatica</i> gen. nov., sp. nov., Isolated from a Freshwater River. <i>Current Microbiology</i> , 2019, 76, 478-484.	1.0	10
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7368	Effects of dietary lysozyme levels on growth performance, intestinal morphology, immunity response and microbiota community of growing pigs. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 1643-1650.	1.7	34
7369	Effects of past and current drought on the composition and diversity of soil microbial communities. <i>Soil Biology and Biochemistry</i> , 2019, 131, 28-39.	4.2	141
7370	Effects of <i>Saccharomyces Cerevisiae</i> Fermentation Products on the Microbial Community throughout the Gastrointestinal Tract of Calves. <i>Animals</i> , 2019, 9, 4.	1.0	9
7371	Diet-Independent Correlations between Bacteria and Dysfunction of Gut, Adipose Tissue, and Liver: A Comprehensive Microbiota Analysis in Feces and Mucosa of the Ileum and Colon in Obese Mice with NAFLD. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1.	1.8	929
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7374	Effects of glucose and starch on the toxicity of nitrobenzene to plants and microbes in constructed wetlands. <i>Science of the Total Environment</i> , 2019, 658, 809-817.	3.9	9

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7377	Which animal type contributes the most to the emission of antibiotic resistance genes in large-scale swine farms in China?. <i>Science of the Total Environment</i> , 2019, 658, 152-159.	3.9	50
7378	Puerariae Lobatae Radix with chuanxiong Rhizoma for treatment of cerebral ischemic stroke by remodeling gut microbiota to regulate the brain-gut barriers. <i>Journal of Nutritional Biochemistry</i> , 2019, 65, 101-114.	1.9	127
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7381	Application of metagenomic analysis for detection of the reduction in the antibiotic resistance genes (ARGs) by the addition of clay during poultry manure composting. <i>Chemosphere</i> , 2019, 220, 137-145.	4.2	41
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7399	Metagenomic profiles of different types of Italian high-moisture Mozzarella cheese. <i>Food Microbiology</i> , 2019, 79, 123-131.	2.1	65
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7401	Deciphering of microbial community and antibiotic resistance genes in activated sludge reactors under high selective pressure of different antibiotics. <i>Water Research</i> , 2019, 151, 388-402.	5.3	229
7402	<i>In vivo</i> screening of multiple bacterial strains identifies <i>Lactobacillus rhamnosus</i> Lb102 and <i>Bifidobacterium animalis</i> ssp. <i>lactis</i> Bf141 as probiotics that improve metabolic disorders in a mouse model of obesity. <i>FASEB Journal</i> , 2019, 33, 4921-4935.	0.2	47
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7461	Understanding the roles of surface proteins in regulation of <i>Lactobacillus pentosus</i> HC-2 to immune response and bacterial diversity in midgut of <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2019, 86, 1194-1206.	1.6	19
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7481	DOM composition alters ecosystem function during microbial processing of isolated sources. <i>Biogeochemistry</i> , 2019, 142, 281-298.	1.7	96
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7485	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
7486	Transitions in microbial communities along a 1600 km freshwater trophic gradient. <i>Journal of Great Lakes Research</i> , 2019, 45, 263-276.	0.8	10
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7491	Pilot study of probiotic/colostrum supplementation on gut function in children with autism and gastrointestinal symptoms. <i>PLoS ONE</i> , 2019, 14, e0210064.	1.1	126
7492	Modulation of fat metabolism and gut microbiota by resveratrol on high-fat diet-induced obese mice. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 97-107.	1.1	58
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7497	Adaptation to Fasting in Crucian Carp (<i>Carassius auratus</i>): Gut Microbiota and Its Correlative Relationship with Immune Function. <i>Microbial Ecology</i> , 2019, 78, 6-19.	1.4	20
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7500	Suppression of banana Panama disease induced by soil microbiome reconstruction through an integrated agricultural strategy. <i>Soil Biology and Biochemistry</i> , 2019, 128, 164-174.	4.2	74

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7502	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
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7504	High-throughput identification and diagnostics of pathogens and pests: Overview and practical recommendations. <i>Molecular Ecology Resources</i> , 2019, 19, 47-76.	2.2	91
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7507	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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7509	Performance of a novel photobioreactor for nutrient removal from piggery biogas slurry: Operation parameters, microbial diversity and nutrient recovery potential. <i>Bioresource Technology</i> , 2019, 272, 421-432.	4.8	30
7510	Fate of microbial pollutants and evolution of antibiotic resistance in three types of soil amended with swine slurry. <i>Environmental Pollution</i> , 2019, 245, 353-362.	3.7	41
7511	Characterization of microbiota diversity of field-collected <i>Haemaphysalis longicornis</i> (Acari: Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.8	40
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7513	Soil pH rather than elevation determines bacterial phylogenetic community assembly on Mt. Norikura. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	22
7514	Bacterial community structure and succession in nests of two megachilid bee genera. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	40
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7935	Characterization of microbial communities in commercial bee pollen used for mass rearing of <i>Bombus impatiens</i> . <i>Journal of Apicultural Research</i> , 2021, 60, 678-682.	0.7	0
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7941	Examining the relationship between maternal body size, gestational glucose tolerance status, mode of delivery and ethnicity on human milk microbiota at three months post-partum. <i>BMC Microbiology</i> , 2020, 20, 219.	1.3	20
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7953	Metagenomic data on bacterial diversity profiling of high-microbial-abundance tropical marine sponges <i>Aaptos aaptos</i> and <i>Xestospongia muta</i> from waters off terengganu, South China Sea. <i>Data in Brief</i> , 2020, 31, 105971.	0.5	4
7954	Irrigation of radish (<i>Raphanus sativus</i> L.) with microcystin-enriched water holds low risk for plants and their associated rhizospheric and epiphytic microbiome. <i>Environmental Pollution</i> , 2020, 266, 115208.	3.7	8
7955	Cocoa diet modulates gut microbiota composition and improves intestinal health in Zucker diabetic rats. <i>Food Research International</i> , 2020, 132, 109058.	2.9	43
7956	A comparative study of artificial cow and sheep rumen fermentation of corn straw and food waste: Batch and continuous operation. <i>Science of the Total Environment</i> , 2020, 745, 140731.	3.9	20
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7959	Phylogenetic Responses of Marine Free-Living Bacterial Community to <i>Phaeocystis globosa</i> Bloom in Beibu Gulf, China. <i>Frontiers in Microbiology</i> , 2020, 11, 1624.	1.5	14
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8008	Phosphorus Reduces Negative Effects of Nitrogen Addition on Soil Microbial Communities and Functions. <i>Microorganisms</i> , 2020, 8, 1828.	1.6	29
8009	Application of next generation sequencing for detection of protozoan pathogens in shellfish. <i>Food and Waterborne Parasitology</i> , 2020, 21, e00096.	1.1	16
8010	The Response of Estuarine Ammonia-Oxidizing Communities to Constant and Fluctuating Salinity Regimes. <i>Frontiers in Microbiology</i> , 2020, 11, 574815.	1.5	5
8011	Carbon and nitrogen cycling in Yedoma permafrost controlled by microbial functional limitations. <i>Nature Geoscience</i> , 2020, 13, 794-798.	5.4	45
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8013	Methanogen Abundance Thresholds Capable of Differentiating In Vitro Methane Production in Human Stool Samples. <i>Digestive Diseases and Sciences</i> , 2020, 66, 3822-3830.	1.1	3
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8024	Effects of Wheat Bran and <i>Clostridium butyricum</i> Supplementation on Cecal Microbiota, Short-Chain Fatty Acid Concentration, pH and Histomorphometry in Broiler Chickens. <i>Animals</i> , 2020, 10, 2230.	1.0	20
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8026	Adjusting Organic Load as a Strategy to Direct Single-Stage Food Waste Fermentation from Anaerobic Digestion to Chain Elongation. <i>Processes</i> , 2020, 8, 1487.	1.3	15
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8048	Evaluation of 16S rRNA Hypervariable Regions for Bioweapon Species Detection by Massively Parallel Sequencing. <i>International Journal of Microbiology</i> , 2020, 2020, 1-11.	0.9	2
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8051	Alterations of Oral Microbiota in Chinese Patients With Esophageal Cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 541144.	1.8	34
8052	Dynamic of Composition and Diversity of Gut Microbiota in <i>Triatoma rubrofasciata</i> in Different Developmental Stages and Environmental Conditions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 587708.	1.8	23
8053	Rumen epithelial transcriptome and microbiome profiles of rumen epithelium and contents of beef cattle with and without liver abscesses. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	10
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8062	Age-related differences in gut microbial community composition of captive spotted seals (<i>Phoca largha</i>). <i>Marine Mammal Science</i> , 2020, 36, 1231-1240.	0.9	13
8063	The Gut Microbiome Associates with Immune Checkpoint Inhibition Outcomes in Patients with Advanced Non-Small Cell Lung Cancer. <i>Cancer Immunology Research</i> , 2020, 8, 1243-1250.	1.6	154
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8066	SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis. <i>BMC Bioinformatics</i> , 2020, 21, 345.	1.2	41
8067	Assessment of polycyclic aromatic hydrocarbon contamination in the Sundarbans, the world's largest tidal mangrove forest and indigenous microbial mixed biofilm-based removal of the contaminants. <i>Environmental Pollution</i> , 2020, 266, 115270.	3.7	24
8068	The effects of abiotic and biotic factors on taxonomic and phylogenetic diversity of stream epilithic bacteria around Qiandao Lake. <i>Aquatic Sciences</i> , 2020, 82, 1.	0.6	4
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8097	The Gut Microbiota Communities of Wild Arboreal and Ground-Feeding Tropical Primates Are Affected Differently by Habitat Disturbance. <i>MSystems</i> , 2020, 5, .	1.7	36
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8109	Effect of increasing precipitation and warming on microbial community in Tibetan alpine steppe. <i>Environmental Research</i> , 2020, 189, 109917.	3.7	32
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8114	Mucosal-associated invariant T cells promote inflammation and intestinal dysbiosis leading to metabolic dysfunction during obesity. <i>Nature Communications</i> , 2020, 11, 3755.	5.8	97
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8117	<i>Bacillus subtilis</i> H2 modulates immune response, fat metabolism and bacterial flora in the gut of grass carp (<i>Ctenopharyngodon idellus</i>). <i>Fish and Shellfish Immunology</i> , 2020, 106, 8-20.	1.6	49
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8125	Probiotic <i>Bifidobacterium breve</i> prevents DOCA-salt hypertension. <i>FASEB Journal</i> , 2020, 34, 13626-13640.	0.2	45
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8133	Effects of Chinese yam (<i>Dioscorea oppositifolia</i> L.) dietary supplementation on intestinal microflora, digestive enzyme activity and immunity in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Aquaculture Research</i> , 2020, 51, 4698-4712.	0.9	11
8134	Root Microbiome Modulates Plant Growth Promotion Induced by Low Doses of Glyphosate. <i>MSphere</i> , 2020, 5, .	1.3	19
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8143	Within-population diversity of bacterial microbiomes in winter ticks (<i>Dermacentor albipictus</i>). <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101535.	1.1	8
8144	Characterization of bacterial community structure in the rhizosphere of <i>Triticum aestivum</i> L.. <i>Genomics</i> , 2020, 112, 4760-4768.	1.3	15
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8157	Reduction of <i>Salmonella Typhimurium</i> Cecal Colonisation and Improvement of Intestinal Health in Broilers Supplemented with Fermented Defatted "Alperujo"™, an Olive Oil By-Product. <i>Animals</i> , 2020, 10, 1931.	1.0	5
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8166	The Role of Phosphorus Limitation in Shaping Soil Bacterial Communities and Their Metabolic Capabilities. <i>MBio</i> , 2020, 11, .	1.8	69
8167	The Rumen Specific Bacteriome in Dry Dairy Cows and Its Possible Relationship with Phenotypes. <i>Animals</i> , 2020, 10, 1791.	1.0	9
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8183	Distinct Polysaccharide Utilization Determines Interspecies Competition between Intestinal <i>Prevotella</i> spp.. <i>Cell Host and Microbe</i> , 2020, 28, 838-852.e6.	5.1	86
8184	<i>Lycium barbarum</i> polysaccharide attenuates myocardial injury in high-fat diet-fed mice through manipulating the gut microbiome and fecal metabolome. <i>Food Research International</i> , 2020, 138, 109778.	2.9	44
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8191	Enhancement of microbial redox cycling of iron in zero-valent iron oxidation coupling with deca-brominated diphenyl ether removal. <i>Science of the Total Environment</i> , 2020, 748, 141328.	3.9	8
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8198	Niche Partitioning between Coastal and Offshore Shelf Waters Results in Differential Expression of Alkane and Polycyclic Aromatic Hydrocarbon Catabolic Pathways. <i>MSystems</i> , 2020, 5, .	1.7	10
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8207	Altered gut microbiota correlated with systemic inflammation in children with Kawasaki disease. <i>Scientific Reports</i> , 2020, 10, 14525.	1.6	21
8208	Oxidation of fish oil exacerbates alcoholic liver disease by enhancing intestinal dysbiosis in mice. <i>Communications Biology</i> , 2020, 3, 481.	2.0	26
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8362	Undernutrition shifted colonic fermentation and digest-associated bacterial communities in pregnant ewes. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 5973-5984.	1.7	12
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8379	Dietary replacement of fish meal with peanut meal in juvenile hybrid grouper (<i>Epinephelus</i>) Tj ETQq0.0.0 rgBT /Overlock 10 Tf 50 267 Td microbiota. <i>Aquaculture Reports</i> , 2020, 17, 100327.	0.7	23
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8435	Persistent organic fertilization reinforces soil-borne disease suppressiveness of rhizosphere bacterial community. <i>Plant and Soil</i> , 2020, 452, 313-328.	1.8	30
8436	Relief of hypersaline stress in Nile tilapia <i>Oreochromis niloticus</i> by dietary supplementation of a host-derived <i>Bacillus subtilis</i> strain. <i>Aquaculture</i> , 2020, 528, 735542.	1.7	22
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8461	Amending microbiota by targeting intestinal inflammation with TNF blockade attenuates development of colorectal cancer. <i>Nature Cancer</i> , 2020, 1, 723-734.	5.7	50
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8469	Host-specific and tissue-dependent orchestration of microbiome community structure in traditional rice paddy ecosystems. <i>Plant and Soil</i> , 2020, 452, 379-395.	1.8	14
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8474	Intercropping with Potato-Onion Enhanced the Soil Microbial Diversity of Tomato. <i>Microorganisms</i> , 2020, 8, 834.	1.6	32
8475	16S rRNA sequencing analysis of the correlation between the intestinal microbiota and body-mass of grass carp (<i>Ctenopharyngodon idella</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100699.	0.4	8

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8477	Short-chain fructo-oligosaccharides supplementation to suckling piglets: Assessment of pre- and post-weaning performance and gut health. <i>PLoS ONE</i> , 2020, 15, e0233910.	1.1	10
8478	Responses of soil and earthworm gut bacterial communities to heavy metal contamination. <i>Environmental Pollution</i> , 2020, 265, 114921.	3.7	44
8479	Bacterial community colonization on tire microplastics in typical urban water environments and associated impacting factors. <i>Environmental Pollution</i> , 2020, 265, 114922.	3.7	58
8480	Characterizing Halloumi cheese's bacterial communities through metagenomic analysis. <i>LWT - Food Science and Technology</i> , 2020, 126, 109298.	2.5	22
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8483	Microbial Community and Short-Chain Fatty Acid Mapping in the Intestinal Tract of Quail. <i>Animals</i> , 2020, 10, 1006.	1.0	20
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8487	Identification of key bacterial populations affecting early embryonic development in cattle uterus. <i>Animal Science Journal</i> , 2020, 91, e13374.	0.6	0
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8489	Heterotrophic Thaumarchaea with Small Genomes Are Widespread in the Dark Ocean. <i>MSystems</i> , 2020, 5, .	1.7	50
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8491	A Two-Way Interaction between Methotrexate and the Gut Microbiota of Male Sprague-Dawley Rats. <i>Journal of Proteome Research</i> , 2020, 19, 3326-3339.	1.8	35
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8497	Assessment of microbial diversity associated with CH ₄ emission from sugarcane vinasse storage and transportation systems. <i>Journal of Environmental Management</i> , 2020, 269, 110748.	3.8	7
8498	Multi-omics analysis on an agroecosystem reveals the significant role of organic nitrogen to increase agricultural crop yield. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14552-14560.	3.3	77
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8500	Soil microbial succession following surface mining is governed primarily by deterministic factors. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
8501	Effects of Dietary Fat Profile on Gut Microbiota in Valproate Animal Model of Autism. <i>Frontiers in Medicine</i> , 2020, 7, 151.	1.2	9
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8506	Depth-related variability in viral communities in highly stratified sulfidic mine tailings. <i>Microbiome</i> , 2020, 8, 89.	4.9	41
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8784	Cloacal bacterial communities of tree swallows (<i>Tachycineta bicolor</i>): Similarity within a population, but not between pair-bonded social partners. <i>PLoS ONE</i> , 2020, 15, e0228982.	1.1	8
8785	Bacterial Exposure Mediates Developmental Plasticity and Resistance to Lethal <i>Vibrio lentus</i> Infection in Purple Sea Urchin (<i>Strongylocentrotus purpuratus</i>) Larvae. <i>Frontiers in Immunology</i> , 2019, 10, 3014.	2.2	16
8786	Microbial and Reactive Transport Modeling Evidence for Hyporheic Flux-Driven Cryptic Sulfur Cycling and Anaerobic Methane Oxidation in a Sulfate-Impacted Wetland-Stream System. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2020, 125, e2019JG005185.	1.3	7
8787	The effects of dietary sodium butyrate supplementation on the growth performance, carcass traits and intestinal microbiota of growing-finishing pigs. <i>Journal of Applied Microbiology</i> , 2020, 128, 1613-1623.	1.4	18
8788	Gut Microbiota Plasticity Influences the Adaptability of Wild and Domestic Animals in Co-inhabited Areas. <i>Frontiers in Microbiology</i> , 2020, 11, 125.	1.5	23
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8791	Intake of a Mixture of Sake Cake and Rice Malt Increases Mucin Levels and Changes in Intestinal Microbiota in Mice. <i>Nutrients</i> , 2020, 12, 449.	1.7	11
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8798	Characterization of Microbial Communities in <i>Ixodes persulcatus</i> (Ixodida: Ixodidae), a Veterinary and Medical Important Tick Species in Northeastern China. <i>Journal of Medical Entomology</i> , 2020, 57, 1270-1276.	0.9	4
8799	Production of lumpfish (<i>Cyclopterus lumpus</i> L.) in RAS with distinct water treatments: Effects on fish survival, growth, gill health and microbial communities in rearing water and biofilm. <i>Aquaculture</i> , 2020, 522, 735097.	1.7	21

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8803	Persistent action of cow rumen microorganisms in enhancing biodegradation of wheat straw by rumen fermentation. <i>Science of the Total Environment</i> , 2020, 715, 136529.	3.9	57
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8806	Culture-Dependent and Culture-Independent Characterization of the Olive Xylem Microbiota: Effect of Sap Extraction Methods. <i>Frontiers in Plant Science</i> , 2019, 10, 1708.	1.7	58
8807	Characterization of Bacterial and Fungal Communities Reveals Novel Consortia in Tropical Oligotrophic Peatlands. <i>Microbial Ecology</i> , 2021, 82, 188-201.	1.4	8
8808	Spatial analysis of bacteria in brackish lake sediment. <i>International Journal of Sediment Research</i> , 2020, 35, 227-236.	1.8	9
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8810	Diversity, compositional and functional differences between gut microbiota of children and adults. <i>Scientific Reports</i> , 2020, 10, 1040.	1.6	89
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8812	Modulation of inflammatory response and gut microbiota in ankylosing spondylitis mouse model by bioactive peptide IQW. <i>Journal of Applied Microbiology</i> , 2020, 128, 1669-1677.	1.4	11
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8815	The effect of different doses of ozone treatments on the postharvest quality and biodiversity of cantaloupes. <i>Postharvest Biology and Technology</i> , 2020, 163, 111124.	2.9	35
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8817	Effects of Dietary Non-Fibrous Carbohydrate (NFC) to Neutral Detergent Fiber (NDF) Ratio Change on Rumen Bacteria in Sheep Based on Three Generations of Full-Length Amplifiers Sequencing. <i>Animals</i> , 2020, 10, 192.	1.0	7

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8819	Who is eating fructose within the <i>Aedes albopictus</i> gut microbiota?. <i>Environmental Microbiology</i> , 2020, 22, 1193-1206.	1.8	22
8820	Assessment of a Machine Learning Model Applied to Harmonized Electronic Health Record Data for the Prediction of Incident Atrial Fibrillation. <i>JAMA Network Open</i> , 2020, 3, e1919396.	2.8	76
8821	Predictive Modeling for Metabolomics Data. <i>Methods in Molecular Biology</i> , 2020, 2104, 313-336.	0.4	32
8822	Characterization of tetracycline effects on microbial community, antibiotic resistance genes and antibiotic resistance of <i>Aeromonas</i> spp. in gut of goldfish <i>Carassius auratus</i> Linnaeus. <i>Ecotoxicology and Environmental Safety</i> , 2020, 191, 110182.	2.9	39
8823	Response of bacterial communities from Kongsfjorden (Svalbard, Arctic Ocean) to macroalgal polysaccharide amendments. <i>Marine Environmental Research</i> , 2020, 155, 104874.	1.1	26
8824	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	4.4	135
8825	Pharyngeal microbiome alterations during <i>Neisseria gonorrhoeae</i> infection. <i>PLoS ONE</i> , 2020, 15, e0227985.	1.1	9
8826	Changes in soil microbial community structure during long-term secondary succession. <i>Land Degradation and Development</i> , 2020, 31, 1151-1166.	1.8	50
8827	The dynamics of bacterial community in a polyculture aquaculture system of <i>Penaeus chinensis</i> , <i>Rhopilema esculenta</i> and <i>Sinonovacula constricta</i> . <i>Aquaculture Research</i> , 2020, 51, 1789-1800.	0.9	18
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8829	Functional dynamics of bacterial species in the mouse gut microbiome revealed by metagenomic and metatranscriptomic analyses. <i>PLoS ONE</i> , 2020, 15, e0227886.	1.1	65
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8831	Selected and Reshaped Early Dominant Microbial Community in the Cecum With Similar Proportions and Better Homogenization and Species Diversity Due to Organic Acids as AGP Alternatives Mediate Their Effects on Broilers Growth. <i>Frontiers in Microbiology</i> , 2019, 10, 2948.	1.5	42
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8833	Integrating hydrochemical and biological approaches to investigate the surface water and groundwater interactions in the hyporheic zone of the Liuxi River basin, southern China. <i>Journal of Hydrology</i> , 2020, 583, 124622.	2.3	29
8834	A pregnancy complication-dependent change in SigA-targeted microbiota during third trimester. <i>Food and Function</i> , 2020, 11, 1513-1524.	2.1	23
8835	Improved Isolation of Uncultured Anaerobic Bacteria using Medium Prepared with Separate Sterilization of Agar and Phosphate. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	9

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8840	Bacterial community profile after the lethal infection of <i>Steinernema</i> – <i>Xenorhabdus</i> pairs into soil-reared <i>Tenebrio molitor</i> larvae. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	13
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8843	Mineralization and nitrification: Archaea dominate ammonia-oxidising communities in grassland soils. <i>Soil Biology and Biochemistry</i> , 2020, 143, 107725.	4.2	44
8844	<i>Klebsiella michiganensis</i> transmission enhances resistance to Enterobacteriaceae gut invasion by nutrition competition. <i>Nature Microbiology</i> , 2020, 5, 630-641.	5.9	67
8845	The complex microbiome from native semen to embryo culture environment in human in vitro fertilization procedure. <i>Reproductive Biology and Endocrinology</i> , 2020, 18, 3.	1.4	37
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8851	The Vaginal Microbiome as a Tool to Predict rASRM Stage of Disease in Endometriosis: a Pilot Study. <i>Reproductive Sciences</i> , 2020, 27, 1064-1073.	1.1	35
8852	Differences in bacterial community structure and potential functions among <i>Eucalyptus</i> plantations with different ages and species of trees. <i>Applied Soil Ecology</i> , 2020, 149, 103515.	2.1	45
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8856	Nitrospira bacteria in paddy soil reduced by biochar application. , 2020, 3, e20009.		4
8857	Insight into the assembly of root-associated microbiome in the medicinal plant <i>Polygonum cuspidatum</i> . <i>Industrial Crops and Products</i> , 2020, 145, 112163.	2.5	38
8858	Study on indoor and outdoor permeability coefficients and bacterial components, sources of fine particles in severe cold region of China. <i>Sustainable Cities and Society</i> , 2020, 55, 102020.	5.1	5
8859	Combination of Chronic Alcohol Consumption and High-Salt Intake Elicits Gut Microbial Alterations and Liver Steatosis in Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 1750-1759.	2.4	13
8860	16S rRNA gene-based primer pair showed high specificity and quantification accuracy in detecting freshwater <i>Brocadiales anammox</i> bacteria. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	14
8861	Evidence for Co-evolutionary History of Early Diverging Lycopodiaceae Plants With Fungi. <i>Frontiers in Microbiology</i> , 2019, 10, 2944.	1.5	18
8862	Construction of Simplified Microbial Consortia to Degrade Recalcitrant Materials Based on Enrichment and Dilution-to-Extinction Cultures. <i>Frontiers in Microbiology</i> , 2019, 10, 3010.	1.5	39
8863	Impact of TCR Diversity on the Development of Transplanted or Chemically Induced Tumors. <i>Cancer Immunology Research</i> , 2020, 8, 192-202.	1.6	15
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8868	Planktonic Bacterial and Archaeal Communities in an Artificially Irrigated Estuarine Wetland: Diversity, Distribution, and Responses to Environmental Parameters. <i>Microorganisms</i> , 2020, 8, 198.	1.6	6
8869	Shifts in the bacterial community of saliva give insights on the relationship between obesity and oral microbiota in adolescents. <i>Archives of Microbiology</i> , 2020, 202, 1085-1095.	1.0	19
8870	Dietary macronutrient intake and molecular-bacterial vaginosis: Role of fiber. <i>Clinical Nutrition</i> , 2020, 39, 3066-3071.	2.3	16
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8874	16S rRNA gene sequencing reveals the relationship between gut microbiota and ovarian development in the swimming crab <i>Portunus trituberculatus</i> . <i>Chemosphere</i> , 2020, 254, 126891.	4.2	20
8875	Diversity of bacteria and archaea in the groundwater contaminated by chlorinated solvents undergoing natural attenuation. <i>Environmental Research</i> , 2020, 185, 109457.	3.7	18
8876	A Diversified Dietary Pattern Is Associated With a Balanced Gut Microbial Composition of Faecalibacterium and Escherichia/Shigella in Patients With Crohn's Disease in Remission. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 1547-1557.	0.6	43
8877	Enrichment and key features of a robust and consistent indigenous marine-cognate microbial consortium growing on oily bilge wastewaters. <i>Biodegradation</i> , 2020, 31, 91-108.	1.5	22
8878	Soybean oligosaccharide, stachyose, and raffinose in broilers diets: effects on odor compound concentration and microbiota in cecal digesta. <i>Poultry Science</i> , 2020, 99, 3532-3539.	1.5	21
8879	Captivity Influences Gut Microbiota in Crocodile Lizards (<i>Shinisaurus crocodilurus</i>). <i>Frontiers in Microbiology</i> , 2020, 11, 550.	1.5	27
8880	Probiotic Consortia: Reshaping the Rhizospheric Microbiome and Its Role in Suppressing Root-Rot Disease of <i>Panax notoginseng</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 701.	1.5	43
8881	Effects of an Eco-Friendly Sanitizing Wash on Spinach Leaf Bacterial Community Structure and Diversity. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 2986.	1.3	4
8882	Host Plants Influence the Symbiont Diversity of Eriosomatinae (Hemiptera: Aphididae). <i>Insects</i> , 2020, 11, 217.	1.0	14
8883	Crypt residing bacteria and proximal colonic carcinogenesis in a mouse model of Lynch syndrome. <i>International Journal of Cancer</i> , 2020, 147, 2316-2326.	2.3	20
8884	Effects of di-n-butyl phthalate and di-2-ethylhexyl phthalate on pollutant removal and microbial community during wastewater treatment. <i>Ecotoxicology and Environmental Safety</i> , 2020, 198, 110665.	2.9	24
8885	Effects of polysaccharides from wild morels on immune response and gut microbiota composition in non-treated and cyclophosphamide-treated mice. <i>Food and Function</i> , 2020, 11, 4291-4303.	2.1	39
8886	Dual oxidase Duox and Toll-like receptor 3 TLR3 in the Toll pathway suppress zoonotic pathogens through regulating the intestinal bacterial community homeostasis in <i>Hermetia illucens</i> L. <i>PLoS ONE</i> , 2020, 15, e0225873.	1.1	19
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8891	Variation of near surface atmosphere microbial communities at an urban and a suburban site in Philadelphia, PA, USA. <i>Science of the Total Environment</i> , 2020, 724, 138353.	3.9	23
8892	Ursodeoxycholic Acid (UDCA) Mitigates the Host Inflammatory Response during <i>Clostridioides difficile</i> Infection by Altering Gut Bile Acids. <i>Infection and Immunity</i> , 2020, 88, .	1.0	47
8893	Contrasting Patterns of Functional Diversity in Coffee Root Fungal Communities Associated with Organic and Conventionally Managed Fields. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	8
8894	The trisaccharide melezitose impacts honey bees and their intestinal microbiota. <i>PLoS ONE</i> , 2020, 15, e0230871.	1.1	18
8895	Comparison of vaginal microbiota in gynecologic cancer patients pre- and post-radiation therapy and healthy women. <i>Cancer Medicine</i> , 2020, 9, 3714-3724.	1.3	23
8896	The effects of eight years of conservation tillage on the soil physicochemical properties and bacterial communities in a rain-fed agroecosystem of the loess plateau, China. <i>Land Degradation and Development</i> , 2020, 31, 2475-2489.	1.8	16
8897	Abnormal gut microbiota composition is associated with experimental autoimmune prostatitis-induced depressive-like behaviors in mice. <i>Prostate</i> , 2020, 80, 663-673.	1.2	15
8898	Dynamic shifts within volatile fatty acid-degrading microbial communities indicate process imbalance in anaerobic digesters. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4563-4575.	1.7	11
8899	Influence of electron acceptor availability and microbial community structure on sedimentary methane oxidation in a boreal estuary. <i>Biogeochemistry</i> , 2020, 148, 291-309.	1.7	28
8900	Rhizosphere bacteria are more strongly related to plant root traits than fungi in temperate montane forests: insights from closed and open forest patches along an elevational gradient. <i>Plant and Soil</i> , 2020, 450, 183-200.	1.8	24
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8902	A formulated diet improved digestive capacity, immune function and intestinal microbiota structure of juvenile hybrid grouper (<i>Epinephelus fuscoguttatus</i> × <i>Epinephelus lanceolatus</i>), when compared with chilled trash fish. <i>Aquaculture</i> , 2020, 523, 735230.	1.7	21
8903	The effect of <i>Lactobacillus plantarum</i> administration on the intestinal microbiota of whiteleg shrimp <i>Penaeus vannamei</i> . <i>Aquaculture</i> , 2020, 526, 735331.	1.7	50
8904	Investigating the composition and distribution of microplastics surface biofilms in coral areas. <i>Chemosphere</i> , 2020, 252, 126565.	4.2	88
8905	Vessel transport of antibiotic resistance genes across oceans and its implications for ballast water management. <i>Chemosphere</i> , 2020, 253, 126697.	4.2	24
8906	An Arabidopsis Secondary Metabolite Directly Targets Expression of the Bacterial Type III Secretion System to Inhibit Bacterial Virulence. <i>Cell Host and Microbe</i> , 2020, 27, 601-613.e7.	5.1	66
8907	Vancomycin exposure caused opportunistic pathogens bloom in intestinal microbiome by simulator of the human intestinal microbial ecosystem (SHIME). <i>Environmental Pollution</i> , 2020, 265, 114399.	3.7	30

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8909	Depauperate soil fungal populations from the St. Helena endemic <i>Commidendrum robustum</i> are dominated by Capnodiales. <i>Fungal Ecology</i> , 2020, 45, 100911.	0.7	6
8910	Assessment of oral ciprofloxacin impaired gut barrier integrity on gut bacteria in mice. <i>International Immunopharmacology</i> , 2020, 83, 106460.	1.7	11
8911	Gut DYSBIOSIS and altered barrier function precedes the appearance of metabolic syndrome in a rat model of nutrient-induced catch-up growth. <i>Journal of Nutritional Biochemistry</i> , 2020, 81, 108383.	1.9	17
8912	Dietary l-arginine supplementation ameliorates inflammatory response and alters gut microbiota composition in broiler chickens infected with <i>Salmonella enterica</i> serovar Typhimurium. <i>Poultry Science</i> , 2020, 99, 1862-1874.	1.5	40
8913	Microbial bloom formation in a high pH spent nuclear fuel pond. <i>Science of the Total Environment</i> , 2020, 720, 137515.	3.9	24
8914	Structural and functional responses of bacterial and fungal communities to multiple heavy metal exposure in arid loess. <i>Science of the Total Environment</i> , 2020, 723, 138081.	3.9	89
8915	Removal of malodorant skatole by two enriched microbial consortia: Performance, dynamic, function prediction and bacteria isolation. <i>Science of the Total Environment</i> , 2020, 725, 138416.	3.9	15
8916	Evaluation and sensitivity analysis of diatom DNA metabarcoding for WFD bioassessment of Mediterranean rivers. <i>Science of the Total Environment</i> , 2020, 727, 138445.	3.9	42
8917	Pioneer trees of <i>Betula pendula</i> at a red gypsum landfill harbour specific structure and composition of root-associated microbial communities. <i>Science of the Total Environment</i> , 2020, 726, 138530.	3.9	14
8918	Root filtering, rather than host identity or age, determines the composition of root-associated fungi and oomycetes in three naturally co-occurring Brassicaceae. <i>Soil Biology and Biochemistry</i> , 2020, 146, 107806.	4.2	28
8919	Biogeography and Assembly of Microbial Communities in Wastewater Treatment Plants in China. <i>Environmental Science & Technology</i> , 2020, 54, 5884-5892.	4.6	34
8920	Macroecological dynamics of gut microbiota. <i>Nature Microbiology</i> , 2020, 5, 768-775.	5.9	62
8921	The cutaneous microbiome in hospitalized patients with pressure ulcers. <i>Scientific Reports</i> , 2020, 10, 5963.	1.6	15
8922	Characterizing the gut microbiota in patients with chronic kidney disease. <i>Postgraduate Medicine</i> , 2020, 132, 495-505.	0.9	57
8923	Effects of copper and zinc sources and inclusion levels of copper on weanling pig performance and intestinal microbiota. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	34
8924	Phylogenetic clustering and rarity imply risk of local species extinction in prospective deep-sea mining areas of the Clarion-Clipperton Fracture Zone. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192666.	1.2	19
8925	Phylogenetic conservation of soil bacterial responses to simulated global changes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190242.	1.8	46

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8927	Isolation and characterization of denitrifiers from woodchip bioreactors for bioaugmentation application. <i>Journal of Applied Microbiology</i> , 2020, 129, 590-600.	1.4	22
8928	Soil Bacterial Community Response and Nitrogen Cycling Variations Associated with Subalpine Meadow Degradation on the Loess Plateau, China. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
8929	Soil Microbial Communities in Diverse Agroecosystems Exposed to the Herbicide Glyphosate. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	33
8930	Reintroducing mothur: 10 Years Later. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	160
8931	Autotoxic Ginsenoside Disrupts Soil Fungal Microbiomes by Stimulating Potentially Pathogenic Microbes. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	38
8932	Human Colon Mucosal Biofilms and Murine Host Communicate via Altered mRNA and microRNA Expression during Cancer. <i>MSystems</i> , 2020, 5, .	1.7	25
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8934	The Gut Microbial Diversity of Newly Diagnosed Diabetics but Not of Prediabetics Is Significantly Different from That of Healthy Nondiabetics. <i>MSystems</i> , 2020, 5, .	1.7	64
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8936	Prokaryotic Community Structure in the Rapeseed (<i>Brassica napus</i> L.) Rhizosphere Depending on Addition of 1-Aminocyclopropane-1-Carboxylate-Utilizing Bacteria. <i>Microbiology</i> , 2020, 89, 115-121.	0.5	6
8937	A Novel "Microbial Bait" Technique for Capturing Fe(III)-Reducing Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 330.	1.5	4
8938	"In situ similis" Culturing of Plant Microbiota: A Novel Simulated Environmental Method Based on Plant Leaf Blades as Nutritional Pads. <i>Frontiers in Microbiology</i> , 2020, 11, 454.	1.5	11
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8941	Radiation Tolerance of <i>Pseudanabaena catenata</i> , a Cyanobacterium Relevant to the First Generation Magnox Storage Pond. <i>Frontiers in Microbiology</i> , 2020, 11, 515.	1.5	13
8942	Crosstalk Between Female Gonadal Hormones and Vaginal Microbiota Across Various Phases of Women's Gynecological Lifecycle. <i>Frontiers in Microbiology</i> , 2020, 11, 551.	1.5	61
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8945	Insights into the Microbiological Safety of Wooden Cutting Boards Used for Meat Processing in Hong Kong's Wet Markets: A Focus on Food-Contact Surfaces, Cross-Contamination and the Efficacy of Traditional Hygiene Practices. <i>Microorganisms</i> , 2020, 8, 579.	1.6	18
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8950	Epithelium intrinsic vitamin A signaling co-ordinates pathogen clearance in the gut via IL-18. <i>PLoS Pathogens</i> , 2020, 16, e1008360.	2.1	20
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8953	The vaginal microbiota associates with the regression of untreated cervical intraepithelial neoplasia 2 lesions. <i>Nature Communications</i> , 2020, 11, 1999.	5.8	111
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8957	Variation of effluent organic matter (EfOM) during anaerobic/anoxic/oxic (A2O) wastewater treatment processes. <i>Water Research</i> , 2020, 178, 115830.	5.3	48
8958	Island biogeography of soil bacteria and fungi: similar patterns, but different mechanisms. <i>ISME Journal</i> , 2020, 14, 1886-1896.	4.4	86
8959	Soil Hg Contamination Impact on Earthworms' Gut Microbiome. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 2565.	1.3	3
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8961	<i>Lactobacillus plantarum</i> LPL-1, a bacteriocin producing strain, changed the bacterial community composition and improved the safety of low-salt fermented sausages. <i>LWT - Food Science and Technology</i> , 2020, 128, 109385.	2.5	26

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8963	Community structure & Ecosystem function relationships in the Congo Basin methane cycle depend on the physiological scale of function. <i>Molecular Ecology</i> , 2020, 29, 1806-1819.	2.0	5
8964	Multiple in situ Nucleic Acid Collections (MISNAC) From Deep-Sea Waters. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	13
8965	Distinct lung microbial community states in patients with pulmonary tuberculosis. <i>Science China Life Sciences</i> , 2020, 63, 1522-1533.	2.3	18
8966	Limiting oxidative DNA damage reduces microbe-induced colitis-associated colorectal cancer. <i>Nature Communications</i> , 2020, 11, 1802.	5.8	58
8967	Altered gut microbial profile is associated with abnormal metabolism activity of Autism Spectrum Disorder. <i>Gut Microbes</i> , 2020, 11, 1246-1267.	4.3	166
8968	Intestinal Enterococcus abundance correlates inversely with excessive weight gain and increased plasma leptin in breastfed infants. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	15
8969	Disentangling the mechanisms shaping the surface ocean microbiota. <i>Microbiome</i> , 2020, 8, 55.	4.9	154
8970	A Molecular Approach to Explore the Background Benthic Fauna Around a Hydrothermal Vent and Their Larvae: Implications for Future Mining of Deep-Sea SMS Deposits. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	10
8971	Bacterial community analysis of floor dust and HEPA filters in air purifiers used in office rooms in ILAS, Beijing. <i>Scientific Reports</i> , 2020, 10, 6417.	1.6	23
8972	Livestock overgrazing disrupts the positive associations between soil biodiversity and nitrogen availability. <i>Functional Ecology</i> , 2020, 34, 1713-1720.	1.7	33
8973	Variation in soil microbial communities: elucidating relationships with vegetation and soil properties, and testing sampling effectiveness. <i>Plant Ecology</i> , 2020, 221, 837-851.	0.7	13
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8978	Different community assembly mechanisms underlie similar biogeography of bacteria and microeukaryotes in Tibetan lakes. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	43
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8982	Carbon turnover and microbial activity in an artificial soil under imposed cyclic drainage and imbibition. <i>Vadose Zone Journal</i> , 2020, 19, e20021.	1.3	12
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8984	The effect of antibiotic cocktails on host immune status is dynamic and does not always correspond to changes in gut microbiota. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4995-5009.	1.7	17
8985	Comparison of the Rhizosphere Soil Microbial Community Structure and Diversity Between Powdery Mildew-Infected and Noninfected Strawberry Plants in a Greenhouse by High-Throughput Sequencing Technology. <i>Current Microbiology</i> , 2020, 77, 1724-1736.	1.0	18
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8987	Screening for electrical conductivity in anaerobic granular sludge from full-scale wastewater treatment reactors. <i>Biochemical Engineering Journal</i> , 2020, 159, 107575.	1.8	10
8988	Investigating the mycobiome of the Holcomb Creosote Superfund Site. <i>Chemosphere</i> , 2020, 252, 126208.	4.2	1
8989	Bambara groundnut soil metagenomics data. <i>Data in Brief</i> , 2020, 30, 105542.	0.5	0
8990	Characteristics of airborne bacterial communities in indoor and outdoor environments during continuous haze events in Beijing: Implications for health care. <i>Environment International</i> , 2020, 139, 105721.	4.8	20
8991	Environmental fate of Bacteroidetes, with particular emphasis on <i>Bacteroides fragilis</i> group bacteria and their specific antibiotic resistance genes, in activated sludge wastewater treatment plants. <i>Journal of Hazardous Materials</i> , 2020, 394, 122544.	6.5	67
8992	Combined photocatalytic pre-oxidation reactor and sequencing batch bioreactor for advanced treatment of industrial wastewater. <i>Journal of Water Process Engineering</i> , 2020, 36, 101259.	2.6	12
8993	Biodegradation of weathered crude oil in seawater with frazil ice. <i>Marine Pollution Bulletin</i> , 2020, 154, 111090.	2.3	10
8994	Extracellular organic matter from <i>Micrococcus luteus</i> containing resuscitation-promoting factor in sequencing batch reactor for effective nutrient and phenol removal. <i>Science of the Total Environment</i> , 2020, 727, 138627.	3.9	11
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8996	Host-microbiota interaction helps to explain the bottom-up effects of climate change on a small rodent species. <i>ISME Journal</i> , 2020, 14, 1795-1808.	4.4	29
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9000	Temporal changes in microbial communities attached to forages with different lignocellulosic compositions in cattle rumen. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	32
9001	Local factors drive bacterial and microeukaryotic community composition in lake surface sediment collected across an altitudinal gradient. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	20
9002	Impacts of Soil Microbiome Variations on Root Colonization by Fungi and Bacteria and on the Metabolome of <i>Populus tremula</i> – <i>Populus alba</i> . <i>Phytobiomes Journal</i> , 2020, 4, 142-155.	1.4	24
9003	Toward a dynamical understanding of microbial communities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190248.	1.8	21
9004	Experimental assessment of tree canopy and leaf litter controls on the microbiome and nitrogen fixation rates of two boreal mosses. <i>New Phytologist</i> , 2020, 227, 1335-1349.	3.5	33
9005	Effects of Spatial Variability and Relic DNA Removal on the Detection of Temporal Dynamics in Soil Microbial Communities. <i>MBio</i> , 2020, 11, .	1.8	70
9006	Long-Term Phytoremediation of Coastal Saline Soil Reveals Plant Species-Specific Patterns of Microbial Community Recruitment. <i>MSystems</i> , 2020, 5, .	1.7	49
9007	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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9019	Rifaximin Alleviates Endotoxemia with Decreased Serum Levels of Soluble CD163 and Mannose Receptor and Partial Modification of Gut Microbiota in Cirrhotic Patients. <i>Antibiotics</i> , 2020, 9, 145.	1.5	33
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9021	Low-gossypol cottonseed protein concentrate used as a replacement of fish meal for juvenile hybrid grouper (<i>Epinephelus fuscoguttatus</i> × <i>Epinephelus lanceolatus</i>): Effects on growth performance, immune responses and intestinal microbiota. <i>Aquaculture</i> , 2020, 524, 735309.	1.7	65
9022	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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9026	Synergetic responses of intestinal microbiota and epithelium to dietary inulin supplementation in pigs. <i>European Journal of Nutrition</i> , 2021, 60, 715-727.	1.8	10
9027	The effect of monoculture and rotation planting on soil bacterial community structure at different elevation in Hubei. <i>Soil Use and Management</i> , 2021, 37, 667-676.	2.6	3
9028	Microbiomics, Metabolomics, Predicted Metagenomics, and Hepatic Steatosis in a Population-Based Study of 1,355 Adults. <i>Hepatology</i> , 2021, 73, 968-982.	3.6	43
9029	Individual and Site-Specific Variation in a Biogeographical Profile of the Coyote Gastrointestinal Microbiota. <i>Microbial Ecology</i> , 2021, 81, 240-252.	1.4	17
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9035	Bacterial diversity associated with a newly described bioeroding sponge, <i>Cliona thomasi</i> , from the coral reefs on the West Coast of India. <i>Folia Microbiologica</i> , 2021, 66, 203-211.	1.1	3
9036	Advanced nitrogen removal in a fixed-bed anaerobic ammonia oxidation reactor following an anoxic/oxic reactor: Nitrogen removal contributions and mechanisms. <i>Bioresource Technology</i> , 2021, 320, 124297.	4.8	8
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9040	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
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9042	Influence of pipe material on biofilm microbial communities found in drinking water supply system. <i>Environmental Research</i> , 2021, 196, 110433.	3.7	21
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9047	Molecular techniques for understanding microbial abundance and activity in clay barriers used for geodisposal. , 2021, , 71-96.		1
9048	Effects of mowing regimes on above- and belowground biota in semi-arid grassland of northern China. <i>Journal of Environmental Management</i> , 2021, 277, 111441.	3.8	22
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9051	Fungal endophyte diversity in table grapes. <i>Canadian Journal of Microbiology</i> , 2021, 67, 29-36.	0.8	12

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9053	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
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9056	Effects of different concentrations of coated nano zinc oxide material on fecal bacterial composition and intestinal barrier in weaned piglets. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 735-745.	1.7	15
9057	Long term natural restoration creates soil-like microbial communities in bauxite residue: A 50-year field study. <i>Land Degradation and Development</i> , 2021, 32, 1606-1617.	1.8	14
9058	Muc2 Mucin and Nonmucin Microbiota Confer Distinct Innate Host Defense in Disease Susceptibility and Colonic Injury. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 11, 77-98.	2.3	28
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9060	Insights on the inhibition of anaerobic digestion performances under short-term exposure of metal-doped nanoplastics via <i>Methanosarcina acetivorans</i> . <i>Environmental Pollution</i> , 2021, 275, 115755.	3.7	22
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9062	Effect of balanced application of boron and phosphorus fertilizers on soil bacterial community, seed yield and phosphorus use efficiency of <i>Brassica napus</i> . <i>Science of the Total Environment</i> , 2021, 751, 141644.	3.9	10
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9064	Power of Microbiome Beta-Diversity Analyses Based on Standard Reference Samples. <i>American Journal of Epidemiology</i> , 2021, 190, 439-447.	1.6	5
9065	Composition of soil bacterial and fungal communities in relation to vegetation composition and soil characteristics along an altitudinal gradient. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	27
9066	<i>Bacillus subtilis</i> and <i>Enterococcus faecium</i> co-fermented feed regulates lactating sow's performance, immune status and gut microbiota. <i>Microbial Biotechnology</i> , 2021, 14, 614-627.	2.0	23
9067	Changes in community structure and metabolic function of soil bacteria depending on the type restoration processing in the degraded alpine grassland ecosystems in Northern Tibet. <i>Science of the Total Environment</i> , 2021, 755, 142619.	3.9	15
9068	Community diversity and abundance of ammonia-oxidizing archaea and bacteria in shrimp pond sediment at different culture stages. <i>Journal of Applied Microbiology</i> , 2021, 130, 1442-1455.	1.4	18
9069	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

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9072	Bacteria in the lakes of the Tibetan Plateau and polar regions. <i>Science of the Total Environment</i> , 2021, 754, 142248.	3.9	16
9073	Gut microbiota in adolescent girls with polycystic ovary syndrome: Effects of randomized treatments. <i>Pediatric Obesity</i> , 2021, 16, e12734.	1.4	16
9074	Characterization of staphylococcal communities on healthy and allergic feline skin. <i>Veterinary Dermatology</i> , 2021, 32, 61.	0.4	3
9075	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
9076	Responses of microbial community and antibiotic resistance genes to the selection pressures of ampicillin, cephalexin and chloramphenicol in activated sludge reactors. <i>Science of the Total Environment</i> , 2021, 755, 142632.	3.9	45
9077	Integrating biological As(III) oxidation with Fe(0) electrocoagulation for arsenic removal from groundwater. <i>Water Research</i> , 2021, 188, 116531.	5.3	23
9078	Host specificity of microbiome assembly and its fitness effects in phytoplankton. <i>ISME Journal</i> , 2021, 15, 774-788.	4.4	48
9079	Distinguishing Between the Impacts of Heat and Drought Stress on the Root Microbiome of <i>Sorghum bicolor</i> . <i>Phytobiomes Journal</i> , 2021, 5, 166-176.	1.4	28
9080	Effects of in vitro metabolism of a broccoli leachate, glucosinolates and S-methylcysteine sulphoxide on the human faecal microbiome. <i>European Journal of Nutrition</i> , 2021, 60, 2141-2154.	1.8	14
9081	Profiling the differences of gut microbial structure between schizophrenia patients with and without violent behaviors based on 16S rRNA gene sequencing. <i>International Journal of Legal Medicine</i> , 2021, 135, 131-141.	1.2	18
9082	The impact of the endophytic bacterial community on mulberry tree growth in the Three Gorges Reservoir ecosystem, China. <i>Environmental Microbiology</i> , 2021, 23, 1858-1875.	1.8	7
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9084	Relationships between nitrogen cycling microbial community abundance and composition reveal the indirect effect of soil pH on oak decline. <i>ISME Journal</i> , 2021, 15, 623-635.	4.4	63
9085	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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9087	Evidence for non-methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i> . <i>Environmental Microbiology</i> , 2021, 23, 340-357.	1.8	19

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9089	Interaction among endophytic bacteria, sweet sorghum (<i>Sorghum bicolor</i>) cultivars and chemical nitrogen fertilization. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
9090	<i>Chlamydia pneumoniae</i> and <i>Mycoplasma pneumoniae</i> in children with cystic fibrosis: impact on bacterial respiratory microbiota diversity. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	6
9091	Microbial networks inferred from environmental DNA data for biomonitoring ecosystem change: Strengths and pitfalls. <i>Molecular Ecology Resources</i> , 2021, 21, 762-780.	2.2	17
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9097	Influence of Environmental Stressors on the Microbiota of Zebra Mussels (<i>Dreissena polymorpha</i>). <i>Microbial Ecology</i> , 2021, 81, 1042-1053.	1.4	6
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9099	Top-down controls on nutrient cycling and population dynamics in a model estuarine photoautotroph-heterotroph co-culture system. <i>Molecular Ecology</i> , 2021, 30, 592-607.	2.0	9
9100	Effects of mild moxibustion on intestinal microbiome and NLRP3 inflammasome in rats with 5-fluorouracil-induced intestinal mucositis. <i>Journal of Integrative Medicine</i> , 2021, 19, 144-157.	1.4	14
9101	Interacting effects of land use type, microbes and plant traits on soil aggregate stability. <i>Soil Biology and Biochemistry</i> , 2021, 154, 108072.	4.2	38
9102	Fate of mercury and methylmercury in full-scale sludge anaerobic digestion combined with thermal hydrolysis. <i>Journal of Hazardous Materials</i> , 2021, 406, 124310.	6.5	10
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9107	A comparison of antibiotics, antibiotic resistance genes, and bacterial community in broiler and layer manure following composting. <i>Environmental Science and Pollution Research</i> , 2021, 28, 14707-14719.	2.7	20
9108	Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology</i> 2000, 2021, 85, 12-27.	6.3	16
9109	Variation of Soil Bacterial and Fungal Communities from Fluvo-Aquic Soil Under Chemical Fertilizer Reduction Combined with Organic Materials in North China Plain. <i>Journal of Soil Science and Plant Nutrition</i> , 2021, 21, 349-363.	1.7	30
9110	Ecological drivers switch from bottom-up to top-down during model microbial community successions. <i>ISME Journal</i> , 2021, 15, 1085-1097.	4.4	21
9111	NLRP6 modulates neutrophil homeostasis in bacterial pneumonia-derived sepsis. <i>Mucosal Immunology</i> , 2021, 14, 574-584.	2.7	25
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9113	Storage period affecting dynamic succession of microbiota and quality changes of strong-flavor Baijiu Daqu. <i>LWT - Food Science and Technology</i> , 2021, 139, 110544.	2.5	26
9114	Characterization of long-range transported bioaerosols in the Central Mediterranean. <i>Science of the Total Environment</i> , 2021, 763, 143010.	3.9	17
9115	Partial fishmeal protein replacement with peptides from swine blood modulates the nutritional status, immune response, and intestinal microbiota of hybrid groupers (female <i>Epinephelus</i>). <i>Tj ETQq1 1 0.784314 ngBT /Overlock 10 Tj</i>		
9116	Stronger impacts of long-term relative to short-term exposure to carbon nanomaterials on soil bacterial communities. <i>Journal of Hazardous Materials</i> , 2021, 410, 124550.	6.5	15
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9118	Changes in the bacterial community structure in soil under conventional and conservation practices throughout a complete maize (<i>Zea mays</i> L.) crop cycle. <i>Applied Soil Ecology</i> , 2021, 157, 103733.	2.1	10
9119	Influence of microbial spatial distribution and activity in an EGSB reactor under high- and low-loading denitrification desulfurization. <i>Environmental Research</i> , 2021, 195, 110311.	3.7	8
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9122	Maize endophytic microbial-communities revealed by removing PCR and 16S rRNA sequencing and their synthetic applications to suppress maize banded leaf and sheath blight. <i>Microbiological Research</i> , 2021, 242, 126639.	2.5	17
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9125	Dynamics of denitrification performance and denitrifying community under high-dose acute oxytetracycline exposure and various biorecovery strategies in polycaprolactone-supported solid-phase denitrification. <i>Journal of Environmental Management</i> , 2021, 279, 111763.	3.8	13
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9128	Propylene glycol-based antifreeze is an effective preservative for DNA metabarcoding of benthic arthropods. <i>Freshwater Science</i> , 2021, 40, 77-87.	0.9	14
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9130	Influence of seasonality on the aerosol microbiome of the Amazon rainforest. <i>Science of the Total Environment</i> , 2021, 760, 144092.	3.9	13
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9132	Contrasting fungal responses to wildfire across different ecosystem types. <i>Molecular Ecology</i> , 2021, 30, 844-854.	2.0	13
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9134	Bacterial epibiont communities of panmictic Antarctic krill are spatially structured. <i>Molecular Ecology</i> , 2021, 30, 1042-1052.	2.0	6
9135	Arid Ecosystem Vegetation Canopy-Gap Dichotomy: Influence on Soil Microbial Composition and Nutrient Cycling Functional Potential. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
9136	Invader-resident relatedness and soil management history shape patterns of invasion of compost microbial populations into agricultural soils. <i>Applied Soil Ecology</i> , 2021, 158, 103795.	2.1	14
9137	Effects of <i>Bacillus megaterium</i> L222 on quality and bacterial diversity of Sichuan paocai. <i>Food Research International</i> , 2021, 140, 109994.	2.9	14
9138	Floral fungal-bacterial community structure and co-occurrence patterns in four sympatric island plant species. <i>Fungal Biology</i> , 2021, 125, 49-61.	1.1	14
9139	Core activated sludge communities are influenced little by immigration: Case study of a membrane bioreactor plant. <i>Journal of Environmental Sciences</i> , 2021, 102, 244-255.	3.2	14
9140	Effect of Gender Bias on Equine Fecal Microbiota. <i>Journal of Equine Veterinary Science</i> , 2021, 97, 103355.	0.4	8
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9143	Large-scale evidence for microbial response and associated carbon release after permafrost thaw. <i>Global Change Biology</i> , 2021, 27, 3218-3229.	4.2	44
9144	Influence of photobioreactor set-up on the survival of microalgae inoculum. <i>Bioresource Technology</i> , 2021, 320, 124408.	4.8	26
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9146	Plant diversity promotes soil fungal pathogen richness under fertilization in an alpine meadow. <i>Journal of Plant Ecology</i> , 2021, 14, 323-336.	1.2	13
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9149	Bacterial dispersal and drift drive microbiome diversity patterns within a population of feral hindgut fermenters. <i>Molecular Ecology</i> , 2021, 30, 555-571.	2.0	22
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9151	Bacterial community dynamics varies with soil management and irrigation practices in grapevines (<i>Vitis vinifera</i> L.). <i>Applied Soil Ecology</i> , 2021, 158, 103807.	2.1	12
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9153	Short-term high-dose gavage of hydroxychloroquine changes gut microbiota but not the intestinal integrity and immunological responses in mice. <i>Life Sciences</i> , 2021, 264, 118450.	2.0	20
9154	Composition and interaction frequencies in soil bacterial communities change in association with urban park age in Beijing. <i>Pedobiologia</i> , 2021, 84, 150699.	0.5	12
9155	Microbiota populations and short-chain fatty acids production in cecum of immunosuppressed broilers consuming diets containing ¹³ C-irradiated <i>Astragalus polysaccharides</i> . <i>Poultry Science</i> , 2021, 100, 273-282.	1.5	35
9156	Effects of grazing mixed-grass pastures on growth performance, immune responses, and intestinal microbiota in free-range Beijing-you chickens. <i>Poultry Science</i> , 2021, 100, 1049-1058.	1.5	13
9157	Endangerment of <i>Ostrya rehderiana</i> Chun and its relationship with rhizosphere soil microflora. <i>Agronomy Journal</i> , 2021, 113, 746-759.	0.9	5
9158	Gut microbiota alteration in adolescent anorexia nervosa does not normalize with short-term weight restoration. <i>International Journal of Eating Disorders</i> , 2021, 54, 969-980.	2.1	43
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9162	Alkalinity gradients in grasslands alter soil bacterial community composition and function. <i>Soil Science Society of America Journal</i> , 2021, 85, 286-298.	1.2	3
9163	Molecular evidence of host-parasite interactions between zooplankton and Syndiniales. <i>Aquatic Ecology</i> , 2021, 55, 125-134.	0.7	15
9164	Large-scale switchable potentiostatically controlled/microbial fuel cell bioelectrochemical wastewater treatment system. <i>Bioelectrochemistry</i> , 2021, 138, 107724.	2.4	18
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9168	Soil Characteristics Constrain the Response of Microbial Communities and Associated Hydrocarbon Degradation Genes during Phytoremediation. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	17
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9171	Postmortem submersion interval (PMSI) estimation from the microbiome of <i>Sus scrofa</i> bone in a freshwater river. <i>Forensic Science International</i> , 2021, 318, 110480.	1.3	18
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9173	Chemotrophic profiling of prokaryotic communities thriving on organic and mineral nutrients in a submerged coastal cave. <i>Science of the Total Environment</i> , 2021, 755, 142514.	3.9	7
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9175	Effects of burning harvested residues on the archaeal and bacterial communities of <i>Eucalyptus urophylla</i> substituting native vegetation. <i>Applied Soil Ecology</i> , 2021, 158, 103796.	2.1	17
9176	Termites Are Associated with External Species-Specific Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	10
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9180	Maternal Diet and Infant Feeding Practices Are Associated with Variation in the Human Milk Microbiota at 3 Months Postpartum in a Cohort of Women with High Rates of Gestational Glucose Intolerance. <i>Journal of Nutrition</i> , 2021, 151, 320-329.	1.3	24
9181	Microbiomes in agricultural and mining soils contaminated with arsenic in Guanajuato, Mexico. <i>Archives of Microbiology</i> , 2021, 203, 499-511.	1.0	1
9182	Interactions between nitrogen availability, bacterial communities, and nematode indicators of soil food web function in response to organic amendments. <i>Applied Soil Ecology</i> , 2021, 157, 103767.	2.1	20
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9184	Type 2 high asthma is associated with a specific indoor mycobiome and microbiome. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1296-1305.e6.	1.5	41
9185	Microbial community changes in the digestive tract of the clam <i>Meretrix petechialis</i> in response to <i>Vibrio parahaemolyticus</i> challenge. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 329-339.	0.6	5
9186	Stochastic processes shape the biogeographic variations in core bacterial communities between aerial and belowground compartments of common bean. <i>Environmental Microbiology</i> , 2021, 23, 949-964.	1.8	25
9187	High-throughput sequencing reveals significant diversity in the gut microbiomes of humpback		

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9199	Only mass migration of fungi runs through the biotopes of soil, phyllosphere, and feces. <i>Journal of Soils and Sediments</i> , 2021, 21, 1151-1164.	1.5	2
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9201	Profiling of Bile Microbiome Identifies District Microbial Population between Cholelithiasis and Cholangiocarcinoma Patients. <i>Asian Pacific Journal of Cancer Prevention</i> , 2021, 22, 233-240.	0.5	11
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9203	Effect of salivary antimicrobial factors on microbial composition of tongue coating in patients with coronary heart disease with phlegm-stasis syndrome. <i>World Journal of Traditional Chinese Medicine</i> , 2021, .	0.9	0
9204	Oral administration of <i>Clostridium butyricum</i> rescues streptomycin-exacerbated respiratory syncytial virus-induced lung inflammation in mice. <i>Virulence</i> , 2021, 12, 2133-2148.	1.8	10
9205	<i>Hyalorbilia oviparasitica</i> Clade Detected in Field Soils Cropped to Sugar Beets and Enriched in the Presence of <i>Heterodera schachtii</i> and a Host Crop. <i>PhytoFrontiers</i> , 2021, 1, 13-20.	0.8	4
9206	Influence of Plant Host and Organ, Management Strategy, and Spore Traits on Microbiome Composition. <i>Phytobiomes Journal</i> , 2021, 5, 202-219.	1.4	13
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9209	First reported quantitative microbiota in different livestock manures used as organic fertilizers in the Northeast of Thailand. <i>Scientific Reports</i> , 2021, 11, 102.	1.6	14
9210	Spatial variations of bacterial community composition in sediments of the Jiaozhou Bay, China. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 865-879.	0.6	4
9211	Effects of Different Vegetation on Soil Microbial Diversity in Karst Area of Northwest Guangxi. <i>Hans Journal of Agricultural Sciences</i> , 2021, 11, 658-677.	0.0	2
9212	Distinct microbial communities colonize tonsillar squamous cell carcinoma. <i>Oncolmmunology</i> , 2021, 10, 1945202.	2.1	13
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9214	Impacts of Invasive Australian Acacias on Soil Bacterial Community Composition, Microbial Enzymatic Activities, and Nutrient Availability in Fynbos Soils. <i>Microbial Ecology</i> , 2021, 82, 704-721.	1.4	19
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9217	Inoculation of Stigma-Colonizing Microbes to Apple Stigmas Alters Microbiome Structure and Reduces the Occurrence of Fire Blight Disease. <i>Phytobiomes Journal</i> , 2021, 5, 156-165.	1.4	18
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9219	Diversity of microbes colonizing forages of varying lignocellulose properties in the sheep rumen. <i>PeerJ</i> , 2021, 9, e10463.	0.9	18
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9222	Deep Learning Based Mineral Image Classification Combined With Visual Attention Mechanism. <i>IEEE Access</i> , 2021, 9, 98091-98109.	2.6	23
9223	Compensatory intestinal immunoglobulin response after vancomycin treatment in humans. <i>Gut Microbes</i> , 2021, 13, 1-14.	4.3	6
9224	Gut Microbiota and Related Metabolites Were Disturbed in Ulcerative Colitis and Partly Restored After Mesalamine Treatment. <i>Frontiers in Pharmacology</i> , 2020, 11, 620724.	1.6	21
9225	Gut microbiota alteration in a mouse model of Anorexia Nervosa. <i>Clinical Nutrition</i> , 2021, 40, 181-189.	2.3	40
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9228	Freshwater monitoring by nanopore sequencing. <i>ELife</i> , 2021, 10, .	2.8	69
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9230	Ameliorative effect of graphene nanosheets against arsenic-induced toxicity in mice by oral exposure. <i>Environmental Science and Pollution Research</i> , 2021, 28, 21577-21588.	2.7	6
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9236	Exploring protocol bias in airway microbiome studies: one versus two PCR steps and 16S rRNA gene region V3 V4 versus V4. <i>BMC Genomics</i> , 2021, 22, 3.	1.2	11
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9245	Comparison of DNA Extraction Methods for Metagenomic Sequencing in Anaerobic Digestion. <i>Daehan Hwan'gyeong Gonghag Hoeji</i> , 2021, 43, 43-50.	0.4	0
9246	Data Mining of Scientometrics for Classifying Science Journals. <i>Intelligent Automation and Soft Computing</i> , 2021, 28, 873-885.	1.6	0
9247	Application of machine learning in prediction of Chemotherapy resistant of Ovarian Cancer based on Gut Microbiota. <i>Journal of Cancer</i> , 2021, 12, 2877-2885.	1.2	8
9248	Comparative analysis of bacterial and fungal endophytes responses to <i>Candidatus Liberibacter asiaticus</i> infection in leaf midribs of <i>Citrus reticulata</i> cv. Shatangju. <i>Physiological and Molecular Plant Pathology</i> , 2021, 113, 101590.	1.3	6
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9275	Norwegian Soils and Waters Contain Mesophilic, Plastic-Degrading Bacteria. <i>Microorganisms</i> , 2021, 9, 94.	1.6	12
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9338	<i>Usitatibacter rugosus</i> gen. nov., sp. nov. and <i>Usitatibacter palustris</i> sp. nov., novel members of Usitatibacteraceae fam. nov. within the order Nitrosomonadales isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	47
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9682	Soil microbiome manipulation triggers direct and possible indirect suppression against <i>Ralstonia solanacearum</i> and <i>Fusarium oxysporum</i> . <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 33.	2.9	33
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9686	Developing a non-destructive metabarcoding protocol for detection of pest insects in bulk trap catches. <i>Scientific Reports</i> , 2021, 11, 7946.	1.6	32
9688	Response to Holmes " practical considerations for vector microbiome studies. <i>Molecular Ecology</i> , 2021, 30, 2214-2219.	2.0	1
9689	<i>Aspergillus oryzae</i> and <i>Aspergillus niger</i> Co-Cultivation Extract Affects In Vitro Degradation, Fermentation Characteristics, and Bacterial Composition in a Diet-Specific Manner. <i>Animals</i> , 2021, 11, 1248.	1.0	12
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9693	A combination of <i>Tropilaelaps mercedesae</i> and imidacloprid negatively affects survival, pollen consumption and midgut bacterial composition of honey bee. <i>Chemosphere</i> , 2021, 268, 129368.	4.2	11
9694	Direct cell extraction from fresh and stored soil samples: Impact on microbial viability and community compositions. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108178.	4.2	12
9695	Individual <i>Microcystis</i> colonies harbour distinct bacterial communities that differ by <i>Microcystis</i> oligotype and with time. <i>Environmental Microbiology</i> , 2021, 23, 3020-3036.	1.8	36
9696	Direct and indirect disturbance impacts in forests. <i>Ecology Letters</i> , 2021, 24, 1225-1236.	3.0	25
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9698	Roles of surface layer proteins in the regulation of <i>Pediococcus pentosaceus</i> on growth performance, intestinal microbiota, and resistance to <i>Aeromonas hydrophila</i> in the freshwater prawn <i>Macrobrachium rosenbergii</i> . <i>Aquaculture International</i> , 2021, 29, 1373-1391.	1.1	5
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9700	Effect of microorganisms on the fingerprint of the volatile compounds in pine nut (<i>Pinus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.2 3		
9701	Sugarcane monoculture drives microbial community composition, activity and abundance of agricultural-related microorganisms. <i>Environmental Science and Pollution Research</i> , 2021, 28, 48080-48096.	2.7	28
9702	Effect of Quicklime on Microbial Community in Strong Acidic Soil. <i>Journal of Soil Science and Plant Nutrition</i> , 2021, 21, 1771-1781.	1.7	8

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9735	Refinement of 16S rRNA gene analysis for low biomass biospecimens. <i>Scientific Reports</i> , 2021, 11, 10741.	1.6	11
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9807	<i>Lactobacillus fermentum</i> CECT5716 ameliorates high fat diet-induced obesity in mice through modulation of gut microbiota dysbiosis. <i>Pharmacological Research</i> , 2021, 167, 105471.	3.1	43
9808	Archaea, bacteria and termite, nitrogen fixation and sustainable plants production. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2021, 49, 12172.	0.5	5
9809	A natural symbiotic bacterium drives mosquito refractoriness to <i>Plasmodium</i> infection via secretion of an antimalarial lipase. <i>Nature Microbiology</i> , 2021, 6, 806-817.	5.9	44
9810	Soil bacterial community composition in rice-fish integrated farming systems with different planting years. <i>Scientific Reports</i> , 2021, 11, 10855.	1.6	16
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9897	Transmission of Seed and Soil Microbiota to Seedling. <i>MSystems</i> , 2021, 6, e0044621.	1.7	38
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9973	Gut Microbiota: Critical Controller and Intervention Target in Brain Aging and Cognitive Impairment. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 671142.	1.7	20
9974	Consuming Different Structural Parts of Bamboo Induce Gut Microbiome Changes in Captive Giant Pandas. <i>Current Microbiology</i> , 2021, 78, 2998-3009.	1.0	9
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9984	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
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10004	Soil microbiome-mediated salinity tolerance in poplar plantlets is source-dependent. <i>Chemosphere</i> , 2021, 272, 129600.	4.2	15
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10031	Bacteriophage classification for assembled contigs using graph convolutional network. <i>Bioinformatics</i> , 2021, 37, i25-i33.	1.8	50
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10072	Pulmonary and intestinal microbiota dynamics during Gram-negative pneumonia-derived sepsis. <i>Intensive Care Medicine Experimental</i> , 2021, 9, 35.	0.9	9
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10074	Administration of All-Trans Retinoic Acid to Pregnant Sows Alters Gut Bacterial Community of Neonatal Piglets With Different <i>Hoxa1</i> Genotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 712212.	1.5	1
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10118	Bacteria associated with vascular wilt of poplar. <i>Archives of Microbiology</i> , 2021, 203, 4829-4838.	1.0	4
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10127	MFGM components promote gut Bifidobacterium growth in infant and in vitro. <i>European Journal of Nutrition</i> , 2022, 61, 277-288.	1.8	12
10128	Microbial community composition controls carbon flux across litter types in early phase of litter decomposition. <i>Environmental Microbiology</i> , 2021, 23, 6676-6693.	1.8	5
10129	Electrocatalytic deep dehalogenation of florfenicol using Fe-doped CoP nanotubes array for blocking resistance gene expression and microbial inhibition during biochemical treatment. <i>Water Research</i> , 2021, 201, 117361.	5.3	19
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10132	The phyllosphere microbiome of host trees contributes more than leaf phytochemicals to variation in the <i>Agrilus planipennis</i> Fairmaire gut microbiome structure. <i>Scientific Reports</i> , 2021, 11, 15911.	1.6	10
10133	Biochar Application Mitigates the Effect of Heat Stress on Rice (<i>Oryza sativa</i> L.) by Regulating the Root-Zone Environment. <i>Frontiers in Plant Science</i> , 2021, 12, 711725.	1.7	14
10134	Influence of metabolic cosubstrates on methanogenic potential and degradation of triclosan and propranolol in sanitary sewage. <i>Environmental Research</i> , 2021, 199, 111220.	3.7	9
10135	Precise head pose estimation on HPD5A database for attention recognition based on convolutional neural network in human-computer interaction. <i>Infrared Physics and Technology</i> , 2021, 116, 103740.	1.3	13
10136	Crude oil biodegradation in upper and supratidal seashores. <i>Journal of Hazardous Materials</i> , 2021, 416, 125919.	6.5	16
10137	The gut microbiome in microscopic polyangiitis with kidney involvement: common and unique alterations, clinical association and values for disease diagnosis and outcome prediction. <i>Annals of Translational Medicine</i> , 2021, 9, 1286-1286.	0.7	7
10139	Urinary metabolomic changes and microbiotic alterations in presenilin1/2 conditional double knockout mice. <i>Journal of Translational Medicine</i> , 2021, 19, 351.	1.8	14
10140	Supplementing Chitosan Oligosaccharide Positively Affects Hybrid Grouper (<i>Epinephelus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Concentrate: Effects on Growth, Gut Microbiota, Antioxidant Function and Immune Response. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
10141	Association of the Maternal Gut Microbiota/Metabolome with Cord Blood CCL17. <i>Nutrients</i> , 2021, 13, 2837.	1.7	4
10142	Dispersal Limitation Plays Stronger Role in the Community Assembly of Fungi Relative to Bacteria in Rhizosphere Across the Arable Area of Medicinal Plant. <i>Frontiers in Microbiology</i> , 2021, 12, 713523.	1.5	17
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10144	Effects of Ocean Acidification, Hypoxia, and Warming on the Gut Microbiota of the Thick Shell Mussel <i>Mytilus coruscus</i> Through 16S rRNA Gene Sequencing. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	7

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10146	Microbial Communities and Physicochemical Characteristics of Traditional Dajiang and Sufu in North China Revealed by High-Throughput Sequencing of 16S rRNA. <i>Frontiers in Microbiology</i> , 2021, 12, 665243.	1.5	6
10147	Analysis of bovine colostrum microbiota at a dairy farm in Ningxia, China. <i>International Dairy Journal</i> , 2021, 119, 104984.	1.5	3
10148	Metagenomic Analysis of Bacterial Diversity in Traditional Fermented Foods Reveals Food-Specific Dominance of Specific Bacterial Taxa. <i>Fermentation</i> , 2021, 7, 167.	1.4	13
10149	Bacterial Diversity in Calcium Carbonate Paleo Accretions (<i>Tosca</i>) in the Southern Pampas, Argentina. <i>Geomicrobiology Journal</i> , 2021, 38, 869-878.	1.0	1
10150	Benchmarking laboratory processes to characterise low-biomass respiratory microbiota. <i>Scientific Reports</i> , 2021, 11, 17148.	1.6	10
10151	Characterization of the Human Oropharyngeal Microbiomes in SARS-CoV-2 Infection and Recovery Patients. <i>Advanced Science</i> , 2021, 8, e2102785.	5.6	27
10152	A Central Role for Atg5 in Microbiota-Dependent Foxp3+ ROR γ ³ t+ Treg Cell Preservation to Maintain Intestinal Immune Homeostasis. <i>Frontiers in Immunology</i> , 2021, 12, 705436.	2.2	5
10153	Community structure and associated networks of endophytic bacteria in pea roots throughout plant life cycle. <i>Plant and Soil</i> , 2021, 468, 225-238.	1.8	7
10154	Activity-Based Cell Sorting Reveals Resistance of Functionally Degenerate <i>Nitrospira</i> during a Press Disturbance in Nitrifying Activated Sludge. <i>MSystems</i> , 2021, 6, e0071221.	1.7	4
10155	Decline in plankton diversity and carbon flux with reduced sea ice extent along the Western Antarctic Peninsula. <i>Nature Communications</i> , 2021, 12, 4948.	5.8	24
10156	Gut and Vagina Microbiota Associated With Estrus Return of Weaning Sows and Its Correlation With the Changes in Serum Metabolites. <i>Frontiers in Microbiology</i> , 2021, 12, 690091.	1.5	8
10157	Mucosal Bacteria Modulate <i>Candida albicans</i> Virulence in Oropharyngeal Candidiasis. <i>MBio</i> , 2021, 12, e0193721.	1.8	22
10158	Aboveground and belowground responses to cyanobacterial biofertilizer supplement in a semi-arid, perennial bioenergy cropping system. <i>GCB Bioenergy</i> , 2021, 13, 1908-1923.	2.5	4
10159	Methane-derived carbon flows into host-virus networks at different trophic levels in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
10161	Safety Assessment of Microbicide 2P23 on the Rectal and Vaginal Microbiota and Its Antiviral Activity on HIV Infection. <i>Frontiers in Immunology</i> , 2021, 12, 702172.	2.2	2
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10163	Microbial assemblages and methanogenesis pathways impact methane production and foaming in manure deep-pit storages. <i>PLoS ONE</i> , 2021, 16, e0254730.	1.1	2

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10165	The biological regulatory activities of <i>Flammulina velutipes</i> polysaccharide in mice intestinal microbiota, immune repertoire and heart transcriptome. <i>International Journal of Biological Macromolecules</i> , 2021, 185, 582-591.	3.6	9
10166	The Spatial and Temporal Characterization of Gut Microbiota in Broilers. <i>Frontiers in Veterinary Science</i> , 2021, 8, 712226.	0.9	26
10167	The Transcriptional Response of Soil Bacteria to Long-Term Warming and Short-Term Seasonal Fluctuations in a Terrestrial Forest. <i>Frontiers in Microbiology</i> , 2021, 12, 666558.	1.5	8
10168	Addition of <i>Trichocladium canadense</i> to an anaerobic membrane bioreactor: evaluation of the microbial composition and reactor performance. <i>Biofouling</i> , 2021, 37, 711-723.	0.8	9
10169	The application of <i>Marinobacter hydrocarbonoclasticus</i> as a bioaugmentation agent for the enhanced treatment of non-sterile fish wastewater. <i>Journal of Environmental Management</i> , 2021, 291, 112658.	3.8	16
10170	Gut Microbial Diversity in Female Patients With Invasive Mole and Choriocarcinoma and Its Differences Versus Healthy Controls. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 704100.	1.8	4
10171	Two community types occur in gut microbiota of large-sample wild plateau pikas (<i>Ochotona</i>) Tj ETQq1 1 0.784314 rgBT/Overlook	1.3	14
10172	Taxonomy, not locality, influences the cloacal microbiota of two nearctic colubrids: a preliminary analysis. <i>Molecular Biology Reports</i> , 2021, 48, 6435-6442.	1.0	0
10173	Anaerobic Microbiota Derived from the Upper Airways Impact <i>Staphylococcus aureus</i> Physiology. <i>Infection and Immunity</i> , 2021, 89, e0015321.	1.0	12
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10176	Conservation Strip Tillage Leads to Persistent Alterations in the Rhizosphere Microbiota of <i>Brassica napus</i> Crops. <i>Frontiers in Soil Science</i> , 2021, 1, .	0.8	0
10177	Diversity and abundance of antibiotic resistance genes in rhizosphere soil and endophytes of leafy vegetables: Focusing on the effect of the vegetable species. <i>Journal of Hazardous Materials</i> , 2021, 415, 125595.	6.5	44
10178	Fungi associated with aeroponic roots in caves and mines of New Brunswick. <i>Fungal Ecology</i> , 2021, 52, 101074.	0.7	2
10179	Characterization of the synergistic relationships between nitrification and microbial regrowth in the chloraminated drinking water supply system. <i>Environmental Research</i> , 2021, 199, 111252.	3.7	10
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10181	Infection Heterogeneity and Microbiota Differences in Chicks Infected by <i>Salmonella enteritidis</i> . <i>Microorganisms</i> , 2021, 9, 1705.	1.6	8

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10183	The Effect of Ryegrass Silage Feeding on Equine Fecal Microbiota and Blood Metabolite Profile. <i>Frontiers in Microbiology</i> , 2021, 12, 715709.	1.5	0
10184	Microbial dysbiosis together with nutrient imbalance cause the replant problem of upper six flue-cured tobacco in Central Henan. <i>Journal of Plant Diseases and Protection</i> , 0, , 1.	1.6	4
10185	Manure derived nutrients alter microbial community composition and increase the presence of potential pathogens in freshwater sediment. <i>Journal of Applied Microbiology</i> , 2021, , .	1.4	0
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10187	Linking soil bacterial diversity to satellite-derived vegetation productivity: a case study in arid and semi-arid desert areas. <i>Environmental Microbiology</i> , 2021, 23, 6137-6147.	1.8	1
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10191	Nitrogen and water addition regulate fungal community and microbial co-occurrence network complexity in the rhizosphere of <i>Alhagi sparsifolia</i> seedlings. <i>Applied Soil Ecology</i> , 2021, 164, 103940.	2.1	24
10192	Gut microbiome is associated with multiple sclerosis activity in children. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 1867-1883.	1.7	21
10193	An Innovative Protocol for Metaproteomic Analyses of Microbial Pathogens in Cystic Fibrosis Sputum. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 724569.	1.8	6
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10195	Meta-omics analysis indicates the saliva microbiome and its proteins associated with the prognosis of oral cancer patients. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140659.	1.1	22
10196	Exploration of the Characteristics of Intestinal Microbiota and Metabolomics in Different Rat Models of Mongolian Medicine. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	0.5	2
10198	Metabarcoding confirms the opportunistic foraging behaviour of Atlantic bluefin tuna and reveals the importance of gelatinous prey. <i>PeerJ</i> , 2021, 9, e11757.	0.9	9
10199	Bacterial Diversity of Water and Sediment Samples from Gull Point State Park (West Okoboji, Iowa) Determined Using 16S rRNA Gene Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0072621.	0.3	0
10200	Influence of different phytoremediation on soil microbial diversity and community composition in saline-alkaline land. <i>International Journal of Phytoremediation</i> , 2022, 24, 507-517.	1.7	9
10201	Skin microbiota dynamics following <i>B. subtilis</i> formulation challenge: an in vivo study in mice. <i>BMC Microbiology</i> , 2021, 21, 231.	1.3	7

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10203	Endophytic bacterial community diversity in two citrus cultivars with different citrus canker disease resistance. <i>Archives of Microbiology</i> , 2021, 203, 5453-5462.	1.0	3
10204	Connection between the Gut Microbiota of Largemouth Bass (<i>Micropterus salmoides</i>) and Microbiota of the Pond Culture Environment. <i>Microorganisms</i> , 2021, 9, 1770.	1.6	18
10205	Spatially resolved correlative microscopy and microbial identification reveal dynamic depth- and mineral-dependent anabolic activity in salt marsh sediment. <i>Environmental Microbiology</i> , 2021, 23, 4756-4777.	1.8	8
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10208	Contributions of meat waste decomposition to the abundance and diversity of pathogens and antibiotic-resistance genes in the atmosphere. <i>Science of the Total Environment</i> , 2021, 784, 147128.	3.9	27
10209	The diversity and antibacterial activity of culturable actinobacteria isolated from the rhizosphere soil of <i>Deschampsia antarctica</i> (Galindez Island, Maritime Antarctic). <i>Polar Biology</i> , 2021, 44, 1859-1868.	0.5	5
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10213	Fecal microbiota transplantation does not alter bacterial translocation and visceral adipose tissue inflammation in individuals with obesity. <i>Obesity Science and Practice</i> , 2022, 8, 56-65.	1.0	4
10214	Functional analysis of pristine estuarine marine sediments. <i>Science of the Total Environment</i> , 2021, 781, 146526.	3.9	16
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10216	Mining the Factors Driving the Evolution of the Pit Mud Microbiome under the Impact of Long-Term Production of Strong-Flavor Baijiu. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0088521.	1.4	36
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10218	Impact of operational conditions on methane yield and microbial community composition during biological methanation in in situ and hybrid reactor systems. <i>Biotechnology for Biofuels</i> , 2021, 14, 170.	6.2	10
10219	Analysis of Porcine Model of Fecal-Induced Peritonitis Reveals the Tropism of Blood Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 676650.	1.8	6

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10226	Effects of a Postbiotic and Prebiotic Mixture on Suckling Ratsâ€™ Microbiota and Immunity. Nutrients, 2021, 13, 2975.	1.7	14
10227	Bacterial communities in paddy soils changed by milk vetch as green manure: A study conducted across six provinces in South China. Pedosphere, 2021, 31, 521-530.	2.1	30
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10233	Local Plants, Not Soils, Are the Primary Source of Foliar Fungal Community Assembly in a C4 Grass. Microbial Ecology, 2022, 84, 122-130.	1.4	4
10234	Chronic Manganese Exposure and the Enteric Nervous System: An <i>in Vitro</i> and Mouse <i>in Vivo</i> Study. Environmental Health Perspectives, 2021, 129, 87005.	2.8	12
10235	Multiple thresholds and trajectories of microbial biodiversity predicted across browning gradients by neural networks and decision tree learning. ISME Communications, 2021, 1, .	1.7	3
10236	Effects of dietary forage to concentrate ratio on nutrient digestibility, ruminal fermentation and rumen bacterial composition in Angus cows. Scientific Reports, 2021, 11, 17023.	1.6	43
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10238	Microbiomes of Field-Grown Maize and Soybean in Southeastern and Central Brazil Inferred by High-Throughput 16S and Internal Transcribed Spacer Amplicon Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0052821.	0.3	1
10239	Unraveling City-Specific Microbial Signatures and Identifying Sample Origins for the Data From CAMDA 2020 Metagenomic Geolocation Challenge. <i>Frontiers in Genetics</i> , 2021, 12, 659650.	1.1	1
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10241	Matrix Effects on the Delivery Efficacy of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 on Fecal Microbiota, Gut Transit Time, and Short-Chain Fatty Acids in Healthy Young Adults. <i>MSphere</i> , 2021, 6, e0008421.	1.3	11
10242	Next-Generation Sequencing Analysis of Root Canal Microbiota Associated with a Severe Endodontic-Periodontal Lesion. <i>Diagnostics</i> , 2021, 11, 1461.	1.3	5
10243	<i>Lactobacillus rhamnosus</i> GG and <i>Saccharomyces cerevisiae</i> boulardii supplementation exert protective effects on human gut microbiome following antibiotic administration in vitro. <i>Beneficial Microbes</i> , 2021, 12, 365-379.	1.0	10
10245	Manganese promoted wheat straw decomposition by regulating microbial communities and enzyme activities. <i>Journal of Applied Microbiology</i> , 2022, 132, 1079-1090.	1.4	5
10246	Forming Consensus To Advance Urobiome Research. <i>MSystems</i> , 2021, 6, e0137120.	1.7	42
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10248	Poultry litter and the environment: Microbial profile of litter during successive flock rotations and after spreading on pastureland. <i>Science of the Total Environment</i> , 2021, 780, 146413.	3.9	10
10249	Investigating the effects of nitrogen deposition and substrates on the microbiome and mycobiome of the millipede <i>Cherokia georgiana georgiana</i> (Diplopoda: Polydesmida). <i>Soil Biology and Biochemistry</i> , 2021, 159, 108285.	4.2	4
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10253	Bio-augmented effect of <i>Bacillus amyloliquefaciens</i> and <i>Candida versatilis</i> on microbial community and flavor metabolites during Chinese horse bean-chili-paste fermentation. <i>International Journal of Food Microbiology</i> , 2021, 351, 109262.	2.1	11
10254	Effects of different antibiotic operation modes on anaerobic digestion of dairy manure: Focus on microbial population dynamics. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 105521.	3.3	7
10255	What's for dinner this time?: DNA authentication of wild mushrooms in food products sold in the USA. <i>PeerJ</i> , 2021, 9, e11747.	0.9	7
10256	A Soybean Resistant Protein-Containing Diet Increased the Production of Reg3 β Through the Regulation of the Gut Microbiota and Enhanced the Intestinal Barrier Function in Mice. <i>Frontiers in Nutrition</i> , 2021, 8, 701466.	1.6	5
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10259	Comparison of Chicken Cecal Microbiota after Metaphylactic Treatment or Following Administration of Feed Additives in a Broiler Farm with Enterococcal Spondylitis History. <i>Pathogens</i> , 2021, 10, 1068.	1.2	5
10260	Endophytic Microbiome Variation Among Single Plant Seeds. <i>Phytobiomes Journal</i> , 2022, 6, 45-55.	1.4	24
10261	The Rhizobial Microbiome from the Tropical Savannah Zones in Northern Côte d'Ivoire. <i>Microorganisms</i> , 2021, 9, 1842.	1.6	7
10262	Diversity, Composition, Taxa Biomarkers, and Functional Genes of Fish Gut Microbes in Peat Swamp Forests and its Converted Areas in North Selangor, Malaysia. <i>Pertanika Journal of Science and Technology</i> , 2021, 44, .	0.1	0
10263	Intake of Koji Amazake Improves Defecation Frequency in Healthy Adults. <i>Journal of Fungi (Basel)</i> , 2022, 7, 1074. Tj ETQq1 1 0.784314 rgBT ₅ Overload	1.5	14
10264	Flavor supplementation during late gestation and lactation periods increases the reproductive performance and alters fecal microbiota of the sows. <i>Animal Nutrition</i> , 2021, 7, 679-687.	2.1	10
10266	High-resolution microbiome analysis enabled by linking of 16S rRNA gene sequences with adjacent genomic contexts. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
10267	The effect of biliary obstruction, biliary drainage and bile reinfusion on bile acid metabolism and gut microbiota in mice. <i>Liver International</i> , 2022, 42, 135-148.	1.9	4
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10271	Evaluation of PCR assays for <i>Campylobacter fetus</i> detection and discrimination between <i>C. fetus</i> subspecies in bovine preputial wash samples. <i>Theriogenology</i> , 2021, 172, 300-306.	0.9	7
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10387	Novel compound FLZ alleviates rotenone-induced PD mouse model by suppressing TLR4/MyD88/NF- κ B pathway through microbiota-gut-brain axis. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 2859-2879.	5.7	36
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10417	Bioemulsification and Microbial Community Reconstruction in Thermally Processed Crude Oil. <i>Microorganisms</i> , 2021, 9, 2054.	1.6	2
10418	Appraisal of paleoclimate indices based on bacterial 3-hydroxy fatty acids in 20 Chinese alkaline lakes. <i>Organic Geochemistry</i> , 2021, 160, 104277.	0.9	4
10419	The diversity of soil mesofauna declines after bamboo invasion in subtropical China. <i>Science of the Total Environment</i> , 2021, 789, 147982.	3.9	14
10420	Inverse fluidised bed bioreactor enabled high-rate selenate reduction for wastewater treatment. <i>Environmental Advances</i> , 2021, 5, 100106.	2.2	4
10421	The effects of <i>Lactobacillus hilgardii</i> 4785 and <i>Lactobacillus buchneri</i> 40788 on the microbiome, fermentation, and aerobic stability of corn silage ensiled for various times. <i>Journal of Dairy Science</i> , 2021, 104, 10678-10698.	1.4	13
10422	Linking microbial taxa and the effect of mineral nitrogen forms on residue decomposition at the early stage in arable soil by DNA-qSIP. <i>Geoderma</i> , 2021, 400, 115127.	2.3	9
10423	Correlation analysis reveals the intensified fermentation via <i>Lactobacillus plantarum</i> improved the flavor of fermented noni juice. <i>Food Bioscience</i> , 2021, 43, 101234.	2.0	9
10424	Key microorganisms mediate soil carbon-climate feedbacks in forest ecosystems. <i>Science Bulletin</i> , 2021, 66, 2036-2044.	4.3	14
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10427	Succession of diversity, functions, and interactions of the fungal community in activated sludge under aromatic hydrocarbon stress. <i>Environmental Research</i> , 2022, 204, 112143.	3.7	26
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10430	Metagenomic analysis of the salivary microbiota in patients with caries, periodontitis and comorbid diseases. <i>Journal of Dental Sciences</i> , 2021, 16, 1264-1273.	1.2	15
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10432	Effects of fish farm activities on the sponge <i>Weberella bursa</i> , and its associated microbiota. <i>Ecological Indicators</i> , 2021, 129, 107879.	2.6	10
10433	Effects of carbohydrate addition methods on Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2021, 543, 736890.	1.7	16
10434	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
10435	Restriction of soil bacteria promoting high yield of super hybrid rice in the Huaihe Valley in central China by conventional ploughing intensity. <i>Soil and Tillage Research</i> , 2021, 214, 105169.	2.6	3
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10437	The Microbial Composition of Lower Genital Tract May Affect the Outcome of in vitro Fertilization-Embryo Transfer. <i>Frontiers in Microbiology</i> , 2021, 12, 729744.	1.5	10
10438	Desert and anthropogenic mixing dust deposition influences microbial communities in surface waters of the western Pacific Ocean. <i>Science of the Total Environment</i> , 2021, 791, 148026.	3.9	12
10439	Immobilization of lead and cadmium in agricultural soil by bioelectrochemical reduction of sulfate in underground water. <i>Chemical Engineering Journal</i> , 2021, 422, 130010.	6.6	16
10440	Quantitative analysis of soil sustainability after applying stabilizing amendments in long-term Cd-contaminated paddy soils. <i>Environmental Pollution</i> , 2021, 286, 117205.	3.7	3
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10443	Crop rotation history constrains soil biodiversity and multifunctionality relationships. <i>Agriculture, Ecosystems and Environment</i> , 2021, 319, 107550.	2.5	48

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10447	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
10448	Mycobiota of <i>Eucommia ulmoides</i> bark: Diversity, rare biosphere and core taxa. <i>Fungal Ecology</i> , 2021, 53, 101090.	0.7	7
10449	Sodium butyrate alleviates cholesterol gallstones by regulating bile acid metabolism. <i>European Journal of Pharmacology</i> , 2021, 908, 174341.	1.7	17
10450	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
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10454	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
10455	Bacterial diversity and community composition changes in paddy soils that have different parent materials and fertility levels. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2797-2806.	1.7	8
10456	Community structures of bacteria and archaea associated with the biodeterioration of sandstone sculptures at the Beishiku Temple. <i>International Biodeterioration and Biodegradation</i> , 2021, 164, 105290.	1.9	34
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10460	Impact of dimethylpyrazole-based nitrification inhibitors on soil-borne bacteria. <i>Science of the Total Environment</i> , 2021, 792, 148374.	3.9	18
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10463	Occurrence of antibiotic resistome in farmland soils near phosphorus chemical industrial area. <i>Science of the Total Environment</i> , 2021, 796, 149053.	3.9	12
10464	Organic amendments, deficit irrigation, and microbial communities impact extracellular polysaccharide content in agricultural soils. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108428.	4.2	11
10465	The effect of atrazine on intestinal histology, microbial community and short chain fatty acids in <i>Pelophylax nigromaculatus</i> tadpoles. <i>Environmental Pollution</i> , 2021, 288, 117702.	3.7	22
10466	Prenatal stress leads to deficits in brain development, mood related behaviors and gut microbiota in offspring. <i>Neurobiology of Stress</i> , 2021, 15, 100333.	1.9	23
10467	Polystyrene microplastics induce microbial dysbiosis and dysfunction in surrounding seawater. <i>Environment International</i> , 2021, 156, 106724.	4.8	47
10468	Soil bacterial community in potato tuberosphere following repeated applications of a common scab suppressive antagonist. <i>Applied Soil Ecology</i> , 2021, 167, 104096.	2.1	12
10469	Magnesium and nitrogen drive soil bacterial community structure under long-term apple orchard cultivation systems. <i>Applied Soil Ecology</i> , 2021, 167, 104103.	2.1	8
10470	Seasonal dynamics of soil microbial diversity and functions along elevations across the treeline. <i>Science of the Total Environment</i> , 2021, 794, 148644.	3.9	22
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10472	Seeding the drainage canal of a wastewater treatment system for the natural rubber industry with rubber for the enhanced removal of organic matter and nitrogen. <i>Chemosphere</i> , 2021, 283, 131233.	4.2	12
10473	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
10474	Field aging alters biochar's effect on antibiotic resistome in manured soil. <i>Environmental Pollution</i> , 2021, 288, 117719.	3.7	16
10475	Treatment with a spore-based probiotic containing five strains of <i>Bacillus</i> induced changes in the metabolic activity and community composition of the gut microbiota in a SHIME [®] model of the human gastrointestinal system. <i>Food Research International</i> , 2021, 149, 110676.	2.9	22
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10477	Alien invasive plant <i>Amaranthus spinosus</i> mainly altered the community structure instead of the β diversity of soil N-fixing bacteria under drought. <i>Acta Oecologica</i> , 2021, 113, 103788.	0.5	6
10478	Microbial colonizers of microplastics in an Arctic freshwater lake. <i>Science of the Total Environment</i> , 2021, 795, 148640.	3.9	35
10479	Pathogenic hitchhiker diversity on international ships' ballast water at West Malaysia port. <i>Marine Pollution Bulletin</i> , 2021, 172, 112850.	2.3	13

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10480	Diversity and composition of soil Acidobacteria and Proteobacteria communities as a bacterial indicator of past land-use change from forest to farmland. <i>Science of the Total Environment</i> , 2021, 797, 148944.	3.9	94
10481	Dynamics of soil bacterial community diversity and composition at aggregate scales in a chronosequence of tea gardens. <i>Catena</i> , 2021, 206, 105486.	2.2	3
10482	Microbial community profiles in soils adjacent to mining and smelting areas: Contrasting potentially toxic metals and co-occurrence patterns. <i>Chemosphere</i> , 2021, 282, 130992.	4.2	33
10483	Supplying silicon alters microbial community and reduces soil cadmium bioavailability to promote health wheat growth and yield. <i>Science of the Total Environment</i> , 2021, 796, 148797.	3.9	35
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10485	Phosphorus elevation erodes ectomycorrhizal community diversity and induces divergence of saprophytic community composition between vegetation types. <i>Science of the Total Environment</i> , 2021, 793, 148502.	3.9	11
10486	Same same, but different: The response of diatoms to environmental gradients in Fennoscandian streams and lakes – barcodes, traits and microscope data compared. <i>Ecological Indicators</i> , 2021, 130, 108088.	2.6	11
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10488	Herbaceous plants influence bacterial communities, while shrubs influence fungal communities in subalpine coniferous forests. <i>Forest Ecology and Management</i> , 2021, 500, 119656.	1.4	9
10489	UV assisted backwashing for fouling control in membrane bioreactor operation. <i>Journal of Membrane Science</i> , 2021, 639, 119751.	4.1	16
10490	Nitrifiers drive successions of particulate organic matter and microbial community composition in a starved macrocosm. <i>Environment International</i> , 2021, 157, 106776.	4.8	8
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10493	Long-term organic fertilizer substitution increases rice yield by improving soil properties and regulating soil bacteria. <i>Geoderma</i> , 2021, 404, 115287.	2.3	145
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10497	Kinetics and scale up of oxygen reducing cathodic biofilms. <i>Biofilm</i> , 2021, 3, 100053.	1.5	3

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10499	NGS-Based Metagenomic Study of Four Traditional Bulgarian Green Cheeses from Tcherni Vit. <i>LWT - Food Science and Technology</i> , 2021, 152, 112278.	2.5	9
10500	Valorization of carbon dioxide and waste (Derived from the site of Eutrophication) into syngas using a catalytic thermo-chemical platform. <i>Bioresource Technology</i> , 2021, 341, 125858.	4.8	1
10501	Evolution of PM2.5 bacterial community structure in Beijing's suburban atmosphere. <i>Science of the Total Environment</i> , 2021, 799, 149387.	3.9	10
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10503	Effects of arbuscular mycorrhizal fungi inoculation and crop sequence on root-associated microbiome, crop productivity and nutrient uptake in wheat-based and flax-based cropping systems. <i>Applied Soil Ecology</i> , 2021, 168, 104136.	2.1	10
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10506	Threshold effects of soil pH on microbial co-occurrence structure in acidic and alkaline arable lands. <i>Science of the Total Environment</i> , 2021, 800, 149592.	3.9	23
10507	Pyrosequencing and phenotypic microarray to decipher bacterial community variation in <i>Sorghum bicolor</i> (L.) Moench rhizosphere. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100025.	1.4	8
10508	Bacterial community demonstrates stronger network connectivity than fungal community in desert-grassland salt marsh. <i>Science of the Total Environment</i> , 2021, 798, 149118.	3.9	24
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10510	Influence of cosubstrate and hydraulic retention time on the removal of drugs and hygiene products in sanitary sewage in an anaerobic Expanded Granular Sludge Bed reactor. <i>Journal of Environmental Management</i> , 2021, 299, 113532.	3.8	10
10511	Effect of rearing systems and dietary probiotic supplementation on the growth and gut microbiota of Nile tilapia (<i>Oreochromis niloticus</i>) larvae. <i>Aquaculture</i> , 2022, 546, 737297.	1.7	24
10512	Linking microbial community composition to farming pattern in selenium-enriched region: Potential role of microorganisms on Se geochemistry. <i>Journal of Environmental Sciences</i> , 2022, 112, 269-279.	3.2	9
10513	Structural characterization of oligosaccharide from <i>Spirulina platensis</i> and its effect on the faecal microbiota in vitro. <i>Food Science and Human Wellness</i> , 2022, 11, 109-118.	2.2	10
10514	Subsoiling and conversion to conservation tillage enriched nitrogen cycling bacterial communities in sandy soils under long-term maize monoculture. <i>Soil and Tillage Research</i> , 2022, 215, 105197.	2.6	29
10515	Restoration of organic-matter-impooverished arable soils through the application of soil conditioner prepared via short-time hydrothermal fermentation. <i>Environmental Research</i> , 2022, 204, 112088.	3.7	4

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10517	Arbuscular mycorrhizal fungal community responses to drought and nitrogen fertilization in switchgrass stands. <i>Applied Soil Ecology</i> , 2022, 169, 104218.	2.1	10
10518	Adaption to hydrogen sulfide-rich environments: Strategies for active detoxification in deep-sea symbiotic mussels, <i>Gigantidas platifrons</i> . <i>Science of the Total Environment</i> , 2022, 804, 150054.	3.9	19
10519	Interactions among heavy metal bioaccessibility, soil properties and microbial community in phyto-remediated soils nearby an abandoned realgar mine. <i>Chemosphere</i> , 2022, 286, 131638.	4.2	32
10520	Biodegradation of water-accommodated aromatic oil compounds in Arctic seawater at 0°C. <i>Chemosphere</i> , 2022, 286, 131751.	4.2	11
10521	Insight into the microbial distribution and succession and biofouling mechanism in membrane distillation for desulfurization wastewater treatment. <i>Chemical Engineering Journal</i> , 2022, 428, 131097.	6.6	11
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10523	Phytoremediation of cadmium-contaminated sediment using <i>Hydrilla verticillata</i> and <i>Elodea canadensis</i> harbor two same keystone rhizobacteria <i>Pedospaeraceae</i> and <i>Parasegetibacter</i> . <i>Chemosphere</i> , 2022, 286, 131648.	4.2	22
10524	Key factors shaping prokaryotic communities in subtropical forest soils. <i>Applied Soil Ecology</i> , 2022, 169, 104162.	2.1	7
10525	Lipid degrading microbe consortium driving micro-ecological evolution of activated sludge for cooking wastewater treatment. <i>Science of the Total Environment</i> , 2022, 804, 150071.	3.9	6
10526	Environmental heterogeneity determines the response patterns of microbially mediated N-reduction processes to sulfamethoxazole in river sediments. <i>Journal of Hazardous Materials</i> , 2022, 421, 126730.	6.5	16
10527	Recovery patterns of soil bacterial and fungal communities in Chinese boreal forests along a fire chronosequence. <i>Science of the Total Environment</i> , 2022, 805, 150372.	3.9	15
10528	A unique microbiome in a highly polluted and alkaline lake in a seasonally frozen area. <i>Environmental Research</i> , 2022, 204, 112056.	3.7	3
10529	Identification of bacterial communities of fermented cereal beverage Boza by metagenomic analysis. <i>LWT - Food Science and Technology</i> , 2022, 153, 112465.	2.5	10
10530	Influence of <i>Bacillus safensis</i> and <i>Bacillus pumilus</i> on the electrochemical behavior of 2024-T3 aluminum alloy. <i>Bioelectrochemistry</i> , 2022, 143, 107950.	2.4	9
10531	Metagenomic and metabolic analyses of poly-extreme microbiome from an active crater volcano lake. <i>Environmental Research</i> , 2022, 203, 111862.	3.7	9
10532	Insight to bacteria community response of organic management in apple orchard-bagasse fertilizer combined with biochar. <i>Chemosphere</i> , 2022, 286, 131693.	4.2	20
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10536	Induced secretion system mutation alters rhizosphere bacterial composition in <i>Sorghum bicolor</i> (L.) Moench. <i>Planta</i> , 2021, 253, 33.	1.6	5
10537	Dysbacteriosis of the Intestinal Flora Is an Important Reason for the Death of Adult House Flies Caused by <i>Beauveria bassiana</i> . <i>Frontiers in Immunology</i> , 2020, 11, 589338.	2.2	5
10538	Investigating the cow skin and teat canal microbiomes of the bovine udder using different sampling and sequencing approaches. <i>Journal of Dairy Science</i> , 2021, 104, 644-661.	1.4	20
10540	Responses of soil microbiome to steel corrosion. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 6.	2.9	28
10541	<i>Paenibacillus silvestris</i> sp. nov., Isolated from Forest Soil. <i>Current Microbiology</i> , 2021, 78, 822-829.	1.0	12
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10543	rANOMALY: Amplicon workflow for Microbial community Analysis. <i>F1000Research</i> , 2021, 10, 7.	0.8	23
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10547	Microbial population selection in integrated fixed-film sequencing batch reactors operated with different lengths of oxic and anoxic conditions. <i>Environmental Science: Water Research and Technology</i> , 2021, 7, 913-926.	1.2	5
10548	Root exudates increase soil respiration and alter microbial community structure in alpine permafrost and active layer soils. <i>Environmental Microbiology</i> , 2021, 23, 2152-2168.	1.8	31
10549	Multi-targeted properties of the probiotic <i>Saccharomyces cerevisiae</i> CNCM I-3856 against enterotoxigenic <i>Escherichia coli</i> (ETEC) H10407 pathogenesis across human gut models. <i>Gut Microbes</i> , 2021, 13, 1953246.	4.3	12
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10552	The intestinal microbiota and metabolites in patients with anorexia nervosa. <i>Gut Microbes</i> , 2021, 13, 1-25.	4.3	58
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10556	Characterization of faecal and caecal microbiota of free-ranging black-tailed prairie dogs (<i>Cynomys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 coab042.		5
10557	Plant and Animal-Type Feedstuff Shape the Gut Microbiota and Metabolic Processes of the Chinese Mitten Crab <i>Eriocheir sinensis</i> . <i>Frontiers in Veterinary Science</i> , 2021, 8, 589624.	0.9	10
10558	Repeated Application of Rice Straw Stabilizes Soil Bacterial Community Composition and Inhibits Clubroot Disease. <i>Agriculture (Switzerland)</i> , 2021, 11, 108.	1.4	4
10559	Effects of <i>Spartina alterniflora</i> Invasion on Soil Microbial Community Structure and Ecological Functions. <i>Microorganisms</i> , 2021, 9, 138.	1.6	23
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10635	Investigating seafood substitution problems and consequences in Taiwan using molecular barcoding and deep microbiome profiling. <i>Scientific Reports</i> , 2020, 10, 21997.	1.6	8
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10652	<i>Roseitalea porphyridii</i> gen. nov., sp. nov., isolated from a red alga, and reclassification of <i>Hoeflea suaedae</i> Chung et al. 2013 as <i>Pseudohoeflea suaedae</i> gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 362-368.	0.8	22
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11906	Pathogen identification in culture-negative cerebrospinal fluid specimens of patients with purulent meningitis using next-generation sequencing technology. <i>International Journal of Clinical and Experimental Pathology</i> , 2020, 13, 2427-2438.	0.5	0
11907	Microbiota alteration at different stages in gastric lesion progression: a population-based study in Linqu, China. <i>American Journal of Cancer Research</i> , 2021, 11, 561-575.	1.4	3
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11910	Differences in gut microbiota structure in patients with stages 4-5 chronic kidney disease. <i>American Journal of Translational Research (discontinued)</i> , 2021, 13, 10056-10074.	0.0	0
11911	Characterization of gut microbiota in captive Himalayan tahr (<i>Hemitragus jemlahicus</i>) and the limited effect of sex on intestinal microorganisms of tahr. , 2021, 88, 1177-1188.		0
11912	The postnatal window is critical for the development of sex-specific metabolic and gut microbiota outcomes in offspring. <i>Gut Microbes</i> , 2021, 13, 2004070.	4.3	6
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11914	Next-generation microbial drugs developed from microbiome's natural products. <i>Advances in Genetics</i> , 2021, 108, 341-382.	0.8	2
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11916	Distribution of antibiotic resistance genes from human and animal origins to their receiving environments: A regional scale survey of urban settings. <i>Environmental Pollution</i> , 2022, 293, 118512.	3.7	13
11917	Correlation analysis between differential metabolites and bacterial endophytes of <i>Ephedra sinica</i> in different years. <i>Industrial Crops and Products</i> , 2022, 175, 114250.	2.5	10
11918	Short- and long-term effects of decabromodiphenyl ether (BDE-209) on sediment denitrification using a semi-continuous microcosm. <i>Environmental Pollution</i> , 2022, 293, 118589.	3.7	5
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11920	Food sources of common carp in a Hani Terrace integrated rice-fish system (Yunnan Province, China). <i>Aquaculture Reports</i> , 2022, 22, 100937.	0.7	1
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11922	Effects of dietary xylooligosaccharide on growth, digestive enzymes activity, intestinal morphology, and the expression of inflammatory cytokines and tight junctions genes in triploid <i>Oncorhynchus mykiss</i> fed a low fishmeal diet. <i>Aquaculture Reports</i> , 2022, 22, 100941.	0.7	7
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11928	Sex Differences in Fecal Microbiota Correlation With Physiological and Biochemical Indices Associated With End-Stage Renal Disease Caused by Immunoglobulin a Nephropathy or Diabetes. <i>Frontiers in Microbiology</i> , 2021, 12, 752393.	1.5	3
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11932	Vaginal Microbiota, Genital Inflammation and Extracellular Matrix Remodelling Collagenase: MMP-9 in Pregnant Women With HIV, a Potential Preterm Birth Mechanism Warranting Further Exploration. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 750103.	1.8	6
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11937	Epigenetic Modulation of Class-Switch DNA Recombination to IgA by miR-146a Through Downregulation of Smad2, Smad3 and Smad4. <i>Frontiers in Immunology</i> , 2021, 12, 761450.	2.2	2
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11943	Metabarcoding Reveals Lacustrine Picocyanobacteria Respond to Environmental Change Through Adaptive Community Structuring. <i>Frontiers in Microbiology</i> , 2021, 12, 757929.	1.5	8
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11955	Trophic niche overlap between round sardinella (<i>Sardinella aurita</i>) and sympatric pelagic fish species in the Western Mediterranean. Ecology and Evolution, 2021, 11, 16126-16142.	0.8	14
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11981	Relevance of the microbial community to Sb and As biogeochemical cycling in natural wetlands. <i>Science of the Total Environment</i> , 2022, 818, 151826.	3.9	11
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11996	Pre-flooding soil used in monocropping increased strawberry biomass and altered bacterial community composition. <i>Soil Science and Plant Nutrition</i> , 2021, 67, 643-652.	0.8	3
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11998	Assessing microplastic exposure of large marine filter-feeders. <i>Science of the Total Environment</i> , 2022, 818, 151815.	3.9	20
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12086	Microbial Diversity in Tobacco Rhizosphere Soil at Different Growth Stages. <i>Journal of Biobased Materials and Bioenergy</i> , 2021, 15, 606-614.	0.1	4
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12092	Characterization of Rhizosphere and Endophytic Microbial Communities Associated with <i>Stipa purpurea</i> and Their Correlation with Soil Environmental Factors. <i>Plants</i> , 2022, 11, 363.	1.6	10
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12107	ExTaxsl: an exploration tool of biodiversity molecular data. <i>GigaScience</i> , 2022, 11, .	3.3	2
12108	Host fruits shape the changes in the gut microbiota and development of <i>Bactrocera dorsalis</i> (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	0.4	6
12109	Meconium Microbiome of Very Preterm Infants across Germany. <i>MSphere</i> , 2022, 7, e0080821.	1.3	15
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12120	Enhanced Biodegradation of High-Salinity and Low-Temperature Crude-Oil Wastewater by Immobilized Crude-Oil Biodegrading Microbiota. <i>Journal of Ocean University of China</i> , 2022, 21, 141-151.	0.6	3
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12128	Physicochemical pretreatment selects microbial communities to produce alcohols through metabolism of volatile fatty acids. <i>Biomass Conversion and Biorefinery</i> , 2024, 14, 2661-2675.	2.9	3
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12154	Effects of Dietary <i>Enterococcus faecalis</i> YFI-G720 on the Growth, Immunity, Serum Biochemical, Intestinal Morphology, Intestinal Microbiota, and Disease Resistance of Crucian Carp (<i>Carassius</i>)	0.0	0
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12460	Assessment of Spoilage Microbiota of Rainbow Trout (<i>Oncorhynchus mykiss</i>) during Storage by 16S rDNA Sequencing. <i>Journal of Food Quality</i> , 2022, 2022, 1-10.	1.4	6
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12499	Comparison between Egg Intake versus Choline Supplementation on Gut Microbiota and Plasma Carotenoids in Subjects with Metabolic Syndrome. <i>Nutrients</i> , 2022, 14, 1179.	1.7	13
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12502	Bacterial Communities in the Feces of Laboratory Reared <i>Gampsocleis gratiosa</i> (Orthoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102	1.0	0
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14284	Gut Microbiota Signatures in Tumor, Para-Cancerous, Normal Mucosa, and Feces in Colorectal Cancer Patients. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	9
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14290	Functional characterization of novel phosphate solubilizing bacteria, <i>Chryseomicrobium imtechense</i> , for enhanced strawberry growth and yield parameters. <i>Arabian Journal of Geosciences</i> , 2022, 15, .	0.6	0
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14457	Thrips Microbiome Study in Commercial Avocado (<i>Persea americana</i> Mill.) from Northwest Colombian Andes (Antioquia, Colombia) Shows the Presence of <i>Wolbachia</i> , <i>Ehrlichia</i> , <i>Enterobacter</i> . <i>Diversity</i> , 2022, 14, 540.	0.7	1
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14460	Supplementation of xylo-oligosaccharides to suckling piglets promotes the growth of fiber-degrading gut bacterial populations during the lactation and nursery periods. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
14461	Effects of Different Organic Fertilizers on Sweet Potato Growth and Rhizosphere Soil Properties in Newly Reclaimed Land. <i>Agronomy</i> , 2022, 12, 1649.	1.3	7
14462	Response of soil bacterial community to biochar application in a boreal pine forest. <i>Journal of Forestry Research</i> , 2023, 34, 749-759.	1.7	6
14463	Characteristics of Fungal Communities and Internal Mildew Occurrence during the Stages of Planting and Storing of Sunflower Seed in China. <i>Microorganisms</i> , 2022, 10, 1434.	1.6	2
14464	Functional Properties of Protein Hydrolysates on Growth, Digestive Enzyme Activities, Protein Metabolism, and Intestinal Health of Larval Largemouth Bass (<i>Micropterus salmoides</i>). <i>Frontiers in Immunology</i> , 0, 13, .	2.2	13
14465	Diversity of endophytic bacteria of mulberry (<i>Morus L.</i>) under cold conditions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
14466	Microbial and Transcriptomic Profiling Reveals Diet-Related Alterations of Metabolism in Metabolic Disordered Mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2

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14469	Effect of <i>Saccharomyces cerevisiae</i> culture mitigates heat stress-related damage in dairy cows by multi-omics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
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14471	Swimming Impedes Intestinal Microbiota and Lipid Metabolites of Tumorigenesis in Colitis-Associated Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
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14504	The Gut Bacterial Community Potentiates <i>Clostridioides difficile</i> Infection Severity. <i>MBio</i> , 2022, 13, .	1.8	18
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14549	Interaction between endometrial microbiota and host gene regulation in recurrent implantation failure. <i>Journal of Assisted Reproduction and Genetics</i> , 0, , .	1.2	2
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14555	Effect of Methionine Supplementation on Serum Metabolism and the Rumen Bacterial Community of Sika Deer (<i>Cervus nippon</i>). <i>Animals</i> , 2022, 12, 1950.	1.0	4
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14557	Microbial and Planktonic Community Characteristics of <i>Eriocheir sinensis</i> Culture Ponds Experiencing Harmful Algal Blooms. <i>Fishes</i> , 2022, 7, 180.	0.7	4
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14575	Effect of Intensity and Duration of Exercise on Gut Microbiota in Humans: A Systematic Review. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 9518.	1.2	20
14576	Changes in the Host Gut Microbiota during Parasitization by Parasitic Wasp <i>Cotesia vestalis</i> . <i>Insects</i> , 2022, 13, 760.	1.0	2
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14586	Reconstruction of a Soil Microbial Network Induced by Stress Temperature. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
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14616	In Situ Genomics and Transcriptomics of SAR202 Subclusters Revealed Subtle Distinct Activities in Deep-Sea Water. <i>Microorganisms</i> , 2022, 10, 1629.	1.6	2
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14648	Electroacupuncture ameliorates peptic ulcer disease in association with gastroduodenal microbiota modulation in mice. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	8
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14740	Effects of different harvest frequencies on microbial community and metabolomic properties of annual ryegrass silage. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	15
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14743	Toxicity and modulation of silver nanoparticles synthesized using abalone viscera hydrolysates on bacterial community in aquatic environment. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
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14757	Long-term cultivation alter soil bacterial community in a forest-grassland transition zone. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
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14761	The response of sugar beet rhizosphere micro-ecological environment to continuous cropping. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
14762	Tropical and Temperate Lineages of <i>Rhipicephalus sanguineus</i> s.l. Ticks (Acari: Ixodidae) Host Different Strains of <i>Coxiella</i> -like Endosymbionts. <i>Journal of Medical Entomology</i> , 0, , .	0.9	0
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14764	Delayed application of N fertilizer mitigates the carbon emissions of pea/maize intercropping via altering soil microbial diversity. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
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14777	Bovine milk with variant β -casein types on immunological mediated intestinal changes and gut health of mice. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	3
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14793	Effects of tillage and biochar on soil physiochemical and microbial properties and its linkage with crop yield. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
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14834	MYBIOTA: A birth cohort on maternal and infant microbiota and its impact on infant health in Malaysia. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	1
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14854	The diversity analysis and gene function prediction of intestinal bacteria in three equine species. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
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14871	Minocycline Prevents the Development of Key Features of Inflammation and Pain in DSS-induced Colitis in Mice. <i>Journal of Pain</i> , 2023, 24, 304-319.	0.7	2
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14875	Effect of Probiotic <i>Lactobacillus plantarum</i> Dad-13 on Metabolic Profiles and Gut Microbiota in Type 2 Diabetic Women: A Randomized Double-Blind Controlled Trial. <i>Microorganisms</i> , 2022, 10, 1806.	1.6	4
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14882	Generalist nematodes dominate the nemabiome of roe deer in sympatry with sheep at a regional level. <i>International Journal for Parasitology</i> , 2022, 52, 751-761.	1.3	8
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14885	Effects of nanoplastic exposure on the immunity and metabolism of red crayfish (<i>Cherax</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2022, 245, 114114.	2.9	7
14886	Eukaryotic diversity of marine biofouling from coastal to offshore areas. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	6
14887	Different gender-derived gut microbiota influence stroke outcomes by mitigating inflammation. <i>Journal of Neuroinflammation</i> , 2022, 19, .	3.1	15
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14890	Ammonia oxidation by novel (Candidatus) <i>Nitrosacidococcus urinae</i> is sensitive to process disturbances at low pH and to iron limitation at neutral pH. <i>Water Research X</i> , 2022, 17, 100157.	2.8	9
14891	Luminal and mucosa-associated caecal microbiota of chickens after experimental <i>Campylobacter jejuni</i> infection in the absence of <i>Campylobacter</i> -specific phages of group II and III. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0

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14896	Differences in the microbiota of oral rinse, lesion, and normal site samples from patients with mucosal abnormalities on the tongue. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
14897	Effects of dietary <i>Clostridium autoethanogenum</i> protein on the growth, disease resistance, intestinal digestion, immunity and microbiota structure of <i>Litopenaeus vannamei</i> reared at different water salinities. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
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14899	Variation in bacterial composition, diversity, and activity across different subglacial basal ice types. <i>Cryosphere</i> , 2022, 16, 4033-4051.	1.5	0
14900	Dietary phosphorus supplementation in the diet of Pacific white shrimp (<i>Litopenaeus vannamei</i>) alleviated the adverse impacts caused by high <i>Clostridium autoethanogenum</i> protein. <i>Fish and Shellfish Immunology</i> , 2022, 131, 137-149.	1.6	5
14902	Structure and diversity of mycorrhizal fungi communities of different part of <i>Bulbophyllum tianguii</i> in three terrestrial environments. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
14903	The rhizosphere microbiome improves the adaptive capabilities of plants under high soil cadmium conditions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
14904	<i>Cornus officinalis</i> prior and post-processing: Regulatory effects on intestinal flora of diabetic nephropathy rats. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	8
14905	Improving earthworm quality and complex metal removal from water by adding aquatic plant residues to cattle manure. <i>Journal of Hazardous Materials</i> , 2023, 443, 130145.	6.5	4
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14943	Sex-based metabolic and microbiota differences in roots and rhizosphere soils of dioecious papaya (<i>Carica papaya</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
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14975	VPsearch: fast exact sequence similarity search for genomic sequences. <i>Journal of Open Source Software</i> , 2022, 7, 4236.	2.0	0
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14998	Investigation of Parasitic Infection in Crocodile Lizards (<i>Shinisaurus crocodilurus</i>) Using High-Throughput Sequencing. <i>Animals</i> , 2022, 12, 2726.	1.0	2
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15007	Bioleaching Test of Polymetallic Nodule Samples from the IOM Exploration Area. <i>Minerals (Basel)</i> Tj ETQq1 1 0.784314 rgBT /Overloc 0.8 2		
15008	Probiotic human alcohol dehydrogenase-4 expressing bacteria protects from diet-induced obesity and metabolic impairment: a new concept of disease prevention. , 0, , 118-136.		0
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15027	Gut microbiome dysbiosis in antibiotic-treated COVID-19 patients is associated with microbial translocation and bacteremia. <i>Nature Communications</i> , 2022, 13, .	5.8	67
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15034	Removal performance and inhibitory effects of combined tetracycline, oxytetracycline, sulfadiazine, and norfloxacin on anaerobic digestion process treating swine manure. <i>Science of the Total Environment</i> , 2023, 857, 159536.	3.9	13
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15052	Experimental warming increases fungal alpha diversity in an oligotrophic maritime Antarctic soil. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
15053	Microbial compost tea properties affect suppression of strawberry grey mould (<i>Botrytis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TTS 0.5	0.5	2
15054	Accelerated gross nitrogen cycling following garlic mustard invasion is linked with abiotic and biotic changes to soils. <i>Frontiers in Forests and Global Change</i> , 0, 5, .	1.0	3
15055	Association of intestinal microbiota markers and dietary pattern in Chinese patients with type 2 diabetes: The Henan rural cohort study. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	2
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15068	Community distribution of rhizosphere and endophytic bacteria of ephemeral plants in desertâ€“oasis ecotone and analysis of environmental driving factors. <i>Land Degradation and Development</i> , 0, , .	1.8	0
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15070	Winogradsky Bioelectrochemical System as a Novel Strategy to Enrich Electrochemically Active Microorganisms from Arsenic-Rich Sediments. <i>Micromachines</i> , 2022, 13, 1953.	1.4	2
15071	Inconsistent Response of Abundant and Rare Bacterial Communities to the Developmental Chronosequence of <i>Pinus massoniana</i> . <i>Forests</i> , 2022, 13, 1904.	0.9	1

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15073	Metagenomic insights into the impacts of phytochemicals on bacterial and archaeal community structure and biogas production patterns during anaerobic digestion of avocado oil processing waste feedstocks. <i>Biomass Conversion and Biorefinery</i> , 0, , .	2.9	4
15074	Effect of Mulberry Leaf Powder of Varying Levels on Growth Performance, Immuno-Antioxidant Status, Meat Quality and Intestinal Health in Finishing Pigs. <i>Antioxidants</i> , 2022, 11, 2243.	2.2	2
15076	Assessment of the Gut Microbiota during Juice Fasting with and without Inulin Supplementation: A Feasibility Study in Healthy Volunteers. <i>Foods</i> , 2022, 11, 3673.	1.9	0
15077	Cow's microbiome from antepartum to postpartum: A long-term study covering two physiological challenges. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
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15079	Overcoming Anxiety Disorder by Probiotic <i>Lactiplantibacillus plantarum</i> LZU-J-TSL6 through Regulating Intestinal Homeostasis. <i>Foods</i> , 2022, 11, 3596.	1.9	6
15080	The incorporation of straw into the subsoil increases C, N, and P enzyme activities and nutrient supply by enriching distinctive functional microorganisms. <i>Land Degradation and Development</i> , 2023, 34, 1297-1310.	1.8	3
15081	Linking Microbial Functional Gene Abundance and Daqu Extracellular Enzyme Activity: Implications for Carbon Metabolism during Fermentation. <i>Foods</i> , 2022, 11, 3623.	1.9	4
15082	Association of Gut Microbiota Composition in Pregnant Women Colonized with Group B <i>Streptococcus</i> with Maternal Blood Routine and Neonatal Blood-Gas Analysis. <i>Pathogens</i> , 2022, 11, 1297.	1.2	0
15083	Effect of marigold (<i>Tagetes erecta</i> L.) on soil microbial communities in continuously cropped tobacco fields. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
15084	Designing a surveillance program for early detection of alien plants and insects in Norway. <i>Biological Invasions</i> , 0, , .	1.2	2
15085	Cradle for the newborn <i>Monochamus saltuarius</i> : Microbial associates to ward off entomopathogens and disarm plant defense. <i>Insect Science</i> , 2023, 30, 1165-1182.	1.5	2
15086	Anaerobic Fermentation of Silage from the Above-Ground Biomass of Jerusalem Artichoke (<i>Helianthus</i>) Tj ETQq1 1 0.784314 rgBT /Over Production. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 11417.	1.3	1
15087	NMN alleviates radiation-induced intestinal fibrosis by modulating gut microbiota. <i>International Journal of Radiation Biology</i> , 2023, 99, 823-834.	1.0	5
15088	Bacterial communities associated with mushrooms in the Qinghai-Tibet Plateau are shaped by soil parameters. <i>International Microbiology</i> , 2023, 26, 231-242.	1.1	2
15089	Abundant bacteria shaped by deterministic processes have a high abundance of potential antibiotic resistance genes in a plateau river sediment. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
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15092	Microbial Community Structure of Colostrum in Women with Antibiotic Exposure Immediately After Delivery. <i>Breastfeeding Medicine</i> , 2022, 17, 940-946.	0.8	0
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15094	Mode of delivery modulates the intestinal microbiota and impacts the response to vaccination. <i>Nature Communications</i> , 2022, 13, .	5.8	9
15095	Correlation between microbial communities and key odourants in fermented capsicum inoculated with <i>Pediococcus pentosaceus</i> and <i>Cyberlindnera rhodanensis</i> . <i>Journal of the Science of Food and Agriculture</i> , 2023, 103, 1139-1151.	1.7	3
15096	Variation in Community Structure of the Root-Associated Fungi of <i>Cinnamomum camphora</i> Forest. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1210.	1.5	2
15097	Cervical Microbiome in Women Infected with HPV16 and High-Risk HPVs. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 14716.	1.2	4
15098	Maize-soybean intercropping facilitates chemical and microbial transformations of phosphorus fractions in a calcareous soil. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
15099	Dietary L-Arginine or N-Carbamylglutamate Alleviates Colonic Barrier Injury, Oxidative Stress, and Inflammation by Modulation of Intestinal Microbiota in Intrauterine Growth-Retarded Suckling Lambs. <i>Antioxidants</i> , 2022, 11, 2251.	2.2	7
15100	Effect of Heat Stress on Rumen Microbial Diversity and Fermentation Pattern in Buffalo. , 2022, 2022, 1-14.		2
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15102	Predominance of <i>Escherichia-Shigella</i> in Gut Microbiome and Its Potential Correlation with Elevated Level of Plasma Tumor Necrosis Factor Alpha in Patients with Tuberculous Meningitis. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	12
15103	Translucent disease outbreak in <i>Penaeus vannamei</i> post-larva accompanies the imbalance of pond water and shrimp gut microbiota homeostasis. <i>Aquaculture Reports</i> , 2022, 27, 101410.	0.7	1
15104	<i>Lactobacillus reuteri</i> normalizes altered fear memory in male <i>Cntnap4</i> knockout mice. <i>EBioMedicine</i> , 2022, 86, 104323.	2.7	6
15105	Relationships between rumen microbes, short-chain fatty acids, and markers of white adipose tissue browning during the cold season in grazing Mongolian sheep (<i>Ovis aries</i>). <i>Journal of Thermal Biology</i> , 2022, 110, 103386.	1.1	3
15106	Effects of Intestinal Bacterial Hydrogen Gas Production on Muscle Recovery following Intense Exercise in Adult Men: A Pilot Study. <i>Nutrients</i> , 2022, 14, 4875.	1.7	1
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15113	Mycorrhizal diversity and community composition in co-occurring <i>Cypripedium</i> species. <i>Mycorrhiza</i> , 0, , .	1.3	0
15114	Triclosan exposure induced disturbance of gut microbiota and exaggerated experimental colitis in mice. <i>BMC Gastroenterology</i> , 2022, 22, .	0.8	4
15115	Methane and nitrous oxide production and their driving factors in <i>Phragmites</i> riparian wetlands of Dianchi Lake, China. <i>Ecological Indicators</i> , 2022, 145, 109696.	2.6	1
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15119	Elevational distribution patterns and drivers of soil microbial diversity in the Sygera Mountains, southeastern Tibet, China. <i>Catena</i> , 2023, 221, 106738.	2.2	7
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15130	Effect of <i>Massa Medicata Fermentata</i> on the intestinal flora of rats with functional dyspepsia. <i>Microbial Pathogenesis</i> , 2023, 174, 105927.	1.3	3
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15134	Benthic bacteria and archaea in the North American Arctic reflect food supply regimes and impacts of coastal and riverine inputs. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2023, 207, 105224.	0.6	5
15135	Use of wood and cork in biofilters for the simultaneous removal of nitrates and pesticides from groundwater. <i>Chemosphere</i> , 2023, 313, 137502.	4.2	3
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15140	An evaluation of different detection methods for anaerobic ammonium-oxidizing (anammox) bacteria inhabiting the oil reservoir systems. <i>International Biodeterioration and Biodegradation</i> , 2023, 177, 105536.	1.9	1
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15144	Alteration of oral microbiome composition in children living with pesticide-exposed farm workers. <i>International Journal of Hygiene and Environmental Health</i> , 2023, 248, 114090.	2.1	0
15145	Which soil microbiome? Bacteria, fungi, and protozoa communities show different relationships with urban green space type and use-intensity. <i>Science of the Total Environment</i> , 2023, 863, 160468.	3.9	2
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15147	Microbial community diversity and enzyme activity varies in response to long-term fertilisation in a continuous potato (<i>Solanum tuberosum</i> L.) cropping system. <i>Soil Research</i> , 2022, , .	0.6	0
15148	IoT-Based Bacillus Number Prediction in Smart Turmeric Farms Using Small Data Sets. <i>IEEE Internet of Things Journal</i> , 2023, 10, 5146-5157.	5.5	1
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15153	Seasonal patterns of rhizosphere microorganisms suggest carbohydrate-degrading and nitrogen-fixing microbes contribute to the attribute of full-year shooting in woody bamboo <i>Cephalostachyum pingbianense</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
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15157	Flavacol and Its Novel Derivative 3- β -Hydroxy Flavacol from <i>Streptomyces</i> sp. Pv 4-95 after the Expression of Heterologous AdpA. <i>Microorganisms</i> , 2022, 10, 2335.	1.6	2
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15165	Challenges of Comparing Marine Microbiome Community Composition Data Provided by Different Commercial Laboratories and Classification Databases. <i>Water (Switzerland)</i> , 2022, 14, 3855.	1.2	0
15166	Mycobiome Diversity of the Cave Church of Sts. Peter and Paul in Serbia—Risk Assessment Implication for the Conservation of Rare Cavern Habitat Housing a Peculiar Fresco Painting. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1263.	1.5	6
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15175	Potential for Polyethylene Terephthalate (PET) Degradation Revealed by Metabarcoding and Bacterial Isolates from Soil Around a Bitumen Source in Southwestern Iran. <i>Journal of Polymers and the Environment</i> , 2023, 31, 1279-1291.	2.4	5
15176	Forest succession improves the complexity of soil microbial interaction and ecological stochasticity of community assembly: Evidence from <i>Phoebe bournei</i> -dominated forests in subtropical regions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
15177	Microbiota Community Structure and Interaction Networks within <i>Dermacentor silvarum</i> , <i>Ixodes persulcatus</i> , and <i>Haemaphysalis concinna</i> . <i>Animals</i> , 2022, 12, 3237.	1.0	0
15178	Interactions between arsenic exposure, high-fat diet and NRF2 shape the complex responses in the murine gut microbiome and hepatic metabolism. , 0, 1, .		0
15180	AMF colonization affects allelopathic effects of <i>Zea mays</i> L. root exudates and community structure of rhizosphere bacteria. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
15181	Altered functional connectivity strength in chronic insomnia associated with gut microbiota composition and sleep efficiency. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	3
15182	Early season soil microbiome best predicts wheat grain quality. <i>FEMS Microbiology Ecology</i> , 2022, 99, .	1.3	2
15183	Dietary Supplementation of Fruit from <i>Nitraria tangutorum</i> Improved Immunity and Abundance of Beneficial Ruminal Bacteria in Hu Sheep. <i>Animals</i> , 2022, 12, 3211.	1.0	3
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15187	Effects of Dietary Oregano Essential Oil on Cecal Microorganisms and Muscle Fatty Acids of Luhua Chickens. <i>Animals</i> , 2022, 12, 3215.	1.0	4
15188	Recommendations for the preservation of environmental samples in diatom metabarcoding studies. <i>Metabarcoding and Metagenomics</i> , 0, 6, .	0.0	6
15189	Microbiome analysis in Lascaux Cave in relation to black stain alterations of rock surfaces and collembola. <i>Environmental Microbiology Reports</i> , 2023, 15, 80-91.	1.0	6
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15191	Oral Administration of the Antimicrobial Peptide Mastoparan X Alleviates Enterohemorrhagic <i>Escherichia coli</i> -Induced Intestinal Inflammation and Regulates the Gut Microbiota. <i>Probiotics and Antimicrobial Proteins</i> , 2024, 16, 138-151.	1.9	0
15192	Association between Fecal Microbiota, SCFA, Gut Integrity Markers and Depressive Symptoms in Patients Treated in the Past with Bariatric Surgery—The Cross-Sectional Study. <i>Nutrients</i> , 2022, 14, 5372.	1.7	4

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15195	Dynamics of rice microbiomes reveal core vertically transmitted seed endophytes. <i>Microbiome</i> , 2022, 10, .	4.9	25
15196	The Bioavailability of Glycyrrhizinic Acid Was Enhanced by Probiotic <i>Lactobacillus rhamnosus</i> R0011 Supplementation in Liver Fibrosis Rats. <i>Nutrients</i> , 2022, 14, 5278.	1.7	4
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15199	Treatment of peanut allergy and colitis in mice via the intestinal release of butyrate from polymeric micelles. <i>Nature Biomedical Engineering</i> , 2023, 7, 38-55.	11.6	36
15200	Response of soil bacterial communities in wheat rhizosphere to straw mulching and N fertilization. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
15201	Bacterial Communities in Informal Dump Sites: A Rich Source of Unique Diversity and Functional Potential for Bioremediation Applications. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 12862.	1.3	1
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15205	Does plastic type matter? Insights into non-indigenous marine larvae recruitment under controlled conditions. <i>PeerJ</i> , 0, 10, e14549.	0.9	0
15206	The harmful intestinal microbial community accumulates during DKD exacerbation and microbiome metabolome combined validation in a mouse model. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	5
15207	Hatchery tanks induce intense reduction in microbiota diversity associated with gills and guts of two endemic species of the San Francisco River. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
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15209	Diversity of Myxobacteria Isolated from Indonesian Mangroves and Their Potential for New Antimicrobial Sources. <i>Current Microbiology</i> , 2023, 80, .	1.0	1
15210	Morphology, phylogeny, mitogenomics and metagenomics reveal a new entomopathogenic fungus <i>Ophiocordyceps nujiangensis</i> (Hypocreales, Ophiocordycipitaceae) from Southwestern China. <i>MycoKeys</i> , 0, 94, 91-108.	0.8	1

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15212	Improving the quality of barren rocky soil by culturing sweetpotato, with special reference to plant-microbes-soil interactions. <i>Microbiological Research</i> , 2023, 268, 127294.	2.5	2
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15214	Sex Differences in Fecal Microbiome Composition and Function of Dromedary Camels in Saudi Arabia. <i>Animals</i> , 2022, 12, 3430.	1.0	2
15215	Microbial community diversity and function analysis of <i>Aconitum carmichaelii</i> Debeaux in rhizosphere soil of farmlands in Southwest China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
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15366	Dynamic changes in intestinal microbiota and metabolite composition of pre-weaned beef calves. <i>Microbial Pathogenesis</i> , 2023, 175, 105991.	1.3	2
15367	TRPC absence induces pro-inflammatory macrophages and gut microbe disorder, sensitizing mice to colitis. <i>International Immunopharmacology</i> , 2023, 115, 109655.	1.7	0
15368	Multi-group biodiversity distributions and drivers of metacommunity organization along a glacial–fluvial–limnic pathway on the Tibetan plateau. <i>Environmental Research</i> , 2023, 220, 115236.	3.7	3
15369	Contrasting responses of microbial diversity and community structure in decaying root bark and xylem to N addition in an alpine shrubland. <i>Soil Biology and Biochemistry</i> , 2023, 178, 108937.	4.2	0
15370	Diversity analysis of vineyards soil bacterial community in different planting years at eastern foot of Helan Mountain, Ningxia. <i>Rhizosphere</i> , 2023, 25, 100650.	1.4	5
15371	Microplastic-induced gut microbiota and serum metabolic disruption in Sprague-Dawley rats. <i>Environmental Pollution</i> , 2023, 320, 121071.	3.7	9
15372	Antibiotic and heavy metal resistance genes in sewage sludge survive during aerobic composting. <i>Science of the Total Environment</i> , 2023, 866, 161386.	3.9	10
15373	Protocol for microbiota analysis of a murine stroke model. <i>STAR Protocols</i> , 2023, 4, 101969.	0.5	1
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15375	Changes in bacterial diversity, co-occurrence pattern, and potential pathogens following digestate fertilization: Extending pathogen management to field for anaerobic digestion of livestock manure. <i>Waste Management</i> , 2023, 158, 107-115.	3.7	4
15376	Distinctive role of soil type and land use in driving bacterial communities and carbon cycling functions down soil profiles. <i>Catena</i> , 2023, 223, 106903.	2.2	6
15377	Total flavonoids of <i>Tetrastigma hemsleyanum</i> Diels et Gilg inhibits colorectal tumor growth by modulating gut microbiota and metabolites. <i>Food Chemistry</i> , 2023, 410, 135361.	4.2	9
15378	The neglected role of micronutrients in predicting soil microbial structure. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	11
15379	Exogenous antibiotic resistance gene contributes to intestinal inflammation by modulating the gut microbiome and inflammatory cytokine responses in mouse. <i>Gut Microbes</i> , 2023, 15, .	4.3	1
15380	Gut microbiota diversity in human strongyloidiasis differs little in two different regions in endemic areas of Thailand. <i>PLoS ONE</i> , 2022, 17, e0279766.	1.1	1
15381	Comparing Transgenic Production to Supplementation of ω -3 PUFA Reveals Distinct But Overlapping Mechanisms Underlying Protection Against Metabolic and Hepatic Disorders. <i>Function</i> , 2023, 4, .	1.1	4
15382	New Insights into the Effect of Fipronil on the Soil Bacterial Community. <i>Microorganisms</i> , 2023, 11, 52.	1.6	2

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15384	Technical versus biological variability in a synthetic human gut community. <i>Gut Microbes</i> , 2023, 15, .	4.3	2
15385	Ameliorative Effects of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> J-12 on Hyperglycemia in Pregnancy and Pregnancy Outcomes in a High-Fat-Diet/Streptozotocin-Induced Rat Model. <i>Nutrients</i> , 2023, 15, 170.	1.7	1
15386	Phytoplankton community structure in the Western Subarctic Gyre of the Pacific Ocean during summer determined by a combined approach of HPLC-pigment CHEMTAX and metabarcoding sequencing. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
15387	Beneficial metabolic transformations and prebiotic potential of hemp bran and its alcalase hydrolysate, after colonic fermentation in a gut model. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
15388	Effect of ospemifene on vaginal microbiome in postmenopausal women with vulvovaginal atrophy. <i>Menopause</i> , 2023, 30, 361-369.	0.8	3
15389	Diagnosis and functional prediction of microbial markers in tumor tissues of sporadic colorectal cancer patients associated with the MLH1 protein phenotype. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
15390	Elevated temperature and CO ₂ strongly affect the growth strategies of soil bacteria. <i>Nature Communications</i> , 2023, 14, .	5.8	10
15391	Data-independent acquisition boosts quantitative metaproteomics for deep characterization of gut microbiota. <i>Npj Biofilms and Microbiomes</i> , 2023, 9, .	2.9	12
15392	Leveraging 16S rRNA data to uncover vaginal microbial signatures in women with cervical cancer. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	0
15393	Viral infection switches the balance between bacterial and eukaryotic recyclers of organic matter during coccolithophore blooms. <i>Nature Communications</i> , 2023, 14, .	5.8	11
15394	A Case of Successful Treatment of Recurrent Urinary Tract Infection by Extended-Spectrum $\hat{2}$ -Lactamase Producing <i>Klebsiella pneumoniae</i> Using Oral Lyophilized Fecal Microbiota Transplant. <i>Microbial Drug Resistance</i> , 2023, 29, 34-38.	0.9	3
15395	Functional metagenomics profiling of symbiotic microbiome. , 2023, , 691-713.		1
15396	Terpene Synthase Gene Amplicons from Subseafloor Sediment. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	2
15397	Nitrogen Fertilizer Type and Genotype as Drivers of P Acquisition and Rhizosphere Microbiota Assembly in Juvenile Maize Plants. <i>Plants</i> , 2023, 12, 544.	1.6	2
15398	Suppression of Banana Fusarium Wilt Disease with Soil Microbial Mechanisms via Pineapple Rotation and Residue Amendment. <i>Agronomy</i> , 2023, 13, 377.	1.3	1
15399	Melibiose- α -X-Gal MacConkey Agar for Presumptive Differentiation of <i>Escherichia albertii</i> from <i>E. coli</i> and <i>Salmonella</i> from Poultry Meat. <i>Applied Microbiology</i> , 2023, 3, 119-130.	0.7	0
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15402	Strengthening and microbial regulation mechanism of <i>Bacillus</i> on purification device for grass carp culture wastewater. <i>Frontiers in Environmental Science</i> , 0, 11, .	1.5	1
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15406	Enhanced phytoremediation of atrazine-contaminated soil by vetiver (<i>Chrysopogon zizanioides</i> L.) and associated bacteria. <i>Environmental Science and Pollution Research</i> , 2023, 30, 44415-44429.	2.7	3
15409	Bacterial communities exhibit apparent phosphate concentration-related patterns of community composition, alpha diversity, and phylogenetic structure in the subtropical Daya Bay. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	4
15410	Effect of Dietary Supplemented with Mulberry Leaf Powder on Growth Performance, Serum Metabolites, Antioxidant Property and Intestinal Health of Weaned Piglets. <i>Antioxidants</i> , 2023, 12, 307.	2.2	4
15411	Coriander (<i>Coriandrum sativum</i>) Cultivation Combined with Arbuscular Mycorrhizal Fungi Inoculation and Steel Slag Application Influences Trace Elements-Polluted Soil Bacterial Functioning. <i>Plants</i> , 2023, 12, 618.	1.6	2
15412	Microbial Changes Associated With Oral Cavity Cancer Progression. <i>Otolaryngology - Head and Neck Surgery</i> , 0, , .	1.1	0
15413	Effects of taurine on rumen fermentation, nutrient digestion, rumen bacterial community and metabolomics and nitrogen metabolism in beef steers. <i>Journal of the Science of Food and Agriculture</i> , 0, , .	1.7	4
15414	Aflatoxin B1 Induced Oxidative Stress and Gut Microbiota Disorder to Increase the Infection of Cyprinid Herpesvirus 2 in Gibel Carp (<i>Carassius auratus gibelio</i>). <i>Antioxidants</i> , 2023, 12, 306.	2.2	3
15415	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
15417	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
15418	Sugarcane Wax Metabolites and Their Toxicity to Silkworms. <i>Life</i> , 2023, 13, 286.	1.1	0
15419	Liver Microbiome in Healthy Rats: The Hidden Inhabitants of Hepatocytes. <i>Cellular Microbiology</i> , 2023, 2023, 1-16.	1.1	0
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15421	Comparison of Bacterial Diversity in the Rhizosphere of <i>Chromolaena odorata</i> (L.) R.M. King and H. Rob. in Different Habitats. <i>Sustainability</i> , 2023, 15, 2315.	1.6	2

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15423	Effects of <i>Cinnamomum camphora</i> coppice planting on soil fertility, microbial community structure and enzyme activity in subtropical China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
15424	The Responses of Sediment Bacterial Communities in Chinese Mitten Crab (<i>Eriocheir sinensis</i>) Culture Ponds to Changes in Physicochemical Properties Caused by Sediment Improvement. <i>Fishes</i> , 2023, 8, 98.	0.7	1
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15426	Potential interactions between diatoms and bacteria are shaped by trace element gradients in the Southern Ocean. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	3
15427	Comparison of methods for biological sequence clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, , 1-24.	1.9	0
15428	Deciphering microeukaryotic bacterial co-occurrence networks in coastal aquaculture ponds. <i>Marine Life Science and Technology</i> , 2023, 5, 44-55.	1.8	5
15429	Ocular conjunctival microbiome profiling in dry eye disease: A case control pilot study. <i>Indian Journal of Ophthalmology</i> , 2023, 71, 1574-1581.	0.5	3
15430	Distinguishable Influence of the Delivery Mode, Feeding Pattern, and Infant Sex on Dynamic Alterations in the Intestinal Microbiota in the First Year of Life. <i>Microbial Ecology</i> , 0, , .	1.4	1
15431	Elevated Temperature-Induced Epimicrobiome Shifts in an Invasive Seaweed <i>Gracilaria vermiculophylla</i> . <i>Microorganisms</i> , 2023, 11, 599.	1.6	1
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15434	Dynamics and diversity of symbiotic bacteria in <i>Apolygus lucorum</i> at different developmental stages. <i>Journal of Cotton Research</i> , 2023, 6, .	1.0	1
15435	Fecal microbiota from MRL/lpr mice exacerbates pristane-induced lupus. <i>Arthritis Research and Therapy</i> , 2023, 25, .	1.6	0
15436	Bacterial communities of <i>Aedes aegypti</i> mosquitoes differ between crop and midgut tissues. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011218.	1.3	5
15437	Evaluation of a novel porous antimicrobial media for industrial and HVAC water biocontrol. <i>Water Science and Technology</i> , 0, , .	1.2	0
15438	Plant species shape the bacterial communities on the phyllosphere in a hyper-arid desert. <i>Microbiological Research</i> , 2023, 269, 127314.	2.5	4
15439	<i>Cordyceps militaris</i> extracts and cordycepin ameliorate type 2 diabetes mellitus by modulating the gut microbiota and metabolites. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	6
15440	Effect of fermented soy beverage in aged female mice model. <i>Food Research International</i> , 2023, 169, 112745.	2.9	2

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15442	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
15443	Composition and function of the skin microbiota were altered of red leg syndrome in cultured bullfrog (<i>Rana catesbeiana</i>). <i>Aquaculture Reports</i> , 2023, 29, 101487.	0.7	2
15444	Plant growth stages covered the legacy effect of rotation systems on microbial community structure and function in wheat rhizosphere. <i>Environmental Science and Pollution Research</i> , 2023, 30, 59632-59644.	2.7	1
15445	<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
15446	Maternal Rumen Bacteriota Shapes the Offspring Rumen Bacteriota, Affecting the Development of Young Ruminants. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
15447	Decision Tree Ensembles Utilizing Multivariate Splits Are Effective at Investigating Beta Diversity in Medically Relevant 16S Amplicon Sequencing Data. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
15448	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
15449	Fishmeal Protein Replacement by Defatted and Full-Fat Black Soldier Fly Larvae Meal in Juvenile Turbot Diet: Effects on the Growth Performance and Intestinal Microbiota. <i>Aquaculture Nutrition</i> , 2023, 2023, 1-14.	1.1	1
15450	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
15451	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
15452	Interrogating the performance and microbial ecology of an enhanced biological phosphorus removal/postâ€œanoxic denitrification process at bench and pilot scales. <i>Water Environment Research</i> , 2023, 95, .	1.3	0
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15454	Combined treatment with glucosamine and chondroitin sulfate improves rheumatoid arthritis in rats by regulating the gut microbiota. <i>Nutrition and Metabolism</i> , 2023, 20, .	1.3	6
15455	The effects of short-term dietary exposure to SiO ₂ nanoparticle on the domesticated lepidopteran insect model silkworm (<i>Bombyx mori</i>): Evidence from the perspective of multi-omics. <i>Chemosphere</i> , 2023, 323, 138257.	4.2	4
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15457	<i>Limosilactobacillus reuteri</i> ameliorates preeclampsia in mice via improving gut dysbiosis and endothelial dysfunction. <i>Biomedicine and Pharmacotherapy</i> , 2023, 161, 114429.	2.5	2
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15460	Elaborating the role of rhamnolipids on the formation of humic substances during rice straw composting based on Fenton pretreatment and fungal inoculation. <i>Bioresource Technology</i> , 2023, 376, 128843.	4.8	7
15461	Multi-factor correlation analysis of the effect of root-promoting practices on tobacco rhizosphere microecology in growth stages. <i>Microbiological Research</i> , 2023, 270, 127349.	2.5	1
15462	Bacterial lipopolysaccharide with different administration routes affects intestinal mucosal morphological, immunological, and microbial barrier functions in goslings. <i>Poultry Science</i> , 2023, 102, 102599.	1.5	2
15463	Adaptive changes of swimming crab (<i>Portunus trituberculatus</i>) associated bacteria helping host against dibutyl phthalate toxification. <i>Environmental Pollution</i> , 2023, 324, 121328.	3.7	3
15464	Gut microbial and metabolic characterization of Atlantic salmon (<i>Salmon salar</i>) challenged with <i>Aeromonas salmonicida</i> . <i>Aquaculture</i> , 2023, 570, 739420.	1.7	0
15465	A comparative study on effects of dietary three strains of lactic acid bacteria on the growth performance, immune responses, disease resistance and intestinal microbiota of Pacific white shrimp, <i>Penaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2023, 136, 108707.	1.6	4
15466	Promotion of astrocyte-neuron glutamate-glutamine shuttle by SCFA contributes to the alleviation of Alzheimer's disease. <i>Redox Biology</i> , 2023, 62, 102690.	3.9	14
15467	Identifying surface water and groundwater interactions using multiple experimental methods in the riparian zone of the polluted and disturbed Shaying River, China. <i>Science of the Total Environment</i> , 2023, 875, 162616.	3.9	4
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15470	Lignite bioorganic fertilizer enhanced microbial co-occurrence network stability and plant-microbe interactions in saline-sodic soil. <i>Science of the Total Environment</i> , 2023, 879, 163113.	3.9	6
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15472	Evaluation of the effects of dietary mycotoxin-degrading adsorbent on juvenile turbot (<i>Scophthalmus maximus</i> L.) fed aflatoxin B1-contaminated diets. <i>Aquaculture Reports</i> , 2023, 30, 101539.	0.7	0
15473	Integrated omics analysis on the bacterial community in the anaerobic digestion of chicken manure materials in biogas production farm. <i>Bioresource Technology Reports</i> , 2023, 22, 101424.	1.5	0
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15475	Deciphering endemic rhizosphere microbiome community's structure towards the host-derived heavy metals tolerance and plant growth promotion functions in serpentine geo-ecosystem. <i>Journal of Hazardous Materials</i> , 2023, 452, 131359.	6.5	4
15476	Changes in soil bacterial communities and functional groups beneath coarse woody debris across a subalpine forest successional series. <i>Global Ecology and Conservation</i> , 2023, 43, e02436.	1.0	1

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15479	Exogenous-organic-matter-driven mobilization of groundwater arsenic. <i>Environmental Science and Ecotechnology</i> , 2023, 15, 100243.	6.7	6
15480	Chemical fumigation combined with soil amendments of contrasting carbon availability alters soil bacterial and fungal community diversity. <i>Applied Soil Ecology</i> , 2023, 188, 104858.	2.1	2
15481	Contributions of abundant and rare bacteria to soil multifunctionality depend on aridity and elevation. <i>Applied Soil Ecology</i> , 2023, 188, 104881.	2.1	2
15482	The composition, function and assembly mechanism of epiphytic microbial communities on <i>Gracilariopsis lemaneiformis</i> . <i>Journal of Experimental Marine Biology and Ecology</i> , 2023, 564, 151909.	0.7	1
15483	Aerobic exercise training-induced alteration of gut microbiota composition affects endurance capacity. <i>Journal of Physiology</i> , 0, , .	1.3	2
15484	Revealing the relative importance among plant species, slope positions, and soil types on rhizosphere microbial communities in northern tropical karst and non-karst seasonal rainforests of China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
15486	Dissolved storage glycans shaped the community composition of abundant bacterioplankton clades during a North Sea spring phytoplankton bloom. <i>Microbiome</i> , 2023, 11, .	4.9	10
15487	Long-term integrated rice-crayfish culture disrupts the microbial communities in paddy soil. <i>Aquaculture Reports</i> , 2023, 29, 101515.	0.7	1
15488	Diversity and dynamics of microbial population during fermentation of gray sufu and their correlation with quality characteristics. <i>LWT - Food Science and Technology</i> , 2023, 180, 114711.	2.5	7
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15490	Combined toxic effects of nanoplastics and norfloxacin on mussel: Leveraging biochemical parameters and gut microbiota. <i>Science of the Total Environment</i> , 2023, 880, 163304.	3.9	7
15495	Effect of granular activated carbon and chloroform on chain elongation with simple substrate ethanol and acetate. <i>Environmental Research</i> , 2023, 221, 115324.	3.7	1
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15497	Effective removal of trace 1,4-dioxane by biological treatments augmented with propanotrophic single culture versus synthetic consortium. <i>Journal of Hazardous Materials Advances</i> , 2023, 9, 100246.	1.2	2
15498	Responses of microbial community to geochemical parameters on vertical depth in bioheap system of low-grade copper sulfide. <i>Science of the Total Environment</i> , 2023, 869, 161752.	3.9	2
15499	Characterization and Hydrocarbon Degradation Potential of <i>Variovorax</i> sp. Strain N23 Isolated from the Antarctic Soil. <i>Microbiology Research</i> , 2023, 14, 91-103.	0.8	1

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15500	Microbial Communities on Samples of Commercially Available Fresh-Consumed Leafy Vegetables and Small Berries. <i>Horticulturae</i> , 2023, 9, 150.	1.2	2
15501	No evidence that modification of soil microbiota by woody invader facilitates subsequent invasion by herbaceous species. <i>Ecological Applications</i> , 2024, 34, .	1.8	4
15502	Fate, uptake and gut toxicity of two colloidal silver products in mice: how micro X-ray fluorescence, micro X-ray absorption spectroscopy and near-infrared spectroscopy provide new insights in food nanotoxicology. <i>Environmental Science: Nano</i> , 2023, 10, 902-921.	2.2	0
15503	Microbiological profile of peri-implantitis: Analyses of microbiome within dental implants. <i>Journal of Prosthodontics</i> , 2023, 32, 783-792.	1.7	5
15504	“ Invited Review ” Assessment of the gastrointestinal microbiota using 16S ribosomal RNA gene amplicon sequencing in ruminant nutrition. <i>Animal Bioscience</i> , 2023, 36, 364-373.	0.8	4
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15506	Short-term feeding of defatted bovine colostrum mitigates inflammation in the gut via changes in metabolites and microbiota in a chicken animal model. <i>Animal Microbiome</i> , 2023, 5, .	1.5	1
15507	Characterization of the Microbiome and Host’s Metabolites of the Lower Respiratory Tract During Acute Community-Acquired Pneumonia Identifies Potential Novel Markers. <i>Infection and Drug Resistance</i> , 0, Volume 16, 581-594.	1.1	2
15508	Parasite Spillover from Domestic Sheep to Wild Reindeer—The Role of Salt Licks. <i>Pathogens</i> , 2023, 12, 186.	1.2	4
15509	Immunomodulatory effects of complex probiotics on the immuno-suppressed mice induced by cyclophosphamide. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
15510	Obeticholic acid protects against methamphetamine-induced anxiety-like behavior by ameliorating microbiota-mediated intestinal barrier impairment. <i>Toxicology</i> , 2023, 486, 153447.	2.0	4
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15681	Responses of bacterioplankton, particle- and colony-attached bacterial communities to <i>Phaeocystis globosa</i> blooms in Mirs Bay, China. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
15683	Temporal dynamics of geothermal microbial communities in Aotearoa-New Zealand. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
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15686	Bioinformatic and Statistical Analysis of Microbiome Data. <i>Methods in Molecular Biology</i> , 2023, , 183-229.	0.4	2
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15694	Richness of arbuscular mycorrhizal fungi increases with ecosystem degradation of temperate eucalypt woodlands. <i>Plant and Soil</i> , 2023, 488, 255-271.	1.8	1
15695	<i>Solitalea lacus</i> sp. nov., isolated from pond sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
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15704	Combining air sampling and DNA metabarcoding to monitor plant pathogens. <i>PhytoFrontiers</i> , 0, , .	0.8	0
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15706	Comparison of the colonization ability of <i>Burkholderia</i> strain B23 in the citrus rhizoplane and rhizosphere and assessment of the underlying mechanisms using full-length 16S rDNA amplicon and metatranscriptomic analyses. <i>Microbial Biotechnology</i> , 0, , .	2.0	1
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15713	Vaginal microbiota of adolescents and their mothers: A preliminary study of vertical transmission and persistence. , 0, 2, .		0
15717	Microbial composition of tumorous and adjacent gastric tissue is associated with prognosis of gastric cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
15718	Dysbiosis of gut microbiota due to diet, alcohol intake, body mass index, and gastrointestinal diseases in India. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 2547-2560.	1.7	0
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15720	<i>Fusobacterium nucleatum</i> Induces Gut Dysbiosis and Inflammasome and Promotes Colonic Inflammation. <i>International Journal of Oral-Medical Sciences</i> , 2023, 21, 60-70.	0.2	0

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15734	Isolation, identification and spoilage capability of dominant spoilage bacteria on Dezhou-braised chicken with different packaging. <i>LWT - Food Science and Technology</i> , 2023, 182, 114710.	2.5	0
15735	Niche Modification by Sulfate-Reducing Bacteria Drives Microbial Community Assembly in Anoxic Marine Sediments. <i>MBio</i> , 0, , .	1.8	1
15736	Alternative stable states, nonlinear behavior, and predictability of microbiome dynamics. <i>Microbiome</i> , 2023, 11, .	4.9	13
15737	Behavioral phenotype, intestinal microbiome, and brain neuronal activity of male serotonin transporter knockout mice. <i>Molecular Brain</i> , 2023, 16, .	1.3	3
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15746	Discrete patterns of microbiome variability across timescales in a wild rodent population. <i>BMC Microbiology</i> , 2023, 23, .	1.3	1
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15748	Characterization of the oral microbiome and gut microbiome of dental caries and extrinsic black stain in preschool children. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
15749	Assessing arthropod diversity metrics derived from stream environmental DNA: spatiotemporal variation and paired comparisons with manual sampling. <i>PeerJ</i> , 0, 11, e15163.	0.9	1
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15751	Biocontrol mechanisms of <i>Bacillus velezensis</i> against <i>Fusarium oxysporum</i> from <i>Panax ginseng</i> . <i>Biological Control</i> , 2023, 182, 105222.	1.4	8
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15756	Links between Soil Bacteriomes and Fungistasis toward Fungi Infecting the Colorado Potato Beetle. <i>Microorganisms</i> , 2023, 11, 943.	1.6	2
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15800	Screening the maize rhizobiome for consortia that improve <i>Azospirillum brasilense</i> root colonization and plant growth outcomes. <i>Frontiers in Sustainable Food Systems</i> , 0, 7, .	1.8	4

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15804	Metagenomic profile of the bacterial communities associated with <i>Ixodes granulatus</i> (Acari: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5)	0.9	0
15805	Surfaces of gymnastic equipment as reservoirs of microbial pathogens with potential for transmission of bacterial infection and antimicrobial resistance. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
15806	Diversity and specificity of orchid mycorrhizal fungi in a leafless epiphytic orchid, <i>Dendrophylax lindenii</i> and the potential role of fungi in shaping its fine-scale distribution. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	0
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15809	Dual use of solar power plants as biocrust nurseries for large-scale arid soil restoration. <i>Nature Sustainability</i> , 2023, 6, 955-964.	11.5	3
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