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Citation Report

#	ARTICLE	IF	CITATIONS
5	Some Principles of Spray Processing. Journal of the SMPTE, 1956, 65, 92-96.	0.3	3
6	Automated group assignment in large phylogenetic trees using GRUNT: GRouping, Ungrouping, Naming Tool. BMC Bioinformatics, 2007, 8, 402.	1.2	9
7	Application of temperature gradient gel electrophoresis technique to monitor changes in the structure of the eukaryotic leaf-epiphytic community of Posidonia oceanica. Marine Biology, 2008, 155, 451-460.	0.7	2
8	The membrane bioreactor: A novel tool to grow anammox bacteria as free cells. Biotechnology and Bioengineering, 2008, 101, 286-294.	1.7	458
9	The diversity of small eukaryotic phytoplankton ($\approx 3 \mu\text{m}$) in marine ecosystems. FEMS Microbiology Reviews, 2008, 32, 795-820.	3.9	363
10	Molecular characterization of bacterial communities mineralizing benzene under sulfate-reducing conditions. FEMS Microbiology Ecology, 2008, 66, 143-157.	1.3	107
11	Potential core species and satellite species in the bacterial community within the rabbit caecum. FEMS Microbiology Ecology, 2008, 66, 620-629.	1.3	76
12	Single-cell identification in microbial communities by improved fluorescence in situ hybridization techniques. Nature Reviews Microbiology, 2008, 6, 339-348.	13.6	647
13	The ecology and biotechnology of sulphate-reducing bacteria. Nature Reviews Microbiology, 2008, 6, 441-454.	13.6	1,737
14	Symbiotic diversity in marine animals: the art of harnessing chemosynthesis. Nature Reviews Microbiology, 2008, 6, 725-740.	13.6	875
15	Wide genetic diversity of picoplanktonic green algae (Chloroplastida) in the Mediterranean Sea uncovered by a phylum-biased PCR approach. Environmental Microbiology, 2008, 10, 1804-1822.	1.8	112
16	A microdiversity study of anammox bacteria reveals a novel <i>Candidatus</i> Scalindua phylotype in marine oxygen minimum zones. Environmental Microbiology, 2008, 10, 3106-3119.	1.8	250
17	probeCheck – a central resource for evaluating oligonucleotide probe coverage and specificity. Environmental Microbiology, 2008, 10, 2894-2898.	1.8	170
18	XplorSeq: A software environment for integrated management and phylogenetic analysis of metagenomic sequence data. BMC Bioinformatics, 2008, 9, 420.	1.2	47
19	The All-Species Living Tree project: A 16S rRNA-based phylogenetic tree of all sequenced type strains. Systematic and Applied Microbiology, 2008, 31, 241-250.	1.2	884
20	Reclassification of Rhodobium marinum and Rhodobium pfennigii as Afifella marina gen. nov. comb. nov. and Afifella pfennigii comb. nov., a new genus of photoheterotrophic Alphaproteobacteria and emended descriptions of Rhodobium, Rhodobium orientis and Rhodobium gokarnense. Systematic and Applied Microbiology, 2008, 31, 339-351.	1.2	111
21	Sulphide oxidation to elemental sulphur in a membrane bioreactor: Performance and characterization of the selected microbial sulphur-oxidizing community. Systematic and Applied Microbiology, 2008, 31, 461-473.	1.2	44
22	A standard operating procedure for phylogenetic inference (SOPPI) using (rRNA) marker genes. Systematic and Applied Microbiology, 2008, 31, 251-257.	1.2	77

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24	The Pervasive Effects of an Antibiotic on the Human Gut Microbiota, as Revealed by Deep 16S rRNA Sequencing. <i>PLoS Biology</i> , 2008, 6, e280.	2.6	2,013
25	A renaissance for the pioneering 16S rRNA gene. <i>Current Opinion in Microbiology</i> , 2008, 11, 442-446.	2.3	418
26	Bacteria from hydrocarbon seep areas growing on short-chain alkanes. <i>Trends in Microbiology</i> , 2008, 16, 138-141.	3.5	19
27	StrainInfo.net Web Services: Enabling Microbiologic Workflows Such as Phylogenetic Tree Building and Biomarker Comparison. , 2008, , .		0
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32	<i>Chlamydiae</i> as Symbionts in Eukaryotes. <i>Annual Review of Microbiology</i> , 2008, 62, 113-131.	2.9	256
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34	Revealing unique properties of the ribosome using a network based analysis. <i>Nucleic Acids Research</i> , 2008, 36, 4641-4652.	6.5	24
35	Pyrosequencing analysis of the Oral Microflora of healthy adults. <i>Journal of Dental Research</i> , 2008, 87, 1016-1020.	2.5	574
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38	Picoplankton diversity in the South-East Pacific Ocean from cultures. <i>Biogeosciences</i> , 2008, 5, 203-214.	1.3	45
39	Environmental and Microbial Ecology in Sulfur Mats Responsible for the Biological Removal of Hydrogen Sulfide from Biogas. <i>Journal of Environmental Conservation Engineering</i> , 2009, 38, 642-651.	0.0	1
40	A Method for Studying Protistan Diversity Using Massively Parallel Sequencing of V9 Hypervariable Regions of Small-Subunit Ribosomal RNA Genes. <i>PLoS ONE</i> , 2009, 4, e6372.	1.1	707
41	A High-Throughput DNA Sequence Aligner for Microbial Ecology Studies. <i>PLoS ONE</i> , 2009, 4, e8230.	1.1	280

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42	<i>Gracilimonas tropica</i> gen. nov., sp. nov., isolated from a <i>Synechococcus</i> culture. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 1167-1172.	0.8	43
43	Free-Living Protozoa in Two Unchlorinated Drinking Water Supplies, Identified by Phylogenetic Analysis of 18S rRNA Gene Sequences. Applied and Environmental Microbiology, 2009, 75, 4736-4746.	1.4	76
44	<i>Glaciibacter superstes</i> gen. nov., sp. nov., a novel member of the family Microbacteriaceae isolated from a permafrost ice wedge. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 482-486.	0.8	41
45	The radiocarbon signature of microorganisms in the mesopelagic ocean. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6513-6518.	3.3	140
46	New Design Strategy for Development of Specific Primer Sets for PCR-Based Detection of <i>Chlorophyceae</i> and <i>Bacillariophyceae</i> in Environmental Samples. Applied and Environmental Microbiology, 2009, 75, 5729-5733.	1.4	40
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52	Asthma and Infections. , 0, , .		0
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61	<i>Desulfovibrio paquesii</i> sp. nov., a hydrogenotrophic sulfate-reducing bacterium isolated from a synthesis-gas-fed bioreactor treating zinc- and sulfate-rich wastewater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 229-233.	0.8	25
62	<i>Demequina lutea</i> sp. nov., isolated from a high Arctic permafrost soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 649-653.	0.8	26
63	Cultivation of Anaerobic and Facultatively Anaerobic Bacteria from Spacecraft-Associated Clean Rooms. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3484-3491.	1.4	100
64	Why Would Phylogeneticists Ignore Computerized Sequence Alignment?. <i>Systematic Biology</i> , 2009, 58, 150-158.	2.7	96
65	<i>Luteibacter anthropi</i> sp. nov., isolated from human blood, and reclassification of <i>Dyella yeojuensis</i> Kim et al. 2006 as <i>Luteibacter yeojuensis</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2884-2887.	0.8	29
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79	Description of <i>Tessaracoccus profundus</i> sp.nov., a deep-subsurface actinobacterium isolated from a Chesapeake impact crater drill core (940m depth). <i>Antonie Van Leeuwenhoek</i> , 2009, 96, 515-526.	0.7	27
80	Members of the Candidate Division OP10 are spread in a variety of environments. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 347-353.	1.7	15
81	Bacterial Community Dynamics in a Seagrass (<i>Posidonia oceanica</i>) Meadow Sediment. <i>Estuaries and Coasts</i> , 2009, 32, 276-286.	1.0	43
82	Diverse communities of active Bacteria and Archaea along oxygen gradients in coral reef sediments. <i>Coral Reefs</i> , 2009, 28, 15-26.	0.9	30
83	Evaluation of the 18S rRNA clone library approach to study the diversity of the macroeukaryotic leaf-epiphytic community of the seagrass <i>Posidonia oceanica</i> (L.) Delile. <i>Marine Biology</i> , 2009, 156, 1963-1976.	0.7	6
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109	DNA-based species level detection of <i>Glomeromycota</i> : one PCR primer set for all arbuscular mycorrhizal fungi. <i>New Phytologist</i> , 2009, 183, 212-223.	3.5	353
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133	Ecology of the rare microbial biosphere of the Arctic Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22427-22432.	3.3	488
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139	Studies on Monitoring and Tracking Genetic Resources: An Executive Summary. <i>Standards in Genomic Sciences</i> , 2009, 1, 78-86.	1.5	8
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143	Abundance and single-cell activity of bacterial groups in Antarctic coastal waters. <i>Limnology and Oceanography</i> , 2010, 55, 2526-2536.	1.6	42
144	Two Types of Endosymbiotic Bacteria in the Enigmatic Marine Worm <i>Xenoturbella bocki</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 2657-2662.	1.4	16
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888	Bacterial community structure and function change in association with colonizer plants during early primary succession in a glacier forefield. <i>Soil Biology and Biochemistry</i> , 2012, 46, 172-180.	4.2	185
889	<i>Duganella phyllosphaerae</i> sp. nov., isolated from the leaf surface of <i>Trifolium repens</i> and proposal to reclassify <i>Duganella violaceinigra</i> into a novel genus as <i>Pseudoduganella violaceinigra</i> gen. nov., comb. nov.. <i>Systematic and Applied Microbiology</i> , 2012, 35, 19-23.	1.2	41
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918	The Bacterial Community Associated with the Marine Polychaete <i>Ophelina</i> sp.1 (Annelida: Opheliidae) Is Altered by Copper and Zinc Contamination in Sediments. <i>Microbial Ecology</i> , 2012, 63, 639-650.	1.4	18
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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970	A novel metatranscriptomic approach to identify gene expression dynamics during extracellular electron transfer. <i>Nature Communications</i> , 2013, 4, 1601.	5.8	162
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#	ARTICLE	IF	CITATIONS
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995	Spatial pattern in Antarctica: what can we learn from Antarctic bacterial isolates?. <i>Extremophiles</i> , 2013, 17, 733-745.	0.9	17
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#	ARTICLE	IF	CITATIONS
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1121	<i>Lutibacter flavus</i> sp. nov., a marine bacterium isolated from a tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 946-951.	0.8	27
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1152	Screening and Expression of Genes from Metagenomes. <i>Advances in Applied Microbiology</i> , 2013, 83, 1-68.	1.3	43
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1154	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	9.4	1,176
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1173	<i>Devosia epidermidihirudinis</i> sp. nov. isolated from the surface of a medical leech. Antonie Van Leeuwenhoek, 2013, 103, 1165-1171.	0.7	26
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1192	Anaerobic oxidation of methane in hypersaline cold seep sediments. <i>FEMS Microbiology Ecology</i> , 2013, 83, 214-231.	1.3	60
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1194	<i>Lysinimonas soli</i> gen. nov., sp. nov., isolated from soil, and reclassification of <i>Leifsonia kribbensis</i> Dastager et al. 2009 as <i>Lysinimonas kribbensis</i> sp. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1403-1410.	0.8	32

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1200	Metagenomic <i>De Novo</i> Assembly of an Aquatic Representative of the Verrucomicrobial Class <i>Spartobacteria</i> . <i>MBio</i> , 2013, 4, e00569-12.	1.8	107
1201	<i>Cloacibacillus porcorum</i> sp. nov., a mucin-degrading bacterium from the swine intestinal tract and emended description of the genus <i>Cloacibacillus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1960-1966.	0.8	75
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1209	<i>Bhargavaea ullalensis</i> sp. nov., isolated from coastal sand. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2450-2456.	0.8	7
1210	Comparative transcriptome analysis of small noncoding RNAs in different stages of <i>Trypanosoma brucei</i> . <i>Rna</i> , 2013, 19, 863-875.	1.6	13
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1219	<i>Brevifollis gellanilyticus</i> gen. nov., sp. nov., a gellan-gum-degrading bacterium of the phylum Verrucomicrobia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3075-3078.	0.8	19
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1225	<i>Rudaecoccus suwonensis</i> gen. nov., sp. nov., an actinobacterium isolated from the epidermal tissue of a root of a <i>Phalaenopsis</i> orchid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1291-1296.	0.8	13
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1271	<i>Arcticibacter svalbardensis</i> gen. nov., sp. nov., of the family Sphingobacteriaceae in the phylum Bacteroidetes, isolated from Arctic soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1627-1632.	0.8	35
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1444	Coprophagous behavior of rabbit pups affects implantation of cecal microbiota and health status. <i>Journal of Animal Science</i> , 2014, 92, 652-665.	0.2	46
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1578	Metagenomic Evidence for Sulfide Oxidation in Extremely Acidic Cave Biofilms. <i>Geomicrobiology Journal</i> , 2014, 31, 194-204.	1.0	41
1579	The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks. <i>Nucleic Acids Research</i> , 2014, 42, D643-D648.	6.5	2,667
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1588	Fluorescence <i>in situ</i> hybridization probing of protozoal <i>Entodinium</i> spp. and their methanogenic colonizers in the rumen of cattle fed alfalfa hay or triticale straw. <i>Journal of Applied Microbiology</i> , 2014, 116, 14-22.	1.4	17
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1804	Permanent draft genome sequence of sulfoquinovose-degrading <i>Pseudomonas putida</i> strain SQ1. <i>Standards in Genomic Sciences</i> , 2015, 10, 42.	1.5	6
1805	High-quality permanent draft genome sequence of the <i>Mimosa asperata</i> - nodulating <i>Cupriavidus</i> sp. strain AMP6. <i>Standards in Genomic Sciences</i> , 2015, 10, 80.	1.5	2

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1806	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolumonas lignolytica</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 106.	1.5	43
1807	Impact of cigarette smoking on the middle meatus microbiome in health and chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2015, 5, 981-989.	1.5	46
1808	Microbial diversity in tanning wastewaters treatment reactors. <i>Environmental Progress and Sustainable Energy</i> , 2015, 34, 401-410.	1.3	8
1809	Draft Genome Sequence of an Alphaproteobacterium Associated with the Mediterranean Sponge <i>Oscarella lobularis</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	11
1810	Draft Genome of <i>Pseudomonas</i> sp. Strain 11/12A, Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
1811	Improved-high-quality draft genome sequence of <i>Rhodococcus</i> sp. JG-3, a eurypsychrophilic Actinobacteria from Antarctic Dry Valley permafrost. <i>Standards in Genomic Sciences</i> , 2015, 10, 61.	1.5	11
1812	High diversity of viable bacteria isolated from lymph nodes of slaughter pigs and its possible impacts for food safety. <i>Journal of Applied Microbiology</i> , 2015, 119, 1420-1432.	1.4	20
1813	Differences in major bacterial populations in the intestines of mature broilers after feeding virginiamycin or bacitracin methylene disalicylate. <i>Journal of Applied Microbiology</i> , 2015, 119, 1515-1526.	1.4	35
1814	Terrestrial origin of bacterial communities in complex boreal freshwater networks. <i>Ecology Letters</i> , 2015, 18, 1198-1206.	3.0	227
1815	Development and application of primers for the class <i>Deltaproteobacteria</i> (phylum <i>Candidatus</i> <i>Halorubrum</i>) enables deep insights into diversity and stratification of subgroups in the marine subsurface. <i>Environmental Microbiology</i> , 2015, 17, 3540-3556.	1.8	22
1816	PhytoREF: a reference database of the plastidial 16S rRNA gene of photosynthetic eukaryotes with curated taxonomy. <i>Molecular Ecology Resources</i> , 2015, 15, 1435-1445.	2.2	198
1817	Arsenic rich Himalayan hot spring metagenomics reveal genetically novel predator-prey genotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 812-823.	1.0	47
1818	Oily waste containing natural radionuclides: does it cause stimulation or inhibition of soil bacterial community?. <i>Journal of Plant Nutrition and Soil Science</i> , 2015, 178, 825-833.	1.1	11
1819	Microbial diversity in shallow water hydrothermal sediments of Kueishan Island, Taiwan as revealed by pyrosequencing. <i>Journal of Basic Microbiology</i> , 2015, 55, 1308-1318.	1.8	34
1820	High-throughput functional screening reveals low frequency of antibiotic resistance genes in DNA recovered from the Upper Mississippi River. <i>Journal of Water and Health</i> , 2015, 13, 693-703.	1.1	20
1821	Exploring the environmental diversity of kinetoplastid flagellates in the high-throughput DNA sequencing era. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2015, 110, 956-965.	0.8	75
1822	Response of soil microorganisms to radioactive oil waste: results from a leaching experiment. <i>Biogeosciences</i> , 2015, 12, 3681-3693.	1.3	12
1823	Hidden biosphere in an oxygen-deficient Atlantic open-ocean eddy: future implications of ocean deoxygenation on primary production in the eastern tropical North Atlantic. <i>Biogeosciences</i> , 2015, 12, 7467-7482.	1.3	29

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1825	Genomics of Methylotrophy in Gram-Positive Methylamine-Utilizing Bacteria. <i>Microorganisms</i> , 2015, 3, 94-112.	1.6	19
1826	A Three-Component Microbial Consortium from Deep-Sea Salt-Saturated Anoxic Lake Thetis Links Anaerobic Glycine Betaine Degradation with Methanogenesis. <i>Microorganisms</i> , 2015, 3, 500-517.	1.6	14
1827	Novel and Unexpected Microbial Diversity in Acid Mine Drainage in Svalbard (78° N), Revealed by Culture-Independent Approaches. <i>Microorganisms</i> , 2015, 3, 667-694.	1.6	44
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1841	Human microbiomes and their roles in dysbiosis, common diseases, and novel therapeutic approaches. <i>Frontiers in Microbiology</i> , 2015, 6, 1050.	1.5	258

#	ARTICLE	IF	CITATIONS
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1843	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1192.	1.5	49
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1846	The Metabolically Active Bacterial Microbiome of Tonsils and Mandibular Lymph Nodes of Slaughter Pigs. <i>Frontiers in Microbiology</i> , 2015, 6, 1362.	1.5	23
1847	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. <i>Frontiers in Microbiology</i> , 2015, 6, 1372.	1.5	24
1848	High-quality permanent draft genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> strain GB30; an effective microsymbiont of <i>Pisum sativum</i> growing in Poland. <i>Standards in Genomic Sciences</i> , 2015, 10, 36.	1.5	3
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1854	Effects of Vaccination with 10-Valent Pneumococcal Non-Typeable Haemophilus influenza Protein D Conjugate Vaccine (PHiD-CV) on the Nasopharyngeal Microbiome of Kenyan Toddlers. <i>PLoS ONE</i> , 2015, 10, e0128064.	1.1	26
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1856	Seasonal Dynamics of Marine Microbial Community in the South Sea of Korea. <i>PLoS ONE</i> , 2015, 10, e0131633.	1.1	67
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1858	Assessment of Zooplankton Community Composition along a Depth Profile in the Central Red Sea. <i>PLoS ONE</i> , 2015, 10, e0133487.	1.1	30
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1868	Interrogation of Chesapeake Bay sediment microbial communities for intrinsic alkane-utilizing potential under anaerobic conditions. FEMS Microbiology Ecology, 2015, 91, 1-14.	1.3	24
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1876	Microbial community composition of a household sand filter used for arsenic, iron, and manganese removal from groundwater in Vietnam. Chemosphere, 2015, 138, 47-59.	4.2	84
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1878	Faster through training: The anammox case. Water Research, 2015, 81, 261-268.	5.3	177

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1880	Elucidating carbon uptake from vinyl chloride using stable isotope probing and Illumina sequencing. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7735-7743.	1.7	25
1881	Diversity of extremely halophilic cultivable prokaryotes in Mediterranean, Atlantic and Pacific solar salterns: Evidence that unexplored sites constitute sources of cultivable novelty. <i>Systematic and Applied Microbiology</i> , 2015, 38, 266-275.	1.2	46
1882	Leprous lesion presents enrichment of opportunistic pathogenic bacteria. <i>SpringerPlus</i> , 2015, 4, 187.	1.2	14
1883	<i>Mesonia hippocampi</i> sp. nov., isolated from the brood pouch of a diseased Barbour's Seahorse (<i>Hippocampus barbouri</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2241-2247.	0.8	15
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1885	Dynamic responses of the benthic bacterial community at the Western English Channel observatory site L4 are driven by deposition of fresh phytodetritus. <i>Progress in Oceanography</i> , 2015, 137, 546-558.	1.5	30
1886	Possible roles of uncultured archaea in carbon cycling in methane-seep sediments. <i>Geochimica Et Cosmochimica Acta</i> , 2015, 164, 35-52.	1.6	31
1887	<i>Chelativorans intermedius</i> sp. nov. and proposal to reclassify <i>Thermovum composti</i> as <i>Chelativorans composti</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1646-1652.	0.8	22
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1889	A longitudinal assessment of changes in bacterial community composition associated with the development of periodontal disease in dogs. <i>Veterinary Microbiology</i> , 2015, 181, 271-282.	0.8	62
1890	Cryptic infection of a broad taxonomic and geographic diversity of tadpoles by <i>Perkinsea</i> protists. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4743-51.	3.3	68
1891	High-quality permanent draft genome sequence of <i>Rhizobium sullae</i> strain WSM1592; a <i>Hedysarum coronarium</i> microsymbiont from Sassari, Italy. <i>Standards in Genomic Sciences</i> , 2015, 10, 44.	1.5	9
1892	Adaptive immunity increases the pace and predictability of evolutionary change in commensal gut bacteria. <i>Nature Communications</i> , 2015, 6, 8945.	5.8	82
1893	Cold adaptive traits revealed by comparative genomic analysis of the eurypsychrophile <i>Rhodococcus</i> sp. JG3 isolated from high elevation McMurdo Dry Valley permafrost, Antarctica. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv154.	1.3	72
1894	Genome Sequence of <i>Methanosarcina soligelidi</i> SMA-21, Isolated from Siberian Permafrost-Affected Soil. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
1895	Complete Genome Sequences of <i>Caldicellulosiruptor</i> sp. Strain Rt8.B8, <i>Caldicellulosiruptor</i> sp. Strain Wai35.B1, and <i>Thermoanaerobacter cellulolyticus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	15
1896	Draft Genome Sequence of <i>Raoultella terrigena</i> R1Gly, a Diazotrophic Endophyte. <i>Genome Announcements</i> , 2015, 3, .	0.8	16

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1898	Genome Sequence of <i>Halomonas</i> sp. Strain MCTG39a, a Hydrocarbon-Degrading and Exopolymeric Substance-Producing Bacterium. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
1899	Draft Genome of <i>Janthinobacterium</i> sp. RA13 Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
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1901	A module tree of Wnt signal transduction pathways. , 2015, , .		0
1902	Complete genome sequence of <i>Thioalkalivibrio paradoxus</i> type strain ARh 1T, an obligately chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium isolated from a Kenyan soda lake. <i>Standards in Genomic Sciences</i> , 2015, 10, 105.	1.5	5
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1907	Genome sequence of <i>Bradyrhizobium</i> sp. WSM1253; a microsymbiont of <i>Ornithopus compressus</i> from the Greek Island of Sifnos. <i>Standards in Genomic Sciences</i> , 2015, 10, 113.	1.5	3
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1909	Biogeochemical environments of streambed-sediment pore waters with and without arsenic enrichment in a sedimentary rock terrain, New Jersey Piedmont, USA. <i>Science of the Total Environment</i> , 2015, 505, 1350-1360.	3.9	3
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1913	Reduced vertical stratification of soil bacterial community structure and composition is associated with <i>Bromus tectorum</i> invasion of sagebrush steppe. <i>Journal of Arid Environments</i> , 2015, 115, 90-99.	1.2	11
1914	Investigation and analysis of microbiological communities in natural <i>Ophiocordyceps sinensis</i> . <i>Canadian Journal of Microbiology</i> , 2015, 61, 104-111.	0.8	37
1915	Quantitative PCR Analysis of Functional Genes in Iron-Rich Microbial Mats at an Active Hydrothermal Vent System (LÅihi Seamount, Hawai'i). <i>Applied and Environmental Microbiology</i> , 2015, 81, 2976-2984.	1.4	32

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1918	Anaerobic membrane bioreactor treatment of domestic wastewater at psychrophilic temperatures ranging from 15 °C to 3 °C. <i>Environmental Science: Water Research and Technology</i> , 2015, 1, 56-64.	1.2	90
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1920	Emerging DNA-based technologies to characterize food ecosystems. <i>Food Research International</i> , 2015, 69, 424-433.	2.9	48
1921	An association network analysis among microeukaryotes and bacterioplankton reveals algal bloom dynamics. <i>Journal of Phycology</i> , 2015, 51, 120-132.	1.0	44
1922	Environmental Metagenomics: The Data Assembly and Data Analysis Perspectives. <i>Journal of the Institution of Engineers (India): Series A</i> , 2015, 96, 71-83.	0.6	5
1923	Methanogenic food web in the gut contents of methane-emitting earthworm <i>Eudrilus eugeniae</i> from Brazil. <i>ISME Journal</i> , 2015, 9, 1778-1792.	4.4	34
1924	RNA Bioinformatics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	3
1925	Bioactive Compounds from Extremophiles. <i>SpringerBriefs in Microbiology</i> , 2015, , .	0.1	2
1926	Effects of ecological engineered oxygenation on the bacterial community structure in an anoxic fjord in western Sweden. <i>ISME Journal</i> , 2015, 9, 656-669.	4.4	18
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1935	Molecular analysis of methanogens involved in methanogenic degradation of tetramethylammonium hydroxide in full-scale bioreactors. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1485-1497.	1.7	22
1936	Grazing livestock are exposed to terrestrial cyanobacteria. <i>Veterinary Research</i> , 2015, 46, 16.	1.1	25
1937	Bacterial and archaeal community structures in the Arctic deep-sea sediment. <i>Acta Oceanologica Sinica</i> , 2015, 34, 93-113.	0.4	16
1938	Metagenomic analysis of the impact of nitrofurantoin treatment on the human faecal microbiota. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1989-1992.	1.3	28
1939	Phytochip: Development of a DNA-microarray for rapid and accurate identification of <i>Pseudo-nitzschia</i> spp and other harmful algal species. <i>Journal of Microbiological Methods</i> , 2015, 112, 55-66.	0.7	21
1940	Correlation between Nasal Microbiome Composition and Remote Purulent Skin and Soft Tissue Infections. <i>Infection and Immunity</i> , 2015, 83, 802-811.	1.0	49
1941	Response of belowground communities to short-term phosphorus addition in a phosphorus-limited woodland. <i>Plant and Soil</i> , 2015, 391, 321-331.	1.8	47
1942	<i>Draconibacterium filum</i> sp. nov., a new species of the genus of <i>Draconibacterium</i> from sediment of the east coast of the Korean Peninsula. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 1049-1056.	0.7	14
1943	Cystic fibrosis mouse model-dependent intestinal structure and gut microbiome. <i>Mammalian Genome</i> , 2015, 26, 222-234.	1.0	33
1944	<i>Saccharomyces cerevisiae</i> transcriptional reprogramming due to bacterial contamination during industrial scale bioethanol production. <i>Microbial Cell Factories</i> , 2015, 14, 13.	1.9	51
1945	Successional Change in Microbial Communities of Benthic Phormidium-Dominated Biofilms. <i>Microbial Ecology</i> , 2015, 69, 254-266.	1.4	44
1946	The interaction of <i>Saccharomyces paradoxus</i> with its natural competitors on oak bark. <i>Molecular Ecology</i> , 2015, 24, 1596-1610.	2.0	39
1947	Anaerobic degradation of cyclohexane by sulfate-reducing bacteria from hydrocarbon-contaminated marine sediments. <i>Frontiers in Microbiology</i> , 2015, 6, 116.	1.5	53
1948	Fungal Communities Respond to Long-Term CO ₂ Elevation by Community Reassembly. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2445-2454.	1.4	48
1949	Assessing the effects of salmon farming seabed enrichment using bacterial community diversity and high-throughput sequencing. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv089.	1.3	77
1950	Effects of Xylo-Oligosaccharides on Broiler Chicken Performance and Microbiota. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5880-5888.	1.4	184
1951	Elucidation of the <i>Photobacterium aerophilum</i> Genome and Generation of a Transposon Mutant Library To Identify Motility Mutants Altered in Pathogenesis. <i>Journal of Bacteriology</i> , 2015, 197, 2201-2216.	1.0	10

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1953	Toolbox Approaches Using Molecular Markers and 16S rRNA Gene Amplicon Data Sets for Identification of Fecal Pollution in Surface Water. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7067-7077.	1.4	68
1954	Lentinula edodes-derived polysaccharide rejuvenates mice in terms of immune responses and gut microbiota. <i>Food and Function</i> , 2015, 6, 2653-2663.	2.1	56
1955	Long-term oil contamination causes similar changes in microbial communities of two distinct soils. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10299-10310.	1.7	34
1956	Effects of plankton net characteristics on metagenetic community analysis of metazoan zooplankton in a coastal marine ecosystem. <i>Journal of Experimental Marine Biology and Ecology</i> , 2015, 469, 36-43.	0.7	28
1957	Elevated CO ₂ induces a bloom of microphytobenthos within a shell gravel mesocosm. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv092.	1.3	2
1958	Ruminal Bacterial Community Composition in Dairy Cows Is Dynamic over the Course of Two Lactations and Correlates with Feed Efficiency. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4697-4710.	1.4	249
1959	Cecal drop reflects the chickens' cecal microbiome, fecal drop does not. <i>Journal of Microbiological Methods</i> , 2015, 117, 164-170.	0.7	41
1960	Influence of 34-years of fertilization on bacterial communities in an intensively cultivated black soil in northeast China. <i>Soil Biology and Biochemistry</i> , 2015, 90, 42-51.	4.2	308
1961	An application of in situ hybridization for the identification of commercially important fish species. <i>Fisheries Research</i> , 2015, 170, 1-8.	0.9	5
1962	Optimization of biostimulant for bioremediation of contaminated coastal sediment by response surface methodology (RSM) and evaluation of microbial diversity by pyrosequencing. <i>Marine Pollution Bulletin</i> , 2015, 98, 235-246.	2.3	16
1963	Phylogenetic Profiling and Diversity of Bacterial Communities in the Death Valley, an Extreme Habitat in the Atacama Desert. <i>Indian Journal of Microbiology</i> , 2015, 55, 392-399.	1.5	14
1964	Census of bacterial microbiota associated with the glacier ice worm <i>Mesenchytraeus solifugus</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	35
1965	Is Planktonic Diversity Well Recorded in Sedimentary DNA? Toward the Reconstruction of Past Protistan Diversity. <i>Microbial Ecology</i> , 2015, 70, 865-875.	1.4	55
1966	High-throughput assessment of bacterial ecology in hog, cow and ovine casings used in sausages production. <i>International Journal of Food Microbiology</i> , 2015, 212, 49-59.	2.1	26
1967	<i>Caldisalibacter kiritimatiensis</i> gen. nov., sp. nov., a Moderately Thermohalophilic Thiosulfate-Reducing Bacterium from a Hypersaline Microbial Mat. <i>Geomicrobiology Journal</i> , 2015, 32, 347-354.	1.0	12
1968	MetaRank: Ranking Microbial Taxonomic Units or Functional Groups for Comparative Analysis of Metagenomes. , 2015, , 442-447.		0
1969	Pyrosequencing revealed highly microbial phylogenetic diversity in ferromanganese nodules from farmland. <i>Environmental Sciences: Processes and Impacts</i> , 2015, 17, 213-224.	1.7	6

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1970	Biotransformation of pink water TNT on the surface of a low-cost adsorbent pine bark. <i>Biodegradation</i> , 2015, 26, 375-386.	1.5	12
1971	Ecophysiology of uncultivated marine euryarchaea is linked to particulate organic matter. <i>ISME Journal</i> , 2015, 9, 1747-1763.	4.4	94
1972	Diversity of methanogens and sulfate-reducing bacteria in the interfaces of five deep-sea anoxic brines of the Red Sea. <i>Research in Microbiology</i> , 2015, 166, 688-699.	1.0	43
1973	Fecal Microbiota Transplantation Eliminates <i>Clostridium difficile</i> in a Murine Model of Relapsing Disease. <i>Infection and Immunity</i> , 2015, 83, 3838-3846.	1.0	116
1974	Understanding the bacterial communities of hard cheese with blowing defect. <i>Food Microbiology</i> , 2015, 52, 106-118.	2.1	72
1975	<i>Lentinula edodes</i> -Derived Polysaccharide Alters the Spatial Structure of Gut Microbiota in Mice. <i>PLoS ONE</i> , 2015, 10, e0115037.	1.1	66
1976	Genomic Applications in the Clinical Management of Infectious Diseases. , 2015, , 581-604.		0
1977	<i>Methanobacterium</i> Dominates Biocathodic Archaeal Communities in Methanogenic Microbial Electrolysis Cells. <i>ACS Sustainable Chemistry and Engineering</i> , 2015, 3, 1668-1676.	3.2	130
1978	High-grain feeding causes strong shifts in ruminal epithelial bacterial community and expression of Toll-like receptor genes in goats. <i>Frontiers in Microbiology</i> , 2015, 6, 167.	1.5	96
1979	Microbial community composition of transiently wetted Antarctic Dry Valley soils. <i>Frontiers in Microbiology</i> , 2015, 6, 9.	1.5	67
1980	Fishing for data and sorting the catch: assessing the data quality, completeness and fitness for use of data in marine biogeographic databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	20
1981	Seasonal dynamics of bacterial and archaeal methanogenic communities in flooded rice fields and effect of drainage. <i>Frontiers in Microbiology</i> , 2014, 5, 752.	1.5	67
1982	Effect of polybrominated diphenyl ether (PBDE) treatment on the composition and function of the bacterial community in the sponge <i>Haliclona cymaeformis</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 799.	1.5	9
1983	Enterolignan-Producing Phenotypes Are Associated with Increased Gut Microbial Diversity and Altered Composition in Premenopausal Women in the United States. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 546-554.	1.1	55
1984	Natural volcanic CO ₂ seeps reveal future trajectories for host-microbial associations in corals and sponges. <i>ISME Journal</i> , 2015, 9, 894-908.	4.4	268
1985	Resuscitation of the rare biosphere contributes to pulses of ecosystem activity. <i>Frontiers in Microbiology</i> , 2015, 6, 24.	1.5	174
1986	Fluorescence in situ hybridization and sequential catalyzed reporter deposition (2C-FISH) for the flow cytometric sorting of freshwater ultramicrobacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 247.	1.5	19
1987	Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. <i>MBio</i> , 2015, 6, .	1.8	126

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1988	Soil carbon content and relative abundance of high affinity H ₂ -oxidizing bacteria predict atmospheric H ₂ soil uptake activity better than soil microbial community composition. <i>Soil Biology and Biochemistry</i> , 2015, 85, 1-9.	4.2	45
1989	Bacterial community structure across environmental gradients in permafrost thaw ponds: methanotroph-rich ecosystems. <i>Frontiers in Microbiology</i> , 2015, 6, 192.	1.5	88
1990	The pig gut microbial diversity: Understanding the pig gut microbial ecology through the next generation high throughput sequencing. <i>Veterinary Microbiology</i> , 2015, 177, 242-251.	0.8	218
1991	Metagenomic analysis of the bacterial microbiota linked to the traditional Algerian date product "Btana". <i>Annals of Microbiology</i> , 2015, 65, 2415-2424.	1.1	1
1992	Microbial Consortium Associated with the Antarctic Marine Ciliate <i>Euplotes focardii</i> : An Investigation from Genomic Sequences. <i>Microbial Ecology</i> , 2015, 70, 484-497.	1.4	42
1993	The Gut Microbiota of Workers of the Litter-Feeding Termite <i>Syntermes wheeleri</i> (Termitidae:). <i>Journal of Biotechnology</i> , 2015, 148, 107-114.	1.4	26
1994	Clostridium cluster I and their pathogenic members in a full-scale operating biogas plant. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 3585-3598.	1.7	9
1995	Short-term changes in total heavy metal concentration and bacterial community composition after replicated and heavy application of pig manure-based compost in an organic vegetable production system. <i>Biology and Fertility of Soils</i> , 2015, 51, 593-603.	2.3	31
1996	Stable isotope probing reveals the importance of <i>Comamonas</i> and <i>Pseudomonadaceae</i> in RDX degradation in samples from a Navy detonation site. <i>Environmental Science and Pollution Research</i> , 2015, 22, 10340-10350.	2.7	17
1997	Application of MetaMesh on the analysis of microbial communities from human associated habitats. <i>Quantitative Biology</i> , 2015, 3, 4-18.	0.3	2
1998	Phylogenetic placement of metagenomic reads using the minimum evolution principle. <i>BMC Genomics</i> , 2015, 16, S13.	1.2	16
1999	Development and pyrosequencing analysis of an in-vitro oral biofilm model. <i>BMC Microbiology</i> , 2015, 15, 24.	1.3	34
2000	Molecular characterization of microbial communities in bioaerosols of a coal mine by 454 pyrosequencing and real-time PCR. <i>Journal of Environmental Sciences</i> , 2015, 30, 241-251.	3.2	31
2001	Metagenomic and Metatranscriptomic Analyses of Bacterial Communities Derived From a Calcifying Karst Water Creek Biofilm and Tufa. <i>Geomicrobiology Journal</i> , 2015, 32, 316-331.	1.0	19
2002	Soils naturally suppressive to banana <i>Fusarium</i> wilt disease harbor unique bacterial communities. <i>Plant and Soil</i> , 2015, 393, 21-33.	1.8	112
2003	Habitat Visualization and Genomic Analysis of <i>Candidatus Pantoea carbekii</i> , the Primary Symbiont of the Brown Marmorated Stink Bug. <i>Genome Biology and Evolution</i> , 2015, 7, 620-635.	1.1	50
2004	A framework for establishing predictive relationships between specific bacterial 16S rRNA sequence abundances and biotransformation rates. <i>Water Research</i> , 2015, 70, 471-484.	5.3	31
2005	16S Classifier: A Tool for Fast and Accurate Taxonomic Classification of 16S rRNA Hypervariable Regions in Metagenomic Datasets. <i>PLoS ONE</i> , 2015, 10, e0116106.	1.1	71

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2006	Evaluation of water sampling methodologies for amplicon-based characterization of bacterial community structure. <i>Journal of Microbiological Methods</i> , 2015, 114, 43-50.	0.7	42
2007	Temperature impacts differentially on the methanogenic food web of cellulose-supplemented peatland soil. <i>Environmental Microbiology</i> , 2015, 17, 720-734.	1.8	60
2008	Calcite-accumulating large sulfur bacteria of the genus <i>Achromatium</i> in Sippewissett Salt Marsh. <i>ISME Journal</i> , 2015, 9, 2503-2514.	4.4	29
2009	Interspecies interactions result in enhanced biofilm formation by co-cultures of bacteria isolated from a food processing environment. <i>Food Microbiology</i> , 2015, 51, 18-24.	2.1	88
2010	Metagenetic tools for the census of marine meiofaunal biodiversity: An overview. <i>Marine Genomics</i> , 2015, 24, 11-20.	0.4	93
2011	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Tv2a.2, a microsymbiont of <i>Tachigali versicolor</i> discovered in Barro Colorado Island of Panama. <i>Standards in Genomic Sciences</i> , 2015, 10, 27.	1.5	5
2012	Parental material and cultivation determine soil bacterial community structure and fertility. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-10.	1.3	37
2013	Phenotypic and Genotypic Description of <i>Sedimenticola selenatireducens</i> Strain CUZ, a Marine (Per)Chlorate-Respiring Gammaproteobacterium, and Its Close Relative the Chlorate-Respiring <i>Sedimenticola</i> Strain NSS. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2717-2726.	1.4	61
2014	Rhizosphere microbial community manipulated by 2 years of consecutive biofertilizer application associated with banana <i>Fusarium</i> wilt disease suppression. <i>Biology and Fertility of Soils</i> , 2015, 51, 553-562.	2.3	175
2015	Environmental diversity of bacteria in a warm monomictic tropical freshwater lake. <i>Annals of Microbiology</i> , 2015, 65, 2099-2108.	1.1	2
2016	<i>Tepidicaulis marinus</i> gen. nov., sp. nov., a marine bacterium that reduces nitrate to nitrous oxide under strictly microaerobic conditions. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1749-1754.	0.8	16
2017	Impacts of bulk soil microbial community structure on rhizosphere microbiomes of <i>Zea mays</i> . <i>Plant and Soil</i> , 2015, 392, 115-126.	1.8	155
2018	Microbial and genetic ecology of tropical Vertisols under intensive chemical farming. <i>Environmental Monitoring and Assessment</i> , 2015, 187, 4081.	1.3	12
2019	Stable Isotope Probing and High-Throughput Sequencing Implicate <i>Xanthomonadaceae</i> and <i>Rhodocyclaceae</i> in Ethylbenzene Degradation. <i>Environmental Engineering Science</i> , 2015, 32, 240-249.	0.8	21
2020	The ecology of pelagic freshwater methylotrophs assessed by a high-resolution monitoring and isolation campaign. <i>ISME Journal</i> , 2015, 9, 2442-2453.	4.4	137
2021	The Perinatal Microbiome and Pregnancy: Moving Beyond the Vaginal Microbiome. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a023051-a023051.	2.9	101
2022	Geological, hydrogeochemical, and microbiological characteristics of the Oil site of the Uzon caldera (Kamchatka). <i>Russian Geology and Geophysics</i> , 2015, 56, 39-63.	0.3	29
2023	Temporal and spatial constraints on community assembly during microbial colonization of wood in seawater. <i>ISME Journal</i> , 2015, 9, 2657-2670.	4.4	35

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2024	Associations between Gut Microbial Colonization in Early Life and Respiratory Outcomes in Cystic Fibrosis. <i>Journal of Pediatrics</i> , 2015, 167, 138-147.e3.	0.9	131
2025	Sinus microbiota varies among chronic rhinosinusitis phenotypes and predicts surgical outcome. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 334-342.e1.	1.5	158
2026	Metagenomic analysis reveals adaptations to a cold-adapted lifestyle in a low-temperature acid mine drainage stream. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	75
2027	Evidence for an active rare biosphere within freshwater protists community. <i>Molecular Ecology</i> , 2015, 24, 1236-1247.	2.0	85
2028	Microbial community structure in the gut of the New Zealand insect Auckland tree weta (<i>Hemideina</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	15
2029	A comparison of six different ballast water treatment systems based on UV radiation, electrochlorination and chlorine dioxide. <i>Environmental Technology (United Kingdom)</i> , 2015, 36, 2094-2104.	1.2	60
2030	Bacterial community structure in the intestinal ecosystem of rainbow trout (<i>Oncorhynchus mykiss</i>) as revealed by pyrosequencing-based analysis of 16S rRNA genes. <i>Research in Veterinary Science</i> , 2015, 100, 8-11.	0.9	62
2031	The human gut microbiome, a taxonomic conundrum. <i>Systematic and Applied Microbiology</i> , 2015, 38, 276-286.	1.2	113
2032	Morphological, genetic and physiological characterization of <i>Hydrocoleum</i> , the most common benthic cyanobacterium in tropical oceans. <i>European Journal of Phycology</i> , 2015, 50, 139-154.	0.9	9
2033	Estimating Protistan Diversity Using High-Throughput Sequencing. <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 688-693.	0.8	66
2034	Metatranscriptomic Analysis of Diminutive Thiomargarita-Like Bacteria (<i>Candidatus Thiopilula</i> spp.) from Abyssal Cold Seeps of the Barbados Accretionary Prism. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3142-3156.	1.4	20
2035	Thermophilic and cellulolytic consortium isolated from composting plants improves anaerobic digestion of cellulosic biomass: Toward a microbial resource management approach. <i>Bioresource Technology</i> , 2015, 189, 138-144.	4.8	66
2036	Physicochemical impacts associated with natural gas development on methanogenesis in deep sand aquifers. <i>ISME Journal</i> , 2015, 9, 436-446.	4.4	19
2037	High Diversity of Culturable Prokaryotes in a Lithifying Hypersaline Microbial Mat. <i>Geomicrobiology Journal</i> , 2015, 32, 332-346.	1.0	46
2038	Influence of age, reproductive cycling status, and menstruation on the vaginal microbiome in baboons (<i>Papio anubis</i>). <i>American Journal of Primatology</i> , 2015, 77, 563-578.	0.8	44
2039	Complementary seminovaginal microbiome in couples. <i>Research in Microbiology</i> , 2015, 166, 440-447.	1.0	164
2040	Clone Libraries of Ribosomal RNA Gene Sequences for Characterization of Microbial Communities. <i>Springer Protocols</i> , 2015, , 127-154.	0.1	2
2041	Rapid response of the active microbial community to CO ₂ exposure from a controlled sub-seabed CO ₂ leak in Ardmucknish Bay (Oban, Scotland). <i>International Journal of Greenhouse Gas Control</i> , 2015, 38, 171-181.	2.3	37

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2043	Bacterial community response to changes in a triâ€trophic cascade during a wholeâ€lake fish manipulation. Ecology, 2016, 97, 684-693.	1.5	7
2044	New Primers Targeting Full-Length Ciliate 18S rRNA Genes and Evaluation of Dietary Effect on Rumen Ciliate Diversity in Dairy Cows. Current Microbiology, 2015, 71, 650-657.	1.0	9
2045	Intercellular wiring enables electron transfer between methanotrophic archaea and bacteria. Nature, 2015, 526, 587-590.	13.7	469
2046	The application of nitric oxide to control biofouling of membrane bioreactors. Microbial Biotechnology, 2015, 8, 549-560.	2.0	13
2047	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp.. Plant Physiology, 2015, 169, 2444-2461.	2.3	111
2048	Microbially influenced corrosion communities associated with fuel-grade ethanol environments. Applied Microbiology and Biotechnology, 2015, 99, 6945-6957.	1.7	24
2049	Inter-comparison of the potentially active prokaryotic communities in the halocline sediments of Mediterranean deep-sea hypersaline basins. Extremophiles, 2015, 19, 949-960.	0.9	13
2050	Assembly independent functional annotation of short-read data using SOFA: Short-ORF functional annotation. , 2015, , .		2
2051	Environmental conditions rather than microbial inoculum composition determine the bacterial composition, microbial biomass and enzymatic activity of reconstructed soil microbial communities. Soil Biology and Biochemistry, 2015, 90, 10-18.	4.2	110
2052	High level of fecal calprotectin at age 2Âmonths as a marker of intestinal inflammation predicts atopic dermatitis and asthma by age 6. Clinical and Experimental Allergy, 2015, 45, 928-939.	1.4	69
2053	Shifts in the mesoâ€and bathypelagic archaea communities composition during recovery and shortâ€term handling of decompressed deepâ€sea samples. Environmental Microbiology Reports, 2015, 7, 450-459.	1.0	27
2054	Microbial Malaise: How Can We Classify the Microbiome?. Trends in Microbiology, 2015, 23, 671-679.	3.5	36
2055	Effect of Exclusive Enteral Nutrition on the Microbiota of Children With Newly Diagnosed Crohn's Disease. Clinical and Translational Gastroenterology, 2015, 6, e71.	1.3	95
2056	The levonorgestrel-releasing intrauterine system is associated with delayed endocervical clearance ofChlamydia trachomatiswithout alterations in vaginal microbiota. Pathogens and Disease, 2015, 73, ftv070.	0.8	9
2057	Adaptation of the Cecal Bacterial Microbiome of Growing Pigs in Response to Resistant Starch Type 4. Applied and Environmental Microbiology, 2015, 81, 8489-8499.	1.4	59
2058	Universal and domain-specific sequences in 23Sâ€28S ribosomal RNA identified by computational phylogenetics. Rna, 2015, 21, 1719-1730.	1.6	29
2059	The dynamics of the bacterial diversity in the redox transition and anoxic zones of the Cariaco Basin assessed by parallel tag sequencing. FEMS Microbiology Ecology, 2015, 91, fiv088.	1.3	13

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2061	Molecular and functional characteristics of streptomycete communities in relation to soil factors and potato common scab. <i>European Journal of Soil Biology</i> , 2015, 70, 58-66.	1.4	11
2062	<i>Enterococcus bulliens</i> sp. nov., a novel lactic acid bacterium isolated from camel milk. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 1257-1265.	0.7	23
2063	Functional and structural responses of methanogenic microbial communities in Uruguayan soils to intermittent drainage. <i>Soil Biology and Biochemistry</i> , 2015, 89, 238-247.	4.2	21
2064	High-Quality draft genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain CJ3Sym. <i>Standards in Genomic Sciences</i> , 2015, 10, 54.	1.5	2
2065	Molecular characterization of microbial communities in the rhizosphere soils and roots of diseased and healthy <i>Panax notoginseng</i> . <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 1059-1074.	0.7	53
2066	Phylogenetic diversity of microbial communities associated with coalbed methane gas from Eastern Ordos Basin, China. <i>International Journal of Coal Geology</i> , 2015, 150-151, 120-126.	1.9	36
2067	The links between ecosystem multifunctionality and above- and belowground biodiversity are mediated by climate. <i>Nature Communications</i> , 2015, 6, 8159.	5.8	471
2068	The microbiome of otitis media with effusion in Indigenous Australian children. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2015, 79, 1548-1555.	0.4	52
2069	<i>Candida albicans</i> commensalism in the gastrointestinal tract. <i>FEMS Yeast Research</i> , 2015, 15, fov081.	1.1	119
2070	The effects of entombment on water chemistry and bacterial assemblages in closed cryoconite holes on Antarctic glaciers. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv144.	1.3	35
2071	Patchy-distributed ciliate (Protozoa) diversity of eight polar communities as determined by 454 amplicon pyrosequencing. <i>Animal Cells and Systems</i> , 2015, 19, 339-349.	0.8	4
2072	Dynamics and Establishment of <i>Clostridium difficile</i> Infection in the Murine Gastrointestinal Tract. <i>Infection and Immunity</i> , 2015, 83, 934-941.	1.0	140
2073	Inconsistent Denoising and Clustering Algorithms for Amplicon Sequence Data. <i>Journal of Computational Biology</i> , 2015, 22, 743-751.	0.8	15
2074	Inoculum selection is crucial to ensure operational stability in anaerobic digestion. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 189-199.	1.7	125
2075	Reappraisal of the phylogeny and fluorescence <i>in situ</i> hybridization probes for the analysis of the <i>Competibacteraceae</i> in wastewater treatment systems. <i>Environmental Microbiology Reports</i> , 2015, 7, 166-174.	1.0	28
2076	Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1375-1386.	1.4	206
2077	Intra- and Interindividual Variations Mask Interspecies Variation in the Microbiota of Sympatric <i>Peromyscus</i> Populations. <i>Applied and Environmental Microbiology</i> , 2015, 81, 396-404.	1.4	54

#	ARTICLE	IF	CITATIONS
2078	Effects of cyclophosphamide on immune system and gut microbiota in mice. <i>Microbiological Research</i> , 2015, 171, 97-106.	2.5	126
2079	Characterization of bacterial community of raw milk from dairy cows during subacute ruminal acidosis challenge by high-throughput sequencing. <i>Journal of the Science of Food and Agriculture</i> , 2015, 95, 1072-1079.	1.7	59
2080	Mechanisms of soil acidification reducing bacterial diversity. <i>Soil Biology and Biochemistry</i> , 2015, 81, 275-281.	4.2	75
2081	<i>Clostridium</i> Species as Metallic Copper-Forming Bacteria in Soil under Reducing Conditions. <i>Geomicrobiology Journal</i> , 2015, 32, 130-139.	1.0	17
2082	Association between specific mucosa-associated microbiota in Crohn's disease at the time of resection and subsequent disease recurrence: A pilot study. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2015, 30, 268-278.	1.4	137
2083	Ammonia-oxidizing microbial communities in reactors with efficient nitrification at low-dissolved oxygen. <i>Water Research</i> , 2015, 70, 38-51.	5.3	209
2084	Pyrosequencing analysis of free-living and attached bacterial communities in Meiliang Bay, Lake Taihu, a large eutrophic shallow lake in China. <i>Canadian Journal of Microbiology</i> , 2015, 61, 22-31.	0.8	40
2085	Spatially resolved sampling reveals dynamic microbial communities in rising hydrothermal plumes across a back-arc basin. <i>ISME Journal</i> , 2015, 9, 1434-1445.	4.4	51
2086	Temporal and Vertical Distributions of Bacterioplankton at the Gray's Reef National Marine Sanctuary. <i>Applied and Environmental Microbiology</i> , 2015, 81, 910-917.	1.4	17
2087	Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. <i>Water Research</i> , 2015, 69, 30-39.	5.3	49
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2095	A metagenetic approach for revealing community structure of marine planktonic copepods. <i>Molecular Ecology Resources</i> , 2015, 15, 68-80.	2.2	82

#	ARTICLE	IF	CITATIONS
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2121	Draft Genome Sequence of <i>Idiomarina woesei</i> Strain W11 ^T (DSM 27808 ^T) Tj ETQq0 0 0 rgBT /Overlock	0.8	1
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2343	Cyanobacteria in lakes on Yungui Plateau, China are assembled via niche processes driven by water physicochemical property, lake morphology and watershed land-use. <i>Scientific Reports</i> , 2016, 6, 36357.	1.6	38
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#	ARTICLE	IF	CITATIONS
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2364	Cellular content of biomolecules in sub-seafloor microbial communities. <i>Geochimica Et Cosmochimica Acta</i> , 2016, 188, 330-351.	1.6	20
2365	Activities and Prevalence of Proteobacteria Members Colonizing <i>Echinacea purpurea</i> Fully Account for Macrophage Activation Exhibited by Extracts of This Botanical. <i>Planta Medica</i> , 2016, 82, 1258-1265.	0.7	11
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2661	<i>Esteya Vermicola</i> , a Nematophagous Fungus Attacking the Pine Wood Nematode, Harbors a Bacterial Endosymbiont Affiliated with <i>Gammaproteobacteria</i> . <i>Microbes and Environments</i> , 2017, 32, 201-209.	0.7	11

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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2808	Microbiome dynamics during ensiling of corn with and without <i>Lactobacillus plantarum</i> inoculant. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4025-4037.	1.7	144
2809	Chloride ion tolerance and pyrite bioleaching capabilities of pure and mixed halotolerant, acidophilic iron- and sulfur-oxidizing cultures. <i>Minerals Engineering</i> , 2018, 120, 87-93.	1.8	22
2810	Dietary changes during weaning shape the gut microbiota of red pandas (<i>Ailurus fulgens</i>). , 2018, 6, cox075.		30
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2818	A randomized trial to determine the impact of a digestion resistant starch composition on the gut microbiome in older and mid-age adults. <i>Clinical Nutrition</i> , 2018, 37, 797-807.	2.3	110
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2823	Habitability analyses of aquatic bacteria. <i>Journal of Oceanography</i> , 2018, 74, 197-207.	0.7	5
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2828	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
2829	Impact of sequence processing and taxonomic classification approaches on eukaryotic community structure from environmental samples with emphasis on diatoms. <i>Molecular Ecology Resources</i> , 2018, 18, 204-216.	2.2	18
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2838	Intestinal microbiota in infants at high risk for allergy: Effects of prebiotics and role in eczema development. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1334-1342.e5.	1.5	128
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2862	Diet tracing in ecology: Method comparison and selection. <i>Methods in Ecology and Evolution</i> , 2018, 9, 278-291.	2.2	320
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2956	Direct oxygen uptake from air by novel glycogen accumulating organism dominated biofilm minimizes excess sludge production. <i>Science of the Total Environment</i> , 2018, 640-641, 80-88.	3.9	11
2957	Relationship between dissolved organic matter quality and microbial community composition across polar glacial environments. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	26
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2965	Bacterial endophyte communities in <i>Pinus flexilis</i> are structured by host age, tissue type, and environmental factors. <i>Plant and Soil</i> , 2018, 428, 335-352.	1.8	32
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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3067	Short-term direct contact with soil and plant materials leads to an immediate increase in diversity of skin microbiota. <i>MicrobiologyOpen</i> , 2019, 8, e00645.	1.2	63
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3078	Improved hemodynamic and liver function in portal hypertensive cirrhotic rats after administration of <i>B. pseudocatenuatum</i> CECT 7765. <i>European Journal of Nutrition</i> , 2019, 58, 1647-1658.	1.8	13

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3087	Biogeographical patterns in soil bacterial communities across the Arctic region. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	53
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3091	Development of quantitative PCR for the detection of <i>Alkalilimnicola ehrlichii</i> , <i>Thioalkalivibrio sulfidophilus</i> and <i>Thioalkalibacter halophilus</i> in gas biodesulfurization processes. <i>AMB Express</i> , 2019, 9, 99.	1.4	5
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#	ARTICLE	IF	CITATIONS
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3100	Contrasting microbial community responses to salinization and straw amendment in a semiarid bare soil and its wheat rhizosphere. <i>Scientific Reports</i> , 2019, 9, 9795.	1.6	20
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3103	Disentangling the complex microbial community of coral reefs using standardized Autonomous Reef Monitoring Structures (ARMS). <i>Molecular Ecology</i> , 2019, 28, 3496-3507.	2.0	31
3104	Diversity of Wadden Sea macrofauna and meiofauna communities highest in DNA from extractions preceded by cell lysis. <i>Journal of Sea Research</i> , 2019, 152, 101764.	0.6	24
3105	Optimization of an in vitro gut microbiome biotransformation platform with chlorogenic acid as model compound: From fecal sample to biotransformation product identification. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 175, 112768.	1.4	12
3106	Durable Long-Term Bacterial Engraftment following Encapsulated Fecal Microbiota Transplantation To Treat <i>Clostridium difficile</i> Infection. <i>MBio</i> , 2019, 10, .	1.8	58
3107	Interaction between high-fat diet and ethanol intake leads to changes on the fecal microbiome. <i>Journal of Nutritional Biochemistry</i> , 2019, 72, 108215.	1.9	16
3108	Administration of antibiotics can cause dysbiosis in fish gut. <i>Aquaculture</i> , 2019, 512, 734330.	1.7	41
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3110	Temporal association of the development of oropharyngeal microbiota with early life wheeze in a population-based birth cohort. <i>EBioMedicine</i> , 2019, 46, 486-498.	2.7	18
3111	Two-Phase Improves Performance of Anaerobic Membrane Bioreactor Treatment of Food Waste at High Organic Loading Rates. <i>Environmental Science & Technology</i> , 2019, 53, 9572-9583.	4.6	42
3112	Diversity of Bacteria in Lakes with Different Chlorophyll Content and Investigation of Their Respiratory Activity through a Long-Term Microcosm Experiment. <i>Water (Switzerland)</i> , 2019, 11, 467.	1.2	7
3113	Insights into the Potential of the Atlantic Cod Gut Microbiome as Biomarker of Oil Contamination in the Marine Environment. <i>Microorganisms</i> , 2019, 7, 209.	1.6	33
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#	ARTICLE	IF	CITATIONS
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3117	Bacterial microbiomes of <i>Ixodes scapularis</i> ticks collected from Massachusetts and Texas, USA. <i>BMC Microbiology</i> , 2019, 19, 138.	1.3	46
3118	Characterization of Anthracite-Degrading Methanogenic Microflora Enriched from Qinshui Basin in China. <i>Energy & Fuels</i> , 2019, 33, 6380-6389.	2.5	31
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3123	Full-length 16S rRNA gene classification of Atlantic salmon bacteria and effects of using different 16S variable regions on community structure analysis. <i>MicrobiologyOpen</i> , 2019, 8, e898.	1.2	28
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3126	Active eukaryotes in drinking water distribution systems of ground and surface waterworks. <i>Microbiome</i> , 2019, 7, 99.	4.9	25
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#	ARTICLE	IF	CITATIONS
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3134	Aerobic and Anaerobic Biodegradation of 1,2-Dibromoethane by a Microbial Consortium under Simulated Groundwater Conditions. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 3775.	1.2	6
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#	ARTICLE	IF	CITATIONS
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3158	Performance and microbial ecology of methane-driven microbial fuel cells at temperatures ranging from 25 to 55°C. <i>Water Research</i> , 2019, 166, 115036.	5.3	19
3159	Distribution patterns of bacterial communities and their potential link to variable viral lysis in temperate freshwater reservoirs. <i>Aquatic Sciences</i> , 2019, 81, 1.	0.6	5
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3163	Upper versus lower airway microbiome and metagenome in children with cystic fibrosis and their correlation with lung inflammation. <i>PLoS ONE</i> , 2019, 14, e0222323.	1.1	17
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#	ARTICLE	IF	CITATIONS
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3179	Antibiotic disturbance affects aquatic microbial community composition and food web interactions but not community resilience. <i>Molecular Ecology</i> , 2019, 28, 1170-1182.	2.0	39
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#	ARTICLE	IF	CITATIONS
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3211	Microbial communities in a former pilot-scale uranium mine in Eastern Finland â€™ Association with radium immobilization. <i>Science of the Total Environment</i> , 2019, 686, 619-640.	3.9	12
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3220	Multidisciplinary investigation on the catfish parasite <i>Hamatopeduncularia Yamaguti</i> , 1953 (Monogeneoidea: Dactylogyridae): description of two new species from India, and phylogenetic considerations. , 2019, 86, 132-155.		9
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3222	Fungal community composition analysis of 24 different urban parks in Shanghai, China. <i>Urban Ecosystems</i> , 2019, 22, 855-863.	1.1	7
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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3252	Anaerobic oxidation of ethane by archaea from a marine hydrocarbon seep. <i>Nature</i> , 2019, 568, 108-111.	13.7	149
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3469	SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis. <i>BMC Bioinformatics</i> , 2020, 21, 345.	1.2	41
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#	ARTICLE	IF	CITATIONS
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3493	Silvopastoral systems in dry Chaco, Argentina: Impact on soil chemical parameters and bacterial communities. <i>Soil Use and Management</i> , 2021, 37, 866-878.	2.6	5
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3498	Modulation of Gut Microbiota in Korean Navy Trainees following a Healthy Lifestyle Change. <i>Microorganisms</i> , 2020, 8, 1265.	1.6	11
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3516	A Subset of Roux-en-Y Gastric Bypass Bacterial Consortium Colonizes the Gut of Nonsurgical Rats without Inducing Host-Microbe Metabolic Changes. <i>MSystems</i> , 2020, 5, .	1.7	5
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#	ARTICLE	IF	CITATIONS
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3519	Gastric Adenocarcinomas and Signet-Ring Cell Carcinoma: Unraveling Gastric Cancer Complexity through Microbiome Analysis—Deepening Heterogeneity for a Personalized Therapy. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9735.	1.8	25
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3525	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	5.8	269
3526	Quantitative stable isotope probing with H ₂ ¹⁸ O to measure taxon-specific microbial growth. <i>Soil Science Society of America Journal</i> , 2020, 84, 1503-1518.	1.2	6
3527	Oral Microbial Species and Virulence Factors Associated with Oral Squamous Cell Carcinoma. <i>Microbial Ecology</i> , 2021, 82, 1030-1046.	1.4	29
3528	Bacterial Communities Show Algal Host (<i>Fucus</i> spp.)/Zone Differentiation Across the Stress Gradient of the Intertidal Zone. <i>Frontiers in Microbiology</i> , 2020, 11, 563118.	1.5	16
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3530	Environmental flexibility in <i>Oulastrea crispata</i> in a highly urbanised environment: a microbial perspective. <i>Coral Reefs</i> , 2020, 39, 649-662.	0.9	13
3531	Seasonal habitat drives intestinal microbiome composition in anadromous Arctic char (<i>Salvelinus</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	19
3532	Phylogenomic Analyses of Members of the Widespread Marine Heterotrophic Genus <i>Pseudovibrio</i> Suggest Distinct Evolutionary Trajectories and a Novel Genus, <i>Polycladidibacter</i> gen. nov. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	6
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3534	Vertical shifts of particle-attached and free-living prokaryotes in the water column above the cold seeps of the South China Sea. <i>Marine Pollution Bulletin</i> , 2020, 156, 111230.	2.3	14
3535	<i>Lactococcus lactis</i> Diversity Revealed by Targeted Amplicon Sequencing of <i>purR</i> Gene, Metabolic Comparisons and Antimicrobial Properties in an Undefined Mixed Starter Culture Used for Soft-Cheese Manufacture. <i>Foods</i> , 2020, 9, 622.	1.9	9

#	ARTICLE	IF	CITATIONS
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3537	Dietary replacement of fish meal with peanut meal in juvenile hybrid grouper (<i>Epinephelus</i>) TJ ETQq1 1 0.784314 rgBT /Overlock 10 T15 microbiota. <i>Aquaculture Reports</i> , 2020, 17, 100327.	0.7	23
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#	ARTICLE	IF	CITATIONS
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3561	Notice of RETRACTION: "Changes in rumen fermentation, bacterial community, and predicted functional pathway in Holstein cows with and without subacute ruminal acidosis during the periparturient period" (<i>J. Dairy Sci.</i> 103:4702-4716). <i>Journal of Dairy Science</i> , 2020, 103, 4702-4716.	1.4	6
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#	ARTICLE	IF	CITATIONS
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3606	Genetic variability, community structure, and horizontal transfer of endosymbionts among three <i>Asiatic Bemisia tabaci</i> mitotypes in Pakistan. <i>Ecology and Evolution</i> , 2020, 10, 2928-2943.	0.8	11
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3612	Impact of sampling and DNA extraction methods on skin microbiota assessment. <i>Journal of Microbiological Methods</i> , 2020, 171, 105880.	0.7	4
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3623	The complex microbiome from native semen to embryo culture environment in human in vitro fertilization procedure. <i>Reproductive Biology and Endocrinology</i> , 2020, 18, 3.	1.4	37
3624	Doing More with Less: A Comparison of 16S Hypervariable Regions in Search of Defining the Shrimp Microbiota. <i>Microorganisms</i> , 2020, 8, 134.	1.6	37
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3632	Respiratory dysbiosis and population-wide temporal dynamics in canine chronic bronchitis and non-inflammatory respiratory disease. <i>PLoS ONE</i> , 2020, 15, e0228085.	1.1	6
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3635	Timescales of variation in diversity and production of bacterioplankton assemblages in the Lower Mississippi River. <i>PLoS ONE</i> , 2020, 15, e0230945.	1.1	4
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3640	A formulated diet improved digestive capacity, immune function and intestinal microbiota structure of juvenile hybrid grouper (<i>Epinephelus fuscoguttatus</i> × <i>Epinephelus lanceolatus</i>) when compared with chilled trash fish. <i>Aquaculture</i> , 2020, 523, 735230.	1.7	21
3641	Gut Microbiota Modulate CD8 ⁺ Cell Responses to Influence Colitis-Associated Tumorigenesis. <i>Cell Reports</i> , 2020, 31, 107471.	2.9	103
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#	ARTICLE	IF	CITATIONS
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3649	A Molecular Approach to Explore the Background Benthic Fauna Around a Hydrothermal Vent and Their Larvae: Implications for Future Mining of Deep-Sea SMS Deposits. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	10
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3660	Metabarcoding reveals distinct microbiotypes in the giant clam <i>Tridacna maxima</i> . <i>Microbiome</i> , 2020, 8, 57.	4.9	23
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3664	Low-gossypol cottonseed protein concentrate used as a replacement of fish meal for juvenile hybrid grouper (<i>Epinephelus fuscoguttatus</i> ^{â™} — <i>Epinephelus lanceolatus</i> ^{â™}): Effects on growth performance, immune responses and intestinal microbiota. <i>Aquaculture</i> , 2020, 524, 735309.	1.7	65
3665	Microbial Diversity and Metabolic Potential in the Stratified Sansha Yongle Blue Hole in the South China Sea. <i>Scientific Reports</i> , 2020, 10, 5949.	1.6	27
3666	Microbial Dysbiosis During Simian Immunodeficiency Virus Infection is Partially Reverted with Combination Anti-retroviral Therapy. <i>Scientific Reports</i> , 2020, 10, 6387.	1.6	11
3667	Nasopharyngeal <i>Haemophilus</i> and local immune response during infant respiratory syncytial virus infection. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1097-1101.e6.	1.5	12
3668	Characterizing Microbial Signatures on Sculptures and Paintings of Similar Provenance. <i>Microbial Ecology</i> , 2021, 81, 1098-1105.	1.4	6
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3671	Alcohol Use Is Associated With Intestinal Dysbiosis and Dysfunctional CD8+ T-Cell Phenotypes in Persons With Human Immunodeficiency Virus. <i>Journal of Infectious Diseases</i> , 2021, 223, 1029-1039.	1.9	8
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3673	Heat waves intensify the effects of drought on bacterial diversity but not community composition in <i>Solanum lycopersicum</i> soil. <i>Journal of Soils and Sediments</i> , 2021, 21, 355-363.	1.5	6
3674	Microbiome analysis and predicted relative metabolomic turnover suggest bacterial heme and selenium metabolism are altered in the gastrointestinal system of zebrafish (<i>Danio rerio</i>) exposed to the organochlorine dieldrin. <i>Environmental Pollution</i> , 2021, 268, 115715.	3.7	13
3675	Allopatric sibling species pair <i>Drosophila nasuta nasuta</i> and <i>Drosophila nasuta albomicans</i> exhibit expression divergence in ovarian transcriptomes. <i>Gene</i> , 2021, 777, 145189.	1.0	2
3676	Bacterial communities in the plant phyllosphere harbour distinct responders to a broad-spectrum pesticide. <i>Science of the Total Environment</i> , 2021, 751, 141799.	3.9	46
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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3830	Common Presence of Phototrophic <i>Gemmatimonadota</i> in Temperate Freshwater Lakes. <i>MSystems</i> , 2021, 6, .	1.7	20
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#	ARTICLE	IF	CITATIONS
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3833	Positive Effects of Crop Diversity on Productivity Driven by Changes in Soil Microbial Composition. <i>Frontiers in Microbiology</i> , 2021, 12, 660749.	1.5	59
3834	<i>Aspergillus oryzae</i> and <i>Aspergillus niger</i> Co-Cultivation Extract Affects In Vitro Degradation, Fermentation Characteristics, and Bacterial Composition in a Diet-Specific Manner. <i>Animals</i> , 2021, 11, 1248.	1.0	12
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3838	Dissecting industrial fermentations of fine flavour cocoa through metagenomic analysis. <i>Scientific Reports</i> , 2021, 11, 8638.	1.6	16
3839	Comparison of bacterial and archaeal communities in two fertilizer doses and soil compartments under continuous cultivation system of garlic. <i>PLoS ONE</i> , 2021, 16, e0250571.	1.1	2
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3843	Decoupling of biotic and abiotic patterns in a coastal area affected by chronic metal micronutrients disturbances. <i>Marine Pollution Bulletin</i> , 2021, 166, 111608.	2.3	2
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3850	Comparison of subgingival and gingival margin plaque microbiota from dogs with healthy gingiva and early periodontal disease.. <i>Research in Veterinary Science</i> , 2021, 136, 396-407.	0.9	5
3851	Investigating variability in microbial community composition in replicate environmental DNA samples down lake sediment cores. <i>PLoS ONE</i> , 2021, 16, e0250783.	1.1	15
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3881	Characterization and phylogenomic analysis of <i>Breznakiella homolactica</i> gen. nov. sp. nov. indicate that termite gut treponemes evolved from non-acetogenic spirochetes in cockroaches. <i>Environmental Microbiology</i> , 2021, 23, 4228-4245.	1.8	15
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3887	Bacterial transfer from <i>Pristionchus entomophagus</i> nematodes to the invasive ant <i>Myrmica rubra</i> and the potential for colony mortality in coastal Maine. <i>iScience</i> , 2021, 24, 102663.	1.9	4
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3890	Intestinal mucositis precedes dysbiosis in a mouse model for pelvic irradiation. <i>ISME Communications</i> , 2021, 1, .	1.7	10
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3898	Description of three new <i>Alteromonas</i> species <i>Alteromonas antoniana</i> sp. nov., <i>Alteromonas lipotruvae</i> sp. nov. and <i>Alteromonas lipotruveiana</i> sp. nov. isolated from marine environments, and proposal for reclassification of the genus <i>Salinimonas</i> as <i>Alteromonas</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126226.	1.2	39
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3905	Organic matter- and temperature-driven deterministic assembly processes govern bacterial community composition and functionality during manure composting. <i>Waste Management</i> , 2021, 131, 31-40.	3.7	30
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3908	<i>Priestia veravalensis</i> sp. nov., isolated from coastal sample. <i>Archives of Microbiology</i> , 2021, 203, 4839-4845.	1.0	5
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3913	An Ecological Basis for Dual Genetic Code Expansion in Marine Deltaproteobacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 680620.	1.5	4
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3915	Bacterial communities in the rumen and feces of lactating Holstein dairy cows are not affected when fed reduced-fat dried distillers' grains with solubles. <i>Animal</i> , 2021, 15, 100281.	1.3	5
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3920	Specific protistan consumers and parasites are responsive to inorganic fertilization in rhizosphere and bulk soils. <i>Journal of Soils and Sediments</i> , 2021, 21, 3801-3812.	1.5	10
3921	Drivers of change and stability in the gut microbiota of an omnivorous avian migrant exposed to artificial food supplementation. <i>Molecular Ecology</i> , 2021, 30, 4723-4739.	2.0	16
3922	Gut Microbiota and Development of Vibrio cholerae-Specific Long-Term Memory B Cells in Adults after Whole-Cell Killed Oral Cholera Vaccine. <i>Infection and Immunity</i> , 2021, 89, e0021721.	1.0	15
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3924	Combining Multiple Markers in Environmental DNA Metabarcoding to Assess Deep-Sea Benthic Biodiversity. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	20
3925	Limited resilience of the soil microbiome to mechanical compaction within four growing seasons of agricultural management. <i>ISME Communications</i> , 2021, 1, .	1.7	30
3926	DNA metabarcoding marker choice skews perception of marine eukaryotic biodiversity. <i>Environmental DNA</i> , 2021, 3, 1229-1246.	3.1	16
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#	ARTICLE	IF	CITATIONS
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3934	Genomic Variation Influences Methanothermococcus Fitness in Marine Hydrothermal Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 714920.	1.5	3
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3937	Characterization of the Genitourinary Microbiome of 1,165 Middle-Aged and Elderly Healthy Individuals. <i>Frontiers in Microbiology</i> , 2021, 12, 673969.	1.5	6
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3939	The Abundance and Taxonomic Diversity of Filterable Forms of Bacteria during Succession in the Soils of Antarctica (Bunger Hills). <i>Microorganisms</i> , 2021, 9, 1728.	1.6	0
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3942	Context-sensitivity of isosteric substitutions of non-Watson-Crick basepairs in recurrent RNA 3D motifs. <i>Nucleic Acids Research</i> , 2021, 49, 9574-9593.	6.5	4
3943	Recovery trajectories and community resilience of biofilms in receiving rivers after wastewater treatment plant upgrade. <i>Environmental Research</i> , 2021, 199, 111349.	3.7	10
3944	Response of Methanogen Communities to the Elevation of Cathode Potentials in Bioelectrochemical Reactors Amended with Magnetite. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0148821.	1.4	1
3945	Fresh Compost Tea Application Does Not Change Rhizosphere Soil Bacterial Community Structure, and Has No Effects on Soybean Growth or Yield. <i>Plants</i> , 2021, 10, 1638.	1.6	5
3946	Ribovore: ribosomal RNA sequence analysis for GenBank submissions and database curation. <i>BMC Bioinformatics</i> , 2021, 22, 400.	1.2	3
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#	ARTICLE	IF	CITATIONS
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3949	Trophic niches reflect compositional differences in microbiota among Caribbean sea urchins. <i>PeerJ</i> , 2021, 9, e12084.	0.9	9
3950	Transcriptomics analysis reveals the high biodegradation efficiency of white-rot fungus <i>Phanerochaete sordida</i> YK-624 on native lignin. <i>Journal of Bioscience and Bioengineering</i> , 2021, 132, 253-257.	1.1	7
3951	Kefir modulates gut microbiota and reduces DMH-associated colorectal cancer via regulation of intestinal inflammation in adulthood offsprings programmed by neonatal overfeeding. <i>Food Research International</i> , 2022, 152, 110708.	2.9	8
3952	High Arsenic Levels Increase Activity Rather than Diversity or Abundance of Arsenic Metabolism Genes in Paddy Soils. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0138321.	1.4	9
3953	Distinct intestinal microbial communities of two sympatric anadromous Arctic salmonids and the effects of migration and feeding. <i>Arctic Science</i> , 2021, 7, 634-654.	0.9	11
3955	Optimizing an enclosed bead beating extraction method for microbial and fish environmental DNA. <i>Environmental DNA</i> , 2022, 4, 291-303.	3.1	6
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3957	DNA Metabarcoding Methods for the Study of Marine Benthic Meiofauna: A Review. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	16
3958	Monocarboxylate Transporter-2 Expression Restricts Tumor Growth in a Murine Model of Lung Cancer: A Multi-Omic Analysis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10616.	1.8	4
3959	Emerging Pathogenic Gammaproteobacteria <i>Wohlfahrtiimonas chitiniclastica</i> and <i>Ignatzschineria</i> Species in a Turkey Vulture (<i>Cathartes aura</i>). , 2021, 35, 280-289.		1
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3964	New Finds on the Systematics of Cycloposthiid Ciliates (Ciliophora: Entodiniomorpha): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (C 2021, 78, 3872-3876.	1.0	1
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3966	Diversity and characteristics of raw milk microbiota from Korean dairy farms using metagenomic and culturomic analysis. <i>Food Control</i> , 2021, 127, 108160.	2.8	12
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#	ARTICLE	IF	CITATIONS
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3970	A Comparative Analysis of the Microbiome of Kiwifruit at Harvest Under Open-Field and Rain-Shelter Cultivation Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 757719.	1.5	9
3971	Capture by hybridization for full-length barcode-based eukaryotic and prokaryotic biodiversity inventories of deep sea ecosystems. <i>Molecular Ecology Resources</i> , 2022, 22, 623-637.	2.2	6
3972	Impact of mechanical Arenicola dredging on the benthic fauna communities: assessed by a morphological and molecular approach. <i>Marine Ecology - Progress Series</i> , 2021, 673, 17-28.	0.9	2
3973	Evaluating the Efficiency of DNA Metabarcoding to Analyze the Diet of <i>Hippocampus guttulatus</i> (Teleostea: Syngnathidae). <i>Life</i> , 2021, 11, 998.	1.1	9
3974	Effects of Dietary Fishmeal Replacement by Poultry By-Product Meal and Hydrolyzed Feather Meal on Liver and Intestinal Histomorphology and on Intestinal Microbiota of Gilthead Seabream (<i>Sparus</i>)	1.0	4
3975	Indigofera tinctoria leaf powder as a promising additive to improve indigo fermentation prepared with sukumo (composted Polygonum tinctorium leaves). <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 179.	1.7	4
3976	Bacterial microbiome of dusky kob <i>Argyrosomus japonicus</i> eggs and rearing water and the bacteriostatic effect of selected disinfectants. <i>Aquaculture</i> , 2021, 542, 736882.	1.7	2
3977	The wastewater protist <i>Rhogostoma minus</i> (Thecofilosea, Rhizaria) is abundant, widespread, and hosts Legionellales. <i>Water Research</i> , 2021, 203, 117566.	5.3	11
3979	Upper respiratory tract bacterial-immune interactions during respiratory syncytial virus infection in infancy. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 966-976.	1.5	11
3980	Structure and Long-Term Stability of the Microbiome in Diverse Diatom Cultures. <i>Microbiology Spectrum</i> , 2021, 9, e0026921.	1.2	8
3981	Profiling the microbial community structure and functional diversity of a dam-regulated river undergoing gravel bar restoration. <i>Freshwater Biology</i> , 2021, 66, 2170-2184.	1.2	5
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3985	Microbial adaptation and response to high ammonia concentrations and precipitates during anaerobic digestion under psychrophilic and mesophilic conditions. <i>Water Research</i> , 2021, 204, 117596.	5.3	11
3986	The "neighbor avoidance effect" of microplastics on bacterial and fungal diversity and communities in different soil horizons. <i>Environmental Science and Ecotechnology</i> , 2021, 8, 100121.	6.7	32

#	ARTICLE	IF	CITATIONS
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3989	MicFunPred: A conserved approach to predict functional profiles from 16S rRNA gene sequence data. <i>Genomics</i> , 2021, 113, 3635-3643.	1.3	22
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3991	Identification of the phylotypes involved in cis-dichloroethene and 1,4-dioxane biodegradation in soil microcosms. <i>Science of the Total Environment</i> , 2021, 794, 148690.	3.9	9
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3999	Kinetics and scale up of oxygen reducing cathodic biofilms. <i>Biofilm</i> , 2021, 3, 100053.	1.5	3
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4003	Perfluorinated compounds (PFCs) in regional industrial rivers: Interactions between pollution flux and eukaryotic community phylosymbiosis. <i>Environmental Research</i> , 2022, 203, 111876.	3.7	10
4004	Infection of oomycetes and bacteria associated with their specific colocalization in chum salmon eggs. <i>Aquaculture</i> , 2022, 546, 737244.	1.7	4

#	ARTICLE	IF	CITATIONS
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4006	Combined Impact of No-Till and Cover Crops with or without Short-Term Water Stress as Revealed by Physicochemical and Microbiological Indicators. <i>Biology</i> , 2021, 10, 23.	1.3	4
4007	Multi-gene phylogeny of the subclass Astomatia (Protista: Ciliophora) refreshed with two rare astome ciliates from the digestive tube of endogeic earthworms. <i>Organisms Diversity and Evolution</i> , 2021, 21, 59-77.	0.7	8
4008	Innate gut microbiota predisposes to high alcohol consumption. <i>Addiction Biology</i> , 2021, 26, e13018.	1.4	19
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4015	Repeated Application of Rice Straw Stabilizes Soil Bacterial Community Composition and Inhibits Clubroot Disease. <i>Agriculture (Switzerland)</i> , 2021, 11, 108.	1.4	4
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4017	Changes in the predicted function of the rumen bacterial community of Japanese Black beef cattle during the fattening stages according to Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses. <i>Journal of Veterinary Medical Science</i> , 2021, 83, 1098-1106.	0.3	5
4018	Contribution of sample processing to gut microbiome analysis in the model Lepidoptera, silkworm <i>Bombyx mori</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4658-4668.	1.9	16
4019	Antimicrobial-specific response from resistance gene carriers studied in a natural, highly diverse microbiome. <i>Microbiome</i> , 2021, 9, 29.	4.9	13
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#	ARTICLE	IF	CITATIONS
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4026	e-DNA Meta-Barcoding: From NGS Raw Data to Taxonomic Profiling. <i>Methods in Molecular Biology</i> , 2015, 1269, 257-278.	0.4	4
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4033	Molecular Biology Techniques for the Identification and Genotyping of Microorganisms. , 2019, , 203-226.		4
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4037	Inhibition of <i>Bacillus cereus</i> by garlic (<i>Allium sativum</i>) essential oil during manufacture of white sufu, a traditional Chinese fermented soybean curd. <i>LWT - Food Science and Technology</i> , 2020, 130, 109634.	2.5	11
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4041	<i>Catenisphaera adipataaccumulans</i> gen. nov., sp. nov., a member of the family Erysipelotrichaceae isolated from an anaerobic digester. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 805-810.	0.8	30
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#	ARTICLE	IF	CITATIONS
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4044	<i>Brevibacterium sandarakinum</i> sp. nov., isolated from a wall of an indoor environment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 909-913.	0.8	21
4045	<i>Archaeoglobus sulfaticallidus</i> sp. nov., a thermophilic and facultatively lithoautotrophic sulfate-reducer isolated from black rust exposed to hot ridge flank crustal fluids. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 2745-2752.	0.8	64
4046	<i>Paenalcaligenes hominis</i> gen. nov., sp. nov., a new member of the family Alcaligenaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 1537-1542.	0.8	28
4047	Description of <i>Undibacterium oligocarboniphilum</i> sp. nov., isolated from purified water, and <i>Undibacterium pigrum</i> strain CCUG 49012 as the type strain of <i>Undibacterium parvum</i> sp. nov., and emended descriptions of the genus <i>Undibacterium</i> and the species <i>Undibacterium pigrum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 384-391.	0.8	42
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4052	<i>Brevirhabdus pacifica</i> gen. nov., sp. nov., isolated from deep-sea sediment in a hydrothermal vent field. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3645-3651.	0.8	35
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4055	<i>Pontibacter amylolyticus</i> sp. nov., isolated from a deep-sea sediment hydrothermal vent field. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1760-1767.	0.8	24
4056	<i>Nocardioides zeicaulis</i> sp. nov., an endophyte actinobacterium of maize. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1869-1874.	0.8	33
4057	<i>Kordiimonas lipolytica</i> sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2198-2204.	0.8	21
4058	<i>Isoptericola cucumis</i> sp. nov., isolated from the root tissue of cucumber (<i>Cucumis sativus</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2784-2788.	0.8	13
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4060	The first representative of the globally widespread subdivision 6 Acidobacteria, <i>Vicinamibacter silvestris</i> gen. nov., sp. nov., isolated from subtropical savannah soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2971-2979.	0.8	59

#	ARTICLE	IF	CITATIONS
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4062	<i>Croceicoccus pelagius</i> sp. nov. and <i>Croceicoccus mobilis</i> sp. nov., isolated from marine environments. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4506-4511.	0.8	18
4063	<i>Saccharibacillus endophyticus</i> sp. nov., an endophyte of cotton. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5134-5139.	0.8	10
4064	“ <i>Streptomyces caelicus</i> ”™, an antibiotic-producing species of the genus <i>Streptomyces</i> , and <i>Streptomyces canchipurensis</i> Li et al. 2015 are later heterotypic synonyms of <i>Streptomyces muensis</i> Ningthoujam et al. 2014. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 548-556.	0.8	14
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4074	<i>Pseudoceanicola lipolyticus</i> sp. nov., a marine alphaproteobacterium, reclassification of <i>Oceanicola flagellatus</i> as <i>Pseudoceanicola flagellatus</i> comb. nov. and emended description of the genus <i>Pseudoceanicola</i> . International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 409-415.	0.8	31
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4083	Pelagicola marinus sp. nov. isolated from deep-sea water. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3961-3966.	0.8	8
4084	Methylotenera oryzisoli sp. nov., a lanthanide-dependent methylotrophic bacteria isolated from rice field soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2713-2718.	0.8	17
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4158	Draft Genome Sequence of Chelatococcus sambhunathii Strain HT4 T (DSM 18167 T) Isolated from a Hot Spring in India. Genome Announcements, 2016, 4, .	0.8	4
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#	ARTICLE	IF	CITATIONS
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5131	Comparative Analysis of <i>Brucepastera parasymphyla</i> gen. nov., sp. nov. and <i>Teretinema zuelzerae</i> gen. nov., comb. nov. (<i>Treponemataceae</i>) Reveals the Importance of Interspecies Hydrogen Transfer in the Energy Metabolism of Spirochetes. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2
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