

Ultra-high-throughput microbial community analysis of platforms

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Citation Report

#	ARTICLE	IF	CITATIONS
6	Therapeutic Helminth Infection of Macaques with Idiopathic Chronic Diarrhea Alters the Inflammatory Signature and Mucosal Microbiota of the Colon. <i>PLoS Pathogens</i> , 2012, 8, e1003000.	2.1	206
7	PCR Biases Distort Bacterial and Archaeal Community Structure in Pyrosequencing Datasets. <i>PLoS ONE</i> , 2012, 7, e43093.	1.1	366
8	Trait-Based Representation of Biological Nitrification: Model Development, Testing, and Predicted Community Composition. <i>Frontiers in Microbiology</i> , 2012, 3, 364.	1.5	94
9	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21390-21395.	3.3	1,260
10	De novo co-assembly of bacterial genomes from multiple single cells. , 2012, , .		15
11	Environmental and Evolutionary Genomics of Microbial Algae: Power and Challenges of Metagenomics. <i>Advances in Botanical Research</i> , 2012, 64, 383-427.	0.5	11
12	Microbial 16S rRNA Ion Tag and community metagenome sequencing using the Ion Torrent (PGM) Platform. <i>Journal of Microbiological Methods</i> , 2012, 91, 80-88.	0.7	187
14	A Direct PCR Approach to Accelerate Analyses of Human-Associated Microbial Communities. <i>PLoS ONE</i> , 2012, 7, e44563.	1.1	60
15	Now and Next-Generation Sequencing Techniques: Future of Sequence Analysis Using Cloud Computing. <i>Frontiers in Genetics</i> , 2012, 3, 280.	1.1	12
16	Predicting microbial distributions in space and time. <i>Nature Methods</i> , 2012, 9, 549-551.	9.0	25
17	Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. <i>GigaScience</i> , 2013, 2, 4.	3.3	227
18	Effects of disturbance scale on soil microbial communities in the Western Cascades of Oregon. <i>Plant and Soil</i> , 2013, 372, 459-471.	1.8	9
19	Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. <i>FEMS Microbiology Ecology</i> , 2013, 86, 557-566.	1.3	86
20	The gut microbiota and obesity: from correlation to causality. <i>Nature Reviews Microbiology</i> , 2013, 11, 639-647.	13.6	665
21	Diversity, distribution and sources of bacteria in residential kitchens. <i>Environmental Microbiology</i> , 2013, 15, 588-596.	1.8	170
22	Comparative metatranscriptomics reveals kingdom level changes in the rhizosphere microbiome of plants. <i>ISME Journal</i> , 2013, 7, 2248-2258.	4.4	468
23	Beyond the genome: community-level analysis of the microbial world. <i>Biology and Philosophy</i> , 2013, 28, 261-282.	0.7	72
24	Microbiota-liberated host sugars facilitate post-antibiotic expansion of enteric pathogens. <i>Nature</i> , 2013, 502, 96-99.	13.7	848

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25	Practical innovations for high-throughput amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 999-1002.	9.0	787
26	Ecological Inferences from a deep screening of the <i>C</i> complex <i>B</i> acterial <i>C</i> onsortia associated with the coral, <i>P</i> orites <i>a</i> streoides. <i>Molecular Ecology</i> , 2013, 22, 4349-4362.	2.0	59
27	Temporal variability and effect of environmental variables on airborne bacterial communities in an urban area of Northern Italy. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6561-6570.	1.7	165
28	Unravelling the bacterial diversity in the atmosphere. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4727-4736.	1.7	138
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30	The Long-Term Stability of the Human Gut Microbiota. <i>Science</i> , 2013, 341, 1237439.	6.0	1,696
31	Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. <i>Nucleic Acids Research</i> , 2013, 41, e1-e1.	6.5	6,268
32	The human mycobiome in health and disease. <i>Genome Medicine</i> , 2013, 5, 63.	3.6	292
33	Cell Size Distributions of Soil Bacterial and Archaeal Taxa. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7610-7617.	1.4	98
34	Environmental bio-monitoring with high-throughput sequencing. <i>Briefings in Bioinformatics</i> , 2013, 14, 575-588.	3.2	26
35	Daily temporal dynamics of vaginal microbiota before, during and after episodes of bacterial vaginosis. <i>Microbiome</i> , 2013, 1, 29.	4.9	258
36	Quantifying and Identifying the Active and Damaged Subsets of Indigenous Microbial Communities. <i>Methods in Enzymology</i> , 2013, 531, 91-107.	0.4	13
37	Assembling Full-Length rRNA Genes from Short-Read Metagenomic Sequence Datasets Using EMIRGE. <i>Methods in Enzymology</i> , 2013, 531, 333-352.	0.4	9
38	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
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41	Advances in computational analysis of metagenome sequences. <i>Environmental Microbiology</i> , 2013, 15, 1-5.	1.8	38
42	Characterisation of the human oral microbiome. <i>Journal of Oral Biosciences</i> , 2013, 55, 143-148.	0.8	39

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44	Analysis of soil fungal communities by amplicon pyrosequencing: current approaches to data analysis and the introduction of the pipeline SEED. <i>Biology and Fertility of Soils</i> , 2013, 49, 1027-1037.	2.3	168
45	Both species sorting and neutral processes drive assembly of bacterial communities in aquatic microcosms. <i>FEMS Microbiology Ecology</i> , 2013, 86, 288-302.	1.3	44
46	Computational meta'omics for microbial community studies. <i>Molecular Systems Biology</i> , 2013, 9, 666.	3.2	253
47	Bacterial community structure on two alpine debris-covered glaciers and biogeography of <i>Polaromonas</i> phylotypes. <i>ISME Journal</i> , 2013, 7, 1483-1492.	4.4	63
49	Illumina metabarcoding of a soil fungal community. <i>Soil Biology and Biochemistry</i> , 2013, 65, 128-132.	4.2	409
50	Significance of the Microbiome in Chronic Obstructive Pulmonary Disease. <i>Annals of the American Thoracic Society</i> , 2013, 10, S170-S179.	1.5	20
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52	Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. <i>Science</i> , 2013, 339, 548-554.	6.0	1,012
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59	Distribution-Based Clustering: Using Ecology To Refine the Operational Taxonomic Unit. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6593-6603.	1.4	140
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63	Gastrointestinal microorganisms in cats and dogs: a brief review. Archivos De Medicina Veterinaria, 2013, 45, 111-124.	0.2	12
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98	Captivity results in disparate loss of gut microbial diversity in closely related hosts. , 2014, 2, cou009-cou009.		132

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164	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	13.5	625
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1092	Efficacy of a high-pressure jet device for excess sludge reduction in a conventional activated sludge process: Pilot-scale demonstration. <i>Chemical Engineering Journal</i> , 2017, 326, 78-86.	6.6	9
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1102	H ₂ O ₂ Production in Microbial Electrochemical Cells Fed with Primary Sludge. <i>Environmental Science & Technology</i> , 2017, 51, 6139-6145.	4.6	44
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1136	Comparison of Microbiomes between Red Poultry Mite Populations (<i>Dermanyssus gallinae</i>): Predominance of Bartonella-like Bacteria. <i>Microbial Ecology</i> , 2017, 74, 947-960.	1.4	51
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1388	Free nitrous acid and pH determine the predominant ammonia-oxidizing bacteria and amount of N ₂ O in a partial nitrifying reactor. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1673-1683.	1.7	44
1389	Enteral High Fat-Polyunsaturated Fatty Acid Blend Alters the Pathogen Composition of the Intestinal Microbiome in Premature Infants with an Enterostomy. <i>Journal of Pediatrics</i> , 2017, 181, 93-101.e6.	0.9	46
1390	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
1391	<i>Microbes and Environment.</i> , 2017, , 43-84.		55
1392	The power of soil microbes: Sustained power production in terrestrial microbial fuel cells under various temperature regimes. <i>Applied Soil Ecology</i> , 2017, 109, 14-22.	2.1	22
1393	An introduction to microbiome analysis for human biology applications. <i>American Journal of Human Biology</i> , 2017, 29, e22931.	0.8	22
1394	Effects of different carriers on biogas production and microbial community structure during anaerobic digestion of cassava ethanol wastewater. <i>Environmental Technology (United Kingdom)</i> , 2017, 38, 2253-2262.	1.2	7
1395	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
1396	Biocharâ€stimulated plant performance is strongly linked to microbial diversity and metabolic potential in the rhizosphere. <i>New Phytologist</i> , 2017, 213, 1393-1404.	3.5	201
1397	Phytoremediation: State-of-the-art and a key role for the plant microbiome in future trends and research prospects. <i>International Journal of Phytoremediation</i> , 2017, 19, 23-38.	1.7	84
1398	Differential specificity between closely related corals and abundant <i>Endozoicomonas</i> endosymbionts across global scales. <i>ISME Journal</i> , 2017, 11, 186-200.	4.4	259
1399	Comprehensive Molecular Characterization of Bacterial Communities in Feces of Pet Birds Using 16S Marker Sequencing. <i>Microbial Ecology</i> , 2017, 73, 224-235.	1.4	28
1400	Indexing Next-Generation Sequencing data. <i>Information Sciences</i> , 2017, 384, 90-109.	4.0	7
1401	The microbiome of a striped dolphin (<i>Stenella coeruleoalba</i>) stranded in Portugal. <i>Research in Microbiology</i> , 2017, 168, 85-93.	1.0	38
1402	Application of Bioorganic Fertilizer Significantly Increased Apple Yields and Shaped Bacterial Community Structure in Orchard Soil. <i>Microbial Ecology</i> , 2017, 73, 404-416.	1.4	90
1403	Shifting Cyanobacterial Diversity in Response to Agricultural Soils Associated with Dust Emission. <i>Land Degradation and Development</i> , 2017, 28, 878-886.	1.8	10
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1406	Using Prokaryotes for Carbon Capture Storage. <i>Trends in Biotechnology</i> , 2017, 35, 22-32.	4.9	44
1407	Molecular diversity of plankton in a tropical crater lake switching from hyposaline to subsaline conditions: Lake Oloidien, Kenya. <i>Hydrobiologia</i> , 2017, 788, 205-229.	1.0	24
1408	Soil resilience and recovery: rapid community responses to management changes. <i>Plant and Soil</i> , 2017, 412, 283-297.	1.8	57
1409	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
1410	Diet-induced changes of redox potential underlie compositional shifts in the rumen archaeal community. <i>Environmental Microbiology</i> , 2017, 19, 174-184.	1.8	53
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1413	Molecular analysis of environmental plant DNA in house dust across the United States. <i>Aerobiologia</i> , 2017, 33, 71-86.	0.7	25
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1415	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
1416	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. <i>Nature Microbiology</i> , 2017, 2, 16221.	5.9	138
1417	Composition and diversity of mucosa-associated microbiota along the entire length of the pig gastrointestinal tract; dietary influences. <i>Environmental Microbiology</i> , 2017, 19, 1425-1438.	1.8	120
1418	Plants, microorganisms, and soil temperatures contribute to a decrease in methane fluxes on a drained Arctic floodplain. <i>Global Change Biology</i> , 2017, 23, 2396-2412.	4.2	54
1419	Oral Vancomycin Followed by Fecal Transplantation Versus Tapering Oral Vancomycin Treatment for Recurrent <i>Clostridium difficile</i> Infection: An Open-Label, Randomized Controlled Trial. <i>Clinical Infectious Diseases</i> , 2017, 64, 265-271.	2.9	145
1420	Is the plant-associated microbiota of <i>Thymus</i> spp. adapted to plant essential oil?. <i>Research in Microbiology</i> , 2017, 168, 276-282.	1.0	35
1421	The role of microbiota in compensatory growth of protein-restricted rats. <i>Microbial Biotechnology</i> , 2017, 10, 480-491.	2.0	16
1422	Field-grown transgenic switchgrass (<i>Panicum virgatum</i> L.) with altered lignin does not affect soil chemistry, microbiology, and carbon storage potential. <i>GCB Bioenergy</i> , 2017, 9, 1100-1109.	2.5	20

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1424	Response of wastewater biofilm to CuO nanoparticle exposure in terms of extracellular polymeric substances and microbial community structure. <i>Science of the Total Environment</i> , 2017, 579, 588-597.	3.9	76
1425	Analysis of bacterial communities in and on concrete. <i>Materials and Structures/Materiaux Et Constructions</i> , 2017, 50, 1.	1.3	18
1426	Experimental metagenomics and ribosomal profiling of the human skin microbiome. <i>Experimental Dermatology</i> , 2017, 26, 211-219.	1.4	34
1427	Interleukin-15 promotes intestinal dysbiosis with butyrate deficiency associated with increased susceptibility to colitis. <i>ISME Journal</i> , 2017, 11, 15-30.	4.4	68
1428	Inhibitory effects of dietary soyasaponin on 2,4-dinitrofluorobenzene-induced contact hypersensitivity in mice. <i>Experimental Dermatology</i> , 2017, 26, 249-254.	1.4	13
1429	Household siblings and nasal and fecal microbiota in infants. <i>Pediatrics International</i> , 2017, 59, 473-481.	0.2	32
1430	Recruitment and establishment of the gut microbiome in arctic shorebirds. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	64
1431	Intraruminal infusion of oligofructose alters ruminal microbiota and induces acute laminitis in sheep ^{1,2} . <i>Journal of Animal Science</i> , 2017, 95, 5407-5419.	0.2	5
1432	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
1433	Comparison of Thaumarchaeotal populations from four deep sea basins. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	15
1434	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. <i>Scientific Reports</i> , 2017, 7, 17686.	1.6	97
1435	Application of <i>Bacillus</i> spp. in Pilot Test of Microbial Huff and Puff to Improve Heavy Oil Recovery. <i>Energy & Fuels</i> , 2017, 31, 13724-13732.	2.5	23
1436	Microbiota Diversification and Crash Induced by Dietary Oxalate in the Mammalian Herbivore <i>Neotoma albigula</i> . <i>MSphere</i> , 2017, 2, .	1.3	22
1437	Bioinformatics in Microbiome Analysis. <i>Methods in Microbiology</i> , 2017, 44, 1-18.	0.4	4
1438	Organismal and spatial partitioning of energy and macronutrient transformations within a hypersaline mat. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	23
1439	The Microbiome in Primary Sclerosing Cholangitis: Current Evidence and Potential Concepts. <i>Seminars in Liver Disease</i> , 2017, 37, 314-331.	1.8	52
1440	Preventive <i>Trichuris suis ova</i> (TSO) treatment protects immunocompetent rabbits from DSS colitis but may be detrimental under conditions of immunosuppression. <i>Scientific Reports</i> , 2017, 7, 16500.	1.6	17

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1442	Genetic influences on the human oral microbiome. <i>BMC Genomics</i> , 2017, 18, 659.	1.2	66
1443	High Organic Loading Treatment of Synthetic Soy-sauce Production Wastewater Using a Combined System Consisting of a Psychrophilic (20 °C) UASB Reactor and a DHS Reactor at Ambient Temperature. <i>Journal of Japan Society on Water Environment</i> , 2017, 40, 67-75.	0.1	1
1444	Anaerobic Baffled Reactor in Treatment of Natural Rubber Processing Wastewater: Reactor Performance and Analysis of Microbial Community. <i>Journal of Water and Environment Technology</i> , 2017, 15, 241-251.	0.3	10
1445	Microbial Community Structure and Enumeration of <i>Bacillus</i> species in Activated Sludge. <i>Journal of Water and Environment Technology</i> , 2017, 15, 233-240.	0.3	18
1446	DNA extraction for streamlined metagenomics of diverse environmental samples. <i>BioTechniques</i> , 2017, 62, 290-293.	0.8	178
1447	Microbial population analysis of the midgut of <i>Melophagus ovinus</i> via high-throughput sequencing. <i>Parasites and Vectors</i> , 2017, 10, 382.	1.0	19
1448	Appendix 3. Waiba Miao Temples. , 2017, , 155-155.		0
1449	Wetland management strategies lead to tradeoffs in ecological structure and function. <i>Elementa</i> , 2017, 5, .	1.1	6
1450	A Combined LC-MS Metabolomics- and 16S rRNA Sequencing Platform to Assess Interactions between Herbal Medicinal Products and Human Gut Bacteria in Vitro: a Pilot Study on Willow Bark Extract. <i>Frontiers in Pharmacology</i> , 2017, 8, 893.	1.6	20
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1452	Exosomes and Metabolic Function in Mice Exposed to Alternating Dark-Light Cycles Mimicking Night Shift Work Schedules. <i>Frontiers in Physiology</i> , 2017, 8, 882.	1.3	46
1453	Root Hair Mutations Displace the Barley Rhizosphere Microbiota. <i>Frontiers in Plant Science</i> , 2017, 8, 1094.	1.7	85
1454	<i>Mycoplasma hominis</i> and <i>Mycoplasma genitalium</i> in the Vaginal Microbiota and Persistent High-Risk Human Papillomavirus Infection. <i>Frontiers in Public Health</i> , 2017, 5, 140.	1.3	55
1455	A Metataxonomic Approach Could Be Considered for Cattle Clinical Mastitis Diagnostics. <i>Frontiers in Veterinary Science</i> , 2017, 4, 36.	0.9	22
1456	Comparison of the Luminal and Mucosa-Associated Microbiota in the Colon of Pigs with and without Swine Dysentery. <i>Frontiers in Veterinary Science</i> , 2017, 4, 139.	0.9	62
1457	Ageing and sarcopenia associate with specific interactions between gut microbes, serum biomarkers and host physiology in rats. <i>Ageing</i> , 2017, 9, 1698-1720.	1.4	82
1458	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

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1460	<i>Wolbachia</i> Affects Reproduction and Population Dynamics of the Coffee Berry Borer (<i>Hypothenemus</i>)	1.0	17
1461	The Role of MicroRNAs in the Chemopreventive Activity of Sulforaphane from Cruciferous Vegetables. <i>Nutrients</i> , 2017, 9, 902.	1.7	20
1462	Modulation of Gut Microbiota of Overweight Mice by Agavins and Their Association with Body Weight Loss. <i>Nutrients</i> , 2017, 9, 821.	1.7	53
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1464	Opportunistic Pathogens and Microbial Communities and Their Associations with Sediment Physical Parameters in Drinking Water Storage Tank Sediments. <i>Pathogens</i> , 2017, 6, 54.	1.2	25
1465	Molecular and Microscopic Insights into the Formation of Soil Organic Matter in a Red Pine Rhizosphere. <i>Soils</i> , 2017, 1, 4.	1.0	12
1466	Cyanobacterial endobionts within a major marine planktonic calcifier (<i>Globigerina</i>)	1.3	42
1467	Application of Molecular Biological Tools to Monitor Process Efficiency. , 2017, , 281-291.		1
1468	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
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1470	Enterotype May Drive the Dietary-Associated Cardiometabolic Risk Factors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 47.	1.8	68
1471	Reducing Viability Bias in Analysis of Gut Microbiota in Preterm Infants at Risk of NEC and Sepsis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 237.	1.8	42
1472	Hot Spring Microbial Community Composition, Morphology, and Carbon Fixation: Implications for Interpreting the Ancient Rock Record. <i>Frontiers in Earth Science</i> , 2017, 5, .	0.8	50
1473	<i>Lactobacillus johnsonii</i> N6.2 Modulates the Host Immune Responses: A Double-Blind, Randomized Trial in Healthy Adults. <i>Frontiers in Immunology</i> , 2017, 8, 655.	2.2	73
1474	Colonial Tube-Dwelling Ciliates Influence Methane Cycling and Microbial Diversity within Methane Seep Ecosystems. <i>Frontiers in Marine Science</i> , 2017, 3, .	1.2	17
1475	Evaluation of Filtration and DNA Extraction Methods for Environmental DNA Biodiversity Assessments across Multiple Trophic Levels. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	160
1476	Acidification Enhances Hybrid N ₂ O Production Associated with Aquatic Ammonia-Oxidizing Microorganisms. <i>Frontiers in Microbiology</i> , 2016, 7, 2104.	1.5	45

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1478	Linking Peripartal Dynamics of Ruminal Microbiota to Dietary Changes and Production Parameters. <i>Frontiers in Microbiology</i> , 2017, 7, 2143.	1.5	58
1479	Human Catestatin Alters Gut Microbiota Composition in Mice. <i>Frontiers in Microbiology</i> , 2016, 7, 2151.	1.5	37
1480	Geological and Geochemical Controls on Subsurface Microbial Life in the Samail Ophiolite, Oman. <i>Frontiers in Microbiology</i> , 2017, 8, 56.	1.5	126
1481	Predominance of Viable Spore-Forming Piezophilic Bacteria in High-Pressure Enrichment Cultures from ~1.5 to 2.4 km-Deep Coal-Bearing Sediments below the Ocean Floor. <i>Frontiers in Microbiology</i> , 2017, 8, 137.	1.5	30
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1483	Sulfur-Oxidizing Bacteria Mediate Microbial Community Succession and Element Cycling in Launched Marine Sediment. <i>Frontiers in Microbiology</i> , 2017, 8, 152.	1.5	32
1484	Changes in Metabolically Active Bacterial Community during Rumen Development, and Their Alteration by Rhubarb Root Powder Revealed by 16S rRNA Amplicon Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 159.	1.5	34
1485	Serpentinization-Influenced Groundwater Harbors Extremely Low Diversity Microbial Communities Adapted to High pH. <i>Frontiers in Microbiology</i> , 2017, 8, 308.	1.5	76
1486	Compositional Stability of the Bacterial Community in a Climate-Sensitive Sub-Arctic Peatland. <i>Frontiers in Microbiology</i> , 2017, 8, 317.	1.5	20
1487	Clustering of Subgingival Microbiota Reveals Microbial Disease Ecotypes Associated with Clinical Stages of Periodontitis in a Cross-Sectional Study. <i>Frontiers in Microbiology</i> , 2017, 08, 340.	1.5	36
1488	The Effect of Increased Loads of Dissolved Organic Matter on Estuarine Microbial Community Composition and Function. <i>Frontiers in Microbiology</i> , 2017, 8, 351.	1.5	119
1489	Temporal Variations in Cigarette Tobacco Bacterial Community Composition and Tobacco-Specific Nitrosamine Content Are Influenced by Brand and Storage Conditions. <i>Frontiers in Microbiology</i> , 2017, 08, 358.	1.5	45
1490	Lack of Evidence That Selenium-Yeast Improves Chicken Health and Modulates the Caecal Microbiota in the Context of Colonization by <i>Campylobacter jejuni</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 451.	1.5	24
1491	<i>Caenorhabditis elegans</i> as a Model for Microbiome Research. <i>Frontiers in Microbiology</i> , 2017, 8, 485.	1.5	177
1492	Inferring Microbial Interactions in the Gut of the Hong Kong Whipping Frog (<i>Polypedates</i>) Tj ETQq1 1 0.784314 rgBT _{1.5} /Overlock 10 Tf 50 37	1.5	37
1493	Protective Effect of Carvacrol against Gut Dysbiosis and <i>Clostridium difficile</i> Associated Disease in a Mouse Model. <i>Frontiers in Microbiology</i> , 2017, 8, 625.	1.5	18
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1496	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
1497	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
1498	Differences in Microbiota Membership along the Gastrointestinal Tract of Piglets and Their Differential Alterations Following an Early-Life Antibiotic Intervention. <i>Frontiers in Microbiology</i> , 2017, 8, 797.	1.5	103
1499	From Vineyard Soil to Wine Fermentation: Microbiome Approximations to Explain the "Terroir" Concept. <i>Frontiers in Microbiology</i> , 2017, 8, 821.	1.5	155
1500	Viral-Induced Mortality of Prokaryotes in a Tropical Monsoonal Estuary. <i>Frontiers in Microbiology</i> , 2017, 8, 895.	1.5	24
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1502	A Small Number of Low-abundance Bacteria Dominate Plant Species-specific Responses during Rhizosphere Colonization. <i>Frontiers in Microbiology</i> , 2017, 8, 975.	1.5	87
1503	Variation in Soil Microbial Community Structure Associated with Different Legume Species Is Greater than that Associated with Different Grass Species. <i>Frontiers in Microbiology</i> , 2017, 8, 1007.	1.5	62
1504	Cesarean or Vaginal Birth Does Not Impact the Longitudinal Development of the Gut Microbiome in a Cohort of Exclusively Preterm Infants. <i>Frontiers in Microbiology</i> , 2017, 8, 1008.	1.5	46
1505	Atribacteria from the Subseafloor Sedimentary Biosphere Disperse to the Hydrosphere through Submarine Mud Volcanoes. <i>Frontiers in Microbiology</i> , 2017, 8, 1135.	1.5	55
1506	Preparing the Gut with Antibiotics Enhances Gut Microbiota Reprogramming Efficiency by Promoting Xenomicrobiota Colonization. <i>Frontiers in Microbiology</i> , 2017, 8, 1208.	1.5	75
1507	Tufts-in-Phosphorylcholine Maintains Normal Gut Microbiota in Collagen Induced Arthritic Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 1222.	1.5	25
1508	Nutrient and Rainfall Additions Shift Phylogenetically Estimated Traits of Soil Microbial Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 1271.	1.5	25
1509	Effect of Nickel and Cobalt on Methanogenic Enrichment Cultures and Role of Biogenic Sulfide in Metal Toxicity Attenuation. <i>Frontiers in Microbiology</i> , 2017, 8, 1341.	1.5	30
1510	Wood Ash Induced pH Changes Strongly Affect Soil Bacterial Numbers and Community Composition. <i>Frontiers in Microbiology</i> , 2017, 8, 1400.	1.5	74
1511	Watershed Urbanization Linked to Differences in Stream Bacterial Community Composition. <i>Frontiers in Microbiology</i> , 2017, 8, 1452.	1.5	94
1512	Personalization of the Microbiota of Donor Human Milk with Mother's Own Milk. <i>Frontiers in Microbiology</i> , 2017, 8, 1470.	1.5	73

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1513	Long-term Fertilization Structures Bacterial and Archaeal Communities along Soil Depth Gradient in a Paddy Soil. <i>Frontiers in Microbiology</i> , 2017, 8, 1516.	1.5	72
1514	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
1515	Community Structure of Lithotrophically-Driven Hydrothermal Microbial Mats from the Mariana Arc and Back-Arc. <i>Frontiers in Microbiology</i> , 2017, 8, 1578.	1.5	32
1516	Microbial Carbonic Anhydrases in Biomimetic Carbon Sequestration for Mitigating Global Warming: Prospects and Perspectives. <i>Frontiers in Microbiology</i> , 2017, 8, 1615.	1.5	68
1517	Composted Cattle Manure Increases Microbial Activity and Soil Fertility More Than Composted Swine Manure in a Submerged Rice Paddy. <i>Frontiers in Microbiology</i> , 2017, 8, 1702.	1.5	134
1518	Enhancing Nitrate Removal from Freshwater Pond by Regulating Carbon/Nitrogen Ratio. <i>Frontiers in Microbiology</i> , 2017, 8, 1712.	1.5	29
1519	Patterns and Processes in Marine Microeukaryotic Community Biogeography from Xiamen Coastal Waters and Intertidal Sediments, Southeast China. <i>Frontiers in Microbiology</i> , 2017, 8, 1912.	1.5	108
1520	<i>Myriophyllum aquaticum</i> Constructed Wetland Effectively Removes Nitrogen in Swine Wastewater. <i>Frontiers in Microbiology</i> , 2017, 8, 1932.	1.5	44
1521	Insights into Microalga and Bacteria Interactions of Selected Phycosphere Biofilms Using Metagenomic, Transcriptomic, and Proteomic Approaches. <i>Frontiers in Microbiology</i> , 2017, 8, 1941.	1.5	97
1522	Diversity and Structure of Diazotrophic Communities in Mangrove Rhizosphere, Revealed by High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2032.	1.5	49
1523	Microbial Taxa Distribution Is Associated with Ecological Trophic Cascades along an Elevation Gradient. <i>Frontiers in Microbiology</i> , 2017, 8, 2071.	1.5	144
1524	A High Grain Diet Dynamically Shifted the Composition of Mucosa-Associated Microbiota and Induced Mucosal Injuries in the Colon of Sheep. <i>Frontiers in Microbiology</i> , 2017, 8, 2080.	1.5	62
1525	Stratified Bacterial and Archaeal Community in Mangrove and Intertidal Wetland Mudflats Revealed by High Throughput 16S rRNA Gene Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2148.	1.5	91
1526	Fungal Community Structure and As-Resistant Fungi in a Decommissioned Gold Mine Site. <i>Frontiers in Microbiology</i> , 2017, 8, 2202.	1.5	18
1527	Effect of Dietary Forage to Concentrate Ratios on Dynamic Profile Changes and Interactions of Ruminal Microbiota and Metabolites in Holstein Heifers. <i>Frontiers in Microbiology</i> , 2017, 8, 2206.	1.5	155
1528	Reduction of Salmonella Shedding by Sows during Gestation in Relation to Its Fecal Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 2219.	1.5	17
1529	Low Microbial Diversity and Abnormal Microbial Succession Is Associated with Necrotizing Enterocolitis in Preterm Infants. <i>Frontiers in Microbiology</i> , 2017, 8, 2243.	1.5	72
1530	Increased Denitrification Rates Associated with Shifts in Prokaryotic Community Composition Caused by Varying Hydrologic Connectivity. <i>Frontiers in Microbiology</i> , 2017, 8, 2304.	1.5	22

#	ARTICLE	IF	CITATIONS
1531	Antibiotic-Induced Alterations in Gut Microbiota Are Associated with Changes in Glucose Metabolism in Healthy Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 2306.	1.5	103
1532	Parallelized, Aerobic, Single Carbon-Source Enrichments from Different Natural Environments Contain Divergent Microbial Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 2321.	1.5	21
1533	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
1534	Fight Fungi with Fungi: Antifungal Properties of the Amphibian Mycobiome. <i>Frontiers in Microbiology</i> , 2017, 8, 2494.	1.5	56
1535	Differential Ecological Specificity of Protist and Bacterial Microbiomes across a Set of Termite Species. <i>Frontiers in Microbiology</i> , 2017, 8, 2518.	1.5	32
1536	Abundance and Diversity of Hydrogenotrophic Microorganisms in the Infant Gut before the Weaning Period Assessed by Denaturing Gradient Gel Electrophoresis and Quantitative PCR. <i>Frontiers in Nutrition</i> , 2017, 4, 29.	1.6	27
1537	Comparison of Oropharyngeal Microbiota from Children with Asthma and Cystic Fibrosis. <i>Mediators of Inflammation</i> , 2017, 2017, 1-10.	1.4	32
1538	Analysis of Microbial Diversity in Soil under Ginger Cultivation. <i>Scientifica</i> , 2017, 2017, 1-4.	0.6	8
1539	The mycobiome of the human urinary tract: potential roles for fungi in urology. <i>Annals of Translational Medicine</i> , 2017, 5, 31-31.	0.7	68
1540	Novel Primer Sets for Next Generation Sequencing-Based Analyses of Water Quality. <i>PLoS ONE</i> , 2017, 12, e0170008.	1.1	8
1541	Community-level physiological profiling analyses show potential to identify the copiotrophic bacteria present in soil environments. <i>PLoS ONE</i> , 2017, 12, e0171638.	1.1	66
1542	<i>Tuber indicum</i> shapes the microbial communities of ectomycorrhizosphere soil and ectomycorrhizae of an indigenous tree (<i>Pinus armandii</i>). <i>PLoS ONE</i> , 2017, 12, e0175720.	1.1	25
1543	Bacterial community and arsenic functional genes diversity in arsenic contaminated soils from different geographic locations. <i>PLoS ONE</i> , 2017, 12, e0176696.	1.1	40
1544	Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716.	1.1	107
1545	Characterization of the juvenile green turtle (<i>Chelonia mydas</i>) microbiome throughout an ontogenetic shift from pelagic to neritic habitats. <i>PLoS ONE</i> , 2017, 12, e0177642.	1.1	59
1546	Biodegradation of di-n-butyl phthalate by bacterial consortium LV-1 enriched from river sludge. <i>PLoS ONE</i> , 2017, 12, e0178213.	1.1	18
1547	Unraveling the environmental and anthropogenic drivers of bacterial community changes in the Estuary of Bilbao and its tributaries. <i>PLoS ONE</i> , 2017, 12, e0178755.	1.1	34
1548	Bacterial communities found in placental tissues are associated with severe chorioamnionitis and adverse birth outcomes. <i>PLoS ONE</i> , 2017, 12, e0180167.	1.1	97

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1549	Species-specific signatures of the microbiome from <i>Camponotus</i> and <i>Colobopsis</i> ants across developmental stages. <i>PLoS ONE</i> , 2017, 12, e0187461.	1.1	36
1550	Fungal communities in ancient peatlands developed from different periods in the Sanjiang Plain, China. <i>PLoS ONE</i> , 2017, 12, e0187575.	1.1	18
1551	Spatiotemporal analysis of microbial community dynamics during seasonal stratification events in a freshwater lake (Grand Lake, OK, USA). <i>PLoS ONE</i> , 2017, 12, e0177488.	1.1	47
1552	The Bacterial and Fungal Microbiota of Hyperaccumulator Plants. <i>Advances in Botanical Research</i> , 2017, 83, 43-86.	0.5	42
1553	Prevalence and extent of heteroresistance by next generation sequencing of multidrug-resistant tuberculosis. <i>PLoS ONE</i> , 2017, 12, e0176522.	1.1	51
1554	Randomized clinical trial to evaluate the effect of fecal microbiota transplant for initial <i>Clostridium difficile</i> infection in intestinal microbiome. <i>PLoS ONE</i> , 2017, 12, e0189768.	1.1	39
1555	The effects of CO ₂ and H ₂ on CO metabolism by pure and mixed microbial cultures. <i>Biotechnology for Biofuels</i> , 2017, 10, 220.	6.2	40
1556	Effect of vitamin A supplementation on gut microbiota in children with autism spectrum disorders - a pilot study. <i>BMC Microbiology</i> , 2017, 17, 204.	1.3	78
1557	Evaluation of prokaryotic diversity of five hot springs in Eritrea. <i>BMC Microbiology</i> , 2017, 17, 203.	1.3	39
1558	Monitoring clinical and microbiological evolution of a cystic fibrosis patient over 26 years: experience of a Brazilian CF Centre. <i>BMC Pulmonary Medicine</i> , 2017, 17, 100.	0.8	2
1559	Effect of acetic acid on ethanol production by <i>Zymomonas mobilis</i> mutant strains through continuous adaptation. <i>BMC Biotechnology</i> , 2017, 17, 63.	1.7	28
1560	Worse inflammatory profile in omnivores than in vegetarians associates with the gut microbiota composition. <i>Diabetology and Metabolic Syndrome</i> , 2017, 9, 62.	1.2	78
1561	Differences in the gut microbiota of dogs (<i>Canis lupus familiaris</i>) fed a natural diet or a commercial feed revealed by the Illumina MiSeq platform. <i>Gut Pathogens</i> , 2017, 9, 68.	1.6	86
1562	A novel ultra high-throughput 16S rRNA gene amplicon sequencing library preparation method for the Illumina HiSeq platform. <i>Microbiome</i> , 2017, 5, 68.	4.9	93
1563	Normal milk microbiome is reestablished following experimental infection with <i>Escherichia coli</i> independent of intramammary antibiotic treatment with a third-generation cephalosporin in bovines. <i>Microbiome</i> , 2017, 5, 74.	4.9	54
1564	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	4.9	138
1565	Blood as a route of transmission of uterine pathogens from the gut to the uterus in cows. <i>Microbiome</i> , 2017, 5, 109.	4.9	80
1566	Microbes and associated soluble and volatile chemicals on periodically wet household surfaces. <i>Microbiome</i> , 2017, 5, 128.	4.9	45

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1568	Microbial biodiversity assessment of the European Space Agency's ExoMars 2016 mission. <i>Microbiome</i> , 2017, 5, 143.	4.9	27
1569	The gut mycobiome of the Human Microbiome Project healthy cohort. <i>Microbiome</i> , 2017, 5, 153.	4.9	609
1570	The gut microbiota in larvae of the housefly <i>Musca domestica</i> and their horizontal transfer through feeding. <i>AMB Express</i> , 2017, 7, 147.	1.4	49
1571	Increasing corn distillers solubles alters the liquid fraction of the ruminal microbiome. <i>Journal of Animal Science</i> , 2017, 95, 3540-3551.	0.2	2
1572	Fungal Communities in Ancient Peatlands at Sanjiang Plain, China. <i>Fungal Genomics & Biology</i> , 2017, 07, .	0.4	2
1573	Fragmentation of Surface Adsorbed and Aligned DNA Molecules using Soft Lithography for Next-Generation Sequencing. <i>Journal of Biosensors & Bioelectronics</i> , 2017, 08, .	0.4	2
1574	Contrasting dynamics and environmental controls of dispersed bacteria along a hydrologic gradient. <i>Advances in Oceanography and Limnology</i> , 2017, 8, .	0.2	13
1575	Understory Dwarf Bamboo Affects Microbial Community Structures and Soil Properties in a <i>Betula ermanii</i> Forest in Northern Japan. <i>Microbes and Environments</i> , 2017, 32, 103-111.	0.7	5
1576	Sex-Specific Effects of Organophosphate Diazinon on the Gut Microbiome and Its Metabolic Functions. <i>Environmental Health Perspectives</i> , 2017, 125, 198-206.	2.8	96
1577	Postmortem succession of gut microbial communities in deceased human subjects. <i>PeerJ</i> , 2017, 5, e3437.	0.9	92
1578	Geochemistry and microbial community composition across a range of acid mine drainage impact and implications for the Neoproterozoic to Paleoproterozoic transition. <i>Journal of Geophysical Research: Biogeosciences</i> , 2017, 122, 1404-1422.	1.3	12
1579	Impact of Roadway Stormwater Runoff on Microbial Contamination in the Receiving Stream. <i>Journal of Environmental Quality</i> , 2017, 46, 1065-1071.	1.0	7
1580	Microbial communities in sediment from <i>Zostera marina</i> patches, but not the <i>Z. marina</i> leaf or root microbiomes, vary in relation to distance from patch edge. <i>PeerJ</i> , 2017, 5, e3246.	0.9	115
1581	Biofilm formation and potential for iron cycling in serpentinization-influenced groundwater of the Zambales and Coast Range ophiolites. <i>Extremophiles</i> , 2018, 22, 407-431.	0.9	9
1582	Comparison of the microbial community structure between inflamed and non-inflamed sites in patients with ulcerative colitis. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2018, 33, 1590-1597.	1.4	87
1583	Drought consistently alters the composition of soil fungal and bacterial communities in grasslands from two continents. <i>Global Change Biology</i> , 2018, 24, 2818-2827.	4.2	221
1584	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018, 8, 3669.	1.6	34

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1586	Acute and repeated exposure to social stress reduces gut microbiota diversity in Syrian hamsters. Behavioural Brain Research, 2018, 345, 39-48.	1.2	57
1587	<i>Mycoplasma</i>-related endobacteria within Mortierellomycotina fungi: diversity, distribution and functional insights into their lifestyle. ISME Journal, 2018, 12, 1743-1757.	4.4	48
1588	Microbial community structure of sea spray aerosols at three California beaches. FEMS Microbiology Ecology, 2018, 94, .	1.3	14
1589	Dog introduction alters the home dust microbiota. Indoor Air, 2018, 28, 539-547.	2.0	46
1590	Arbuscular mycorrhizal fungi in two vertical-flow wetlands constructed for heavy metal-contaminated wastewater bioremediation. Environmental Science and Pollution Research, 2018, 25, 12830-12840.	2.7	24
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1592	Spatial Organization of the Gastrointestinal Microbiota in Urban Canada Geese. Scientific Reports, 2018, 8, 3713.	1.6	23
1593	Draft genome of the protandrous Chinese black porgy, Acanthopagrus schlegelii. GigaScience, 2018, 7, 1-7.	3.3	70
1594	The divergence between fungal and bacterial communities in seasonal and spatial variations of wastewater treatment plants. Science of the Total Environment, 2018, 628-629, 969-978.	3.9	79
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1598	Estimating taxonâ€specific population dynamics in diverse microbial communities. Ecosphere, 2018, 9, e02090.	1.0	85
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1601	Gammaproteobacterial Diversity and Carbon Utilization in Response to Salinity in the Lakes on the Qinghaiâ€Tibetan Plateau. Geomicrobiology Journal, 2018, 35, 392-403.	1.0	19
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1605	Cycad-feeding insects share a core gut microbiome. Biological Journal of the Linnean Society, 2018, 123, 728-738.	0.7	23
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1609	Impact of gut colonization with butyrate producing microbiota on respiratory viral infection following allo-HCT. Blood, 2018, 131, blood-2018-01-828996.	0.6	155
1610	Stabilization of Cd-, Pb-, Cu- and Zn-contaminated calcareous agricultural soil using red mud: a field experiment. Environmental Geochemistry and Health, 2018, 40, 2143-2153.	1.8	34
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1615	Circular permutation profiling by deep sequencing libraries created using transposon mutagenesis. Nucleic Acids Research, 2018, 46, e76-e76.	6.5	23
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1626	Nematode-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
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1628	High diversity and variability in the bacterial microbiota of the coffee berry borer (<i>Coleoptera</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4.	1.4	15
1629	Changes in soil physicochemical properties and soil bacterial community in mulberry (<i>Morus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4.	1.2	67
1630	Host species effects on bacterial communities associated with the fruiting bodies of Tuber species from the Sichuan Province in Southwest China. <i>Mycological Progress</i> , 2018, 17, 833-840.	0.5	22
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1645	Delayed gut microbiota development in high-risk for asthma infants is temporarily modifiable by <i>Lactobacillus</i> supplementation. <i>Nature Communications</i> , 2018, 9, 707.	5.8	158
1646	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
1647	<i>Agrobacterium bohemicum</i> sp. nov. isolated from poppy seed wastes in central Bohemia. <i>Systematic and Applied Microbiology</i> , 2018, 41, 184-190.	1.2	14
1648	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
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1658	Screening and bioprospecting of anaerobic consortia for biohydrogen and volatile fatty acid production in a vinasse based medium through dark fermentation. <i>Process Biochemistry</i> , 2018, 67, 1-7.	1.8	38
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1665	Microbial Diversity of Hypersaline Sediments from Lake Lucero Playa in White Sands National Monument, New Mexico, USA. <i>Microbial Ecology</i> , 2018, 76, 404-418.	1.4	19
1666	Gut Microbial Diversity in Women With Polycystic Ovary Syndrome Correlates With Hyperandrogenism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 1502-1511.	1.8	224
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1668	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
1669	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
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1673	Bolus Weekly Vitamin D3 Supplementation Impacts Gut and Airway Microbiota in Adults With Cystic Fibrosis: A Double-Blind, Randomized, Placebo-Controlled Clinical Trial. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 564-574.	1.8	82
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1677	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
1678	Shifts in prokaryotic communities under forest and grassland within a tropical mosaic landscape. <i>Applied Soil Ecology</i> , 2018, 125, 156-161.	2.1	2
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1681	The nasal microbiome mirrors and potentially shapes olfactory function. <i>Scientific Reports</i> , 2018, 8, 1296.	1.6	76
1682	Effects of weight loss with a moderate-protein, high-fiber diet on body composition, voluntary physical activity, and fecal microbiota of obese cats. <i>American Journal of Veterinary Research</i> , 2018, 79, 181-190.	0.3	25
1683	Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig (<i>Sus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 T	0.8	63
1684	Investigating Fish Larvae-Microbe Interactions in the 21st Century: Old Questions Studied with New Tools. , 2018, , 1-35.		7
1685	Occurrence and Distribution of Urban Dust-Associated Bacterial Antibiotic Resistance in Northern China. <i>Environmental Science and Technology Letters</i> , 2018, 5, 50-55.	3.9	42
1686	Nonalcoholic fatty liver disease is associated with dysbiosis independent of body mass index and insulin resistance. <i>Scientific Reports</i> , 2018, 8, 1466.	1.6	196
1687	Shift in the subgingival microbiome following scaling and root planing in generalized aggressive periodontitis. <i>Journal of Clinical Periodontology</i> , 2018, 45, 440-452.	2.3	36
1688	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
1689	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
1690	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
1691	Associations between <i>Escherichia coli</i> O157 shedding and the faecal microbiota of dairy cows. <i>Journal of Applied Microbiology</i> , 2018, 124, 881-898.	1.4	15
1692	Nutrient content affects the turnover of fungal biomass in forest topsoil and the composition of associated microbial communities. <i>Soil Biology and Biochemistry</i> , 2018, 118, 187-198.	4.2	64

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1694	Changes in mouse gut bacterial community in response to different types of drinking water. <i>Water Research</i> , 2018, 132, 79-89.	5.3	47
1695	In vitro fermentation of <i>Clostridium speciosum</i> glucans stimulates the growth of the butyrogenic <i>Clostridium</i> cluster XIVa in a targeted way. <i>Carbohydrate Polymers</i> , 2018, 183, 219-229.	5.1	45
1696	Differential soil microbial community responses to the linkage of soil organic carbon fractions with respiration across land-use changes. <i>Forest Ecology and Management</i> , 2018, 409, 170-178.	1.4	119
1697	Changes in soil microbial community are linked to soil carbon fractions after afforestation. <i>European Journal of Soil Science</i> , 2018, 69, 370-379.	1.8	43
1698	The Microbial Community of Tardigrades: Environmental Influence and Species Specificity of Microbiome Structure and Composition. <i>Microbial Ecology</i> , 2018, 76, 467-481.	1.4	28
1699	Enrichment and characterization of a bacterial mixture capable of utilizing C-mannosyl tryptophan as a carbon source. <i>Glycoconjugate Journal</i> , 2018, 35, 165-176.	1.4	14
1700	Shifts in soil bacterial and archaeal communities during freeze-thaw cycles in a seasonal frozen marsh, Northeast China. <i>Science of the Total Environment</i> , 2018, 625, 782-791.	3.9	56
1701	Shifts in spinach microbial communities after chlorine washing and storage at compliant and abusive temperatures. <i>Food Microbiology</i> , 2018, 73, 73-84.	2.1	50
1702	Urban stream microbial communities show resistance to pharmaceutical exposure. <i>Ecosphere</i> , 2018, 9, e02041.	1.0	46
1703	Unravelling the Identity, Metabolic Potential and Global Biogeography of the Atmospheric Methane-Oxidizing Upland Soil Cluster 1. <i>Environmental Microbiology</i> , 2018, 20, 1016-1029.	1.8	103
1704	Investigation of probiotics in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2018, 24, 58-63.	1.4	112
1705	Nitrifiers activity and community characteristics under stress conditions in partial nitrification systems treating ammonium-rich wastewater. <i>Journal of Environmental Sciences</i> , 2018, 73, 1-8.	3.2	19
1706	Plant community and soil conditions individually affect soil microbial community assembly in experimental mesocosms. <i>Ecology and Evolution</i> , 2018, 8, 1196-1205.	0.8	31
1707	Shift of uterine microbiota associated with antibiotic treatment and cure of metritis in dairy cows. <i>Veterinary Microbiology</i> , 2018, 214, 132-139.	0.8	35
1708	Respiratory Syncytial Virus and Rhinovirus Bronchiolitis Are Associated With Distinct Metabolic Pathways. <i>Journal of Infectious Diseases</i> , 2018, 217, 1160-1169.	1.9	50
1709	The commensal microbiome is associated with anti-PD-1 efficacy in metastatic melanoma patients. <i>Science</i> , 2018, 359, 104-108.	6.0	2,027
1710	Greatest soil microbial diversity found in micro-habitats. <i>Soil Biology and Biochemistry</i> , 2018, 118, 217-226.	4.2	248

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1712	Nutrient dynamics and stream order influence microbial community patterns along a 2914 kilometer transect of the Mississippi River. <i>Limnology and Oceanography</i> , 2018, 63, 1837-1855.	1.6	48
1713	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	6.0	447
1714	SGLT2 inhibition via dapagliflozin improves generalized vascular dysfunction and alters the gut microbiota in type 2 diabetic mice. <i>Cardiovascular Diabetology</i> , 2018, 17, 62.	2.7	178
1715	Walnut Consumption Alters the Gastrointestinal Microbiota, Microbially Derived Secondary Bile Acids, and Health Markers in Healthy Adults: A Randomized Controlled Trial. <i>Journal of Nutrition</i> , 2018, 148, 861-867.	1.3	118
1716	Marine-influenced microbial communities inhabit terrestrial hot springs on a remote island volcano. <i>Extremophiles</i> , 2018, 22, 687-698.	0.9	10
1717	Effect of hydraulic retention time on microbial community structure in wastewater treatment electrobioreactors. <i>MicrobiologyOpen</i> , 2018, 7, e00590.	1.2	16
1718	The effects of sequencing platforms on phylogenetic resolution in 16S rRNA gene profiling of human feces. <i>Scientific Data</i> , 2018, 5, 180068.	2.4	22
1719	Regional feature extraction of various fishes based on chemical and microbial variable selection using machine learning. <i>Analytical Methods</i> , 2018, 10, 2160-2168.	1.3	11
1720	Continuous application of inorganic and organic fertilizers over 47 years in paddy soil alters the bacterial community structure and its influence on rice production. <i>Agriculture, Ecosystems and Environment</i> , 2018, 262, 65-75.	2.5	120
1721	High-rate anaerobic treatment system for solid/lipid-rich wastewater using anaerobic baffled reactor with scum recovery. <i>Bioresource Technology</i> , 2018, 263, 145-152.	4.8	33
1722	Differential susceptibility of whitefly-associated bacteria to antibiotic as revealed by metagenomics analysis. <i>Infection, Genetics and Evolution</i> , 2018, 63, 24-29.	1.0	11
1723	Contrasting responses of bacterial and fungal communities to aggregate-size fractions and long-term fertilizations in soils of northeastern China. <i>Science of the Total Environment</i> , 2018, 635, 784-792.	3.9	80
1724	Semi-passive in-situ pilot scale bioreactor successfully removed sulfate and metals from mine impacted water under subarctic climatic conditions. <i>Water Research</i> , 2018, 140, 268-279.	5.3	36
1725	Peyer's patch-specific <i>Lactobacillus reuteri</i> strains increase extracellular microbial DNA and antimicrobial peptide expression in the mouse small intestine. <i>Food and Function</i> , 2018, 9, 2989-2997.	2.1	4
1726	Accurate O ₂ delivery enabled benzene biodegradation through aerobic activation followed by denitrification-coupled mineralization. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1988-1999.	1.7	30
1727	Bacterial population dynamics in recycled mushroom compost leachate. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5335-5342.	1.7	9
1728	Long-Term Coffee Monoculture Alters Soil Chemical Properties and Microbial Communities. <i>Scientific Reports</i> , 2018, 8, 6116.	1.6	102

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1729	Urea hydrolysis by gut bacteria in a hibernating frog: evidence for urea-nitrogen recycling in Amphibia. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180241.	1.2	38
1730	Elucidation of bacterial species during childhood diarrhea through 16S rRNA Illumina Miseq approach. <i>Meta Gene</i> , 2018, 16, 234-240.	0.3	3
1731	Biocrust-forming mosses mitigate the impact of aridity on soil microbial communities in drylands: observational evidence from three continents. <i>New Phytologist</i> , 2018, 220, 824-835.	3.5	46
1732	Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats. <i>Environmental Science and Pollution Research</i> , 2018, 25, 14743-14751.	2.7	3
1733	A Lachnospiraceae-dominated bacterial signature in the fecal microbiota of HIV-infected individuals from Colombia, South America. <i>Scientific Reports</i> , 2018, 8, 4479.	1.6	34
1734	Long-term fire management history affects N-fertilization sensitivity, but not seasonality, of grassland soil microbial communities. <i>Soil Biology and Biochemistry</i> , 2018, 121, 231-239.	4.2	29
1735	Similar Batch Process Monitoring With Orthogonal Subspace Alignment. <i>IEEE Transactions on Industrial Electronics</i> , 2018, 65, 8173-8183.	5.2	14
1736	Phylum-Level Archaeal Distributions in the Sediments of Chinese Lakes With a Large Range of Salinity. <i>Geomicrobiology Journal</i> , 2018, 35, 404-410.	1.0	14
1737	Structural Variation in the Bacterial Community Associated with Airborne Particulate Matter in Beijing, China, during Hazy and Nonhazy Days. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	64
1738	Effect of exogenous inoculants on enhancing oil recovery and indigenous bacterial community dynamics in long-term field pilot of low permeability reservoir. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 53.	1.7	13
1739	Using mock communities of arbuscular mycorrhizal fungi to evaluate fidelity associated with Illumina sequencing. <i>Fungal Ecology</i> , 2018, 33, 52-64.	0.7	33
1740	Degradation shaped bacterial and archaeal communities with predictable taxa and their association patterns in Zoige wetland at Tibet plateau. <i>Scientific Reports</i> , 2018, 8, 3884.	1.6	42
1741	The Pancreatic Cancer Microbiome Promotes Oncogenesis by Induction of Innate and Adaptive Immune Suppression. <i>Cancer Discovery</i> , 2018, 8, 403-416.	7.7	834
1742	The nasal microbiome in patients with chronic rhinosinusitis: Analyzing the effects of atopy and bacterial functional pathways in 111 patients. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 287-290.e4.	1.5	55
1743	Salinity shifts in marine sediment: Importance of number of fluctuation rather than their intensities on bacterial denitrifying community. <i>Marine Pollution Bulletin</i> , 2018, 130, 76-83.	2.3	13
1744	Reproducibility and repeatability of six high-throughput 16S rDNA sequencing protocols for microbiota profiling. <i>Journal of Microbiological Methods</i> , 2018, 147, 76-86.	0.7	30
1745	Lower dietary concentrate level increases bacterial diversity in the rumen of <i>Cervus elaphus</i> <i>yarkandensis</i> . <i>Canadian Journal of Microbiology</i> , 2018, 64, 501-509.	0.8	10
1746	â€˜Cyclical Biasâ€™™ in Microbiome Researchâ€˜Revealed byâ€™A Portable Germ-Free Housing System Usingâ€™Nested Isolation. <i>Scientific Reports</i> , 2018, 8, 3801.	1.6	40

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1748	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
1749	Galactooligosaccharide and a combination of yeast and β -glucan supplements enhance growth and improve intestinal condition in striped catfish <i>Pangasianodon hypophthalmus</i> fed soybean meal diets. <i>Fisheries Science</i> , 2018, 84, 523-533.	0.7	10
1750	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
1751	Influence of fecal collection conditions and 16S rRNA gene sequencing at two centers on human gut microbiota analysis. <i>Scientific Reports</i> , 2018, 8, 4386.	1.6	46
1752	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
1753	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018, 3, .	1.7	123
1754	Gut microbial communities of American pikas (<i>Ochotona princeps</i>): Evidence for phyllosymbiosis and adaptations to novel diets. <i>Journal of Animal Ecology</i> , 2018, 87, 323-330.	1.3	85
1755	Effects of residual organics in municipal wastewater on hydrogenotrophic denitrifying microbial communities. <i>Journal of Environmental Sciences</i> , 2018, 65, 262-270.	3.2	94
1756	First evaluation of the microbiome of built cultural heritage by using the Ion Torrent next generation sequencing platform. <i>International Biodeterioration and Biodegradation</i> , 2018, 131, 11-18.	1.9	61
1757	Enrichments of methanotrophic heterotrophic cultures with high poly- β -hydroxybutyrate (PHB) accumulation capacities. <i>Journal of Environmental Sciences</i> , 2018, 65, 133-143.	3.2	28
1758	Assessment of bacterial community composition, methanotrophic and nitrogen-cycling bacteria in three soils with different biochar application rates. <i>Journal of Soils and Sediments</i> , 2018, 18, 148-158.	1.5	70
1759	Effects of coexisting BDE-47 on the migration and biodegradation of BDE-99 in river-based aquifer media recharged with reclaimed water. <i>Environmental Science and Pollution Research</i> , 2018, 25, 5140-5153.	2.7	11
1760	The microbiota of diapause: How host-microbe associations are formed after dormancy in an aquatic crustacean. <i>Journal of Animal Ecology</i> , 2018, 87, 400-413.	1.3	40
1761	A nitrogen removal system to limit water exchange for recirculating freshwater aquarium using DHS-USB reactor. <i>Environmental Technology (United Kingdom)</i> , 2018, 39, 1577-1585.	1.2	15
1762	Gastrointestinal Colonization of <i>Candida Albicans</i> Increases Serum β -D-Glucan, without Candidemia, and Worsens Cecal Ligation and Puncture Sepsis in Murine Model. <i>Shock</i> , 2018, 49, 62-70.	1.0	50
1763	Using Illumina-Based Sequence Analysis to Guide Probiotic Candidate Selection and Isolation. <i>Probiotics and Antimicrobial Proteins</i> , 2018, 10, 478-484.	1.9	3
1764	Metagenomic Analysis of Subtidal Sediments from Polar and Subpolar Coastal Environments Highlights the Relevance of Anaerobic Hydrocarbon Degradation Processes. <i>Microbial Ecology</i> , 2018, 75, 123-139.	1.4	30

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1766	Microbial Community Structure and Function Decoupling Across a Phosphorus Gradient in Streams. <i>Microbial Ecology</i> , 2018, 75, 64-73.	1.4	33
1767	Hyphospheric impacts of earthworms and arbuscular mycorrhizal fungus on soil bacterial community to promote oxytetracycline degradation. <i>Journal of Hazardous Materials</i> , 2018, 341, 346-354.	6.5	49
1768	Unravelling biocomplexity of electroactive biofilms for producing hydrogen from biomass. <i>Microbial Biotechnology</i> , 2018, 11, 84-97.	2.0	26
1769	Microbial community structures and functions of wastewater treatment systems in plateau and cold regions. <i>Bioresource Technology</i> , 2018, 249, 684-693.	4.8	178
1770	The taxonomic composition of the donor intestinal microbiota is a major factor influencing the efficacy of faecal microbiota transplantation in therapy refractory ulcerative colitis. <i>Alimentary Pharmacology and Therapeutics</i> , 2018, 47, 67-77.	1.9	154
1771	Estimating Population Turnover Rates by Relative Quantification Methods Reveals Microbial Dynamics in Marine Sediment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	31
1772	Impact of Age-Related Mitochondrial Dysfunction and Exercise on Intestinal Microbiota Composition. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 571-578.	1.7	28
1773	Co-selection of antibiotic resistance via copper shock loading on bacteria from a drinking water bio-filter. <i>Environmental Pollution</i> , 2018, 233, 132-141.	3.7	52
1774	Bacterial communities in soil become sensitive to drought under intensive grazing. <i>Science of the Total Environment</i> , 2018, 618, 1638-1646.	3.9	33
1775	The organophosphate malathion disturbs gut microbiome development and the quorum-Sensing system. <i>Toxicology Letters</i> , 2018, 283, 52-57.	0.4	28
1776	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018, 359, 97-103.	6.0	3,126
1777	Microbial community differentiation between active and inactive sulfide chimneys of the Kolumbo submarine volcano, Hellenic Volcanic Arc. <i>Extremophiles</i> , 2018, 22, 13-27.	0.9	21
1778	Mediation of effects of biofiltration on bacterial regrowth, <i>Legionella pneumophila</i> , and the microbial community structure under hot water plumbing conditions. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 183-194.	1.2	12
1779	Wastewater treatment plant effluent introduces recoverable shifts in microbial community composition in receiving streams. <i>Science of the Total Environment</i> , 2018, 613-614, 1104-1116.	3.9	67
1780	Microbial sequence typing in the genomic era. <i>Infection, Genetics and Evolution</i> , 2018, 63, 346-359.	1.0	50
1781	Priority effects can persist across floral generations in nectar microbial metacommunities. <i>Oikos</i> , 2018, 127, 345-352.	1.2	68
1782	Community Structure of Active Aerobic Methanotrophs in Red Mangrove (<i>Kandelia obovata</i>) Soils Under Different Frequency of Tides. <i>Microbial Ecology</i> , 2018, 75, 761-770.	1.4	30

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1783	In Vitro Response of Rumen Microbiota to the Antimethanogenic Red Macroalga <i>Asparagopsis taxiformis</i> . <i>Microbial Ecology</i> , 2018, 75, 811-818.	1.4	42
1784	Do host-associated gut microbiota mediate the effect of an herbicide on disease risk in frogs?. <i>Journal of Animal Ecology</i> , 2018, 87, 489-499.	1.3	45
1785	Impact of carbon monoxide partial pressures on methanogenesis and medium chain fatty acids production during ethanol fermentation. <i>Biotechnology and Bioengineering</i> , 2018, 115, 341-350.	1.7	33
1786	Application of compost and clay under water-stressed conditions influences functional diversity of rhizosphere bacteria. <i>Biology and Fertility of Soils</i> , 2018, 54, 55-70.	2.3	53
1787	Transmission of a common intestinal neoplasm in zebrafish by cohabitation. <i>Journal of Fish Diseases</i> , 2018, 41, 569-579.	0.9	24
1788	Vertical distribution of archaeal communities associated with anaerobic degradation of pentabromodiphenyl ether (BDE-99) in river-based groundwater recharge with reclaimed water. <i>Environmental Science and Pollution Research</i> , 2018, 25, 5154-5163.	2.7	4
1789	Soil fungal abundance and plant functional traits drive fertile island formation in global drylands. <i>Journal of Ecology</i> , 2018, 106, 242-253.	1.9	123
1790	A comparative study of composting the solid fraction of dairy manure with or without bulking material: Performance and microbial community dynamics. <i>Bioresource Technology</i> , 2018, 247, 443-452.	4.8	135
1791	Effect of hydraulic retention time on microbial community in biochemical passive reactors during treatment of acid mine drainage. <i>Bioresource Technology</i> , 2018, 247, 624-632.	4.8	46
1792	Biodiversity of soil bacteria exposed to sub-lethal concentrations of phosphonium-based ionic liquids: Effects of toxicity and biodegradation. <i>Ecotoxicology and Environmental Safety</i> , 2018, 147, 157-164.	2.9	37
1793	Fe(III) Reducing Microorganisms from Iron Ore Caves Demonstrate Fermentative Fe(III) Reduction and Promote Cave Formation. <i>Geomicrobiology Journal</i> , 2018, 35, 311-322.	1.0	36
1794	The Influence of Oyster Farming on Sediment Bacterial Communities. <i>Estuaries and Coasts</i> , 2018, 41, 800-814.	1.0	15
1795	Role of earthworms' mucus in vermicomposting system: Biodegradation tests based on humification and microbial activity. <i>Science of the Total Environment</i> , 2018, 610-611, 703-708.	3.9	75
1796	Functional redundancy ensures performance robustness in 3-stage PHA-producing mixed cultures under variable feed operation. <i>New Biotechnology</i> , 2018, 40, 207-217.	2.4	28
1797	Biochar and biomass organic amendments shaped different dominance of lithoautotrophs and organoheterotrophs in microbial communities colonizing neutral copper(Cu)-molybdenum(Mo)-gold(Au) tailings. <i>Geoderma</i> , 2018, 309, 100-110.	2.3	20
1798	Long and short term effects of solarization on soil microbiome and agricultural production. <i>Applied Soil Ecology</i> , 2018, 124, 54-61.	2.1	26
1799	Gut microbes limit growth in house sparrow nestlings (<i>Passer domesticus</i>) but not through limitations in digestive capacity. <i>Integrative Zoology</i> , 2018, 13, 139-151.	1.3	42
1800	Organic amendments shift the phosphorus-correlated microbial co-occurrence pattern in the peanut rhizosphere network during long-term fertilization regimes. <i>Applied Soil Ecology</i> , 2018, 124, 229-239.	2.1	48

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1802	Microbial communities exhibit host species distinguishability and phyllosymbiosis along the length of the gastrointestinal tract. <i>Molecular Ecology</i> , 2018, 27, 1874-1883.	2.0	73
1803	Sampling, Extraction, and High-Throughput Sequencing Methods for Environmental Microbial and Viral Communities. <i>Methods in Molecular Biology</i> , 2018, 1712, 163-173.	0.4	2
1804	Tales from the tomb: the microbial ecology of exposed rock surfaces. <i>Environmental Microbiology</i> , 2018, 20, 958-970.	1.8	63
1805	Identifying protist consumers of photosynthetic picoeukaryotes in the surface ocean using stable isotope probing. <i>Environmental Microbiology</i> , 2018, 20, 815-827.	1.8	51
1806	A Microbial Analysis Primer for Biogeochemists. , 2018, , 599-609.		3
1807	Frankia Diversity in Host Plant Root Nodules Is Independent of Abundance or Relative Diversity of Frankia Populations in Corresponding Rhizosphere Soils. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	13
1808	Next Generation Sequencing. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	2
1809	Effect of microbially mediated iron mineral transformation on temporal variation of arsenic in the Pleistocene aquifers of the central Yangtze River basin. <i>Science of the Total Environment</i> , 2018, 619-620, 1247-1258.	3.9	65
1810	Quality of Irrigation Water Affects Soil Functionality and Bacterial Community Stability in Response to Heat Disturbance. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	19
1811	Social behaviour and gut microbiota in red-bellied lemurs (<i>Eulemur rubriventer</i>): In search of the role of immunity in the evolution of sociality. <i>Journal of Animal Ecology</i> , 2018, 87, 388-399.	1.3	57
1812	Composition of gut microbiota in obese and normal-weight Mexican school-age children and its association with metabolic traits. <i>Pediatric Obesity</i> , 2018, 13, 381-388.	1.4	69
1813	Gut microbiota composition is associated with environmental landscape in honey bees. <i>Ecology and Evolution</i> , 2018, 8, 441-451.	0.8	106
1814	Influence of the intestinal microbiota on the immunogenicity of oral rotavirus vaccine given to infants in south India. <i>Vaccine</i> , 2018, 36, 264-272.	1.7	88
1815	Active migration is associated with specific and consistent changes to gut microbiota in <i>Calidris</i> shorebirds. <i>Journal of Animal Ecology</i> , 2018, 87, 428-437.	1.3	73
1816	Bacterial, archaeal, and fungal community responses to acid mine drainage-laden pollution in a rice paddy soil ecosystem. <i>Science of the Total Environment</i> , 2018, 616-617, 107-116.	3.9	93
1817	Physicochemical characteristics of stored cattle manure affect methane emissions by inducing divergence of methanogens that have different interactions with bacteria. <i>Agriculture, Ecosystems and Environment</i> , 2018, 253, 38-47.	2.5	16
1818	Anaerobic co-digestion of pig manure and food waste; effects on digestate biosafety, dewaterability, and microbial community dynamics. <i>Waste Management</i> , 2018, 71, 532-541.	3.7	72

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1819	Common Cutaneous Bacteria Isolated from Snakes Inhibit Growth of <i>Ophidiomyces ophiodiicola</i> . <i>EcoHealth</i> , 2018, 15, 109-120.	0.9	22
1820	Detecting macroecological patterns in bacterial communities across independent studies of global soils. <i>Nature Microbiology</i> , 2018, 3, 189-196.	5.9	136
1821	Contrasting effects of inorganic and organic fertilisation regimes on shifts in Fe redox bacterial communities in red soils. <i>Soil Biology and Biochemistry</i> , 2018, 117, 56-67.	4.2	48
1822	Differences in bacterial composition between menâ€™s and womenâ€™s restrooms and other common areas within a public building. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 551-561.	0.7	9
1823	Exposure to predicted precipitation patterns decreases population size and alters community structure of cyanobacteria in biological soil crusts from the Chihuahuan Desert. <i>Environmental Microbiology</i> , 2018, 20, 259-269.	1.8	83
1824	Sympatric kelp species share a large portion of their surface bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 658-670.	1.8	65
1825	Heterogeneity of methane seep biomes in the Northeast Pacific. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 150, 195-209.	0.6	17
1826	Exposure to the fungicide propamocarb causes gut microbiota dysbiosis and metabolic disorder in mice. <i>Environmental Pollution</i> , 2018, 237, 775-783.	3.7	71
1827	Characterization of microbial community in high-pressure treated oysters by high-throughput sequencing technology. <i>Innovative Food Science and Emerging Technologies</i> , 2018, 45, 241-248.	2.7	36
1828	Influence of soil bacteria and carbonic anhydrase on karstification intensity and regulatory factors in a typical karst area. <i>Geoderma</i> , 2018, 313, 17-24.	2.3	4
1829	Treatment impacts on temporal microbial community dynamics during phytostabilization of acid-generating mine tailings in semiarid regions. <i>Science of the Total Environment</i> , 2018, 618, 357-368.	3.9	32
1830	Effects of biochar on CH ₄ emission with straw application on paddy soil. <i>Journal of Soils and Sediments</i> , 2018, 18, 599-609.	1.5	40
1831	PCB dechlorination hotspots and reductive dehalogenase genes in sediments from a contaminated wastewater lagoon. <i>Environmental Science and Pollution Research</i> , 2018, 25, 16376-16388.	2.7	27
1832	Differential responses of soil microbial biomass, diversity, and compositions to altitudinal gradients depend on plant and soil characteristics. <i>Science of the Total Environment</i> , 2018, 610-611, 750-758.	3.9	205
1833	The TLR9 agonist MGN1703 triggers a potent type I interferon response in the sigmoid colon. <i>Mucosal Immunology</i> , 2018, 11, 449-461.	2.7	31
1834	Diversity and community structure of marine microbes around the Benham Rise underwater plateau, northeastern Philippines. <i>PeerJ</i> , 2018, 6, e4781.	0.9	19
1835	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. <i>PeerJ</i> , 2018, 6, e6075.	0.9	64
1836	Active Ooid Growth Driven By Sediment Transport in a High-Energy Shoal, Little Ambergris Cay, Turks and Caicos Islands. <i>Journal of Sedimentary Research</i> , 2018, 88, 1132-1151.	0.8	43

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1838	Microbial and Small Eukaryotes Associated With Reefs in the Upper Gulf of Thailand. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	8
1839	Microbial processes in the weathering crust aquifer of a temperate glacier. <i>Cryosphere</i> , 2018, 12, 3653-3669.	1.5	17
1840	Witchesâ€™ broom resistant genotype CCN51 shows greater diversity of symbiont bacteria in its phylloplane than susceptible genotype catongo. <i>BMC Microbiology</i> , 2018, 18, 194.	1.3	9
1841	Spatial and Seasonal Variability of Reef Bacterial Communities in the Upper Gulf of Thailand. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	23
1842	Effects of tobacco smoke and electronic cigarette vapor exposure on the oral and gut microbiota in humans: a pilot study. <i>PeerJ</i> , 2018, 6, e4693.	0.9	84
1843	Minimal Influence of Extracellular DNA on Molecular Surveys of Marine Sedimentary Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 2969.	1.5	57
1844	Effects of acute exposures of 2,4,6-trinitrotoluene and inorganic lead on the fecal microbiome of the green anole (<i>Anolis carolinensis</i>). <i>PLoS ONE</i> , 2018, 13, e0208281.	1.1	8
1845	Heterogeneity of Microbial Communities on Deep-Sea Ferromanganese Crusts in the Takuyo-Daigo Seamount. <i>Microbes and Environments</i> , 2018, 33, 366-377.	0.7	18
1846	Traits of Exogenous Species and Indigenous Community Contribute to the Species Colonization and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 3087.	1.5	9
1847	Composition of Rumen Bacterial Community in Dairy Cows With Different Levels of Somatic Cell Counts. <i>Frontiers in Microbiology</i> , 2018, 9, 3217.	1.5	39
1848	Culture-independent Profiling of the Fecal Microbiome to Identify Microbial Species Associated with a Diarrheal Outbreak in Immunocompromised Mice. <i>Comparative Medicine</i> , 2018, 68, 261-268.	0.4	6
1849	An adaptive microbiome \pm -diversity-based association analysis method. <i>Scientific Reports</i> , 2018, 8, 18026.	1.6	34
1850	Chalcopyrite bioleaching of an <i>in situ</i> leaching system by introducing different functional oxidizers. <i>RSC Advances</i> , 2018, 8, 37040-37049.	1.7	12
1851	Biofilm diversity, structure and matrix seasonality in a full-scale cooling tower. <i>Biofouling</i> , 2018, 34, 1093-1109.	0.8	3
1852	Run-to-Run Sequencing Variation Can Introduce Taxon-Specific Bias in the Evaluation of Fungal Microbiomes. <i>Phytobiomes Journal</i> , 2018, 2, 165-170.	1.4	13
1853	Transfer of Qualitative and Quantitative Knowledge for Similar Batch Process Monitoring. <i>IEEE Access</i> , 2018, 6, 73856-73870.	2.6	8
1855	Evaluation of Microbial Communities Associated With the Liquid and Solid Phases of the Rumen of Cattle Offered a Diet of Perennial Ryegrass or White Clover. <i>Frontiers in Microbiology</i> , 2018, 9, 2389.	1.5	27

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1857	Butyrate Producers as Potential Next-Generation Probiotics: Safety Assessment of the Administration of <i>Butyricoccus pullicaecorum</i> to Healthy Volunteers. <i>MSystems</i> , 2018, 3, .	1.7	99
1858	Cervicovaginal Fungi and Bacteria Associated With Cervical Intraepithelial Neoplasia and High-Risk Human Papillomavirus Infections in a Hispanic Population. <i>Frontiers in Microbiology</i> , 2018, 9, 2533.	1.5	67
1859	Microbial Community Changes in a Chlorinated Solvents Polluted Aquifer Over the Field Scale Treatment With Poly-3-Hydroxybutyrate as Amendment. <i>Frontiers in Microbiology</i> , 2018, 9, 1664.	1.5	31
1860	Fecal microbiota transplantation for refractory immune checkpoint inhibitor-associated colitis. <i>Nature Medicine</i> , 2018, 24, 1804-1808.	15.2	521
1861	Microbiomes and chemical components of feed water and membrane-attached biofilm in reverse osmosis system to treat membrane bioreactor effluents. <i>Scientific Reports</i> , 2018, 8, 16805.	1.6	12
1862	Gut microbiome transition across a lifestyle gradient in Himalaya. <i>PLoS Biology</i> , 2018, 16, e2005396.	2.6	128
1863	Human milk oligosaccharides, milk microbiome and infant gut microbiome modulate neonatal rotavirus infection. <i>Nature Communications</i> , 2018, 9, 5010.	5.8	130
1864	Interpersonal Variations in Gut Microbiota Profiles Supersedes the Effects of Differing Fecal Storage Conditions. <i>Scientific Reports</i> , 2018, 8, 17367.	1.6	46
1865	Demystifying Dysbiosis: Can the Gut Microbiome Promote Oral Tolerance Over IgE-mediated Food Allergy?. <i>Current Pediatric Reviews</i> , 2018, 14, 156-163.	0.4	22
1866	Island Biogeography of Cryoconite Hole Bacteria in Antarctica's Taylor Valley and Around the World. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	29
1867	NanoAmpli-Seq: a workflow for amplicon sequencing for mixed microbial communities on the nanopore sequencing platform. <i>GigaScience</i> , 2018, 7, .	3.3	85
1868	Diazotrophs and N ₂ -Fixation Associated With Particles in Coastal Estuarine Waters. <i>Frontiers in Microbiology</i> , 2018, 9, 2759.	1.5	36
1869	Photoperiod and Soil Muniton Constituent Effects on Phytoaccumulation and Rhizosphere Interactions in Boreal Vegetation. <i>Water, Air, and Soil Pollution</i> , 2018, 229, 1.	1.1	5
1870	Coral-associated bacteria demonstrate phyllosymbiosis and cophylogeny. <i>Nature Communications</i> , 2018, 9, 4921.	5.8	264
1871	Comparative Microbiome Signatures and Short-Chain Fatty Acids in Mouse, Rat, Non-human Primate, and Human Feces. <i>Frontiers in Microbiology</i> , 2018, 9, 2897.	1.5	170
1872	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. <i>MSystems</i> , 2018, 3, .	1.7	56
1873	Dynamic linear models guide design and analysis of microbiota studies within artificial human guts. <i>Microbiome</i> , 2018, 6, 202.	4.9	54

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1875	Terminal restriction fragment length polymorphism is an "old school" reliable technique for swift microbial community screening in anaerobic digestion. <i>Scientific Reports</i> , 2018, 8, 16818.	1.6	48
1876	Impact of DNA extraction method and targeted 16S-rRNA hypervariable region on oral microbiota profiling. <i>Scientific Reports</i> , 2018, 8, 16321.	1.6	126
1877	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018, 3, .	1.7	58
1878	In situ visualisation of the abundant Chloroflexi populations in full-scale anaerobic digesters and the fate of immigrating species. <i>PLoS ONE</i> , 2018, 13, e0206255.	1.1	37
1879	Low Salivary Amylase Gene (AMY1) Copy Number Is Associated with Obesity and Gut Prevotella Abundance in Mexican Children and Adults. <i>Nutrients</i> , 2018, 10, 1607.	1.7	36
1880	Role of gut microbiota in intestinal wound healing and barrier function. <i>Tissue Barriers</i> , 2018, 6, 1539595.	1.6	94
1881	Specific Effect of Trace Metals on Marine Heterotrophic Microbial Activity and Diversity: Key Role of Iron and Zinc and Hydrocarbon-Degrading Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 3190.	1.5	15
1882	Assessment of Bioleaching Microbial Community Structure and Function Based on Next-Generation Sequencing Technologies. <i>Minerals (Basel, Switzerland)</i> , 2018, 8, 596.	0.8	8
1883	Bacterial diversity and community in Qula from the Qinghai "Tibetan Plateau in China. <i>PeerJ</i> , 2018, 6, e6044.	0.9	22
1884	Studying safe storage time of orange peel (<i>Citrus reticulata</i>) using high-throughput sequencing and conventional pure culture. <i>Food Science and Nutrition</i> , 2018, 6, 2545-2552.	1.5	6
1885	Formal description of sequence-based voucherless Fungi: promises and pitfalls, and how to resolve them. <i>IMA Fungus</i> , 2018, 9, 143-165.	1.7	42
1886	Variations of Bacterial Community Composition and Functions in an Estuary Reservoir during Spring and Summer Alternation. <i>Toxins</i> , 2018, 10, 315.	1.5	6
1887	Absolute Configurations of Naturally Occurring [5]- and [3]-Ladderanoic Acids: Isolation, Chiroptical Spectroscopy, and Crystallography. <i>Journal of Natural Products</i> , 2018, 81, 2654-2666.	1.5	8
1888	Microbial community diversity of Jinghong laying hens at peak production based on 16S rRNA sequencing. <i>Journal of Applied Animal Research</i> , 2018, 46, 1430-1436.	0.4	6
1889	Phosphorus-mineralizing Communities Reflect Nutrient-Rich Characteristics in Japanese Arable Andisols. <i>Microbes and Environments</i> , 2018, 33, 282-289.	0.7	17
1890	A Phylogeny-Regularized Sparse Regression Model for Predictive Modeling of Microbial Community Data. <i>Frontiers in Microbiology</i> , 2018, 9, 3112.	1.5	20
1891	Both the intratumoral immune and microbial microenvironment are linked to recurrence in human colon cancer: results from a prospective, multicenter nodal ultrastaging trial. <i>Oncotarget</i> , 2018, 9, 23564-23576.	0.8	7

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1893	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , 2018, 9, 5353.	5.8	48
1894	Microbial subnetworks related to short-term diel O ₂ fluxes within geochemically distinct freshwater wetlands. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	2
1895	Scaling up <sc>DNA</sc> metabarcoding for freshwater macrozoobenthos monitoring. <i>Freshwater Biology</i> , 2019, 64, 380-387.	1.2	76
1896	Diet, physical activity and screen time but not body mass index are associated with the gut microbiome of a diverse cohort of college students living in university housing: a cross-sectional study. <i>BMC Microbiology</i> , 2018, 18, 210.	1.3	51
1897	An alternative storage method for characterization of the intestinal microbiota through next generation sequencing. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2018, 60, e77.	0.5	8
1898	Deep-sea anthropogenic macrodebris harbours rich and diverse communities of bacteria and archaea. <i>PLoS ONE</i> , 2018, 13, e0206220.	1.1	38
1899	Effects of Gut Bacteria Depletion and High-Na ⁺ and Low-K ⁺ Intake on Circulating Levels of Biogenic Amines. <i>Molecular Nutrition and Food Research</i> , 2018, 63, 1801184.	1.5	12
1900	Gut microbiota diversity across ethnicities in the United States. <i>PLoS Biology</i> , 2018, 16, e2006842.	2.6	216
1901	Marginal Zinc Deficiency and Environmentally Relevant Concentrations of Arsenic Elicit Combined Effects on the Gut Microbiome. <i>MSphere</i> , 2018, 3, .	1.3	34
1902	Microbiota-Induced TNF-like Ligand 1A Drives Group 3 Innate Lymphoid Cell-Mediated Barrier Protection and Intestinal T Cell Activation during Colitis. <i>Immunity</i> , 2018, 49, 1077-1089.e5.	6.6	108
1903	Use of sugarcane-soybean intercropping in acid soil impacts the structure of the soil fungal community. <i>Scientific Reports</i> , 2018, 8, 14488.	1.6	29
1904	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
1905	Accounting for Bacterial Overlap Between Raw Water Communities and Contaminating Sources Improves the Accuracy of Signature-Based Microbial Source Tracking. <i>Frontiers in Microbiology</i> , 2018, 9, 2364.	1.5	16
1906	Microbial Community Composition and Predicted Functional Attributes of Antarctic Lithobionts Using Targeted Next-Generation Sequencing and Bioinformatics Tools. <i>Methods in Microbiology</i> , 2018, , 243-290.	0.4	3
1907	Estimating bacteria diversity in different organs of nine species of mosquito by next generation sequencing. <i>BMC Microbiology</i> , 2018, 18, 126.	1.3	81
1908	Methods and Strategies to Examine the Human Breastmilk Microbiome. <i>Methods in Molecular Biology</i> , 2018, 1849, 63-86.	0.4	15
1909	Reconstitution of the gut microbiota of antibiotic-treated patients by autologous fecal microbiota transplant. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	258

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1910	Obesity-Linked Gut Microbiome Dysbiosis Associated with Derangements in Gut Permeability and Intestinal Cellular Homeostasis Independent of Diet. <i>Journal of Diabetes Research</i> , 2018, 2018, 1-9.	1.0	116
1911	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
1912	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
1913	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
1914	Analysis of microbial communities in heavy metals-contaminated soils using the metagenomic approach. <i>Ecotoxicology</i> , 2018, 27, 1281-1291.	1.1	94
1915	Patterns of root colonization by arbuscular mycorrhizal fungi and dark septate endophytes across a mostly-unvegetated, high-elevation landscape. <i>Fungal Ecology</i> , 2018, 36, 63-74.	0.7	55
1916	The gut of the finch: uniqueness of the gut microbiome of the Galápagos vampire finch. <i>Microbiome</i> , 2018, 6, 167.	4.9	63
1917	Comparative study on treatment performance, membrane fouling, and microbial community profile between conventional and hybrid sequencing batch membrane bioreactors for municipal wastewater treatment. <i>Environmental Science and Pollution Research</i> , 2018, 25, 32767-32782.	2.7	10
1918	Microbiome and Blood Analyte Differences Point to Community and Metabolic Signatures in Lean and Obese Horses. <i>Frontiers in Veterinary Science</i> , 2018, 5, 225.	0.9	55
1919	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
1920	The effects of amine-modified single-walled carbon nanotubes on the mouse microbiota. <i>International Journal of Nanomedicine</i> , 2018, Volume 13, 5275-5286.	3.3	2
1921	Cellulose acetate, a new candidate feed supplement for ruminant animals: In vitro evaluations. <i>Journal of Dairy Science</i> , 2018, 101, 10929-10938.	1.4	17
1922	Effects of Phytoremediation Treatment on Bacterial Community Structure and Diversity in Different Petroleum-Contaminated Soils. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 2168.	1.2	26
1923	Air and waterborne microbiome of a pharmaceutical plant provide insights on spatiotemporal variations and community resilience after disturbance. <i>BMC Microbiology</i> , 2018, 18, 124.	1.3	5
1924	NIK signaling axis regulates dendritic cell function in intestinal immunity and homeostasis. <i>Nature Immunology</i> , 2018, 19, 1224-1235.	7.0	32
1925	Impact of foliar fungicides on target and non-target soil microbial communities in cucumber crops. <i>Ecotoxicology and Environmental Safety</i> , 2018, 166, 78-85.	2.9	30
1926	Decoupling between sulfate reduction and the anaerobic oxidation of methane in the shallow methane seep of the Black sea. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	13
1927	Using pseudoalignment and base quality to accurately quantify microbial community composition. <i>PLoS Computational Biology</i> , 2018, 14, e1006096.	1.5	20

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1928	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
1929	Compositional and Temporal Changes in the Gut Microbiome of Pediatric Ulcerative Colitis Patients Are Linked to Disease Course. <i>Cell Host and Microbe</i> , 2018, 24, 600-610.e4.	5.1	193
1930	Pathogen elimination by probiotic <i>Bacillus</i> via signalling interference. <i>Nature</i> , 2018, 562, 532-537.	13.7	389
1931	Do apes smell like humans? The role of skin bacteria and volatiles of primates in mosquito host selection. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	24
1932	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
1933	Pathogenicity of <i>Serratia marcescens</i> Strains in Honey Bees. <i>MBio</i> , 2018, 9, .	1.8	90
1934	Relationships Between Fungal and Plant Communities Differ Between Desert and Grassland in a Typical Dryland Region of Northwest China. <i>Frontiers in Microbiology</i> , 2018, 9, 2327.	1.5	20
1935	Australian dryland soils are acidic and nutrientâ€depleted, and have unique microbial communities compared with other drylands. <i>Journal of Biogeography</i> , 2018, 45, 2803-2814.	1.4	35
1936	Enteric infection coupled with chronic Notch pathway inhibition alters colonic mucus composition leading to dysbiosis, barrier disruption and colitis. <i>PLoS ONE</i> , 2018, 13, e0206701.	1.1	20
1937	Safety and preliminary efficacy of orally administered lyophilized fecal microbiota product compared with frozen product given by enema for recurrent <i>Clostridium difficile</i> infection: A randomized clinical trial. <i>PLoS ONE</i> , 2018, 13, e0205064.	1.1	77
1938	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	13.7	1,220
1939	Transmission modes of the mammalian gut microbiota. <i>Science</i> , 2018, 362, 453-457.	6.0	189
1940	In situ responses of the sponge microbiome to ocean acidification. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	6
1941	Diversity of fungi and bacteria in species-rich grasslands increases with plant diversity in shoots but not in roots and soil. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	24
1942	Biochar Modulates Methanogenesis through Electron Syntrophy of Microorganisms with Ethanol as a Substrate. <i>Environmental Science & Technology</i> , 2018, 52, 12198-12207.	4.6	172
1943	Community profiling of the urinary microbiota: considerations for low-biomass samples. <i>Nature Reviews Urology</i> , 2018, 15, 735-749.	1.9	87
1944	The gut bacteria across life stages in the synanthropic fly <i>Chrysomya megacephala</i> . <i>BMC Microbiology</i> , 2018, 18, 131.	1.3	20
1945	Efficient coffee beans mucilage layer removal using lactic acid fermentation in a stirred-tank bioreactor: Kinetic, metabolic and sensorial studies. <i>Food Bioscience</i> , 2018, 26, 80-87.	2.0	39

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1946	Liver Injury, Endotoxemia, and Their Relationship to Intestinal Microbiota Composition in Alcohol-Preferring Rats. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2313-2325.	1.4	29
1947	Microbial nitrogen limitation in the mammalian large intestine. <i>Nature Microbiology</i> , 2018, 3, 1441-1450.	5.9	107
1948	The gut microbiome participates in transgenerational inheritance of low-temperature responses in <i>Drosophila melanogaster</i> . <i>FEBS Letters</i> , 2018, 592, 4078-4086.	1.3	23
1949	Generation of axenic <i>Aedes aegypti</i> demonstrate live bacteria are not required for mosquito development. <i>Nature Communications</i> , 2018, 9, 4464.	5.8	84
1950	Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. <i>Clinical Transplantation</i> , 2018, 32, e13436.	0.8	24
1951	Temperature-controlled thermophilic bacterial communities in hot springs of western Sichuan, China. <i>BMC Microbiology</i> , 2018, 18, 134.	1.3	45
1952	Antigen discovery and specification of immunodominance hierarchies for MHCII-restricted epitopes. <i>Nature Medicine</i> , 2018, 24, 1762-1772.	15.2	64
1953	Dichotomous development of the gut microbiome in preterm infants. <i>Microbiome</i> , 2018, 6, 157.	4.9	53
1954	Phosphorus and Nitrogen Drive the Seasonal Dynamics of Bacterial Communities in Pinus Forest Rhizospheric Soil of the Qinling Mountains. <i>Frontiers in Microbiology</i> , 2018, 9, 1930.	1.5	25
1955	Bioelectricity generation using microalgal biomass as electron donor in a bio-anode microbial fuel cell. <i>Bioresource Technology</i> , 2018, 270, 286-293.	4.8	55
1956	Spatial structuring of bacterial communities in epilithic biofilms in the Acquarossa river (Italy). <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	15
1957	Effect of different grain sizes of hydroxyapatite on soil heavy metal bioavailability and microbial community composition. <i>Agriculture, Ecosystems and Environment</i> , 2018, 267, 165-173.	2.5	82
1958	Smoking is associated with quantifiable differences in the human lung DNA virome and metabolome. <i>Respiratory Research</i> , 2018, 19, 174.	1.4	28
1959	Microbial community analysis of sulfate-reducing passive bioreactor for treating acid mine drainage under failure conditions after long-term continuous operation. <i>Journal of Environmental Chemical Engineering</i> , 2018, 6, 5795-5800.	3.3	15
1960	Profiling of the Microbiome Associated With Nitrogen Removal During Vermifiltration of Wastewater From a Commercial Dairy. <i>Frontiers in Microbiology</i> , 2018, 9, 1964.	1.5	9
1961	Protocols for Investigating the Leaf Mycobiome Using High-Throughput DNA Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1848, 39-51.	0.4	11
1962	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (<i>Oreochromis shiranus</i>) and North African catfish (<i>Clarias gariepinus</i>). <i>MicrobiologyOpen</i> , 2018, 7, e00716.	1.2	23
1963	Plant roots alter microbial functional genes supporting root litter decomposition. <i>Soil Biology and Biochemistry</i> , 2018, 127, 90-99.	4.2	35

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1965	Diverse Bacteria Utilize Alginate Within the Microbiome of the Giant Kelp <i>Macrocystis pyrifera</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1914.	1.5	38
1966	Microbial community structure and functions differ between native and novel (exotic-dominated) grassland ecosystems in an 8-year experiment. <i>Plant and Soil</i> , 2018, 432, 359-372.	1.8	22
1967	Airway Microbiota Dynamics Uncover a Critical Window for Interplay of Pathogenic Bacteria and Allergy in Childhood Respiratory Disease. <i>Cell Host and Microbe</i> , 2018, 24, 341-352.e5.	5.1	146
1968	Bacterial communities and potential waterborne pathogens within the typical urban surface waters. <i>Scientific Reports</i> , 2018, 8, 13368.	1.6	54
1969	Quantification of variation and the impact of biomass in targeted 16S rRNA gene sequencing studies. <i>Microbiome</i> , 2018, 6, 155.	4.9	44
1970	Effect of Pressure, Reconstituted RTE Meat Microbiota, and Antimicrobials on Survival and Post-pressure Growth of <i>Listeria monocytogenes</i> on Ham. <i>Frontiers in Microbiology</i> , 2018, 9, 1979.	1.5	22
1971	Characterization of the Functional Changes in Mouse Gut Microbiome Associated with Increased <i>Akkermansia muciniphila</i> Population Modulated by Dietary Black Raspberries. <i>ACS Omega</i> , 2018, 3, 10927-10937.	1.6	49
1972	Time Radically Alters Ex Situ Evidentiary Soil 16S Bacterial Profiles Produced Via Next-Generation Sequencing. <i>Journal of Forensic Sciences</i> , 2018, 63, 1356-1365.	0.9	10
1973	Microbial Transplantation With Human Gut Commensals Containing CutC Is Sufficient to Transmit Enhanced Platelet Reactivity and Thrombosis Potential. <i>Circulation Research</i> , 2018, 123, 1164-1176.	2.0	122
1974	Abundant and Rare Microbial Biospheres Respond Differently to Environmental and Spatial Factors in Tibetan Hot Springs. <i>Frontiers in Microbiology</i> , 2018, 9, 2096.	1.5	45
1975	Dysbiosis and early mortality in zebrafish larvae exposed to subclinical concentrations of streptomycin. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	48
1976	Long-term anaerobic digestion of food waste at semi-pilot scale: Relationship between microbial community structure and process performances. <i>Biomass and Bioenergy</i> , 2018, 118, 55-64.	2.9	41
1977	Synergistic inhibition of anaerobic ammonium oxidation (anammox) activity by phenol and thiocyanate. <i>Chemosphere</i> , 2018, 213, 498-506.	4.2	29
1978	A Review of Prebiotics Against Salmonella in Poultry: Current and Future Potential for Microbiome Research Applications. <i>Frontiers in Veterinary Science</i> , 2018, 5, 191.	0.9	79
1979	A Vegetable Fermentation Facility Hosts Distinct Microbiomes Reflecting the Production Environment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	27
1980	CO ₂ conversion to CH ₄ using Zero Valent Iron (ZVI) and anaerobic granular sludge: Optimum batch conditions and microbial pathways. <i>Journal of CO₂ Utilization</i> , 2018, 27, 415-422.	3.3	44
1981	Conditional Regression Based on a Multivariate Zero-Inflated Logistic-Normal Model for Microbiome Relative Abundance Data. <i>Statistics in Biosciences</i> , 2018, 10, 587-608.	0.6	22

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1982	Evaluation of trophic transfer in the microbial food web during sludge degradation based on 13C and 15N natural abundance. <i>Water Research</i> , 2018, 146, 30-36.	5.3	13
1983	Abundant and Rare Bacterioplankton in Freshwater Lakes Subjected to Different Levels of Tourism Disturbances. <i>Water (Switzerland)</i> , 2018, 10, 1075.	1.2	18
1984	Environmental temperature alters the digestive performance and gut microbiota of a terrestrial amphibian. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	98
1985	Composici3n de la microbiota intestinal en pacientes con esclerosis m4ltiple. Influencia del tratamiento con interfer3n 12-1b. <i>Neurolog4a</i> , 2021, 36, 495-503.	0.3	22
1986	Effects of dietary supplementation of formaldehyde and crystalline amino acids on gut microbial composition of nursery pigs. <i>Scientific Reports</i> , 2018, 8, 8164.	1.6	5
1987	Practical applications of PCR primers in detection of anammox bacteria effectively from different types of samples. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5859-5871.	1.7	21
1988	Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water. <i>Science of the Total Environment</i> , 2018, 639, 1126-1137.	3.9	43
1989	Resilience to fire of phylogenetic diversity across biological domains. <i>Molecular Ecology</i> , 2018, 27, 2896-2908.	2.0	49
1990	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
1991	Interleukin 11-Deficient Mice Have an Altered Gut Microbiota Leading to Protection from Dextran Sodium Sulfate-Induced Colitis. <i>MSystems</i> , 2018, 3, .	1.7	33
1992	Signatures of diversifying selection and convergence acting on passerine Toll4like receptor 4 in an evolutionary context. <i>Molecular Ecology</i> , 2018, 27, 2871-2883.	2.0	11
1993	Nature-derived microbiota exposure as a novel immunomodulatory approach. <i>Future Microbiology</i> , 2018, 13, 737-744.	1.0	50
1994	Crop rotational diversity increases disease suppressive capacity of soil microbiomes. <i>Ecosphere</i> , 2018, 9, e02235.	1.0	134
1995	Microbial communities in soil profile are more responsive to legacy effects of wheat-cover crop rotations than tillage systems. <i>Soil Biology and Biochemistry</i> , 2018, 123, 126-135.	4.2	61
1996	Bangladeshi children with acute diarrhoea show faecal microbiomes with increased <i>Streptococcus</i> abundance, irrespective of diarrhoea aetiology. <i>Environmental Microbiology</i> , 2018, 20, 2256-2269.	1.8	33
1997	Cadmium phytoextraction potential of king grass (<i>Pennisetum sinese</i> Roxb.) and responses of rhizosphere bacterial communities to a cadmium pollution gradient. <i>Environmental Science and Pollution Research</i> , 2018, 25, 21671-21681.	2.7	17
1998	Culture-independent Characterization of the Microbiome of Healthy Pulp. <i>Journal of Endodontics</i> , 2018, 44, 1132-1139.e2.	1.4	21
1999	Paddy-upland rotation for sustainable agriculture with regards to diverse soil microbial community. <i>Scientific Reports</i> , 2018, 8, 7966.	1.6	33

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2000	Phosphorus, not nitrogen, limits plants and microbial primary producers following glacial retreat. <i>Science Advances</i> , 2018, 4, eaaq0942.	4.7	86
2001	Iron Sequestration in Microbiota Biofilms As A Novel Strategy for Treating Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 1493-1502.	0.9	30
2002	Enrichment of Clinically Relevant Organisms in Spontaneous Preterm-Delivered Placentas and Reagent Contamination across All Clinical Groups in a Large Pregnancy Cohort in the United Kingdom. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
2003	Effect of bamboo vinegar powder as an antibiotic alternative on the digesta bacteria communities of finishing pigs. <i>Canadian Journal of Microbiology</i> , 2018, 64, 732-743.	0.8	4
2004	The gut microbiome is associated with behavioural task in honey bees. <i>Insectes Sociaux</i> , 2018, 65, 419-429.	0.7	90
2005	Dysbiosis of microbiome and probiotic treatment in a genetic model of autism spectrum disorders. <i>Brain, Behavior, and Immunity</i> , 2018, 73, 310-319.	2.0	130
2006	Cold adaptation and replicable microbial community development during long-term low-temperature anaerobic digestion treatment of synthetic sewage. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	34
2007	Ecological features of feather microbiota in breeding common swifts. <i>Ethology Ecology and Evolution</i> , 2018, 30, 569-581.	0.6	5
2008	Litter chemistry influences decomposition through activity of specific microbial functional guilds. <i>Ecological Monographs</i> , 2018, 88, 429-444.	2.4	87
2009	Biofilm and planktonic population distribution. Key aspects in carbonaceous anodes for microbial fuel cells. <i>Journal of Chemical Technology and Biotechnology</i> , 2018, 93, 3436-3443.	1.6	7
2010	Entomopathogenic fungal infection leads to temporospatial modulation of the mosquito immune system. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006433.	1.3	50
2011	Comparison of the oral microbiome in mouthwash and whole saliva samples. <i>PLoS ONE</i> , 2018, 13, e0194729.	1.1	36
2012	Shift of soil bacterial community and decrease of metals bioavailability after immobilization of a multi-metal contaminated acidic soil by inorganic-organic mixed amendments: A field study. <i>Applied Soil Ecology</i> , 2018, 130, 104-119.	2.1	33
2013	Increases in temperature and nutrient availability positively affect methane cycling microorganisms in Arctic thermokarst lake sediments. <i>Environmental Microbiology</i> , 2018, 20, 4314-4327.	1.8	51
2014	Microbial distribution and turnover in Antarctic microbial mats highlight the relevance of heterotrophic bacteria in low-nutrient environments. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	19
2015	<i>Enterococcus faecium</i> WEFA23 from infants lessens high-fat-diet-induced hyperlipidemia via cholesterol 7-alpha-hydroxylase gene by altering the composition of gut microbiota in rats. <i>Journal of Dairy Science</i> , 2018, 101, 7757-7767.	1.4	29
2016	Successive transitory distribution of Thaumarchaeota and partitioned distribution of Bathyarchaeota from the Pearl River estuary to the northern South China Sea. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8035-8048.	1.7	20
2017	Seasonal distribution of nitrifiers and denitrifiers in urban river sediments affected by agricultural activities. <i>Science of the Total Environment</i> , 2018, 642, 1282-1291.	3.9	38

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2019	Distinct biogeographic patterns of rhizobia and non-rhizobial endophytes associated with soybean nodules across China. <i>Science of the Total Environment</i> , 2018, 643, 569-578.	3.9	39
2020	Integrated methodological approach reveals microbial diversity and functions in aerobic groundwater microcosms adapted to vinyl chloride. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	11
2021	How, When, and Where Relic DNA Affects Microbial Diversity. <i>MBio</i> , 2018, 9, .	1.8	151
2022	Plant growth stages and fertilization regimes drive soil fungal community compositions in a wheat-rice rotation system. <i>Biology and Fertility of Soils</i> , 2018, 54, 731-742.	2.3	57
2023	Characterization of Wild and Captive Baboon Gut Microbiota and Their Antibiotic Resistomes. <i>MSystems</i> , 2018, 3, .	1.7	51
2024	Gastrointestinal Microbial Ecology With Perspectives on Health and Disease. , 2018, , 737-753.		3
2025	Phylogenetically distinct methanotrophs modulate methane oxidation in rice paddies across Taiwan. <i>Soil Biology and Biochemistry</i> , 2018, 124, 59-69.	4.2	63
2026	Antibiotic-induced changes in the microbiota disrupt redox dynamics in the gut. <i>ELife</i> , 2018, 7, .	2.8	121
2027	Next Generation Sequencing and mass spectrometry reveal high taxonomic diversity and complex phytoplankton-phycotoxins patterns in Southeastern Pacific fjords. <i>Toxicon</i> , 2018, 151, 5-14.	0.8	11
2028	Identification of active and taxonomically diverse 1,4-dioxane degraders in a full-scale activated sludge system by high-sensitivity stable isotope probing. <i>ISME Journal</i> , 2018, 12, 2376-2388.	4.4	42
2029	Predators and nutrient availability favor protozoa-resisting bacteria in aquatic systems. <i>Scientific Reports</i> , 2018, 8, 8415.	1.6	20
2030	Effects of different management regimes on microbial biodiversity in vineyard soils. <i>Scientific Reports</i> , 2018, 8, 9393.	1.6	71
2031	Perennials but not slope aspect affect the diversity of soil bacterial communities in the northern Negev Desert, Israel. <i>Soil Research</i> , 2018, 56, 123.	0.6	5
2032	Rectal and Naris Swabs: Practical and Informative Samples for Analyzing the Microbiota of Critically Ill Patients. <i>MSphere</i> , 2018, 3, .	1.3	15
2033	Early-life antibiotics attenuate regulatory T cell generation and increase the severity of murine house dust mite-induced asthma. <i>Pediatric Research</i> , 2018, 84, 426-434.	1.1	23
2034	Spring drying and intensified summer rainfall affected soil microbial community composition but not enzyme activity in a subtropical forest. <i>Applied Soil Ecology</i> , 2018, 130, 219-225.	2.1	21
2035	The effects of marine farm-scale sequentially integrated multi-trophic aquaculture systems on microbial community composition, prevalence of sulfonamide-resistant bacteria and sulfonamide resistance gene <i>sul1</i> . <i>Science of the Total Environment</i> , 2018, 643, 681-691.	3.9	33

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2037	Resilience of small intestinal beneficial bacteria to the toxicity of soybean oil fatty acids. <i>ELife</i> , 2018, 7, .	2.8	14
2038	Network Analyses Can Advance Above-Belowground Ecology. <i>Trends in Plant Science</i> , 2018, 23, 759-768.	4.3	60
2039	Astrovirus infections induce age-dependent dysbiosis in gut microbiomes of bats. <i>ISME Journal</i> , 2018, 12, 2883-2893.	4.4	38
2040	Shifts in intestinal microbiota after duodenal exclusion favor glycemic control and weight loss: a randomized controlled trial. <i>Surgery for Obesity and Related Diseases</i> , 2018, 14, 1748-1754.	1.0	27
2041	Topical ferumoxylol nanoparticles disrupt biofilms and prevent tooth decay in vivo via intrinsic catalytic activity. <i>Nature Communications</i> , 2018, 9, 2920.	5.8	129
2042	Alternate life history phases of a common seaweed have distinct microbial surface communities. <i>Molecular Ecology</i> , 2018, 27, 3555-3568.	2.0	41
2043	Amazon basin pasture soils reveal susceptibility to phytopathogens and lower fungal community dissimilarity than forest. <i>Applied Soil Ecology</i> , 2018, 131, 1-11.	2.1	13
2044	Nasal microbiota clusters associate with inflammatory response, viral load, and symptom severity in experimental rhinovirus challenge. <i>Scientific Reports</i> , 2018, 8, 11411.	1.6	51
2045	Effects of prebiotic inulin-type fructans on blood metabolite and hormone concentrations and faecal microbiota and metabolites in overweight dogs. <i>British Journal of Nutrition</i> , 2018, 120, 711-720.	1.2	46
2046	Fouling Development in A/O-MBR under Low Organic Loading Condition and Identification of Key Bacteria for Biofilm Formations. <i>Scientific Reports</i> , 2018, 8, 11427.	1.6	21
2047	Fiber Supplements Derived From Sugarcane Stem, Wheat Dextrin and Psyllium Husk Have Different In Vitro Effects on the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 1618.	1.5	25
2048	Distinct Oceanic Microbiomes From Viruses to Protists Located Near the Antarctic Circumpolar Current. <i>Frontiers in Microbiology</i> , 2018, 9, 1474.	1.5	23
2049	Tuning culturing conditions towards the production of neutral lipids from lubricant-based wastewater in open mixed bacterial communities. <i>Water Research</i> , 2018, 144, 532-542.	5.3	11
2050	Intestinal microbiota lipid metabolism varies across rainbow trout (<i>Oncorhynchus mykiss</i>) phylogeographic divide. <i>Journal of Applied Microbiology</i> , 2018, 125, 1614-1625.	1.4	13
2051	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. <i>PLoS Biology</i> , 2018, 16, e2006352.	2.6	236
2052	TRIM31 Deficiency Is Associated with Impaired Glucose Metabolism and Disrupted Gut Microbiota in Mice. <i>Frontiers in Physiology</i> , 2018, 9, 24.	1.3	16
2053	Long-Term Irrigation Affects the Dynamics and Activity of the Wheat Rhizosphere Microbiome. <i>Frontiers in Plant Science</i> , 2018, 9, 345.	1.7	73

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2054	Inferences of gut bacterial diversity from next-generation sequencing of 16S rDNA in deep sea blind ray - <i>Benthobatis moresbyi</i> . <i>Ecological Genetics and Genomics</i> , 2018, 9, 1-6.	0.3	2
2055	Assessment of Rumen Microbiota from a Large Dairy Cattle Cohort Reveals the Pan and Core Bacteriomes Contributing to Varied Phenotypes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	97
2056	Tree species mixture inhibits soil organic carbon mineralization accompanied by decreased r-selected bacteria. <i>Plant and Soil</i> , 2018, 431, 203-216.	1.8	24
2057	Gut microbiota components are associated with fixed airway obstruction in asthmatic patients living in the tropics. <i>Scientific Reports</i> , 2018, 8, 9582.	1.6	16
2058	Microbial Ecology and Water Chemistry Impact Regrowth of Opportunistic Pathogens in Full-Scale Reclaimed Water Distribution Systems. <i>Environmental Science & Technology</i> , 2018, 52, 9056-9068.	4.6	59
2059	Effects of phenolic acids from ginseng rhizosphere on soil fungi structure, richness and diversity in consecutive monoculturing of ginseng. <i>Saudi Journal of Biological Sciences</i> , 2018, 25, 1788-1794.	1.8	37
2060	Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. <i>Scientific Reports</i> , 2018, 8, 11159.	1.6	60
2061	Metagenomics of pigmented and cholesterol gallstones: the putative role of bacteria. <i>Scientific Reports</i> , 2018, 8, 11218.	1.6	26
2062	Gut microbes contribute to variation in solid organ transplant outcomes in mice. <i>Microbiome</i> , 2018, 6, 96.	4.9	49
2063	A two-stage microbial association mapping framework with advanced FDR control. <i>Microbiome</i> , 2018, 6, 131.	4.9	29
2064	Intestinal Microbiota Disruption Reduces Regulatory T Cells and Increases Respiratory Viral Infection Mortality Through Increased IFN γ Production. <i>Frontiers in Immunology</i> , 2018, 9, 1587.	2.2	52
2065	Anaerobic Fungi in Gorilla (<i>Gorilla gorilla gorilla</i>) Feces: an Adaptation to a High-Fiber Diet?. <i>International Journal of Primatology</i> , 2018, 39, 567-580.	0.9	6
2066	Comparing 16S rDNA amplicon sequencing and hybridization capture for pea aphid microbiota diversity analysis. <i>BMC Research Notes</i> , 2018, 11, 461.	0.6	10
2067	Enhanced preservation of the human intestinal microbiota by ridinilazole, a novel <i>Clostridium difficile</i> -targeting antibacterial, compared to vancomycin. <i>PLoS ONE</i> , 2018, 13, e0199810.	1.1	44
2068	Dysbiosis of the Vaginal Microbiota and Higher Vaginal Kynurenine/Tryptophan Ratio Reveals an Association with <i>Chlamydia trachomatis</i> Genital Infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 1.	1.8	155
2069	Ecological Restoration of Antibiotic-Disturbed Gastrointestinal Microbiota in Foregut and Hindgut of Cows. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 79.	1.8	31
2070	Clay Flocculation Effect on Microbial Community Composition in Water and Sediment. <i>Frontiers in Environmental Science</i> , 2018, 6, .	1.5	8
2071	The Green Roof Microbiome: Improving Plant Survival for Ecosystem Service Delivery. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	36

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2072	A Short Comparison of Two Marine Planktonic Diazotrophic Symbioses Highlights an Un-quantified Disparity. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	15
2073	Differential Responses of Eukaryotic Phytoplankton to Nitrogenous Nutrients in the North Pacific Subtropical Gyre. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	16
2074	Characterization of the Skin Microbiota of the Cane Toad <i>Rhinella cf. marina</i> in Puerto Rico and Costa Rica. <i>Frontiers in Microbiology</i> , 2017, 8, 2624.	1.5	20
2075	Spatial Heterogeneity and Co-occurrence of Mucosal and Luminal Microbiome across Swine Intestinal Tract. <i>Frontiers in Microbiology</i> , 2018, 9, 48.	1.5	172
2076	Urbanization Reduces Transfer of Diverse Environmental Microbiota Indoors. <i>Frontiers in Microbiology</i> , 2018, 9, 84.	1.5	95
2077	Community Composition of Nitrous Oxide-Related Genes in Salt Marsh Sediments Exposed to Nitrogen Enrichment. <i>Frontiers in Microbiology</i> , 2018, 9, 170.	1.5	22
2078	Environmental and Host Effects on Skin Bacterial Community Composition in Panamanian Frogs. <i>Frontiers in Microbiology</i> , 2018, 9, 298.	1.5	49
2079	Metatranscriptomics and Amplicon Sequencing Reveal Mutualisms in Seagrass Microbiomes. <i>Frontiers in Microbiology</i> , 2018, 9, 388.	1.5	113
2080	Exploring Biogeochemistry and Microbial Diversity of Extant Microbialites in Mexico and Cuba. <i>Frontiers in Microbiology</i> , 2018, 9, 510.	1.5	29
2081	Benthic Algal Community Structures and Their Response to Geographic Distance and Environmental Variables in the Qinghai-Tibetan Lakes With Different Salinity. <i>Frontiers in Microbiology</i> , 2018, 9, 578.	1.5	23
2082	Urea Amendment Decreases Microbial Diversity and Selects for Specific Nitrifying Strains in Eight Contrasting Agricultural Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 634.	1.5	37
2083	Rapid Formation of Microbe-Oil Aggregates and Changes in Community Composition in Coastal Surface Water Following Exposure to Oil and the Dispersant Corexit. <i>Frontiers in Microbiology</i> , 2018, 9, 689.	1.5	72
2084	Tillage Changes Vertical Distribution of Soil Bacterial and Fungal Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 699.	1.5	126
2085	Evaluation of Primers Targeting the Diazotroph Functional Gene and Development of NifMAP – A Bioinformatics Pipeline for Analyzing nifH Amplicon Data. <i>Frontiers in Microbiology</i> , 2018, 9, 703.	1.5	50
2086	Energy Gradients Structure Microbial Communities Across Sediment Horizons in Deep Marine Sediments of the South China Sea. <i>Frontiers in Microbiology</i> , 2018, 9, 729.	1.5	19
2087	16S rRNA Gene Sequencing for Deciphering the Colorectal Cancer Gut Microbiome: Current Protocols and Workflows. <i>Frontiers in Microbiology</i> , 2018, 9, 767.	1.5	39
2088	Extracellular Enzyme Activity Profile in a Chemically Enhanced Water Accommodated Fraction of Surrogate Oil: Toward Understanding Microbial Activities After the Deepwater Horizon Oil Spill. <i>Frontiers in Microbiology</i> , 2018, 9, 798.	1.5	30
2089	Conditionally Rare Taxa Contribute but Do Not Account for Changes in Soil Prokaryotic Community Structure. <i>Frontiers in Microbiology</i> , 2018, 9, 809.	1.5	12

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2091	Variation in Bat Guano Bacterial Community Composition With Depth. <i>Frontiers in Microbiology</i> , 2018, 9, 914.	1.5	20
2092	Enrichment of Bacteria From Eastern Mediterranean Sea Involved in Lignin Degradation via the Phenylacetyl-CoA Pathway. <i>Frontiers in Microbiology</i> , 2018, 9, 922.	1.5	22
2093	Taxonomic and Functional Responses of Soil Microbial Communities to Annual Removal of Aboveground Plant Biomass. <i>Frontiers in Microbiology</i> , 2018, 9, 954.	1.5	11
2094	Effect of Limit-Fed Diets With Different Forage to Concentrate Ratios on Fecal Bacterial and Archaeal Community Composition in Holstein Heifers. <i>Frontiers in Microbiology</i> , 2018, 9, 976.	1.5	37
2095	Changes in Rumen Microbial Profiles and Subcutaneous Fat Composition When Feeding Extruded Flaxseed Mixed With or Before Hay. <i>Frontiers in Microbiology</i> , 2018, 9, 1055.	1.5	25
2096	Clean Low-Biomass Procedures and Their Application to Ancient Ice Core Microorganisms. <i>Frontiers in Microbiology</i> , 2018, 9, 1094.	1.5	24
2097	Marked Response in Microbial Community and Metabolism in the Ileum and Cecum of Suckling Piglets After Early Antibiotics Exposure. <i>Frontiers in Microbiology</i> , 2018, 9, 1166.	1.5	67
2098	Sediment Microbial Communities Influenced by Cool Hydrothermal Fluid Migration. <i>Frontiers in Microbiology</i> , 2018, 9, 1249.	1.5	14
2099	Comparison of Database Search Methods for the Detection of <i>Legionella pneumophila</i> in Water Samples Using Metagenomic Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 1272.	1.5	13
2100	Exposure to Arsenic Alters the Microbiome of Larval Zebrafish. <i>Frontiers in Microbiology</i> , 2018, 9, 1323.	1.5	42
2101	Metagenomic Analysis of Cyanobacteria in an Oligotrophic Tropical Estuary, South Atlantic. <i>Frontiers in Microbiology</i> , 2018, 9, 1393.	1.5	17
2102	Diversity of Fungal Communities in Heshang Cave of Central China Revealed by Mycobiome-Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 1400.	1.5	23
2103	Gut Microbiome Composition in Non-human Primates Consuming a Western or Mediterranean Diet. <i>Frontiers in Nutrition</i> , 2018, 5, 28.	1.6	125
2104	Absolute quantitation of microbiota abundance in environmental samples. <i>Microbiome</i> , 2018, 6, 110.	4.9	203
2105	Schwertmannite transformation via direct or indirect electron transfer by a sulfate reducing enrichment culture. <i>Environmental Pollution</i> , 2018, 242, 738-748.	3.7	20
2106	Enterococcal Concentrations in a Coastal Ecosystem Are a Function of Fecal Source Input, Environmental Conditions, and Environmental Sources. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	21
2107	Quantitative PCR Analysis of Gut Disease-Discriminatory Phyla for Determining Shrimp Disease Incidence. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	10

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2109	Variation in Soil Methane Fluxes and Comparison between Two Forests in China. <i>Forests</i> , 2018, 9, 204.	0.9	7
2110	Microbial Community Analysis of Sauerkraut Fermentation Reveals a Stable and Rapidly Established Community. <i>Foods</i> , 2018, 7, 77.	1.9	73
2111	Identification of Major Rhizobacterial Taxa Affected by a Glyphosate-Tolerant Soybean Line via Shotgun Metagenomic Approach. <i>Genes</i> , 2018, 9, 214.	1.0	9
2112	Dynamics of Bacterial and Fungal Communities during the Outbreak and Decline of an Algal Bloom in a Drinking Water Reservoir. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 361.	1.2	48
2113	Water Bacterial and Fungal Community Compositions Associated with Urban Lakes, Xi'an, China. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 469.	1.2	57
2114	Survey of Soil Fungal Communities in Strawberry Fields by Illumina Amplicon Sequencing. <i>Eurasian Soil Science</i> , 2018, 51, 682-691.	0.5	13
2115	Endophytic Microbes as a Novel Source for Producing Anticancer Compounds as Multidrug Resistance Modulators. , 2018, , 343-381.		1
2116	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
2117	Microbial Community Cohesion Mediates Community Turnover in Unperturbed Aquifers. <i>MSystems</i> , 2018, 3, .	1.7	63
2118	Flavin monooxygenase 3, the host hepatic enzyme in the metaorganismal trimethylamine N-oxide-generating pathway, modulates platelet responsiveness and thrombosis risk. <i>Journal of Thrombosis and Haemostasis</i> , 2018, 16, 1857-1872.	1.9	104
2119	Effects of corn stover management on soil quality. <i>European Journal of Soil Biology</i> , 2018, 88, 57-64.	1.4	29
2120	Shifts of Faecal Microbiota During Sporadic Colorectal Carcinogenesis. <i>Scientific Reports</i> , 2018, 8, 10329.	1.6	99
2121	Linking Uncultivated Microbial Populations and Benthic Carbon Turnover by Using Quantitative Stable Isotope Probing. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	37
2122	Almond Consumption and Processing Affects the Composition of the Gastrointestinal Microbiota of Healthy Adult Men and Women: A Randomized Controlled Trial. <i>Nutrients</i> , 2018, 10, 126.	1.7	86
2123	The Effects of Antibiotics on Microbial Community Composition in an Estuary Reservoir during Spring and Summer Seasons. <i>Water (Switzerland)</i> , 2018, 10, 154.	1.2	10
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2125	Early-life skin microbiota in hospitalized preterm and full-term infants. <i>Microbiome</i> , 2018, 6, 98.	4.9	63

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2133	The short-term impact of probiotic consumption on the oral cavity microbiome. <i>Scientific Reports</i> , 2018, 8, 10476.	1.6	36
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2140	Effects of tannins on population dynamics of sympatric seed-eating rodents: the potential role of gut tannin-degrading bacteria. <i>Oecologia</i> , 2018, 187, 667-678.	0.9	9
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2262	Prevalence of <i>Arcobacter</i> and Other Pathogenic Bacteria in River Water in Nepal. <i>Water (Switzerland)</i> , 2019, 11, 1416.	1.2	14
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2264	Prokaryotic and eukaryotic microbial community responses to N and P nutrient addition in oligotrophic Mediterranean coastal waters: Novel insights from DNA metabarcoding and network analysis. <i>Marine Environmental Research</i> , 2019, 150, 104752.	1.1	27
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2421	Conventional and organic soil management as divergent drivers of resident and active fractions of major soil food web constituents. <i>Scientific Reports</i> , 2019, 9, 13521.	1.6	54
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2425	Characterization and Comparison of Microbiota in the Gastrointestinal Tracts of the Goat (<i>Capra</i>) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50	1.5	67
2426	Minor increases in <i>Phyllostachys edulis</i> (Moso bamboo) biomass despite evident alterations of soil bacterial community structure after phosphorus fertilization alone: Based on field studies at different altitudes. <i>Forest Ecology and Management</i> , 2019, 451, 117561.	1.4	19
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2428	Identification of Microbial Profiles in Heavy-Metal-Contaminated Soil from Full-Length 16S rRNA Reads Sequenced by a PacBio System. <i>Microorganisms</i> , 2019, 7, 357.	1.6	18
2429	Effects of dietary supplementation of inulin on rumen fermentation and bacterial microbiota, inflammatory response and growth performance in finishing beef steers fed high or low-concentrate diet. <i>Animal Feed Science and Technology</i> , 2019, 258, 114299.	1.1	29
2430	Letrozole treatment of pubertal female mice results in activational effects on reproduction, metabolism and the gut microbiome. <i>PLoS ONE</i> , 2019, 14, e0223274.	1.1	37
2431	The Gut Microbiome Derived From Anorexia Nervosa Patients Impairs Weight Gain and Behavioral Performance in Female Mice. <i>Endocrinology</i> , 2019, 160, 2441-2452.	1.4	72
2432	Food Preservatives Induce Proteobacteria Dysbiosis in Human-Microbiota Associated Nod2-Deficient Mice. <i>Microorganisms</i> , 2019, 7, 383.	1.6	40

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2434	Lactulose drives a reversible reduction and qualitative modulation of the faecal microbiota diversity in healthy dogs. <i>Scientific Reports</i> , 2019, 9, 13350.	1.6	11
2435	Intermittent micro-aeration: New strategy to control volatile fatty acid accumulation in high organic loading anaerobic digestion. <i>Water Research</i> , 2019, 166, 115080.	5.3	122
2436	Rice bran supplementation modulates growth, microbiota and metabolome in weaning infants: a clinical trial in Nicaragua and Mali. <i>Scientific Reports</i> , 2019, 9, 13919.	1.6	31
2437	Nitrogen flow and microbial community in the anoxic reactor of α -Sulfate Reduction, Denitrification/Anammox and Partial Nitrification process. <i>Biochemical Engineering Journal</i> , 2019, 151, 107304.	1.8	16
2438	Effects of dietary Gelsemium elegans alkaloids on intestinal morphology, antioxidant status, immune responses and microbiota of <i>Megalobrama amblycephala</i> . <i>Fish and Shellfish Immunology</i> , 2019, 94, 464-478.	1.6	32
2439	Performance of sulfur-based autotrophic denitrification and denitrifiers for wastewater treatment under acidic conditions. <i>Bioresource Technology</i> , 2019, 294, 122176.	4.8	52
2440	Soil Microbial Communities Involved in Reductive Dissolution of Arsenic from Arsenate-Laden Minerals with Different Carbon Sources. <i>Environmental Science & Technology</i> , 2019, 53, 12398-12406.	4.6	21
2441	Bacterial Community Structure Applied to Hormone Degradation. <i>Journal of Environmental Engineering, ASCE</i> , 2019, 145, 04019086.	0.7	5
2442	Insight Into the Microbial Co-occurrence and Diversity of 73 Grapevine (<i>Vitis vinifera</i>) Crown Galls Collected Across the Northern Hemisphere. <i>Frontiers in Microbiology</i> , 2019, 10, 1896.	1.5	15
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2444	Chitoooligosaccharides Prevents the Development of Colitis-Associated Colorectal Cancer by Modulating the Intestinal Microbiota and Mycobiota. <i>Frontiers in Microbiology</i> , 2019, 10, 2101.	1.5	58
2445	Mesophilic microorganisms build terrestrial mats analogous to Precambrian microbial jungles. <i>Nature Communications</i> , 2019, 10, 4323.	5.8	15
2446	Composition and Drivers of Gut Microbial Communities in Arctic-Breeding Shorebirds. <i>Frontiers in Microbiology</i> , 2019, 10, 2258.	1.5	49
2447	Fast response of fungal and prokaryotic communities to climate change manipulation in two contrasting tundra soils. <i>Environmental Microbiomes</i> , 2019, 14, 6.	2.2	15
2448	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
2449	Bacteria Associated With <i>Shiraia</i> Fruiting Bodies Influence Fungal Production of Hypocrellin A. <i>Frontiers in Microbiology</i> , 2019, 10, 2023.	1.5	21
2450	Effect of blending landfill leachate with activated sludge on the domestic wastewater treatment process. <i>Environmental Science: Water Research and Technology</i> , 2019, 5, 268-276.	1.2	18

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2452	Microbial and macroinvertebrate communities, but not leaf decomposition, change along a mining-induced salinity gradient. <i>Freshwater Biology</i> , 2019, 64, 671-684.	1.2	25
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2458	Changes in the Active, Dead, and Dormant Microbial Community Structure across a Pleistocene Permafrost Chronosequence. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	63
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2462	Hydrogen production efficiency and microbial community of ethanol-type fermentation. <i>Journal of Renewable and Sustainable Energy</i> , 2019, 11, 013105.	0.8	3
2463	Structural and functional differentiation of the microbial community in the surface and subsurface peat of two minerotrophic fens in China. <i>Plant and Soil</i> , 2019, 437, 21-40.	1.8	22
2464	Effect of temperature on the microbial community responsible for methane production in alkaline NamCo wetland soil. <i>Soil Biology and Biochemistry</i> , 2019, 132, 69-79.	4.2	32
2465	The Purple Sea Urchin <i>Strongylocentrotus purpuratus</i> Demonstrates a Compartmentalization of Gut Bacterial Microbiota, Predictive Functional Attributes, and Taxonomic Co-Occurrence. <i>Microorganisms</i> , 2019, 7, 35.	1.6	24
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2467	Green Tea Polyphenols Modify the Gut Microbiome in <i>db/db</i> Mice as Co-Abundance Groups Correlating with the Blood Glucose Lowering Effect. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1801064.	1.5	69
2468	A comparison of dynamic distributions of intestinal microbiota between Large White and Chinese Shanxi Black pigs. <i>Archives of Microbiology</i> , 2019, 201, 357-367.	1.0	14

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2483	Effects of Lactic Acid Bacteria-Fermented Soymilk on Isoflavone Metabolites and Short-Chain Fatty Acids Excretion and Their Modulating Effects on Gut Microbiota. <i>Journal of Food Science</i> , 2019, 84, 1854-1863.	1.5	39
2484	Gut microbial-derived butyrate is inversely associated with IgE responses to allergens in childhood asthma. <i>Pediatric Allergy and Immunology</i> , 2019, 30, 689-697.	1.1	89
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2488	Endocrine disruption and commensal bacteria alteration associated with gaseous and soil PAH contamination among daycare children. <i>Environment International</i> , 2019, 130, 104894.	4.8	32
2489	Enhanced nitrate removal in an Fe ⁰ -driven autotrophic denitrification system using hydrogen-rich water. <i>Environmental Science: Water Research and Technology</i> , 2019, 5, 1380-1388.	1.2	11
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2491	Effect of cashew nut shell liquid feeding on fermentation and microbiota in the rumen of Thai native cattle and swamp buffaloes. <i>Livestock Science</i> , 2019, 226, 99-106.	0.6	12
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2503	Host genetic determinants of the gut microbiota of wild mice. <i>Molecular Ecology</i> , 2019, 28, 3197-3207.	2.0	76
2504	Soil bacterial and fungal diversity and compositions respond differently to forest development. <i>Catena</i> , 2019, 181, 104071.	2.2	62

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2511	Impact of <i>Artemisia absinthium</i> hydrolate extracts with nematicidal activity on non-target soil organisms of different trophic levels. <i>Ecotoxicology and Environmental Safety</i> , 2019, 180, 565-574.	2.9	20
2512	Predominance of Anaerobic, Spore-Forming Bacteria in Metabolically Active Microbial Communities from Ancient Siberian Permafrost. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	25
2513	Realgar (As ₄ S ₄) bioprecipitation in microcosm fed by a natural groundwater and organic matter. <i>Environmental Science and Pollution Research</i> , 2019, 26, 18766-18776.	2.7	8
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2517	Disrupted Maturation of the Microbiota and Metabolome among Extremely Preterm Infants with Postnatal Growth Failure. <i>Scientific Reports</i> , 2019, 9, 8167.	1.6	64
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2538	Vermicompost can suppress <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> via generation of beneficial bacteria in a long-term tomato monoculture soil. <i>Plant and Soil</i> , 2019, 440, 491-505.	1.8	66
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2545	Use of a filter cartridge combined with intra-cartridge bead-beating improves detection of microbial DNA from water samples. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1142-1156.	2.2	34
2546	Anaerobic biodegradation of catechol by sediment microorganisms: Interactive roles of N reduction and S cycling. <i>Journal of Cleaner Production</i> , 2019, 230, 80-89.	4.6	14
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2551	High-Throughput Illumina MiSeq Amplicon Sequencing of Yeast Communities Associated With Indigenous Dairy Products From Republics of Benin and Niger. <i>Frontiers in Microbiology</i> , 2019, 10, 594.	1.5	16
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2553	Source Environments of the Microbiome in Perennially Ice-Covered Lake Untersee, Antarctica. <i>Frontiers in Microbiology</i> , 2019, 10, 1019.	1.5	26
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2555	Comparison of Co-housing and Littermate Methods for Microbiota Standardization in Mouse Models. <i>Cell Reports</i> , 2019, 27, 1910-1919.e2.	2.9	134
2556	A comparative study of gut microbiomes in captive nocturnal strepsirrhines. <i>American Journal of Primatology</i> , 2019, 81, e22986.	0.8	15
2557	The spatial scale dependence of diazotrophic and bacterial community assembly in paddy soil. <i>Global Ecology and Biogeography</i> , 2019, 28, 1093-1105.	2.7	42
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2561	Tracking of the activity of individual bacteria in temperate forest soils shows guild-specific responses to seasonality. <i>Soil Biology and Biochemistry</i> , 2019, 135, 275-282.	4.2	36
2562	Soil Bacterial Function Associated With Stylo (Legume) and Bahiagrass (Grass) Is Affected More Strongly by Soil Chemical Property Than by Bacterial Community Composition. <i>Frontiers in Microbiology</i> , 2019, 10, 798.	1.5	20
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2565	<i>Candida albicans</i> induces mucosal bacterial dysbiosis that promotes invasive infection. <i>PLoS Pathogens</i> , 2019, 15, e1007717.	2.1	127
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2575	Resource heterogeneity structures aquatic bacterial communities. <i>ISME Journal</i> , 2019, 13, 2183-2195.	4.4	93
2576	High-throughput phenotyping of cell-to-cell interactions in gel microdroplet pico-cultures. <i>BioTechniques</i> , 2019, 66, 218-224.	0.8	24

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2598	Belowground Consequences of Intracontinental Range-Expanding Plants and Related Natives in Novel Environments. <i>Frontiers in Microbiology</i> , 2019, 10, 505.	1.5	5
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2635	Comparison of Microbial Communities in the Sediments and Water Columns of Frozen Cryoconite Holes in the McMurdo Dry Valleys, Antarctica. <i>Frontiers in Microbiology</i> , 2019, 10, 65.	1.5	36
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2637	Different bioreactors for treating secondary effluent from recycled paper mill. <i>Science of the Total Environment</i> , 2019, 667, 49-56.	3.9	22
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2643	Subchronic low-dose 2,4-D exposure changed plasma acylcarnitine levels and induced gut microbiome perturbations in mice. <i>Scientific Reports</i> , 2019, 9, 4363.	1.6	22
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2647	Bacterial colonisation of reeds and cottonseed hulls in the rumen of Tarim red deer (<i>Cervus elaphus</i>)	8.7	12
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2650	Root traits and belowground herbivores relate to plant-soil feedback variation among congeners. <i>Nature Communications</i> , 2019, 10, 1564.	5.8	71
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2655	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
2656	Denitrifying Bacteria Active in Woodchip Bioreactors at Low-Temperature Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 635.	1.5	33
2657	Taxonomic and functional responses of soil microbial communities to slag-based fertilizer amendment in rice cropping systems. <i>Environment International</i> , 2019, 127, 531-539.	4.8	43
2658	Microbiota encompassing putative spoilage bacteria in retail packaged broiler meat and commercial broiler abattoir. <i>International Journal of Food Microbiology</i> , 2019, 300, 14-21.	2.1	50
2659	A 16S rDNA PCR-based theoretical to actual delta approach on culturable mock communities revealed severe losses of diversity information. <i>BMC Microbiology</i> , 2019, 19, 74.	1.3	50
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2661	Assessing Microbial Community Patterns During Incipient Soil Formation From Basalt. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 941-958.	1.3	16
2662	Structural equation modeling of a winnowed soil microbiome identifies how invasive plants re-structure microbial networks. <i>ISME Journal</i> , 2019, 13, 1988-1996.	4.4	57
2663	Microbial Community Analysis Provides Insights into the Effects of Tetrahydrofuran on 1,4-Dioxane Biodegradation. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
2664	High-rate stabilization of primary sludge in a single-chamber microbial hydrogen peroxide producing cell. <i>Environmental Science: Water Research and Technology</i> , 2019, 5, 1124-1131.	1.2	7
2665	Microbial diversity of an Antarctic subglacial community and high-resolution replicate sampling inform hydrological connectivity in a polar desert. <i>Environmental Microbiology</i> , 2019, 21, 2290-2306.	1.8	20
2666	Startup, performance, and microbial communities of an anammox reactor inoculated with indigenous sludge for the treatment of high-salinity and mesophilic underground brine. <i>Clean Technologies and Environmental Policy</i> , 2019, 21, 1001-1011.	2.1	2

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2669	Localized production of defence chemicals by intracellular symbionts of <i>Haliclona</i> sponges. <i>Nature Microbiology</i> , 2019, 4, 1149-1159.	5.9	69
2670	Improvement of terrestrial groundwater sampling method affects microbial community analysis. <i>Geomicrobiology Journal</i> , 2019, 36, 303-316.	1.0	1
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2672	Strategy of rapid start-up and the mechanism of de-nitrogen in landfill bioreactor. <i>Journal of Environmental Management</i> , 2019, 240, 126-135.	3.8	5
2673	Gut microbial dysbiosis is associated with allergen-specific IgE responses in young children with airway allergies. <i>World Allergy Organization Journal</i> , 2019, 12, 100021.	1.6	77
2674	Hepatic glycogen storage diseases are associated to microbial dysbiosis. <i>PLoS ONE</i> , 2019, 14, e0214582.	1.1	17
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2677	Defining Dysbiosis in Patients with Urolithiasis. <i>Scientific Reports</i> , 2019, 9, 5425.	1.6	69
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2680	Grazing and enclosure alter the vertical distribution of organic nitrogen pools and bacterial communities in semiarid grassland soils. <i>Plant and Soil</i> , 2019, 439, 525-539.	1.8	15
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2682	Gut microbiome patterns correlate with higher postoperative complication rates after pancreatic surgery. <i>BMC Microbiology</i> , 2019, 19, 42.	1.3	40
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2686	Impact of 5 fluorouracil chemotherapy on gut inflammation, functional parameters, and gut microbiota. <i>Brain, Behavior, and Immunity</i> , 2019, 80, 44-55.	2.0	63
2687	The Microbiome in Lung Cancer Tissue and Recurrence-Free Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 731-740.	1.1	109
2688	Microbial communities are sensitive indicators for freshwater sediment copper contamination. <i>Environmental Pollution</i> , 2019, 247, 1028-1038.	3.7	38
2689	Detection of Natural Products and Their Producers in Ocean Sediments. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	33
2690	A mole rat's gut microbiota suggests selective influence of diet on microbial niche space and evolution. <i>Experimental Biology and Medicine</i> , 2019, 244, 471-483.	1.1	2
2691	Microbial species and biodiversity in settling dust within and between pig farms. <i>Environmental Research</i> , 2019, 171, 558-567.	3.7	49
2692	Impact of routine sanitation on the microbiomes in a fresh produce processing facility. <i>International Journal of Food Microbiology</i> , 2019, 294, 31-41.	2.1	22
2693	Association between rhinovirus species and nasopharyngeal microbiota in infants with severe bronchiolitis. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1925-1928.e7.	1.5	26
2694	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
2695	Spatial distribution of prokaryotic communities in hypersaline soils. <i>Scientific Reports</i> , 2019, 9, 1769.	1.6	33
2696	Effect of tacrolimus on skin microbiome in atopic dermatitis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 1400-1406.	2.7	16
2697	Distinct microbiotas of anatomical gut regions display idiosyncratic seasonal variation in an avian folivore. <i>Animal Microbiome</i> , 2019, 1, 2.	1.5	21
2698	Effect of the extraction and purification of soil DNA and pooling of PCR amplification products on the description of bacterial and archaeal communities. <i>Journal of Applied Microbiology</i> , 2019, 126, 1454-1467.	1.4	26
2699	Performance of Microbiome Sequence Inference Methods in Environments with Varying Biomass. <i>MSystems</i> , 2019, 4, .	1.7	118
2700	Effect of pegbovigrastim administration on the microbiome found in the vagina of cows postpartum. <i>Journal of Dairy Science</i> , 2019, 102, 3439-3451.	1.4	11
2701	Effects of a <i>Saccharomyces cerevisiae</i> fermentation product on liver abscesses, fecal microbiome, and resistome in feedlot cattle raised without antibiotics. <i>Scientific Reports</i> , 2019, 9, 2559.	1.6	41
2702	Successful operation performance and syntrophic micro-granule in partial nitritation and anammox reactor treating low-strength ammonia wastewater. <i>Water Research</i> , 2019, 155, 288-299.	5.3	174

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2703	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
2704	Leukemia multiclass assessment and classification from Microarray and RNA-seq technologies integration at gene expression level. <i>PLoS ONE</i> , 2019, 14, e0212127.	1.1	31
2705	Watershed hydrology and salinity, but not nutrient chemistry, are associated with arid-land stream microbial diversity. <i>Freshwater Science</i> , 2019, 38, 77-91.	0.9	5
2706	The NLRP3 inflammasome mediates DSS-induced intestinal inflammation in <i>Nod2</i> knockout mice. <i>Innate Immunity</i> , 2019, 25, 132-143.	1.1	27
2707	Community ecology across bacteria, archaea and microbial eukaryotes in the sediment and seawater of coastal Puerto Nuevo, Baja California. <i>PLoS ONE</i> , 2019, 14, e0212355.	1.1	44
2708	Successional Dynamics and Seascape-Level Patterns of Microbial Communities on the Canopy-Forming Kelps <i>Nereocystis luetkeana</i> and <i>Macrocystis pyrifera</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 346.	1.5	77
2709	Anammox response to natural and anthropogenic impacts over the Yangtze River. <i>Science of the Total Environment</i> , 2019, 665, 171-180.	3.9	34
2710	Effects of a <i>Saccharomyces cerevisiae</i> fermentation product on fecal characteristics, nutrient digestibility, fecal fermentative end-products, fecal microbial populations, immune function, and diet palatability in adult dogs. <i>Journal of Animal Science</i> , 2019, 97, 1586-1599.	0.2	43
2711	Cave Drip Water-Related Samples as a Natural Environment for Aromatic Hydrocarbon-Degrading Bacteria. <i>Microorganisms</i> , 2019, 7, 33.	1.6	25
2712	Composition and Variation of the Human Milk Microbiota Are Influenced by Maternal and Early-Life Factors. <i>Cell Host and Microbe</i> , 2019, 25, 324-335.e4.	5.1	343
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2860	Gut bacterial and fungal communities in ground-dwelling beetles are associated with host food habit and habitat. <i>ISME Journal</i> , 2019, 13, 676-685.	4.4	54
2861	The Mouse Microbiome Is Required for Sex-Specific Diurnal Rhythms of Gene Expression and Metabolism. <i>Cell Metabolism</i> , 2019, 29, 362-382.e8.	7.2	178
2862	Transmaternal <i>Helicobacter pylori</i> exposure reduces allergic airway inflammation in offspring through regulatory T cells. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1496-1512.e11.	1.5	38
2863	Comparative Analysis of Anuran Amphibian Skin Microbiomes Across Inland and Coastal Wetlands. <i>Microbial Ecology</i> , 2019, 78, 348-360.	1.4	16
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2872	Using Partial Nitrification and Anammox To Remove Nitrogen from Low-Strength Wastewater by Co-immobilizing Biofilm inside a Moving Bed Bioreactor. <i>ACS Sustainable Chemistry and Engineering</i> , 2019, 7, 1353-1361.	3.2	35
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2876	Remediation of deterioration in microbial structure in continuous <i>Pinellia ternata</i> cropping soil by crop rotation. <i>Canadian Journal of Microbiology</i> , 2019, 65, 282-295.	0.8	20
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2927	Alterations in Oral Microbiota in HIV Are Related to Decreased Pulmonary Function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 445-457.	2.5	42
2928	Novel probiotic approach to counter <i>Paenibacillus larvae</i> infection in honey bees. <i>ISME Journal</i> , 2020, 14, 476-491.	4.4	95
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2939	Bacterial Community Dynamics During Nursery Rearing of Pacific White Shrimp (<i>Litopenaeus vannamei</i>) Revealed via High-Throughput Sequencing. <i>Indian Journal of Microbiology</i> , 2020, 60, 214-221.	1.5	9
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2976	Peanut plant growth was altered by monocropping-associated microbial enrichment of rhizosphere microbiome. <i>Plant and Soil</i> , 2020, 446, 655-669.	1.8	20
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2995	Endophytic Microbiome of Biofuel Plant <i>Miscanthus sinensis</i> (Poaceae) Interacts with Environmental Gradients. <i>Microbial Ecology</i> , 2020, 80, 133-144.	1.4	9
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3576	Endophytes enhance Asia minor bluegrass (<i>Polypogon fugax</i>) resistance to quizalofop-p-ethyl. <i>Plant and Soil</i> , 2020, 450, 373-384.	1.8	5
3577	Persistent Diarrhea in Patients With Crohn's Disease After Mucosal Healing Is Associated With Lower Diversity of the Intestinal Microbiome and Increased Dysbiosis. <i>Clinical Gastroenterology and Hepatology</i> , 2021, 19, 296-304.e3.	2.4	19
3578	Alterations of the Oral Microbiome and Cumulative Carbapenem Exposure Are Associated With <i>Stenotrophomonas maltophilia</i> Infection in Patients With Acute Myeloid Leukemia Receiving Chemotherapy. <i>Clinical Infectious Diseases</i> , 2021, 72, 1507-1513.	2.9	19
3579	House dust microbiota in relation to adult asthma and atopy in a US farming population. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 910-920.	1.5	21
3580	Effect of organic micropollutants on biofouling in a forward osmosis process integrating seawater desalination and wastewater reclamation. <i>Journal of Hazardous Materials</i> , 2021, 401, 123386.	6.5	18
3581	Long-term agricultural contamination shaped diversity response of sediment microbiome. <i>Journal of Environmental Sciences</i> , 2021, 99, 90-99.	3.2	13
3582	Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2021, 27, 366-379.	1.4	24
3583	Reduction of alkalinity supplementation for acid-based wastewater treatment using a thermophilic multi-feed upflow anaerobic sludge blanket reactor. <i>Environmental Technology (United Kingdom)</i> , 2021, 42, 32-42.	1.2	3
3584	Adsorption and biodegradation removal of methylene blue in a down-flow hanging filter reactor incorporating natural adsorbent. <i>Environmental Technology (United Kingdom)</i> , 2021, 42, 410-418.	1.2	6
3585	The human gut microbiota in people with amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2021, 22, 186-194.	1.1	49

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3587	Low root functional dispersion enhances functionality of plant growth by influencing bacterial activities in European forest soils. <i>Environmental Microbiology</i> , 2021, 23, 1889-1906.	1.8	16
3588	Chemical and microbial characterization for fermentation of water-soluble cellulose acetate in human stool cultures. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 2950-2960.	1.7	5
3589	Profiling microbial community structures and functions in bioremediation strategies for treating 1,4-dioxane-contaminated groundwater. <i>Journal of Hazardous Materials</i> , 2021, 408, 124457.	6.5	21
3590	Pulp and paper mill sludges decrease soil erodibility. <i>Journal of Environmental Quality</i> , 2021, 50, 172-184.	1.0	22
3591	Biochar affects taxonomic and functional community composition of protists. <i>Biology and Fertility of Soils</i> , 2021, 57, 15-29.	2.3	26
3592	Microbiomic and transcriptomic insight into the pathogenesis of meningitis-like disease in cultured <i>Pelophylax nigromaculatus</i> . <i>Aquaculture</i> , 2021, 530, 735736.	1.7	8
3593	Ecological insights into assembly processes and network structures of bacterial biofilms in full-scale biologically active carbon filters under ozone implementation. <i>Science of the Total Environment</i> , 2021, 751, 141409.	3.9	16
3594	A new Illumina MiSeq high-throughput sequencing-based method for evaluating the composition of the <i>Bacteroides</i> community in the intestine using the rpsD gene sequence. <i>Microbial Biotechnology</i> , 2021, 14, 577-586.	2.0	9
3595	Effects of the inoculum source, electron donor, and immobilization on the microbial community of sulfidogenic bioreactors. <i>Chemical Engineering Journal</i> , 2021, 404, 126549.	6.6	10
3596	Prebiotics enhance the biotransformation and bioavailability of ginsenosides in rats by modulating gut microbiota. <i>Journal of Ginseng Research</i> , 2021, 45, 334-343.	3.0	29
3597	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
3598	What Could Explain $\delta^{13}C$ Signatures in Biocrust Cyanobacteria of Drylands?. <i>Microbial Ecology</i> , 2021, 81, 134-145.	1.4	1
3599	Fecal Microbiota Transplantation Reduces Symptoms in Some Patients With Irritable Bowel Syndrome With Predominant Abdominal Bloating: Short- and Long-term Results From a Placebo-Controlled Randomized Trial. <i>Gastroenterology</i> , 2021, 160, 145-157.e8.	0.6	109
3600	Bacterial community dynamics and functional profiling of soils from conventional and organic cropping systems. <i>Applied Soil Ecology</i> , 2021, 157, 103734.	2.1	20
3601	Sewage sludge application alters the composition and co-occurrence pattern of the soil bacterial community in southern China forestlands. <i>Applied Soil Ecology</i> , 2021, 157, 103744.	2.1	18
3602	Effect of antibiotic type and vegetable species on antibiotic accumulation in soil-vegetable system, soil microbiota, and resistance genes. <i>Chemosphere</i> , 2021, 263, 128099.	4.2	60
3603	Response of syntrophic bacterial and methanogenic archaeal communities in paddy soil to soil type and phenological period of rice growth. <i>Journal of Cleaner Production</i> , 2021, 278, 123418.	4.6	8

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3605	Comparison of the microbial communities of alpacas and sheep fed diets with three different ratios of corn stalk to concentrate. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2021, 105, 26-34.	1.0	6
3606	Microbial community assembly in a multi-layer dendritic metacommunity. <i>Oecologia</i> , 2021, 195, 13-24.	0.9	16
3607	Natural attenuation of lead by microbial manganese oxides in a karst aquifer. <i>Science of the Total Environment</i> , 2021, 754, 142312.	3.9	11
3608	Toxic trace element resistance genes and systems identified using the shotgun metagenomics approach in an Iranian mine soil. <i>Environmental Science and Pollution Research</i> , 2021, 28, 4845-4856.	2.7	6
3609	Response of the green June beetle and its gut microbiome to RDX and phenanthrene. <i>International Journal of Environmental Science and Technology</i> , 2021, 18, 1785-1792.	1.8	2
3610	Contrasting patterns of microbial community and enzyme activity between rhizosphere and bulk soil along an elevation gradient. <i>Catena</i> , 2021, 196, 104921.	2.2	59
3611	Alterations of stool metabolome, phenome, and microbiome of the marine fish, red sea bream, <i>Pagrus major</i> , following exposure to phenanthrene: A non-invasive approach for exposure assessment. <i>Science of the Total Environment</i> , 2021, 752, 141796.	3.9	12
3612	A symbiotic nutrient exchange within the cyanosphere microbiome of the biocrust cyanobacterium, <i>Microcoleus vaginatus</i> . <i>ISME Journal</i> , 2021, 15, 282-292.	4.4	44
3613	Fifteen-year no tillage of a Mollisol with residue retention indirectly affects topsoil bacterial community by altering soil properties. <i>Soil and Tillage Research</i> , 2021, 205, 104804.	2.6	28
3614	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
3615	Airborne bacterial communities over the Tibetan and Mongolian Plateaus: variations and their possible sources. <i>Atmospheric Research</i> , 2021, 247, 105215.	1.8	11
3616	Evaluating the effect of air flow rate on hybrid and conventional membrane bioreactors: Implications on performance, microbial activity and membrane fouling. <i>Science of the Total Environment</i> , 2021, 755, 142563.	3.9	21
3617	Performance evaluation of down-flow hanging sponge reactor for direct treatment of actual textile wastewater; Effect of effluent recirculation to performance and microbial community. <i>Journal of Water Process Engineering</i> , 2021, 39, 101724.	2.6	19
3618	Application of down-flow hanging sponge "Upflow sludge blanket system for nitrogen removal in <i>Epinephelus bruneus</i> closed recirculating aquaculture system. <i>Aquaculture</i> , 2021, 532, 735997.	1.7	13
3619	Rock varnish in La Proveedora/Sonora in the context of desert geobiological processes and landscape evolution. <i>Journal of South American Earth Sciences</i> , 2021, 105, 102959.	0.6	4
3620	Soil bacterial diversities and response to deforestation, land use and burning in North Amazon, Brazil. <i>Applied Soil Ecology</i> , 2021, 158, 103775.	2.1	13
3621	Contrasting seasonal variations of geochemistry and microbial community in two adjacent acid mine drainage lakes in Anhui Province, China. <i>Environmental Pollution</i> , 2021, 268, 115826.	3.7	24

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3623	Specific enrichment of hydrocarbonclastic bacteria from diesel-amended soil on biochar particles. <i>Science of the Total Environment</i> , 2021, 762, 143084.	3.9	9
3624	Characterization of gut microbiota in polycystic ovary syndrome: Findings from a lean population. <i>European Journal of Clinical Investigation</i> , 2021, 51, e13417.	1.7	30
3625	Changes in rhizosphere microbial diversity and composition due to NaCl addition to the soil modify the outcome of maize-weed interactions. <i>Applied Soil Ecology</i> , 2021, 159, 103818.	2.1	2
3626	Biomarkers associated with cheese quality uncovered by integrative multi-omic analysis. <i>Food Control</i> , 2021, 123, 107752.	2.8	15
3627	Compositional changes of sedimentary microbes in the Yangtze River Estuary and their roles in the biochemical cycle. <i>Science of the Total Environment</i> , 2021, 760, 143383.	3.9	25
3628	Maintaining microbial diversity mitigates membrane fouling of an anoxic/oxic membrane bioreactor under starvation condition. <i>Science of the Total Environment</i> , 2021, 759, 143474.	3.9	19
3629	DNA metabarcoding provides insights into seasonal diet variations in Chinese mole shrew (<i>Tupaia chiroptera</i>). <i>Evolution</i> , 2021, 11, 376-389.	0.8	8
3630	Effects of the insecticide fipronil in freshwater model organisms and microbial and periphyton communities. <i>Science of the Total Environment</i> , 2021, 764, 142820.	3.9	14
3631	Startup and performance of a novel single-stage partial nitritation/anammox system for reject water treatment. <i>Bioresource Technology</i> , 2021, 321, 124432.	4.8	26
3632	Characterization of microbial communities in sediments of the South Yellow Sea. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 846-864.	0.6	8
3633	Characterization of the bacterial communities associated with biofilters in two full-scale recirculating aquaculture systems. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1143-1150.	0.6	7
3634	Topographic heterogeneity of lung microbiota in end-stage idiopathic pulmonary fibrosis: the Microbiome in Lung Explants-2 (MiLEs-2) study. <i>Thorax</i> , 2021, 76, 239-247.	2.7	11
3635	Combined ozonation and solarization for the removal of pesticides from soil: Effects on soil microbial communities. <i>Science of the Total Environment</i> , 2021, 758, 143950.	3.9	18
3636	Co-culturing fructophilic lactic acid bacteria and yeast enhanced sugar metabolism and aroma formation during cocoa beans fermentation. <i>International Journal of Food Microbiology</i> , 2021, 339, 109015.	2.1	35
3637	Seasonal changes and the unexpected impact of environmental disturbance on skin bacteria of individual amphibians in a natural habitat. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	10
3638	Plant-microbial feedback in secondary succession of semiarid grasslands. <i>Science of the Total Environment</i> , 2021, 760, 143389.	3.9	10
3639	Abnormal food timing and predisposition to weight gain: Role of barrier dysfunction and microbiota. <i>Translational Research</i> , 2021, 231, 113-123.	2.2	13

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3641	Preparatory immunity: Seasonality of mucosal skin defences and <i>Batrachochytrium</i> infections in Southern leopard frogs. <i>Journal of Animal Ecology</i> , 2021, 90, 542-554.	1.3	18
3642	Age Patterning in Wild Chimpanzee Gut Microbiota Diversity Reveals Differences from Humans in Early Life. <i>Current Biology</i> , 2021, 31, 613-620.e3.	1.8	31
3643	Optimizing the quality of clinical studies on oral microbiome: A practical guide for planning, performing, and reporting. <i>Periodontology 2000</i> , 2021, 85, 210-236.	6.3	51
3644	Nitrate promotes the transfer of methane-derived carbon from the methanotroph <i>Methylobacter</i> sp. to the methylotroph <i>Methylothermobacter</i> sp. in eutrophic lake water. <i>Limnology and Oceanography</i> , 2021, 66, 878-891.	1.6	29
3645	Inter-trophic Interaction of Gut Microbiota in a Tripartite System. <i>Microbial Ecology</i> , 2021, 81, 1075-1087.	1.4	5
3646	Altered bacteria community dominance reduces tolerance to resident fungus and seed to seedling growth performance in maize (<i>Zea mays</i> L. var. DKB 177). <i>Microbiological Research</i> , 2021, 243, 126643.	2.5	4
3647	Gut microbiomes of bigheaded carps and hybrids provide insights into invasion: A hologenome perspective. <i>Evolutionary Applications</i> , 2021, 14, 735-745.	1.5	16
3648	<i>Clostridium bolteae</i> is elevated in neuromyelitis optica spectrum disorder in India and shares sequence similarity with AQP4. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2021, 8, .	3.1	26
3649	Lower Airway Dysbiosis Affects Lung Cancer Progression. <i>Cancer Discovery</i> , 2021, 11, 293-307.	7.7	139
3650	Impacts of ammonia loading and biofilm age on the prevalence of nitrogen-cycling microorganisms in a full-scale submerged attached-growth reactor. <i>Water Environment Research</i> , 2021, 93, 787-796.	1.3	2
3651	Dishwashing sponges and brushes: Consumer practices and bacterial growth and survival. <i>International Journal of Food Microbiology</i> , 2021, 337, 108928.	2.1	20
3652	Native plant <i>Maireana brevifolia</i> drives prokaryotic microbial community development in alkaline Fe ore tailings under semi-arid climatic conditions. <i>Science of the Total Environment</i> , 2021, 760, 144019.	3.9	15
3653	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
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3655	Subseafloor Archaea reflect 139 kyrs of paleodepositional changes in the northern Red Sea. <i>Geobiology</i> , 2021, 19, 162-172.	1.1	6
3656	Coinfection and infection duration shape how pathogens affect the African buffalo gut microbiota. <i>ISME Journal</i> , 2021, 15, 1359-1371.	4.4	17
3657	Novel Fecal Biomarkers That Precede Clinical Diagnosis of Ulcerative Colitis. <i>Gastroenterology</i> , 2021, 160, 1532-1545.	0.6	94

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3659	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. <i>Molecular Ecology</i> , 2021, 30, 1072-1085.	2.0	43
3660	Soil rehabilitation shaped different patterns of bacterial and archaeal community in AMD-irrigated paddy soil. <i>Chemosphere</i> , 2021, 263, 128259.	4.2	9
3661	Genomic investigations of acute munitions exposures on the health and skin microbiome composition of leopard frog (<i>Rana pipiens</i>) tadpoles. <i>Environmental Research</i> , 2021, 192, 110245.	3.7	8
3662	Effective Se reduction by lactate-stimulated indigenous microbial communities in excavated waste rocks. <i>Journal of Hazardous Materials</i> , 2021, 403, 123908.	6.5	4
3663	Comparison of intestinal permeability, morphology, and ileal microbial communities of commercial hens housed in conventional cages and cage-free housing systems. <i>Poultry Science</i> , 2021, 100, 1178-1191.	1.5	21
3664	Interplay of microbial communities with mineral environments in coralline algae. <i>Science of the Total Environment</i> , 2021, 757, 143877.	3.9	6
3665	Evidence of sporulation capability of the ubiquitous oil reservoir microbe <i>Halanaerobium congolense</i> . <i>Geomicrobiology Journal</i> , 2021, 38, 283-293.	1.0	5
3666	Invasive freshwater snails form novel microbial relationships. <i>Evolutionary Applications</i> , 2021, 14, 770-780.	1.5	9
3667	Can switchgrass increase carbon accrual in marginal soils? The importance of site selection. <i>GCB Bioenergy</i> , 2021, 13, 320-335.	2.5	11
3668	Long-term fertilisation reveals close associations between soil organic carbon composition and microbial traits at aggregate scales. <i>Agriculture, Ecosystems and Environment</i> , 2021, 306, 107169.	2.5	32
3669	Use of compost and phosphate-solubilizing bacteria affect sugarcane mineral nutrition, phosphorus availability, and the soil bacterial community. <i>Applied Soil Ecology</i> , 2021, 157, 103760.	2.1	53
3670	Probiotic <i>Carnobacterium divergens</i> increase growth parameters and disease resistance in farmed Atlantic cod (<i>Gadus morhua</i>) larvae without influencing the microbiota.. <i>Aquaculture</i> , 2021, 532, 736072.	1.7	17
3671	Community assembly processes underlying the temporal dynamics of glacial stream and lake bacterial communities. <i>Science of the Total Environment</i> , 2021, 761, 143178.	3.9	22
3672	Methamphetamine exposure and its cessation alter gut microbiota and induce depressive-like behavioral effects on rats. <i>Psychopharmacology</i> , 2021, 238, 281-292.	1.5	25
3673	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. <i>Brain, Behavior, and Immunity</i> , 2021, 91, 245-256.	2.0	44
3674	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
3675	Enrichment of potential pathogens in marine microbiomes with different degrees of anthropogenic activity. <i>Environmental Pollution</i> , 2021, 268, 115757.	3.7	12

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3677	Effects of Urbanization and Landscape on Gut Microbiomes in White-Crowned Sparrows. <i>Microbial Ecology</i> , 2021, 81, 253-266.	1.4	24
3678	A hole in the nematosphere: tardigrades and rotifers dominate the cryoconite hole environment, whereas nematodes are missing. <i>Journal of Zoology</i> , 2021, 313, 18-36.	0.8	36
3679	Western-type diet influences mortality from necrotising pancreatitis and demonstrates a central role for butyrate. <i>Gut</i> , 2021, 70, 915-927.	6.1	66
3680	Niche Partitioning of Microbial Communities at an Ancient Vitrified Hillfort: Implications for Vitrified Radioactive Waste Disposal. <i>Geomicrobiology Journal</i> , 2021, 38, 36-56.	1.0	5
3681	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
3682	The quest for absolute abundance: The use of internal standards for DNA-based community ecology. <i>Molecular Ecology Resources</i> , 2021, 21, 30-43.	2.2	42
3683	The effect of Np-magnetite on the granulation process of an SBR reactor used for domestic wastewater treatment. <i>Bioprocess and Biosystems Engineering</i> , 2021, 44, 161-171.	1.7	3
3684	Depth-Dependent Variables Shape Community Structure and Functionality in the Prince Edward Islands. <i>Microbial Ecology</i> , 2021, 81, 396-409.	1.4	5
3685	Effects of Oil Pollution on Indigenous Bacterial Diversity and Community Structure of Soil in Fushun, Liaoning Province, China. <i>Geomicrobiology Journal</i> , 2021, 38, 115-126.	1.0	6
3686	Alterations of the salivary and fecal microbiome in patients with primary sclerosing cholangitis. <i>Hepatology International</i> , 2021, 15, 191-201.	1.9	28
3687	Microbial Communities of Stored Product Mites: Variation by Species and Population. <i>Microbial Ecology</i> , 2021, 81, 506-522.	1.4	12
3688	The effects of straw incorporation with plastic film mulch on soil properties and bacterial community structure on the loess plateau. <i>European Journal of Soil Science</i> , 2021, 72, 979-994.	1.8	40
3689	Characterization of Microbial Community in Cold-Chain Hairtail Fish by High-Throughput Sequencing Technology. <i>Journal of Food Protection</i> , 2021, 84, 1080-1087.	0.8	5
3690	Methane recovery from acidic tofu wastewater using an anaerobic fixed-bed reactor with bamboo as the biofilm carrier. <i>Journal of Material Cycles and Waste Management</i> , 2021, 23, 537-547.	1.6	6
3692	Self-Crossing Leads to Weak Co-Variation of the Bacterial and Fungal Communities in the Rice Rhizosphere. <i>Microorganisms</i> , 2021, 9, 175.	1.6	9
3693	Wastewater treatment alters microbial colonization of microplastics. <i>PLoS ONE</i> , 2021, 16, e0244443.	1.1	72
3694	Impact of long-term fertilizer and summer warming treatments on bulk soil and birch rhizosphere microbial communities in mesic arctic tundra. <i>Arctic, Antarctic, and Alpine Research</i> , 2021, 53, 196-211.	0.4	2

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3695	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
3696	Dynamics and Complexity of Dark Fermentation Microbial Communities Producing Hydrogen From Sugar Beet Molasses in Continuously Operating Packed Bed Reactors. <i>Frontiers in Microbiology</i> , 2020, 11, 612344.	1.5	19
3697	The Apple Microbiome: Structure, Function, and Manipulation for Improved Plant Health. <i>Compendium of Plant Genomes</i> , 2021, , 341-382.	0.3	8
3698	Identification of degrader bacteria and fungi enriched in rhizosphere soil from a toluene phytoremediation site using DNA stable isotope probing. <i>International Journal of Phytoremediation</i> , 2021, 23, 846-856.	1.7	2
3699	Microbiomics and cloud-based analytics advance sustainable soil management. <i>Frontiers in Bioscience - Landmark</i> , 2021, 26, 478-495.	3.0	4
3700	Cervicovaginal bacterial communities in reproductive-aged Tanzanian women with <i>Schistosoma mansoni</i> , <i>Schistosoma haematobium</i> , or without schistosome infection. <i>ISME Journal</i> , 2021, 15, 1539-1550.	4.4	4
3701	Examination of population genetics of the Coconut Rhinoceros Beetle (<i>Oryctes rhinoceros</i>) and the incidence of its biocontrol agent (<i>Oryctes rhinoceros nudivirus</i>) in the South Pacific Islands. <i>Current Research in Insect Science</i> , 2021, 1, 100015.	0.8	15
3702	Mesopelagic microbial carbon production correlates with diversity across different marine particle fractions. <i>ISME Journal</i> , 2021, 15, 1695-1708.	4.4	31
3703	Revealing interactions between root phenolic metabolomes and rhizosphere bacterial communities in <i>Populus euphratica</i> plantations. <i>Biology and Fertility of Soils</i> , 2021, 57, 421-434.	2.3	24
3704	<i>Lactobacillus plantarum</i> HAC01 ameliorates type 2 diabetes in high-fat diet and streptozotocin-induced diabetic mice in association with modulating the gut microbiota. <i>Food and Function</i> , 2021, 12, 6363-6373.	2.1	40
3705	Boosting the value of insoluble dietary fiber to increase gut fermentability through food processing. <i>Food and Function</i> , 2021, 12, 10658-10666.	2.1	13
3706	Nitrogen cycling in coastal sediment microbial communities with seasonally variable benthic nutrient fluxes. <i>Aquatic Microbial Ecology</i> , 2021, 86, 1-19.	0.9	10
3707	Cast iron drinking water pipe biofilms support diverse microbial communities containing antibiotic resistance genes, metal resistance genes, and class 1 integrons. <i>Environmental Science: Water Research and Technology</i> , 2021, 7, 584-598.	1.2	10
3708	Profiling the Gastrointestinal Microbiota. <i>Methods in Molecular Biology</i> , 2021, 2283, 83-92.	0.4	3
3709	Live and ultrasound-inactivated <i>Lactobacillus casei</i> modulate the intestinal microbiota and improve biochemical and cardiovascular parameters in male rats fed a high-fat diet. <i>Food and Function</i> , 2021, 12, 5287-5300.	2.1	15
3710	Early life gut microbiota is associated with rapid infant growth in Hispanics from Southern California. <i>Gut Microbes</i> , 2021, 13, 1961203.	4.3	32
3711	Accurate identification and quantification of commensal microbiota bound by host immunoglobulins. <i>Microbiome</i> , 2021, 9, 33.	4.9	29
3712	Progressive Shifts in the Gut Microbiome Reflect Prediabetes and Diabetes Development in a Treatment-Naive Mexican Cohort. <i>Frontiers in Endocrinology</i> , 2020, 11, 602326.	1.5	13

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3713	Application of molecular biological tools to monitor process efficiency. , 2021, , 475-498.		0
3714	Roux-en-Y gastric bypass surgery in Zucker rats induces bacterial and systemic metabolic changes independent of caloric restriction-induced weight loss. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	18
3715	Breastfeeding promotes early neonatal regulatory T cell expansion and immune tolerance of non-inherited maternal antigens. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 2447-2460.	2.7	40
3716	The emerging roles of the gut microbiome in allogeneic hematopoietic stem cell transplantation. <i>Gut Microbes</i> , 2021, 13, 1966262.	4.3	4
3717	Feeding cashew nut shell liquid decreases methane production from feces by altering fecal bacterial and archaeal communities in Thai local ruminants. <i>Animal Science Journal</i> , 2021, 92, e13569.	0.6	3
3718	Introduction to Forensic DNA Typing and Current Trends. , 2021, , 1-21.		0
3719	Anthelmintic drugs modulate the acute phase immune response but not the microbiota in wild Song Sparrows. <i>Auk</i> , 2021, 138, .	0.7	1
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3806	Characteristics of gut microbiota in pigs with different breeds, growth periods and genders. <i>Microbial Biotechnology</i> , 2022, 15, 793-804.	2.0	20
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3821	The Structure of Rhizosphere Fungal Communities of Wild and Domesticated Rice: Changes in Diversity and Co-occurrence Patterns. <i>Frontiers in Microbiology</i> , 2021, 12, 610823.	1.5	29
3822	Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. <i>International Journal of Cancer</i> , 2021, 148, 2712-2723.	2.3	33
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3841	Methotrexate impacts conserved pathways in diverse human gut bacteria leading to decreased host immune activation. <i>Cell Host and Microbe</i> , 2021, 29, 362-377.e11.	5.1	70
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3846	Dynamics of Gut Microbiota Recovery after Antibiotic Exposure in Young and Old Mice (A Pilot Study). <i>Microorganisms</i> , 2021, 9, 647.	1.6	15
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3853	Evaluating a Laboratory Flume Microbiome as a Window Into Natural Riverbed Biogeochemistry. <i>Frontiers in Water</i> , 2021, 3, .	1.0	3
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3856	Dysregulated Free Fatty Acid Receptor 2 Exacerbates Colonic Adenoma Formation in <i>Apc^{Min/+}</i> Mice: Relation to Metabolism and Gut Microbiota Composition. <i>Journal of Cancer Prevention</i> , 2021, 26, 32-40.	0.8	5
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3868	Compilation of longitudinal microbiota data and hospitalome from hematopoietic cell transplantation patients. <i>Scientific Data</i> , 2021, 8, 71.	2.4	19
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3874	Persistent microbiome members in the common bean rhizosphere: an integrated analysis of space, time, and plant genotype. <i>ISME Journal</i> , 2021, 15, 2708-2722.	4.4	76
3875	A guide to minimize contamination issues in microbiome restoration studies. <i>Restoration Ecology</i> , 2021, 29, e13358.	1.4	6
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3881	Bacterial diversity and flavor profile of Zha-Chili, a traditional fermented food in China. <i>Food Research International</i> , 2021, 141, 110112.	2.9	57
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3960	Microbiota populations in supragingival plaque, subgingival plaque, and saliva habitats of adult dogs. <i>Animal Microbiome</i> , 2021, 3, 38.	1.5	13
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3988	Intestinal Microbes of Hooded Cranes (<i>Grus monacha</i>) Wintering in Three Lakes of the Middle and Lower Yangtze River Floodplain. <i>Animals</i> , 2021, 11, 1390.	1.0	3
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3995	Taxonomic classification of the bacterial endosymbiont <i>Wolbachia</i> based on next-generation sequencing: is there molecular evidence for its presence in tardigrades?. <i>Genome</i> , 2021, 64, 951-958.	0.9	13
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4007	Red Fluorescence of European Hedgehog (<i>Erinaceus europaeus</i>) Spines Results from Free-Base Porphyrins of Potential Microbial Origin. <i>Journal of Chemical Ecology</i> , 2021, 47, 588-596.	0.9	10
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4012	Effects of foraging site distances on the intestinal bacterial community compositions of the sympatric wintering Hooded Crane (<i>Grus monacha</i>) and Domestic Duck (<i>Anas platyrhynchos</i>)	0.7	10
4013	Antibiotic resistance, antimicrobial residues and bacterial community diversity in pasture-raised poultry, swine and beef cattle manures. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	13
4014	Characterization of bacterial community and flavor differences of different types of Douchi. <i>Food Science and Nutrition</i> , 2021, 9, 3460-3469.	1.5	14
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4019	Editorial: Microbial Utilization and Transformation of Dissolved Organic Matter in Aquatic Environments—From Streams to the Deep Ocean. <i>Frontiers in Microbiology</i> , 2021, 12, 668560.	1.5	1
4020	Microbial communities of wild-captured Kemp's ridley (<i>Lepidochelys kempii</i>) and green sea turtles (<i>Chelonia mydas</i>). <i>Endangered Species Research</i> , 2021, 45, 21-36.	1.2	7
4022	Illumina Sequencing of 18S/16S rRNA Reveals Microbial Community Composition, Diversity, and Potential Pathogens in 17 Turfgrass Seeds. <i>Plant Disease</i> , 2021, 105, 1328-1338.	0.7	3
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4033	Effects of the dietary grain content on rumen and fecal microbiota of dairy cows. <i>Canadian Journal of Animal Science</i> , 2021, 101, 274-286.	0.7	10
4034	Selection of lactic acid bacteria with promising probiotic aptitudes from fruit and ability to survive in different food matrices. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 2257-2269.	0.8	13
4036	Distinct microbial communities alter litter decomposition rates in a fertilized coastal plain wetland. <i>Ecosphere</i> , 2021, 12, e03619.	1.0	6
4037	Markers of metabolic health and gut microbiome diversity: findings from two population-based cohort studies. <i>Diabetologia</i> , 2021, 64, 1749-1759.	2.9	30
4038	Influence of shrub willow buffers strategically integrated in an Illinois corn-soybean field on soil health and microbial community composition. <i>Science of the Total Environment</i> , 2021, 772, 145674.	3.9	6
4039	Phage vB_PaeS-PAJD-1 Rescues Murine Mastitis Infected With Multidrug-Resistant <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 689770.	1.8	7
4040	Aerobic bacterial methane synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	36
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4044	<i>Miscanthus</i> Grass as a Novel Functional Fiber Source in Extruded Feline Diets. <i>Frontiers in Veterinary Science</i> , 2021, 8, 668288.	0.9	4
4045	Natural genetic variation drives microbiome selection in the <i>Caenorhabditis elegans</i> gut. <i>Current Biology</i> , 2021, 31, 2603-2618.e9.	1.8	48
4046	Dental Biofilm and Saliva Microbiome and Its Interplay with Pediatric Allergies. <i>Microorganisms</i> , 2021, 9, 1330.	1.6	9

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4053	Association of biochar properties with changes in soil bacterial, fungal and fauna communities and nutrient cycling processes. <i>Biochar</i> , 2021, 3, 239-254.	6.2	112
4054	Intermittent Hypoxia and Hypercapnia Alter Diurnal Rhythms of Luminal Gut Microbiome and Metabolome. <i>MSystems</i> , 2021, 6, e0011621.	1.7	27
4055	Nasopharyngeal Microbiota in SARS-CoV-2 Positive and Negative Patients. <i>Biological Procedures Online</i> , 2021, 23, 10.	1.4	26
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4061	Detection of cell-free microbial DNA using a contaminant-controlled analysis framework. <i>Genome Biology</i> , 2021, 22, 187.	3.8	22
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4079	Fecal Methylmercury Correlates With Gut Microbiota Taxa in Pacific Walruses (<i>Odobenus rosmarus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.5	7
4080	Gut Microbiota Dynamics in Natural Populations of <i>Pintomyia evansi</i> under Experimental Infection with <i>Leishmania infantum</i> . <i>Microorganisms</i> , 2021, 9, 1214.	1.6	6
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4085	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	4.9	37
4086	Use of Legumes and Yeast as Novel Dietary Protein Sources in Extruded Canine Diets. <i>Frontiers in Veterinary Science</i> , 2021, 8, 667642.	0.9	9
4088	Editorial: The Wildlife Gut Microbiome and Its Implication for Conservation Biology. <i>Frontiers in Microbiology</i> , 2021, 12, 697499.	1.5	20

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4091	Chronic Stress-Induced Depression and Anxiety Priming Modulated by Gut-Brain-Axis Immunity. <i>Frontiers in Immunology</i> , 2021, 12, 670500.	2.2	54
4092	Comparative Genomics Reveals Potential Mechanisms of Plant Beneficial Effects of a Novel Bamboo-Endophytic Bacterial Isolate <i>Paraburkholderia sacchari</i> Suichang626. <i>Frontiers in Microbiology</i> , 2021, 12, 686998.	1.5	5
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4095	Projection of Gut Microbiome Pre- and Post-Bariatric Surgery To Predict Surgery Outcome. <i>MSystems</i> , 2021, 6, e0136720.	1.7	14
4096	Metagenomic Exploration of Bacterial Community Structure of Earthwormsâ€™ Gut. <i>Journal of Pure and Applied Microbiology</i> , 2021, 15, 1156-1172.	0.3	5
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4102	Ditching Nutrients: Roadside Drainage Networks are Hotspots for Microbial Nitrogen Removal. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2020JG006115.	1.3	9
4103	Crop rotation reduces the frequency of anaerobic soil bacteria in Red Latosol of Brazil. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 2169-2177.	0.8	3
4104	Captivity reduces diversity and shifts composition of the Brown Kiwi microbiome. <i>Animal Microbiome</i> , 2021, 3, 48.	1.5	36
4105	Diet-induced microbiome shifts of sympatric overwintering birds. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5993-6005.	1.7	17
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4107	Protistan grazing impacts microbial communities and carbon cycling at deep-sea hydrothermal vents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
4108	Depth-dependent influence of biochar application on the abundance and community structure of diazotrophic under sugarcane growth. <i>PLoS ONE</i> , 2021, 16, e0253970.	1.1	16

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4110	Effect of Increasing C/N Ratio on Performance and Microbial Community Structure in a Membrane Bioreactor with a High Ammonia Load. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 8070.	1.2	2
4111	Microbial Chain Elongation and Subsequent Fermentation of Elongated Carboxylates as H ₂ -Producing Processes for Sustained Reductive Dechlorination of Chlorinated Ethenes. <i>Environmental Science & Technology</i> , 2021, 55, 10398-10410.	4.6	30
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4113	Digital soil science and beyond. <i>Soil Science Society of America Journal</i> , 2021, 85, 1313-1331.	1.2	11
4114	<i>Lactobacillus plantarum</i> HAC01 Supplementation Improves Glycemic Control in Prediabetic Subjects: A Randomized, Double-Blind, Placebo-Controlled Trial. <i>Nutrients</i> , 2021, 13, 2337.	1.7	22
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4116	Microbial Interventions to Control and Reduce Blood Pressure in Australia (MICRoBIA): rationale and design of a double-blinded randomised cross-over placebo controlled trial. <i>Trials</i> , 2021, 22, 496.	0.7	17
4117	Drivers of soil microbial community assembly during recovery from selective logging and clear-cutting. <i>Journal of Applied Ecology</i> , 2021, 58, 2231-2242.	1.9	3
4119	Haploflow: strain-resolved de novo assembly of viral genomes. <i>Genome Biology</i> , 2021, 22, 212.	3.8	16
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4123	Responses of cucumber (<i>Cucumis sativus</i> L.) rhizosphere microbial community to some agronomic management practices. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	4
4124	Protective Effect of Baicalin against <i>Clostridioides difficile</i> Infection in Mice. <i>Antibiotics</i> , 2021, 10, 926.	1.5	4
4125	Dynamics of dark fermentation microbial communities in the light of lactate and butyrate production. <i>Microbiome</i> , 2021, 9, 158.	4.9	47
4126	Distribution of Hydrogen-Producing Bacteria in Tibetan Hot Springs, China. <i>Frontiers in Microbiology</i> , 2021, 12, 569020.	1.5	4
4127	Changes in the Microbial Community in Soybean Plots Treated with Biochar and Poultry Litter. <i>Agronomy</i> , 2021, 11, 1428.	1.3	6
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4131	Chemical composition controls the decomposition of organic amendments and influences the microbial community structure in agricultural soils. <i>Carbon Management</i> , 2021, 12, 359-376.	1.2	10
4133	High-throughput sequencing of the microbial community associated with the physicochemical properties of meju (dried fermented soybean) and doenjang (traditional Korean fermented soybean) Tj ETQq1 1 0.784314 rgB6 /Overfoc		
4135	Biodegradation kinetics of organic micropollutants and microbial community dynamics in a moving bed biofilm reactor. <i>Chemical Engineering Journal</i> , 2021, 415, 128963.	6.6	22
4136	Comparison of Preservation and Extraction Methods on Five Taxonomically Disparate Coral Microbiomes. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
4138	Bioconversion of food waste to volatile fatty acids: Impact of microbial community, pH and retention time. <i>Chemosphere</i> , 2021, 275, 129981.	4.2	69
4139	Microbiomes of Various Maternal Body Systems Are Predictive of Calf Digestive Bacterial Ecology. <i>Animals</i> , 2021, 11, 2210.	1.0	5
4140	Minimal-moderate variation of human oral virome and microbiome in IgA deficiency. <i>Scientific Reports</i> , 2021, 11, 14913.	1.6	5
4141	Molecular characterization of the bacterial communities present in sheep's milk and cheese produced in South Brazilian Region via 16S rRNA gene metabarcoding sequencing. <i>LWT - Food Science and Technology</i> , 2021, 147, 111579.	2.5	11
4142	Competition and community succession link N transformation and greenhouse gas emissions in urine patches. <i>Science of the Total Environment</i> , 2021, 779, 146318.	3.9	6
4143	Local vegetation and hydroperiod influence spatial and temporal patterns of carbon and microbe response to wetland rehabilitation. <i>Applied Soil Ecology</i> , 2021, 163, 103917.	2.1	6
4144	Administration of All-Trans Retinoic Acid to Pregnant Sows Alters Gut Bacterial Community of Neonatal Piglets With Different Hoxa1 Genotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 712212.	1.5	1
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4148	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021, 373, 181-186.	6.0	126
4149	Changes in Soil Microbial Community Structure Following Different Tree Species Functional Traits Afforestation. <i>Forests</i> , 2021, 12, 1018.	0.9	2

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4151	Prokaryotic community diversity in the sediments of saline lagoons and its resistance to seasonal disturbances by water level cycles. <i>Journal of Soils and Sediments</i> , 2021, 21, 3169-3184.	1.5	5
4152	Assessing age, breeding stage, and mating activity as drivers of variation in the reproductive microbiome of female tree swallows. <i>Ecology and Evolution</i> , 2021, 11, 11398-11413.	0.8	9
4154	High ambient temperature exposure during late gestation disrupts glycolipid metabolism and hepatic mitochondrial function tightly related to gut microbial dysbiosis in pregnant mice. <i>Microbial Biotechnology</i> , 2021, 14, 2116-2129.	2.0	9
4155	Bioelectrochemical anoxic ammonium nitrogen removal by an MFC driven single chamber microbial electrolysis cell. <i>Chemosphere</i> , 2021, 274, 129715.	4.2	39
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4159	Simultaneous nitrification-denitrification (SND) using a thermoplastic gel as support: pollutants removal and microbial community in a pilot-scale biofilm membrane bioreactor. <i>Environmental Technology (United Kingdom)</i> , 2022, 43, 4411-4425.	1.2	11
4160	Vertical Stratification of Dissolved Organic Matter Linked to Distinct Microbial Communities in Subtropic Estuarine Sediments. <i>Frontiers in Microbiology</i> , 2021, 12, 697860.	1.5	12
4161	MYCOBACTERIA IN SKIN LESIONS AND THE HABITAT OF THE ENDANGERED HOUSTON TOAD (ANAXYRUS TIGRIS) IN THE OVERLOOK	0.3	0
4162	Low-Level Anorectal HIV Shedding despite Effective Antiretroviral Therapy Is Not Driven by Mucosal Inflammation. <i>Journal of Immunology</i> , 2021, 207, 685-695.	0.4	0
4163	Influenza A virus infection in turkeys induces respiratory and enteric bacterial dysbiosis correlating with cytokine gene expression. <i>PeerJ</i> , 2021, 9, e11806.	0.9	2
4164	Interactions between <i>Teladorsagia circumcincta</i> Infections and Microbial Composition of Sheep with or without Successful Monepantel Treatment—A Preliminary Study. <i>Ruminants</i> , 2021, 1, 31-45.	0.4	2
4165	Disentangling the Complexity of the Rumen Microbial Diversity Through Fractionation Using a Sucrose Density Gradient. <i>Frontiers in Microbiology</i> , 2021, 12, 664754.	1.5	2
4166	Landscape analyses using eDNA metabarcoding and Earth observation predict community biodiversity in California. <i>Ecological Applications</i> , 2021, 31, e02379.	1.8	23
4167	Boreal soil microbial diversity and seed onion mycorrhizal colonization is unaffected by preceding one season crop cultivation. <i>European Journal of Soil Biology</i> , 2021, 105, 103335.	1.4	2
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4171	Auto-selection of microorganisms of sewage sludge used as an inoculum for fermentative hydrogen production from different substrates. <i>International Journal of Hydrogen Energy</i> , 2021, 46, 29834-29845.	3.8	18
4172	<i>Vibrio cholerae</i> Infection Induces Strain-Specific Modulation of the Zebrafish Intestinal Microbiome. <i>Infection and Immunity</i> , 2021, 89, e0015721.	1.0	8
4173	Influence of Recycled Waste Compost on Soil Food Webs, Nutrient Cycling and Tree Growth in a Young Almond Orchard. <i>Agronomy</i> , 2021, 11, 1745.	1.3	1
4174	Herbivory shapes the rhizosphere bacterial microbiota in potato plants. <i>Environmental Microbiology Reports</i> , 2021, 13, 805-811.	1.0	16
4176	Changes in the Gut Bacteria Composition of Healthy Men with the Same Nutritional Profile Undergoing 10-Week Aerobic Exercise Training: A Randomized Controlled Trial. <i>Nutrients</i> , 2021, 13, 2839.	1.7	17
4177	The Impact of Enriched Resistant Starch Type 2 Cookies on the Gut Microbiome in Hemodialysis Patients: A Randomized Controlled Trial. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2100374.	1.5	19
4178	Mucosal Bacteria Modulate <i>Candida albicans</i> Virulence in Oropharyngeal Candidiasis. <i>MBio</i> , 2021, 12, e0193721.	1.8	22
4179	Soil biota shift with land use change from pristine rainforest and Savannah (Cerrado) to agriculture in southern Amazonia. <i>Molecular Ecology</i> , 2021, 30, 4899-4912.	2.0	10
4180	Lactic microbiota of the minas artisanal cheese produced in the serro region, Minas Gerais, Brazil. <i>LWT - Food Science and Technology</i> , 2021, 148, 111698.	2.5	9
4181	Variations in bacterial and archaeal community structure and diversity along the soil profiles of a peatland in Southwest China. <i>Environmental Science and Pollution Research</i> , 2022, 29, 2276-2286.	2.7	5
4182	Geographic source estimation using airborne plant environmental DNA in dust. <i>Scientific Reports</i> , 2021, 11, 16238.	1.6	10
4183	Oral Microbiota Identifies Patients in Early Onset Rheumatoid Arthritis. <i>Microorganisms</i> , 2021, 9, 1657.	1.6	23
4184	Assessment of microbial α -diversity in one meter squared topsoil. <i>Soil Ecology Letters</i> , 2022, 4, 224-236.	2.4	10
4185	Protocol of the Snuggle Bug/Acurrucadito Study: a longitudinal study investigating the influences of sleep-wake patterns and gut microbiome development in infancy on rapid weight gain, an early risk factor for obesity. <i>BMC Pediatrics</i> , 2021, 21, 374.	0.7	4
4186	The influence of electrokinetic bioremediation on subsurface microbial communities at a perchloroethylene contaminated site. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 6489-6497.	1.7	3
4187	Production of Two Highly Abundant 2-Methyl-Branched Fatty Acids by Blooms of the Globally Significant Marine Cyanobacteria <i>Trichodesmium erythraeum</i> . <i>ACS Omega</i> , 2021, 6, 22803-22810.	1.6	2
4188	Metagenomic Investigation Uncovers Presence of Probiotic-Type Microbiome in Kalparasa® (Fresh) Tj ETQq1 1 0.784314 rgBT /Over 1.5	1.5	8

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4189	Divergent drivers determine soil bacterial β -diversity of forest and grassland ecosystems in Northwest China. <i>Global Ecology and Conservation</i> , 2021, 28, e01622.	1.0	4
4190	Plumage manipulation alters associations between behaviour, physiology, the internal microbiome and fitness. <i>Animal Behaviour</i> , 2021, 178, 11-36.	0.8	10
4191	The <i>Vibrio cholerae</i> Type Six Secretion System Is Dispensable for Colonization but Affects Pathogenesis and the Structure of Zebrafish Intestinal Microbiome. <i>Infection and Immunity</i> , 2021, 89, e0015121.	1.0	10
4192	PD-L1+ and XCR1+ dendritic cells are region-specific regulators of gut homeostasis. <i>Nature Communications</i> , 2021, 12, 4907.	5.8	18
4193	The Light-to-Nutrient Ratio in Alpine Lakes: Different Scenarios of Bacterial Nutrient Limitation and Community Structure in Lakes Above and Below the Treeline. <i>Microbial Ecology</i> , 2022, 83, 837-849.	1.4	0
4195	Changes in bacterial community and expression of genes involved in intestinal innate immunity in the jejunum of newborn lambs during the first 24 hours of life. <i>Journal of Dairy Science</i> , 2021, 104, 9263-9275.	1.4	6
4196	Healthy Oral Lifestyle Behaviours Are Associated with Favourable Composition and Function of the Oral Microbiota. <i>Microorganisms</i> , 2021, 9, 1674.	1.6	5
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5075	Alone Yet Not Alone: Frankia Lives Under the Same Roof With Other Bacteria in Actinorhizal Nodules. <i>Frontiers in Microbiology</i> , 2021, 12, 749760.	1.5	10
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5077	The Diversity and Function of Soil Bacteria and Fungi Mediated by Plant and Soil Process Under Altered Nitrogen and Rainfall Patterns in a Temperate Steppe. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
5078	Long-Term Metal Pollution Shifts Microbial Functional Profiles of Nitrification and Denitrification in Agricultural Soils. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
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5081	Metagenomic analysis of rhizosphere microbiome provides insights into occurrence of iron deficiency chlorosis in field of Asian pears. <i>BMC Microbiology</i> , 2022, 22, 18.	1.3	2
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5089	Age-Associated Gut Dysbiosis, Marked by Loss of Butyrogenic Potential, Correlates With Altered Plasma Tryptophan Metabolites in Older People Living With HIV. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2022, 89, S56-S64.	0.9	7
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5094	Biodegradation of PFOA in microbial electrolysis cells by <i>Acidimicrobiaceae</i> sp. strain A6. <i>Chemosphere</i> , 2022, 292, 133506.	4.2	26
5095	The effect of tea fermented with <i>Lactobacillus pentosus</i> OLL203984 on gastrointestinal transit time and gut microbiota in Ncx/Hox11L1-deficient mice. <i>Japanese Journal of Lactic Acid Bacteria</i> , 2020, 31, 99-104.	0.1	0
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5109	Predicting fungal infection rate and severity with skin-associated microbial communities on amphibians. <i>Molecular Ecology</i> , 2022, 31, 2140-2156.	2.0	7
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5114	Degradation of Sugarcane Bagasse by Cockroach Consortium Bacteria. <i>Bioenergy Research</i> , 2022, 15, 1144-1156.	2.2	3
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5119	Bovine respiratory microbiota of feedlot cattle and its association with disease. <i>Veterinary Research</i> , 2022, 53, 4.	1.1	28
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5133	Quinoa Soluble Fiber and Quercetin Alter the Composition of the Gut Microbiome and Improve Brush Border Membrane Morphology In Vivo (<i>Gallus gallus</i>). <i>Nutrients</i> , 2022, 14, 448.	1.7	10
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5136	Metagenomic Insights into the Composition and Function of Microbes Associated with the Rootzone of <i>Datura innoxia</i> . <i>BioTech</i> , 2022, 11, 1.	1.3	4
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5138	Salivary Microbial Dysbiosis Is Associated With Peri-Implantitis: A Case-Control Study in a Brazilian Population. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 696432.	1.8	8

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5149	Environmental filtering controls soil biodiversity in wet tropical ecosystems. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108571.	4.2	3
5150	Polar soils exhibit distinct patterns in microbial diversity and dominant phylotypes. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108550.	4.2	19
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5217	iMeta: Integrated meta-omics for biology and environments. , 2022, 1, .		13
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6243	Microbiota responses to different prebiotics are conserved within individuals and associated with habitual fiber intake. <i>Microbiome</i> , 2022, 10, .	4.9	33
6244	Evolved high aerobic capacity has context-specific effects on gut microbiota. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
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6286	The Effect of Intensity-Modulated Radiotherapy to the Head and Neck Region on the Oral Innate Immune Response and Oral Microbiome: A Prospective Cohort Study of Head and Neck Tumour Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9594.	1.8	4
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6311	Microbiome analysis: An emerging forensic investigative tool. <i>Forensic Science International</i> , 2022, 340, 111462.	1.3	7
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6353	Plant Endophytes in Growth Promotion and Sustainable Management of Crop Pests. , 2022, , 429-454.		0
6354	Dynamics of microbial community and enzyme activities during preparation of <i>Agaricus bisporus</i> compost substrate. <i>ISME Communications</i> , 2022, 2, .	1.7	5
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6363	Obligate Gut Symbiotic Association with <i>Caballeronia</i> in the Mulberry Seed Bug <i>Paradiseus dissimilis</i> (Lygaeoidea: Rhyparochromidae). <i>Microbial Ecology</i> , 2023, 86, 1307-1318.	1.4	3
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6368	Effects of biochar on soil microbial diversity and community structure in clay soil. <i>Annals of Microbiology</i> , 2022, 72, .	1.1	12
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6375	Long-term fertilization has different impacts on bacterial communities and phosphorus forms in sugarcane rhizosphere and bulk soils under low-P stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
6377	Impact of key parameters involved with plant-microbe interaction in context to global climate change. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6379	Management-induced shifts in rhizosphere bacterial communities contribute to the control of pathogen causing citrus greening disease. , 2022, 1, 275-286.		4
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6384	Dynamic gill and mucus microbiomes during a gill disease episode in farmed Atlantic salmon. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
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6386	Temporal variation in the prokaryotic community of a nearshore marine environment. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
6388	Variation in bacterial composition, diversity, and activity across different subglacial basal ice types. <i>Cryosphere</i> , 2022, 16, 4033-4051.	1.5	0
6389	Effects of lactic acid bacteria-fermented formula milk supplementation on ileal microbiota, transcriptomic profile, and mucosal immunity in weaned piglets. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	1
6391	Relation Between Dietary Protein Intake and Gut Microbiome Composition in Community-Dwelling Older Men: Findings from the Osteoporotic Fractures in Men Study (MrOS). <i>Journal of Nutrition</i> , 2022, 152, 2877-2887.	1.3	6
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6394	An increase in sludge loading rate induces gel fouling in membrane bioreactors treating real sewage. <i>Chemosphere</i> , 2022, 309, 136557.	4.2	1
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6396	<i>Plectus</i> of the Prairie: A Case Study of Taxonomic Resolution from a Nematode Biodiversity Survey. <i>Journal of Nematology</i> , 2022, 54, .	0.4	1
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6398	Effects of antibacterial peptide-producing <i>Bacillus subtilis</i> , gallic acid, and cellulase on fermentation quality and bacterial community of whole-plant corn silage. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
6399	Exploratory analysis of one versus two-day intermittent fasting protocols on the gut microbiome and plasma metabolome in adults with overweight/obesity. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	8
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6406	Functional differentiation determines the molecular basis of the symbiotic lifestyle of <i>Ca. Nanohaloarchaeota</i> . <i>Microbiome</i> , 2022, 10, .	4.9	8
6407	Plant and Soil Core Mycobiomes in a Two-Year Sorghumâ€“Legume Intercropping System of Underutilized Crops in South Africa. <i>Microorganisms</i> , 2022, 10, 2079.	1.6	2
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6412	Strain level and comprehensive microbiome analysis in inflammatory bowel disease via multi-technology meta-analysis identifies key bacterial influencers of disease. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
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6415	Effect of <i>Lactobacillus casei</i> fermented milk on fracture healing in osteoporotic mice. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
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6427	Global airborne bacterial community interactions with Earth's microbiomes and anthropogenic activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	29
6428	Oral gut bacterial profiles discriminate between periodontal health and diseases. <i>Journal of Periodontal Research</i> , 2022, 57, 1227-1237.	1.4	4
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6456	Antibiotic properties of <i>Satureja montana</i> L. hydrolate in bacteria and fungus of clinical interest and its impact in non-target environmental microorganisms. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
6457	Effect of chia flour associated with high fat diet on intestinal health in female ovariectomized Wistar rats. <i>European Journal of Nutrition</i> , 0, , .	1.8	3
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6557	Internal and external microbiota of home-caught <i>Anopheles coluzzii</i> (Diptera: Culicidae) from Côte d'Ivoire, Africa: Mosquitoes are filthy. <i>PLoS ONE</i> , 2022, 17, e0278912.	1.1	2
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