

Uniting the classification of cultured and uncultured bacterial gene sequences

Nature Reviews Microbiology

12, 635-645

DOI: [10.1038/nrmicro3330](https://doi.org/10.1038/nrmicro3330)

Citation Report

#	ARTICLE	IF	CITATIONS
2	<i>Oenococcus alcoholitolerans</i> sp. nov., a lactic acid bacteria isolated from cachaça and ethanol fermentation processes. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 1259-1267.	0.7	28
3	The Need for Change. <i>Methods in Microbiology</i> , 2014, , 1-12.	0.4	10
4	<i>Celeribacter indicus</i> sp. nov., a polycyclic aromatic hydrocarbon-degrading bacterium from deep-sea sediment and reclassification of <i>Huaishuia halophila</i> as <i>Celeribacter halophilus</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 4160-4167.	0.8	61
5	Localized electron transfer rates and microelectrode-based enrichment of microbial communities within a phototrophic microbial mat. <i>Frontiers in Microbiology</i> , 2014, 5, 11.	1.5	31
6	Towards an integrated phylogenetic classification of the <i>Tremellomycetes</i> . <i>Studies in Mycology</i> , 2015, 81, 85-147.	4.5	393
7	Biodiversity for biocatalysis: A review of the β -hydrolase fold superfamily of esterases-lipases discovered in metagenomes. <i>Biocatalysis and Biotransformation</i> , 2015, 33, 235-249.	1.1	48
8	Microbiology: Create a global microbiome effort. <i>Nature</i> , 2015, 526, 631-634.	13.7	107
9	Back to Basics – The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. <i>PLoS ONE</i> , 2015, 10, e0132783.	1.1	437
10	Complete genome sequence of the thermophilic Acidobacteria, <i>Pyrimomonas methylaliphatogenes</i> type strain K22T. <i>Standards in Genomic Sciences</i> , 2015, 10, 101.	1.5	17
11	The microbiome of the human lower airways: a next generation sequencing perspective. <i>World Allergy Organization Journal</i> , 2015, 8, 23.	1.6	36
12	Identification and analysis of the bacterial endosymbiont specialized for production of the chemotherapeutic natural product <i>ET</i> . <i>Environmental Microbiology</i> , 2015, 17, 3964-3975.	1.8	78
13	MiDAS: the field guide to the microbes of activated sludge. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav062.	1.4	213
14	Whole-cell-based identification of electrochemically active bacteria in microbial fuel cells by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2015, 29, 2211-2218.	0.7	8
15	Fungal specificity and selectivity for algae play a major role in determining lichen partnerships across diverse ecogeographic regions in the lichen-forming family Parmeliaceae (Ascomycota). <i>Molecular Ecology</i> , 2015, 24, 3779-3797.	2.0	94
16	The 16S rRNA gene in the study of marine microbial communities. <i>Ciencias Marinas</i> , 2015, 41, 297-313.	0.4	8
17	Challenging the anthropocentric emphasis on phenotypic testing in prokaryotic species descriptions: rip it up and start again. <i>Frontiers in Genetics</i> , 2015, 6, 218.	1.1	57
18	The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. <i>Frontiers in Genetics</i> , 2015, 6, 348.	1.1	252
19	A taxonomic framework for emerging groups of ecologically important marine gammaproteobacteria based on the reconstruction of evolutionary relationships using genome-scale data. <i>Frontiers in Microbiology</i> , 2015, 6, 281.	1.5	168

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20	Metatranscriptome analysis reveals host-microbiome interactions in traps of carnivorous Genlisea species. <i>Frontiers in Microbiology</i> , 2015, 6, 526.	1.5	23
21	Culturable diversity and antimicrobial activity of Actinobacteria from marine sediments in Valparaíso bay, Chile. <i>Frontiers in Microbiology</i> , 2015, 6, 737.	1.5	61
22	Abundant Atribacteria in deep marine sediment from the Adálie Basin, Antarctica. <i>Frontiers in Microbiology</i> , 2015, 6, 872.	1.5	83
23	Seasonal and spatial patterns of microbial diversity along a trophic gradient in the interconnected lakes of the Osterseen Lake District, Bavaria. <i>Frontiers in Microbiology</i> , 2015, 6, 1168.	1.5	48
24	Microbial Contaminants of Cord Blood Units Identified by 16S rRNA Sequencing and by API Test System, and Antibiotic Sensitivity Profiling. <i>PLoS ONE</i> , 2015, 10, e0141152.	1.1	5
25	Thermophilic prokaryotic communities inhabiting the biofilm and well water of a thermal karst system located in Budapest (Hungary). <i>Extremophiles</i> , 2015, 19, 787-797.	0.9	12
26	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
27	Does a Barcoding Gap Exist in Prokaryotes? Evidences from Species Delimitation in Cyanobacteria. <i>Life</i> , 2015, 5, 50-64.	1.1	16
28	Insights into the life of an oxygenic phototroph. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14747-14748.	3.3	1
29	Complete Genome Sequence of the Bacterium Aalborg_AAW-1, Representing a Novel Family within the Candidate Phylum SR1. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
30	Giving microbes their due “animal life in a microbially dominant world. <i>Journal of Experimental Biology</i> , 2015, 218, 1968-1973.	0.8	46
31	Classifying the uncultivated microbial majority: A place for metagenomic data in the Candidatus proposal. <i>Systematic and Applied Microbiology</i> , 2015, 38, 223-230.	1.2	61
32	Emendation of the family Chlamydiaceae: Proposal of a single genus, Chlamydia, to include all currently recognized species. <i>Systematic and Applied Microbiology</i> , 2015, 38, 99-103.	1.2	156
33	Identification and Characterization of Carboxyl Esterases of Gill Chamber-Associated Microbiota in the Deep-Sea Shrimp <i>Rimicaris exoculata</i> by Using Functional Metagenomics. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2125-2136.	1.4	35
34	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	4.4	88
35	Improved pipeline for reducing erroneous identification by 16S rRNA sequences using the Illumina MiSeq platform. <i>Journal of Microbiology</i> , 2015, 53, 60-69.	1.3	41
36	Genome sequences as the type material for taxonomic descriptions of prokaryotes. <i>Systematic and Applied Microbiology</i> , 2015, 38, 217-222.	1.2	107
37	<i>Emcibacter nanhaiensis</i> gen. nov. sp. nov., isolated from sediment of the South China Sea. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 893-900.	0.7	18

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38	<i>Pseudobowmanella zhangzhouensis</i> gen. nov., sp. nov., isolated from the surface freshwater of the Jiulong River in China. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 741-748.	0.7	13
39	Crohn associated microbial communities associated to colonic mucosal biopsies in patients of the western Mediterranean. <i>Systematic and Applied Microbiology</i> , 2015, 38, 442-452.	1.2	37
40	Uncultivated thermophiles: current status and spotlight on <i>Aigarchaeota</i> TM . <i>Current Opinion in Microbiology</i> , 2015, 25, 136-145.	2.3	70
41	Moderate halophilic bacteria colonizing the phylloplane of halophytes of the subfamily <i>Salicornioideae</i> (<i>Amaranthaceae</i>). <i>Systematic and Applied Microbiology</i> , 2015, 38, 406-416.	1.2	58
42	Selection Maintains Low Genomic GC Content in Marine SAR11 Lineages. <i>Molecular Biology and Evolution</i> , 2015, 32, 2738-2748.	3.5	47
43	A phylogenomic and molecular markers based analysis of the phylum <i>Chlamydiae</i> : proposal to divide the class <i>Chlamydia</i> into two orders, <i>Chlamydiales</i> and <i>Parachlamydiales</i> ord. nov., and emended description of the class <i>Chlamydia</i> . <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 765-781.	0.7	38
44	<i>Bacillus stamsii</i> sp. nov., a facultatively anaerobic sugar degrader that is numerically dominant in freshwater lake sediment. <i>Systematic and Applied Microbiology</i> , 2015, 38, 379-389.	1.2	17
45	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	13.7	1,050
46	Isolation of diverse members of the <i>Aquificales</i> from geothermal springs in Tengchong, China. <i>Frontiers in Microbiology</i> , 2015, 6, 157.	1.5	31
47	Physiological and evolutionary potential of microorganisms from the Canterbury Basin subseafloor, a metagenomic approach. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	16
48	Characterization of mucosa-associated bacterial communities in abomasal ulcers by pyrosequencing. <i>Veterinary Microbiology</i> , 2015, 177, 132-141.	0.8	15
49	<i>Savagea faecisuis</i> gen. nov., sp. nov., a tylosin- and tetracycline-resistant bacterium isolated from a swine-manure storage pit. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 151-161.	0.7	16
50	Microbial Diversity: A Bonanza of Phyla. <i>Current Biology</i> , 2015, 25, R227-R230.	1.8	18
51	The changing landscape of microbial biodiversity exploration and its implications for systematics. <i>Systematic and Applied Microbiology</i> , 2015, 38, 231-236.	1.2	26
52	The human gut microbiome, a taxonomic conundrum. <i>Systematic and Applied Microbiology</i> , 2015, 38, 276-286.	1.2	113
53	Archaeal community diversity and abundance changes along a natural salinity gradient in estuarine sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-18.	1.3	77
54	Biogas Upgrading via Hydrogenotrophic Methanogenesis in Two-Stage Continuous Stirred Tank Reactors at Mesophilic and Thermophilic Conditions. <i>Environmental Science & Technology</i> , 2015, 49, 12585-12593.	4.6	287
55	Generating Enriched Metagenomes from Active Microorganisms with DNA Stable Isotope Probing. <i>Springer Protocols</i> , 2015, , 163-180.	0.1	2

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56	From culturomics to taxonomogenomics: A need to change the taxonomy of prokaryotes in clinical microbiology. <i>Anaerobe</i> , 2015, 36, 73-78.	1.0	119
57	Mechanosensitive channel MSL8 regulates osmotic forces during pollen hydration and germination. <i>Science</i> , 2015, 350, 438-441.	6.0	184
58	Microbial ecology-based methods to characterize the bacterial communities of non-model insects. <i>Journal of Microbiological Methods</i> , 2015, 119, 110-125.	0.7	14
59	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. <i>Science</i> , 2015, 350, 434-438.	6.0	677
60	Out of sight, out of mind. <i>Environmental Microbiology Reports</i> , 2015, 7, 29-30.	1.0	2
61	Cable Bacteria in Freshwater Sediments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6003-6011.	1.4	112
62	Diversity of <i>Rhodopirellula</i> and related planctomycetes in a North Sea coastal sediment employing <i>carB</i> as molecular marker. <i>FEMS Microbiology Letters</i> , 2015, 362, fnv127.	0.7	7
63	Prokaryotic microbiota in the digestive cavity of the jellyfish <i>Cotylorhiza tuberculata</i> . <i>Systematic and Applied Microbiology</i> , 2015, 38, 494-500.	1.2	21
64	How to use molecular biology tools for the study of the anaerobic digestion process?. <i>Reviews in Environmental Science and Biotechnology</i> , 2015, 14, 555-593.	3.9	60
65	Uncultured <i>D</i> and <i>esulfobacteraceae</i> and <i>C</i> renarchaeotal group <i>C</i> 3 incorporate ¹³ <i>C</i> acetate in coastal marine sediment. <i>Environmental Microbiology Reports</i> , 2015, 7, 614-622.	1.0	51
66	Macroecological patterns of archaeal ammonia oxidizers in the Atlantic Ocean. <i>Molecular Ecology</i> , 2015, 24, 4931-4942.	2.0	34
67	Novel isolates double the number of chemotrophic species and allow the first description of higher taxa in Acidobacteria subdivision 4. <i>Systematic and Applied Microbiology</i> , 2015, 38, 534-544.	1.2	121
68	Classifying the bacterial gut microbiota of termites and cockroaches: A curated phylogenetic reference database (DictDb). <i>Systematic and Applied Microbiology</i> , 2015, 38, 472-482.	1.2	87
69	Analyses of Intestinal Microbiota: Culture versus Sequencing: Figure 1. <i>ILAR Journal</i> , 2015, 56, 228-240.	1.8	156
70	Sulfur Reduction in Acid Rock Drainage Environments. <i>Environmental Science & Technology</i> , 2015, 49, 11746-11755.	4.6	59
71	Molecular studies of anaerobic strains from Antarctica and their taxonomic identifications. <i>Proceedings of SPIE</i> , 2015, , .	0.8	0
72	Faecalibaculum rodentium gen. nov., sp. nov., isolated from the faeces of a laboratory mouse. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 1309-1318.	0.7	57
73	Anoxybacter fermentans gen. nov., sp. nov., a piezophilic, thermophilic, anaerobic, fermentative bacterium isolated from a deep-sea hydrothermal vent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 710-715.	0.8	19

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74	Dealing with the Data Deluge – New Strategies in Prokaryotic Genome Analysis. , 0, , .		1
75	Freshwater Metaviromics and Bacteriophages: A Current Assessment of the State of the Art in Relation to Bioinformatic Challenges. <i>Evolutionary Bioinformatics</i> , 2016, 12s1, EBO.S38549.	0.6	20
76	Gene content dissimilarity for subclassification of highly similar microbial strains. <i>BMC Genomics</i> , 2016, 17, 647.	1.2	12
77	A Dormant Microbial Component in the Development of Preeclampsia. <i>Frontiers in Medicine</i> , 2016, 3, 60.	1.2	64
78	High Diversity of Anaerobic Alkane-Degrading Microbial Communities in Marine Seep Sediments Based on (1-methylalkyl)succinate Synthase Genes. <i>Frontiers in Microbiology</i> , 2015, 6, 1511.	1.5	47
79	Expanding the World of Marine Bacterial and Archaeal Clades. <i>Frontiers in Microbiology</i> , 2015, 6, 1524.	1.5	122
80	Metabolic Capabilities of Microorganisms Involved in and Associated with the Anaerobic Oxidation of Methane. <i>Frontiers in Microbiology</i> , 2016, 7, 46.	1.5	99
81	Novel, Deep-Branching Heterotrophic Bacterial Populations Recovered from Thermal Spring Metagenomes. <i>Frontiers in Microbiology</i> , 2016, 7, 304.	1.5	48
82	Phenotypic and Genomic Properties of <i>Chitinispirillum alkaliphilum</i> gen. nov., sp. nov., A Haloalkaliphilic Anaerobic Chitinolytic Bacterium Representing a Novel Class in the Phylum Fibrobacteres. <i>Frontiers in Microbiology</i> , 2016, 7, 407.	1.5	33
83	A Novel Extracellular Gut Symbiont in the Marine Worm <i>Priapulus caudatus</i> (Priapulida) Reveals an Alphaproteobacterial Symbiont Clade of the Ecdysozoa. <i>Frontiers in Microbiology</i> , 2016, 7, 539.	1.5	19
84	Endozoicomonas Are Specific, Facultative Symbionts of Sea Squirts. <i>Frontiers in Microbiology</i> , 2016, 7, 1042.	1.5	43
85	Insights into Broilers' Gut Microbiota Fed with Phosphorus, Calcium, and Phytase Supplemented Diets. <i>Frontiers in Microbiology</i> , 2016, 7, 2033.	1.5	86
86	<i>Fuerstia marisgermanicae</i> gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 2079.	1.5	49
87	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. <i>Frontiers in Nutrition</i> , 2016, 3, 26.	1.6	40
88	Rare Freshwater Ciliate <i>Paramecium chlorelligerum</i> Kahl, 1935 and Its Macronuclear Symbiotic Bacterium – <i>Candidatus Holospora parva</i> –. <i>PLoS ONE</i> , 2016, 11, e0167928.	1.1	42
89	Bacterial Communities of Three Saline Meromictic Lakes in Central Asia. <i>PLoS ONE</i> , 2016, 11, e0150847.	1.1	56
90	Assessing Bacterial Diversity in the Rhizosphere of <i>Thymus zygis</i> Growing in the Sierra Nevada National Park (Spain) through Culture-Dependent and Independent Approaches. <i>PLoS ONE</i> , 2016, 11, e0146558.	1.1	47
91	Reclassification of <i>Clostridium difficile</i> as <i>Clostridioides difficile</i> (Hall and Oâ™Toole 1935) PrÃ©vot 1938. <i>Anaerobe</i> , 2016, 40, 95-99.	1.0	510

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92	Cultivating microbial dark matter in benzene-degrading methanogenic consortia. <i>Environmental Microbiology</i> , 2016, 18, 2923-2936.	1.8	54
93	<i>Candidatus</i> <i>Desulfofervidus auxilii</i> , a hydrogenotrophic sulfate-reducing bacterium involved in the thermophilic anaerobic oxidation of methane. <i>Environmental Microbiology</i> , 2016, 18, 3073-3091.	1.8	115
97	Draft Genome Sequence of <i>Criibacterium bergeronii</i> gen. nov., sp. nov., Strain CCRI-22567 T, Isolated from a Vaginal Sample from a Woman with Bacterial Vaginosis. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
98	Next-generation systematics: An innovative approach to resolve the structure of complex prokaryotic taxa. <i>Scientific Reports</i> , 2016, 6, 38392.	1.6	114
99	Nested Machine Learning Facilitates Increased Sequence Content for Large-Scale Automated High Resolution Melt Genotyping. <i>Scientific Reports</i> , 2016, 6, 19218.	1.6	34
100	Analysis and Interpretation of the Human Microbiome. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 1713-1722.	0.9	12
101	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. <i>ISME Journal</i> , 2016, 10, 2352-2364.	4.4	62
102	Revised phylogeny of Bacteroidetes and proposal of sixteen new taxa and two new combinations including <i>Rhodothermaeaota</i> phyl. nov.. <i>Systematic and Applied Microbiology</i> , 2016, 39, 281-296.	1.2	214
103	A New Genomics-Driven Taxonomy of Bacteria and Archaea: Are We There Yet?. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1956-1963.	1.8	62
104	Gene and whole genome analyses reveal that the mycobacterial strain JS 623 is not a member of the species <i>Mycobacterium smegmatis</i> . <i>Microbial Biotechnology</i> , 2016, 9, 269-274.	2.0	2
105	Divorcing Strain Classification from Species Names. <i>Trends in Microbiology</i> , 2016, 24, 431-439.	3.5	27
106	Ribosomal Tag Pyrosequencing of DNA and RNA Reveals "Rare" Taxa with High Protein Synthesis Potential in the Sediment of a Hypersaline Lake in Western Australia. <i>Geomicrobiology Journal</i> , 2016, 33, 426-440.	1.0	22
107	Estimating the success of enzyme bioprospecting through metagenomics: current status and future trends. <i>Microbial Biotechnology</i> , 2016, 9, 22-34.	2.0	175
108	Soil biochar amendment shapes the composition of N ₂ O-reducing microbial communities. <i>Science of the Total Environment</i> , 2016, 562, 379-390.	3.9	117
109	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in <i>Opisthorchis viverrini</i> Associated Cholangiocarcinoma. <i>EBioMedicine</i> , 2016, 8, 195-202.	2.7	94
110	Single-Cell Genome and Group-Specific <i>dsrAB</i> Sequencing Implicate Marine Members of the Class <i>Dehalococcoidia</i> (Phylum <i>Chloroflexi</i>) in Sulfur Cycling. <i>MBio</i> , 2016, 7, .	1.8	78
111	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5022-5033.	6.5	97
112	Unusual Butane- and Pentanetriol-Based Tetraether Lipids in <i>Methanomassiliicoccus luminyensis</i> , a Representative of the Seventh Order of Methanogens. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4505-4516.	1.4	64

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113	Evaluating community–environment relationships along fine to broad taxonomic resolutions reveals evolutionary forces underlying community assembly. <i>ISME Journal</i> , 2016, 10, 2867-2878.	4.4	31
114	Seasonal dynamics of extremely halophilic microbial communities in three Argentinian salterns. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw184.	1.3	34
115	Phylogenomic re-assessment of the thermophilic genus <i>Geobacillus</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 527-533.	1.2	116
116	Structural and Functional Characterization of a Ruminant β -Glycosidase Defines a Novel Subfamily of Glycoside Hydrolase Family 3 with Permuted Domain Topology. <i>Journal of Biological Chemistry</i> , 2016, 291, 24200-24214.	1.6	21
117	98 The cystic fibrosis lower airways microbial metagenome. <i>Journal of Cystic Fibrosis</i> , 2016, 15, S76.	0.3	3
118	Composition and immunological significance of the upper respiratory tract microbiota. <i>FEBS Letters</i> , 2016, 590, 3705-3720.	1.3	72
119	Analysis of the duodenal microbiotas of weaned piglet fed with epidermal growth factor-expressed <i>Saccharomyces cerevisiae</i> . <i>BMC Microbiology</i> , 2016, 16, 166.	1.3	13
120	Gene Sequence Analyses of the Healthy Oral Microbiome in Humans and Companion Animals. <i>Journal of Veterinary Dentistry</i> , 2016, 33, 97-107.	0.1	22
121	The microbiome–systemic diseases connection. <i>Oral Diseases</i> , 2016, 22, 719-734.	1.5	96
122	A taxonomic framework for cable bacteria and proposal of the candidate genera <i>Electrothrix</i> and <i>Electronema</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 297-306.	1.2	151
123	<i>Telluribacter humicola</i> gen. nov., sp. nov., a new member of the family <i>Cytophagaceae</i> isolated from soil in South Korea. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 1525-1533.	0.7	10
124	The Bacterial Cell. , 2016, , 3-29.		0
125	A novel isolate and widespread abundance of the candidate alphaproteobacterial order (Ellin 329), in southern Appalachian peatlands. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw151.	0.7	21
126	Microbial communities associated with Antarctic snow pack and their biogeochemical implications. <i>Microbiological Research</i> , 2016, 192, 192-202.	2.5	65
127	After All, Only Millions?. <i>MBio</i> , 2016, 7, .	1.8	38
128	A specific and widespread association between deep-sea <i>Bathymodiolus</i> mussels and a novel family of Epsilonproteobacteria. <i>Environmental Microbiology Reports</i> , 2016, 8, 805-813.	1.0	43
129	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	5.8	994
130	Disentangling the Taxonomy of Rickettsiales and Description of Two Novel Symbionts (–Candidatus) <i>Tj ETQq1</i> 1 0.784314 rgBT /Cve Protist <i>Paramecium biaurelia</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 7236-7247.	1.4	106

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131	Seasonal and altitudinal changes of culturable bacterial and yeast diversity in Alpine forest soils. <i>Extremophiles</i> , 2016, 20, 855-873.	0.9	43
132	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	5.9	207
133	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	5.9	1,823
134	The Underestimation of Global Microbial Diversity. <i>MBio</i> , 2016, 7, .	1.8	23
135	Reply to "The Underestimation of Global Microbial Diversity". <i>MBio</i> , 2016, 7, .	1.8	6
136	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. <i>Nature Microbiology</i> , 2016, 1, 16131.	5.9	465
137	Single sample resolution of rare microbial dark matter in a marine invertebrate metagenome. <i>Scientific Reports</i> , 2016, 6, 34362.	1.6	34
138	Molecular Phylogenetics: Concepts for a Newcomer. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2016, 160, 185-196.	0.6	13
139	Label-free isolation and deposition of single bacterial cells from heterogeneous samples for clonal culturing. <i>Scientific Reports</i> , 2016, 6, 32837.	1.6	27
140	Metabolic traits of an uncultured archaeal lineage -MSBL1- from brine pools of the Red Sea. <i>Scientific Reports</i> , 2016, 6, 19181.	1.6	66
141	TACO: Taxonomic prediction of unknown OTUs through OTU co-abundance networks. <i>Quantitative Biology</i> , 2016, 4, 149-158.	0.3	4
142	Species-specific diversity of novel bacterial lineages and differential abundance of predicted pathways for toxic compound degradation in scorpion gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 1364-1378.	1.8	20
143	<i>Calculibacillus koreensis</i> gen. nov., sp. nov., an anaerobic Fe(III)-reducing bacterium isolated from sediment of mine tailings. <i>Journal of Microbiology</i> , 2016, 54, 413-419.	1.3	9
144	Description of <i>Hydrogenophaga laconesensis</i> sp. nov. isolated from tube well water. <i>Archives of Microbiology</i> , 2016, 198, 637-644.	1.0	21
145	Application of urea-agarose gel electrophoresis to select non-redundant 16S rRNAs for taxonomic studies: palladium(II) removal bacteria. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 2721-2735.	1.7	0
146	Impact of genomics on the understanding of microbial evolution and classification: the importance of Darwin's views on classification. <i>FEMS Microbiology Reviews</i> , 2016, 40, 520-553.	3.9	73
147	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. <i>Genome Biology</i> , 2016, 17, 111.	3.8	152
148	Diversity of methanogenic archaea from the 2012 terrestrial hot spring (Valley of Geysers, Kamchatka). <i>Microbiology</i> , 2016, 85, 342-349.	0.5	7

#	ARTICLE	IF	CITATIONS
149	The cystic fibrosis lower airways microbial metagenome. ERJ Open Research, 2016, 2, 00096-2015.	1.1	59
150	The bright side of microbial dark matter: lessons learned from the uncultivated majority. Current Opinion in Microbiology, 2016, 31, 217-226.	2.3	241
151	Gut microbial communities associated with the molting stages of the giant freshwater prawn <i>Macrobrachium rosenbergii</i> . Aquaculture, 2016, 463, 181-188.	1.7	19
152	<i>Abyssicoccus albus</i> gen. nov., sp. nov., a novel member of the family Staphylococcaceae isolated from marine sediment of the Indian Ocean. Antonie Van Leeuwenhoek, 2016, 109, 1153-1160.	0.7	12
153	Characterization of the first cultured representative of <i>Verrucomicrobia</i> subdivision 5 indicates the proposal of a novel phylum. ISME Journal, 2016, 10, 2801-2816.	4.4	173
154	MALDI-TOF MS as a Novel Tool for Dereplication and Characterization of Microbiota in Bacterial Diversity Studies. , 2016, , 235-256.		9
155	To split or not to split: an opinion on dividing the genus <i>Burkholderia</i> . Annals of Microbiology, 2016, 66, 1303-1314.	1.1	90
156	Applications of Mass Spectrometry in Microbiology. , 2016, , .		9
157	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. Applied and Environmental Microbiology, 2016, 82, 992-1003.	1.4	36
158	Genome-Based Microbial Taxonomy Coming of Age. Cold Spring Harbor Perspectives in Biology, 2016, 8, a018085.	2.3	69
159	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. Environmental Microbiology, 2016, 18, 159-173.	1.8	164
160	Ecological Genomics of the Uncultivated Marine <i>Roseobacter</i> Lineage CHAB-I-5. Applied and Environmental Microbiology, 2016, 82, 2100-2111.	1.4	50
161	High-resolution phylogenetic microbial community profiling. ISME Journal, 2016, 10, 2020-2032.	4.4	232
162	<i>Haematospirillum jordaniae</i> gen. nov., sp. nov., isolated from human blood samples.. Antonie Van Leeuwenhoek, 2016, 109, 493-500.	0.7	22
163	Genomic and <i>in situ</i> investigations of the novel uncultured <i>Chloroflexi</i> associated with 0092 morphotype filamentous bulking in activated sludge. ISME Journal, 2016, 10, 2223-2234.	4.4	88
164	Microbial diversity in European alpine permafrost and active layers. FEMS Microbiology Ecology, 2016, 92, fiw018.	1.3	266
165	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular β -proteobacteria. ISME Journal, 2016, 10, 1791-1803.	4.4	34
166	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. Nature Communications, 2016, 7, 10476.	5.8	189

#	ARTICLE	IF	CITATIONS
167	Studying long 16S rDNA sequences with ultrafast-metagenomic sequence classification using exact alignments (Kraken). <i>Journal of Microbiological Methods</i> , 2016, 122, 38-42.	0.7	34
168	<i>Halorhabdus rudnickae</i> sp. nov., a halophilic archaeon isolated from a salt mine borehole in Poland. <i>Systematic and Applied Microbiology</i> , 2016, 39, 100-105.	1.2	23
169	Phylogenetic and genomic analysis of <i>Methanomassiliicoccales</i> in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv149.	1.3	110
170	Metabolic network-guided binning of metagenomic sequence fragments. <i>Bioinformatics</i> , 2016, 32, 867-874.	1.8	8
171	Phylogeny and physiology of candidate phylum <i>Atribacteria</i> ™ (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	4.4	166
172	Evolution of the archaeal and mammalian information processing systems: towards an archaeal model for human disease. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 183-212.	2.4	12
173	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO ₂ concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
174	Endophytic bacteria in <i>Miscanthus</i> seed: implications for germination, vertical inheritance of endophytes, plant evolution and breeding. <i>GCB Bioenergy</i> , 2017, 9, 57-77.	2.5	99
175	Genomic repertoire of the <i>Woeseiaceae</i> /JTB255, cosmopolitan and abundant core members of microbial communities in marine sediments. <i>ISME Journal</i> , 2017, 11, 1276-1281.	4.4	176
176	<i>Enterovirga rhinocerotis</i> gen. nov., sp. nov., isolated from <i>Rhinoceros unicornis</i> faeces. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 553-562.	0.7	18
177	Permeability shapes bacterial communities in sublittoral surface sediments. <i>Environmental Microbiology</i> , 2017, 19, 1584-1599.	1.8	84
178	<i>Olegusella massiliensis</i> gen. nov., sp. nov., strain KHD7 T, a new bacterial genus isolated from the female genital tract of a patient with bacterial vaginosis. <i>Anaerobe</i> , 2017, 44, 87-95.	1.0	14
179	Metataxonomics reveal vultures as a reservoir for <i>Clostridium perfringens</i> . <i>Emerging Microbes and Infections</i> , 2017, 6, 1-8.	3.0	40
180	Microbial community changes during different empty bed residence times and operational fluctuations in an air diffusion reactor for odor abatement. <i>Science of the Total Environment</i> , 2017, 590-591, 352-360.	3.9	16
181	Description of new genera and species of marine cyanobacteria from the Portuguese Atlantic coast. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 18-34.	1.2	92
182	Biological and Ecological Features, Trophic Structure and Energy Flow in Meromictic Lakes. <i>Ecological Studies</i> , 2017, , 61-86.	0.4	9
183	Symbiosis in eukaryotic evolution. <i>Journal of Theoretical Biology</i> , 2017, 434, 20-33.	0.8	113
184	Fish intestinal microbiome: diversity and symbiosis unravelled by metagenomics. <i>Journal of Applied Microbiology</i> , 2017, 123, 2-17.	1.4	290

#	ARTICLE	IF	CITATIONS
185	Distinct Biogeographic Patterns for Archaea, Bacteria, and Fungi along the Vegetation Gradient at the Continental Scale in Eastern China. <i>MSystems</i> , 2017, 2, .	1.7	116
186	<i>Inediibacterium massiliense</i> gen. nov., sp. nov., a new bacterial species isolated from the gut microbiota of a severely malnourished infant. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 737-750.	0.7	12
187	Deciphering composition and function of the root microbiome of a legume plant. <i>Microbiome</i> , 2017, 5, 2.	4.9	152
188	Effects of feeding Original XPCâ„¢ to broilers with a live coccidiosis vaccine under industrial conditions: Part 2. Cecal microbiota analysis. <i>Poultry Science</i> , 2017, 96, 2400-2411.	1.5	16
190	Salivary microbiome of an urban Indian cohort and patterns linked to subclinical inflammation. <i>Oral Diseases</i> , 2017, 23, 926-940.	1.5	26
191	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. <i>Gut Microbes</i> , 2017, 8, 493-503.	4.3	79
192	The low diverse gastric microbiome of the jellyfish <i>Cotylorhiza tuberculata</i> is dominated by four novel taxa. <i>Environmental Microbiology</i> , 2017, 19, 3039-3058.	1.8	62
193	The novel bacterial phylum <i>Calditrichaeota</i> is diverse, widespread and abundant in marine sediments and has the capacity to degrade detrital proteins. <i>Environmental Microbiology Reports</i> , 2017, 9, 397-403.	1.0	39
195	The completely annotated genome and comparative genomics of the <i>Peptoniphilaceae</i> bacterium str. ING2-D1G, a novel acidogenic bacterium isolated from a mesophilic biogas reactor. <i>Journal of Biotechnology</i> , 2017, 257, 178-186.	1.9	2
196	<i>Planctomycetes</i> —New Models for Microbial Cells and Activities. , 2017, , 1-27.		16
197	Modern Natural Products Drug Discovery and Its Relevance to Biodiversity Conservation. , 2017, , 103-120.		9
198	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, 17081.	5.9	213
199	Long-term P fertilisation of pasture soil did not increase soil organic matter stocks but increased microbial biomass and activity. <i>Biology and Fertility of Soils</i> , 2017, 53, 511-521.	2.3	32
200	A phylogenetic framework for the kingdom <i>Fungi</i> based on 18S rRNA gene sequences. <i>Marine Genomics</i> , 2017, 36, 33-39.	0.4	47
201	<i>Bacillus thuringiensis</i> Characterization: Morphology, Physiology, Biochemistry, Pathotype, Cellular, and Molecular Aspects. , 2017, , 1-18.		2
202	Bioaugmentation with hydrolytic microbes to improve the anaerobic biodegradability of lignocellulosic agricultural residues. <i>Bioresource Technology</i> , 2017, 234, 350-359.	4.8	91
203	Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. <i>ISME Journal</i> , 2017, 11, 1545-1558.	4.4	168
204	The Microbiome and Human Biology. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 65-86.	2.5	266

#	ARTICLE	IF	CITATIONS
205	Molecular analysis of the human faecal archaea in a southern Indian population. <i>Journal of Biosciences</i> , 2017, 42, 113-119.	0.5	5
206	Comammox in drinking water systems. <i>Water Research</i> , 2017, 116, 332-341.	5.3	163
207	<i>Jacksonvillea apiculata</i> (Oscillatoriales, Cyanobacteria) gen. nov. & sp. nov.: a new genus of filamentous, epipsamic cyanobacteria from North Florida. <i>Phycologia</i> , 2017, 56, 284-295.	0.6	19
208	Ex-situ biogas upgrading and enhancement in different reactor systems. <i>Bioresource Technology</i> , 2017, 225, 429-437.	4.8	249
209	â€ˆ Candidatus <i>Dichloromethanomonas elyunquensis</i> gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the Peptococcaceae family. <i>Systematic and Applied Microbiology</i> , 2017, 40, 150-159.	1.2	50
210	Bacterial community structure in simultaneous nitrification, denitrification and organic matter removal process treating saline mustard tuber wastewater as revealed by 16S rRNA sequencing. <i>Bioresource Technology</i> , 2017, 228, 31-38.	4.8	147
211	High taxonomic variability despite stable functional structure across microbial communities. <i>Nature Ecology and Evolution</i> , 2017, 1, 15.	3.4	378
212	Characterization of the first cultured representative of a <i>Bacteroidetes</i> clade specialized on the scavenging of cyanobacteria. <i>Environmental Microbiology</i> , 2017, 19, 1134-1148.	1.8	50
213	Microbial community changes in methanogenic granules during the transition from mesophilic to thermophilic conditions. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1313-1322.	1.7	51
214	Viruses in Soil Ecosystems: An Unknown Quantity Within an Unexplored Territory. <i>Annual Review of Virology</i> , 2017, 4, 201-219.	3.0	270
215	Adaptability as the key to success for the ubiquitous marine nitrite oxidizer <i>Nitrococcus</i> . <i>Science Advances</i> , 2017, 3, e1700807.	4.7	74
216	Molecular and Functional Ecology of Sponges and Their Microbial Symbionts. , 2017, , 105-142.		16
217	Porcine intestinal microbiota is shaped by diet composition based on rye or triticale. <i>Journal of Applied Microbiology</i> , 2017, 123, 1571-1583.	1.4	8
218	The Induction of Oxalate Metabolism <i>In Vivo</i> Is More Effective with Functional Microbial Communities than with Functional Microbial Species. <i>MSystems</i> , 2017, 2, .	1.7	33
219	Integrated Bacterial Identification and Antimicrobial Susceptibility Testing Using PCR and High-Resolution Melt. <i>Analytical Chemistry</i> , 2017, 89, 11529-11536.	3.2	61
220	The microbiome beyond the horizon of ecological and evolutionary theory. <i>Nature Ecology and Evolution</i> , 2017, 1, 1606-1615.	3.4	216
221	How to boost marine fungal research: A first step towards a multidisciplinary approach by combining molecular fungal ecology and natural products chemistry. <i>Marine Genomics</i> , 2017, 36, 57-75.	0.4	41
222	Microbial taxonomy in the era of OMICS: application of DNA sequences, computational tools and techniques. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1357-1371.	0.7	54

#	ARTICLE	IF	CITATIONS
223	Transient exposure to oxygen or nitrate reveals ecophysiology of fermentative and sulfate-reducing benthic microbial populations. <i>Environmental Microbiology</i> , 2017, 19, 4866-4881.	1.8	26
224	Culture independent assessment of human milk microbial community in lactational mastitis. <i>Scientific Reports</i> , 2017, 7, 7804.	1.6	133
225	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , 2017, 2, 1533-1542.	5.9	1,465
226	Multiple <i>Streptomyces</i> species with distinct secondary metabolomes have identical 16S rRNA gene sequences. <i>Scientific Reports</i> , 2017, 7, 11089.	1.6	96
228	Comparative RNA function analysis reveals high functional similarity between distantly related bacterial 16 S rRNAs. <i>Scientific Reports</i> , 2017, 7, 9993.	1.6	28
229	Uncultivated microbes in need of their own taxonomy. <i>ISME Journal</i> , 2017, 11, 2399-2406.	4.4	572
230	Patterns of seasonality and group membership characterize the gut microbiota in a longitudinal study of wild Verreaux's sifakas (<i>Propithecus verreauxi</i>). <i>Ecology and Evolution</i> , 2017, 7, 5732-5745.	0.8	90
231	Luciferase-Zinc-Finger System for the Rapid Detection of Pathogenic Bacteria. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 6674-6681.	2.4	15
233	Type II chaperonin gene as a complementary barcode for 16S rRNA gene in study of Archaea diversity of petroleum reservoirs. <i>International Biodeterioration and Biodegradation</i> , 2017, 123, 113-120.	1.9	8
234	Comparison of the active and resident community of a coastal microbial mat. <i>Scientific Reports</i> , 2017, 7, 2969.	1.6	43
235	Description of <i>Absiella argi</i> gen. nov., sp. nov., and transfer of <i>Eubacterium dolichum</i> and <i>Eubacterium tortuosum</i> to the genus <i>Absiella</i> as <i>Absiella dolichum</i> comb. nov. and <i>Absiella tortuosum</i> comb. nov. <i>Anaerobe</i> , 2017, 48, 70-75.	1.0	33
236	Bacterial community composition in Adelie (<i>Pygoscelis adeliae</i>) and Chinstrap (<i>Pygoscelis antarctica</i>) Penguin stomach contents from Signy Island, South Orkney Islands. <i>Polar Biology</i> , 2017, 40, 2517-2530.	0.5	12
237	First description of a new uncultured epsilon sulfur bacterium colonizing marine mangrove sediment in the Caribbean: <i>Thiovulum</i> sp. strain karukerense. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	6
238	The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. <i>ISME Journal</i> , 2017, 11, 2407-2425.	4.4	320
239	A flourishing field: going back to the roots of the Archaea. <i>Nature Reviews Microbiology</i> , 2017, 15, 705-705.	13.6	0
240	Increased Biosynthetic Gene Dosage in a Genome-Reduced Defensive Bacterial Symbiont. <i>MSystems</i> , 2017, 2, .	1.7	46
241	Biogeography at the limits of life: Do extremophilic microbial communities show biogeographical regionalization?. <i>Global Ecology and Biogeography</i> , 2017, 26, 1435-1446.	2.7	18
242	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	1.8	82

#	ARTICLE	IF	CITATIONS
243	Saccharomyces Identifier, SID: strain-level analysis of <i>Saccharomyces cerevisiae</i> populations by using microsatellite meta-patterns. <i>Scientific Reports</i> , 2017, 7, 15343.	1.6	5
244	An Important Role for Purifying Selection in Archaeal Genome Evolution. <i>MSystems</i> , 2017, 2, .	1.7	5
245	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <i>Environmental Microbiology</i> , 2017, 19, 4939-4952.	1.8	107
246	Molecular phylogeny of Bradyrhizobium bacteria isolated from root nodules of tribe Genisteae plants growing in southeast Poland. <i>Systematic and Applied Microbiology</i> , 2017, 40, 482-491.	1.2	19
247	25 years of serving the community with ribosomal RNA gene reference databases and tools. <i>Journal of Biotechnology</i> , 2017, 261, 169-176.	1.9	679
248	Recovery of Previously Uncultured Bacterial Genera from Three Mediterranean Sponges. <i>Marine Biotechnology</i> , 2017, 19, 454-468.	1.1	29
249	Complete genome sequence and whole-genome phylogeny of <i>Kosmotoga pacifica</i> type strain SLHJ1T from an East Pacific hydrothermal sediment. <i>Standards in Genomic Sciences</i> , 2017, 12, 3.	1.5	4
250	Recycled Paper Sludge Microbial Community as a Potential Source of Cellulase and Xylanase Enzymes. <i>Waste and Biomass Valorization</i> , 2017, 8, 1907-1917.	1.8	11
251	<i>Candidatus Cochliophilus cryoturris</i> ™ (Coxiellaceae), a symbiont of the testate amoeba <i>Cochliopodium minus</i> . <i>Scientific Reports</i> , 2017, 7, 3394.	1.6	24
252	Phylogenomics and comparative genomic studies delineate six main clades within the family Enterobacteriaceae and support the reclassification of several polyphyletic members of the family. <i>Infection, Genetics and Evolution</i> , 2017, 54, 108-127.	1.0	112
253	Lifestyles in transition: evolution and natural history of the genus <i>Lactobacillus</i> . <i>FEMS Microbiology Reviews</i> , 2017, 41, S27-S48.	3.9	400
254	Identification of a new cyanobacterium, <i>Toxifilum mysidocida</i> gen. nov. & sp. nov. (Cyanobacteria, Cyanophyceae). <i>Journal of Phycology</i> , 2017, 53, 188-197.	1.0	33
255	High-resolution characterization of the human microbiome. <i>Translational Research</i> , 2017, 179, 7-23.	2.2	55
256	Metagenomics and the Search for Industrial Enzymes. , 2017, , 167-184.		4
257	WIsH: who is the host? Predicting prokaryotic hosts from metagenomic phage contigs. <i>Bioinformatics</i> , 2017, 33, 3113-3114.	1.8	197
258	Eikelboom filamentous morphotypes 0675 and 0041 embrace members of the Chloroflexi: resolving their phylogeny, and design of fluorescence in situ hybridisation probes for their identification. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	17
259	Bioinformatics in Microbiome Analysis. <i>Methods in Microbiology</i> , 2017, 44, 1-18.	0.4	4
260	Reconciliation between operational taxonomic units and species boundaries. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	71

#	ARTICLE	IF	CITATIONS
261	Functionalization and Modification of Hydrocarbon-Like Molecules Guided by Metagenomics: Enzymes Most Requested at the Industrial Scale for Chemical Synthesis as Study Cases. , 2017, , 309-329.		0
262	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	4.9	102
263	Optimisation of 16S rRNA gut microbiota profiling of extremely low birth weight infants. <i>BMC Genomics</i> , 2017, 18, 841.	1.2	47
264	16S rRNA Gene-Based Metagenomic Analysis of Ozark Cave Bacteria. <i>Diversity</i> , 2017, 9, 31.	0.7	30
265	Phylogenetic Analysis and Antimicrobial Profiles of Cultured Emerging Opportunistic Pathogens (Phyla Actinobacteria and Proteobacteria) Identified in Hot Springs. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 1070.	1.2	52
266	Reciprocal Interactions between Nematodes and Their Microbial Environments. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 144.	1.8	63
267	Distinctive Gut Microbiota Is Associated with Diarrheagenic <i>Escherichia coli</i> Infections in Chilean Children. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 424.	1.8	26
268	Volcanic Soils as Sources of Novel CO-Oxidizing Paraburkholderia and Burkholderia: Paraburkholderia hiiakae sp. nov., Paraburkholderia metrosideri sp. nov., Paraburkholderia paradisi sp. nov., Paraburkholderia peleae sp. nov., and Burkholderia alpina sp. nov. a Member of the Burkholderia cepacia Complex. <i>Frontiers in Microbiology</i> , 2017, 8, 207.	1.5	78
269	Ca. Similichlamydia in Epitheliocystis Co-infection of Gilthead Seabream Gills: Unique Morphological Features of a Deep Branching Chlamydial Family. <i>Frontiers in Microbiology</i> , 2017, 8, 508.	1.5	16
270	Stratified Bacterial Diversity along Physico-chemical Gradients in High-Altitude Modern Stromatolites. <i>Frontiers in Microbiology</i> , 2017, 8, 646.	1.5	24
271	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	1.5	409
272	Effect of Environmental Variation on Estimating the Bacterial Species Richness. <i>Frontiers in Microbiology</i> , 2017, 8, 690.	1.5	8
273	Microbial Community Response to Simulated Petroleum Seepage in Caspian Sea Sediments. <i>Frontiers in Microbiology</i> , 2017, 8, 764.	1.5	19
274	Novel Large Sulfur Bacteria in the Metagenomes of Groundwater-Fed Chemosynthetic Microbial Mats in the Lake Huron Basin. <i>Frontiers in Microbiology</i> , 2017, 8, 791.	1.5	29
275	Bacterial Communities in Boreal Forest Mushrooms Are Shaped Both by Soil Parameters and Host Identity. <i>Frontiers in Microbiology</i> , 2017, 8, 836.	1.5	62
276	Culture-Independent Analyses Reveal Novel Anaerolineaceae as Abundant Primary Fermenters in Anaerobic Digesters Treating Waste Activated Sludge. <i>Frontiers in Microbiology</i> , 2017, 8, 1134.	1.5	158
277	A Multilocus Sequence Analysis Scheme for Phylogeny of Thioclava Bacteria and Proposal of Two Novel Species. <i>Frontiers in Microbiology</i> , 2017, 8, 1321.	1.5	24
278	Benzene and Naphthalene Degrading Bacterial Communities in an Oil Sands Tailings Pond. <i>Frontiers in Microbiology</i> , 2017, 8, 1845.	1.5	37

#	ARTICLE	IF	CITATIONS
279	Genomic Comparison of Two Family-Level Groups of the Uncultivated NAG1 Archaeal Lineage from Chemically and Geographically Disparate Hot Springs. <i>Frontiers in Microbiology</i> , 2017, 8, 2082.	1.5	19
280	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	1.5	142
281	A Functional Perspective Analysis of Macroalgae and Epiphytic Bacterial Community Interaction. <i>Frontiers in Microbiology</i> , 2017, 8, 2561.	1.5	65
282	Marine Actinobacteria as a source of compounds for phytopathogen control: An integrative metabolic-profiling / bioactivity and taxonomical approach. <i>PLoS ONE</i> , 2017, 12, e0170148.	1.1	51
283	Genomic diversity within the haloalkaliphilic genus <i>Thioalkalivibrio</i> . <i>PLoS ONE</i> , 2017, 12, e0173517.	1.1	42
284	Phylogenetic analysis of family Neisseriaceae based on genome sequences and description of <i>Populibacter corticis</i> gen. nov., sp. nov., a member of the family Neisseriaceae, isolated from symptomatic bark of <i>Populus</i> Å— euramericana canker. <i>PLoS ONE</i> , 2017, 12, e0174506.	1.1	36
285	Modified RNA-seq method for microbial community and diversity analysis using rRNA in different types of environmental samples. <i>PLoS ONE</i> , 2017, 12, e0186161.	1.1	15
286	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologistâ€™s Perspective - Not Only Size Matters!. <i>PLoS ONE</i> , 2017, 12, e0169662.	1.1	186
287	Metagenomic Mining of Enzyme Diversity. , 2017, , 245-269.		2
288	Use of a mixed culture strategy to isolate halophilic bacteria with antibacterial and cytotoxic activity from the Manaure solar saltern in Colombia. <i>BMC Microbiology</i> , 2017, 17, 230.	1.3	12
289	Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. <i>Microbiome</i> , 2017, 5, 112.	4.9	118
290	Quinones are growth factors for the human gut microbiota. <i>Microbiome</i> , 2017, 5, 161.	4.9	73
291	Draft Genome Sequence of a Sporulating and Motile Strain of <i>Lachnotalea glycerini</i> Isolated from Water in QuÃ©bec City, Canada. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
292	Interpreting Microbial Biosynthesis in the Genomic Age: Biological and Practical Considerations. <i>Marine Drugs</i> , 2017, 15, 165.	2.2	21
293	Characterization of Alkaliphilic Bacteria Isolated from Bauxite Residue in the Southern Region of Minas Gerais, Brazil. <i>Brazilian Archives of Biology and Technology</i> , 2017, 60, .	0.5	14
294	Characterization of a Novel Laccase-producing <i>Bacillus</i> sp. A4 and its Application in <i>Miscanthus</i> Degradation. <i>BioResources</i> , 2017, 12, .	0.5	14
295	How conserved are the conserved 16S-rRNA regions?. <i>PeerJ</i> , 2017, 5, e3036.	0.9	39
296	The divergence between fungal and bacterial communities in seasonal and spatial variations of wastewater treatment plants. <i>Science of the Total Environment</i> , 2018, 628-629, 969-978.	3.9	79

#	ARTICLE	IF	CITATIONS
297	Updating the 97% identity threshold for 16S ribosomal RNA OTUs. <i>Bioinformatics</i> , 2018, 34, 2371-2375.	1.8	513
298	Growth and Population Dynamics of the Anaerobic Fe(II)-Oxidizing and Nitrate-Reducing Enrichment Culture KS. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	46
299	Coupling MALDI-TOF mass spectrometry protein and specialized metabolite analyses to rapidly discriminate bacterial function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4981-4986.	3.3	68
300	Biodegradation of CuTETA, an effluent by-product in mineral processing. <i>Environmental Science and Pollution Research</i> , 2018, 25, 17393-17401.	2.7	2
301	Spatial and temporal dynamics of a freshwater eukaryotic plankton community revealed via 18S rRNA gene metabarcoding. <i>Hydrobiologia</i> , 2018, 818, 71-86.	1.0	45
302	Methodological Strategies in Microbiome Research and their Explanatory Implications. <i>Perspectives on Science</i> , 2018, 26, 239-265.	0.3	14
303	Phylogenetic relationships among endosymbiotic R-body producer: Bacteria providing their host the killer trait. <i>Systematic and Applied Microbiology</i> , 2018, 41, 213-220.	1.2	57
304	<i>Nodosilinea chupicuarensis</i> sp. nov. (Leptolyngbyaceae, Synechococcales) a subaerial cyanobacterium isolated from a stone monument in central Mexico. <i>Phytotaxa</i> , 2018, 334, 167.	0.1	36
305	<i>Abditibacterium utsteinense</i> sp. nov., the first cultivated member of candidate phylum FBP, isolated from ice-free Antarctic soil samples. <i>Systematic and Applied Microbiology</i> , 2018, 41, 279-290.	1.2	58
306	<i>Corynebacterium fournierii</i> sp. nov., isolated from the female genital tract of a patient with bacterial vaginosis. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1165-1174.	0.7	15
307	Genomic comparison between members of the <i>Salinibacteraceae</i> family, and description of a new species of <i>Salinibacter</i> (<i>Salinibacter altiplanensis</i> sp. nov.) isolated from high altitude hypersaline environments of the Argentinian Altiplano. <i>Systematic and Applied Microbiology</i> , 2018, 41, 198-212.	1.2	29
308	Biogeographical patterns of bacterial and archaeal communities from distant hypersaline environments. <i>Systematic and Applied Microbiology</i> , 2018, 41, 139-150.	1.2	39
309	Airway microbial metagenomics. <i>Microbes and Infection</i> , 2018, 20, 536-542.	1.0	6
310	Methods for the Characterization of Plant-Growth Promoting Rhizobacteria. <i>Methods in Molecular Biology</i> , 2018, 1734, 307-328.	0.4	2
311	<i>Ereboglobus luteus</i> gen. nov. sp. nov. from cockroach guts, and new insights into the oxygen relationship of the genera <i>Opiritutus</i> and <i>Didymococcus</i> (Verrucomicrobia : Opiritutaceae). <i>Systematic and Applied Microbiology</i> , 2018, 41, 101-112.	1.2	30
312	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. <i>Nature Biotechnology</i> , 2018, 36, 190-195.	9.4	165
313	Host-Pathogen Interactions. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
314	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018, 8, 525.	1.6	102

#	ARTICLE	IF	CITATIONS
315	Prokaryote composition and predicted metagenomic content of two <i>Cinachyrella</i> Morphospecies and water from West Papuan Marine Lakes. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	32
316	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
317	Hybrid biogas upgrading in a two-stage thermophilic reactor. <i>Energy Conversion and Management</i> , 2018, 168, 1-10.	4.4	71
318	Metagenome, metatranscriptome, and metaproteome approaches unraveled compositions and functional relationships of microbial communities residing in biogas plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5045-5063.	1.7	128
319	<i>Burkholderia alba</i> sp. nov., isolated from a soil sample on Halla mountain in Jeju island. <i>Journal of Microbiology</i> , 2018, 56, 312-316.	1.3	3
320	Genome biology of a novel lineage of planctomycetes widespread in anoxic aquatic environments. <i>Environmental Microbiology</i> , 2018, 20, 2438-2455.	1.8	57
321	Complex life cycle, broad host range and adaptation strategy of the intranuclear <i>Paramecium</i> symbiont <i>Preeria caryophila</i> comb. nov. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	24
322	Protein- and RNA-Enhanced Fermentation by Gut Microbiota of the Earthworm <i>Lumbricus terrestris</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	14
323	<i>Aidingibacillus halophilus</i> gen. nov., sp. nov., a novel member of the family Bacillaceae. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 601-608.	0.7	9
324	Current Perspectives of the Chicken Gastrointestinal Tract and Its Microbiome. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 131-139.	1.9	181
325	Community structure and distribution of benthic cyanobacteria in Antarctic lacustrine microbial mats. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
326	The multi-omics promise in context: from sequence to microbial isolate. <i>Critical Reviews in Microbiology</i> , 2018, 44, 212-229.	2.7	158
327	Characterization of bacterial diversity in contaminated groundwater using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Science of the Total Environment</i> , 2018, 622-623, 1562-1571.	3.9	17
328	<i>In Vitro</i> Evolution of Unmodified 16S rRNA for Simple Ribosome Reconstitution. <i>ACS Synthetic Biology</i> , 2018, 7, 576-583.	1.9	21
329	Multilocus and SSU rRNA gene phylogenetic analyses of available cyanobacterial genomes, and their relation to the current taxonomic system. <i>Hydrobiologia</i> , 2018, 811, 19-34.	1.0	55
330	Microbial ecology-based engineering of Microbial Electrochemical Technologies. <i>Microbial Biotechnology</i> , 2018, 11, 22-38.	2.0	27
331	Isolation, purification, structural elucidation and antimicrobial activities of kocumarin, a novel antibiotic isolated from actinobacterium <i>Kocuria marina</i> CMG S2 associated with the brown seaweed <i>Pelvetia canaliculata</i> . <i>Microbiological Research</i> , 2018, 206, 186-197.	2.5	47
332	Exploring the links between groundwater quality and bacterial communities near oil and gas extraction activities. <i>Science of the Total Environment</i> , 2018, 618, 165-173.	3.9	23

#	ARTICLE	IF	CITATIONS
333	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. ISME Journal, 2018, 12, 756-775.	4.4	91
334	Phylogeny and genomics of SAUL, an enigmatic bacterial lineage frequently associated with marine sponges. Environmental Microbiology, 2018, 20, 561-576.	1.8	32
335	Year-Round Shotgun Metagenomes Reveal Stable Microbial Communities in Agricultural Soils and Novel Ammonia Oxidizers Responding to Fertilization. Applied and Environmental Microbiology, 2018, 84, .	1.4	121
336	Metagenomic Protocols and Strategies. , 2018, , 15-54.		7
337	Fungi in the Wound Microbiome. Advances in Wound Care, 2018, 7, 247-255.	2.6	71
338	Relative abundance of <i>Candidatus Tenderia electrophaga</i> TM is linked to cathodic current in an aerobic biocathode community. Microbial Biotechnology, 2018, 11, 98-111.	2.0	30
339	Comparative 16SrDNA Gene-Based Microbiota Profiles of the Pacific Oyster (<i>Crassostrea gigas</i>) and the Mediterranean Mussel (<i>Mytilus galloprovincialis</i>) from a Shellfish Farm (Ligurian Sea, Italy). Microbial Ecology, 2018, 75, 495-504.	1.4	101
340	Using Core Genome Alignments To Assign Bacterial Species. MSystems, 2018, 3, .	1.7	54
341	Bacterial Epibiotic Communities of Ubiquitous and Abundant Marine Diatoms Are Distinct in Short- and Long-Term Associations. Frontiers in Microbiology, 2018, 9, 2879.	1.5	33
342	Assessment of Molecular Markers for Classification of Bacterial Phyla using Topological Dissimilarity of Phylogenetic Trees. Journal of Phylogenetics & Evolutionary Biology, 2018, 06, .	0.2	0
343	A new connection between wood saprobism and beetle endosymbiosis: the rarely reported saprobic discomycete <i>Tromeropsis</i> is congeneric with the symbiotic yeast <i>Symbiotaphrina</i> (Symbiotaphrinales). Tj ETQq0 0 0 rgBT /Overlock 10 T 215-254.	0.5	18
344	Endophytic and endolichenic fungal diversity in maritime Antarctica based on cultured material and their evolutionary position among Dikarya. Fungal Systematics and Evolution, 2018, 2, 263-272.	0.9	12
346	The first complete genomic structure of <i>Butyrivibrio fibrisolvens</i> and its chromid. Microbial Genomics, 2018, 4, .	1.0	9
347	Cryptic diversity within the <i>Scytonema</i> complex: Characterization of the paralytic shellfish toxin producer <i>Heteroscytonema crispum</i> , and the establishment of the family Heteroscytonemataceae (Cyanobacteria/Nostocales). Harmful Algae, 2018, 80, 158-170.	2.2	21
348	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, .	1.7	293
349	Whole genome sequencing of <i>Moraxella bovoculi</i> reveals high genetic diversity and evidence for interspecies recombination at multiple loci. PLoS ONE, 2018, 13, e0209113.	1.1	19
350	Walking Ecosystems in Microbiome-Inspired Green Infrastructure: An Ecological Perspective on Enhancing Personal and Planetary Health. Challenges, 2018, 9, 40.	0.9	56
351	Influence of CO ₂ Degassing on the Microbial Community in a Dry Mofette Field in HartouÁjov, Czech Republic (Western Eger Rift). Frontiers in Microbiology, 2018, 9, 2787.	1.5	8

#	ARTICLE	IF	CITATIONS
352	Intestinal microbiota mediates Enterotoxigenic Escherichia coli-induced diarrhea in piglets. BMC Veterinary Research, 2018, 14, 385.	0.7	92
353	Genomic Analysis of Lactic Acid Bacteria and Their Applications. , 2018, , 21-49.		1
354	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. Nature Communications, 2018, 9, 5114.	5.8	2,816
355	Co-culture of a Novel Fermentative Bacterium, <i>Lucifera butyrlica</i> gen. nov. sp. nov., With the Sulfur Reducer <i>Desulfurella amilsii</i> for Enhanced Sulfidogenesis. Frontiers in Microbiology, 2018, 9, 3108.	1.5	22
356	<i>Rivularia halophila</i> sp. nov. (Nostocales, Cyanobacteria): the first species of <i>Rivularia</i> described with the modern polyphasic approach. European Journal of Phycology, 2018, 53, 537-548.	0.9	19
357	Characterization of a phenanthrene-degrading methanogenic community. Frontiers of Environmental Science and Engineering, 2018, 12, 1.	3.3	8
358	Sulfur Respiration in a Group of Facultatively Anaerobic Natronoarchaea Ubiquitous in Hypersaline Soda Lakes. Frontiers in Microbiology, 2018, 9, 2359.	1.5	30
359	Single-Cell Genomics Reveals a Diverse Metabolic Potential of Uncultivated Desulfatiglans-Related Deltaproteobacteria Widely Distributed in Marine Sediment. Frontiers in Microbiology, 2018, 9, 2038.	1.5	69
360	Revisiting the Taxonomy of the Genus <i>Arcobacter</i> : Getting Order From the Chaos. Frontiers in Microbiology, 2018, 9, 2077.	1.5	245
361	Sizing Up the Uncultured Microbial Majority. MSystems, 2018, 3, .	1.7	13
362	The molecular and phenotypic characterization of fructophilic lactic acid bacteria isolated from the guts of <i>Apis mellifera</i> L. derived from a Polish apiary. Journal of Applied Genetics, 2018, 59, 503-514.	1.0	23
363	Genome-Based Analysis Reveals the Taxonomy and Diversity of the Family <i>Idiomarinaceae</i> . Frontiers in Microbiology, 2018, 9, 2453.	1.5	48
364	Phylogenetically Novel Uncultured Microbial Cells Dominate Earth Microbiomes. MSystems, 2018, 3, .	1.7	273
365	Exclusivity offers a sound yet practical species criterion for bacteria despite abundant gene flow. BMC Genomics, 2018, 19, 724.	1.2	14
366	Planktonic prokaryote and protist communities in a submarine canyon system in the Ligurian Sea (NW) Tj ETQq0 0,0,rgBT /Overlock 10	1.5	19
367	Precise Fecal Microbiome of the Herbivorous Tibetan Antelope Inhabiting High-Altitude Alpine Plateau. Frontiers in Microbiology, 2018, 9, 2321.	1.5	33
368	High-Quality Draft Single-Cell Genome Sequence Belonging to the Archaeal Candidate Division SA1, Isolated from <i>Nereus</i> Deep in the Red Sea. Genome Announcements, 2018, 6, .	0.8	6
369	G3 PhyloChip Analysis Confirms the Promise of Plant-Based Culture Media for Unlocking the Composition and Diversity of the Maize Root Microbiome and for Recovering Unculturable Candidate Divisions/Phyla. Microbes and Environments, 2018, 33, 317-325.	0.7	21

#	ARTICLE	IF	CITATIONS
370	Genomic Description of <i>Candidatus Abyssubacteria</i> , a Novel Subsurface Lineage Within the Candidate Phylum Hydrogenedentes. <i>Frontiers in Microbiology</i> , 2018, 9, 1993.	1.5	36
371	Ecophylogenetics Clarifies the Evolutionary Association between Mammals and Their Gut Microbiota. <i>MBio</i> , 2018, 9, .	1.8	67
372	Time Radically Alters Ex Situ Evidentiary Soil 16S Bacterial Profiles Produced Via Next-Generation Sequencing. <i>Journal of Forensic Sciences</i> , 2018, 63, 1356-1365.	0.9	10
373	Inhibition of anammox by sludge thermal hydrolysis and metagenomic insights. <i>Bioresource Technology</i> , 2018, 270, 46-54.	4.8	26
374	First case report of bacteremia caused by <i>Dysgonomonas mossii</i> . <i>Anaerobe</i> , 2018, 54, 111-114.	1.0	5
375	Bloom of a denitrifying methanotroph, <i>Candidatus Methylopirabilis limnetica</i> , in a deep stratified lake. <i>Environmental Microbiology</i> , 2018, 20, 2598-2614.	1.8	87
376	Bathyarchaeota: globally distributed metabolic generalists in anoxic environments. <i>FEMS Microbiology Reviews</i> , 2018, 42, 639-655.	3.9	206
377	Description of <i>Mediterraneibacter massiliensis</i> , gen. nov., sp. nov., a new genus isolated from the gut microbiota of an obese patient and reclassification of <i>Ruminococcus faecis</i> , <i>Ruminococcus lactaris</i> , <i>Ruminococcus torques</i> , <i>Ruminococcus gnavus</i> and <i>Clostridium glycyrrhizinilyticum</i> as <i>Mediterraneibacter faecis</i> comb. nov., <i>Mediterraneibacter lactaris</i> comb. nov., <i>Mediterraneibacter torques</i> comb. nov., <i>Mediterraneibacter gnavus</i> comb. nov. and <i>Mediterraneibacter glycyrrhizinilyticus</i> comb. nov., <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2107-2128.	0.7	87
378	Case study on the soil antibiotic resistome in an urban community garden. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 241-250.	1.1	14
379	<i>Steinernema poinari</i> (Nematoda: Steinernematidae): a new symbiotic host of entomopathogenic bacteria <i>Xenorhabdus bovienii</i> . <i>Archives of Microbiology</i> , 2018, 200, 1307-1316.	1.0	14
380	Analytic Methods in Microbiome Studies. , 2018, , 29-42.		0
381	Galacturonate Metabolism in Anaerobic Chemostat Enrichment Cultures: Combined Fermentation and Acetogenesis by the Dominant sp. nov. <i>Candidatus Galacturonibacter soehngeni</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	16
382	Screening and Molecular Identification of Pectinase Producing Microbes from Coffee Pulp. <i>BioMed Research International</i> , 2018, 2018, 1-7.	0.9	55
383	Effect of temperature and dietary lipid proportion on gut microbiota in yellowtail kingfish <i>Seriola lalandi</i> juveniles. <i>Aquaculture</i> , 2018, 497, 269-277.	1.7	59
384	Description of <i>Candidatus Methylocucumis oryzae</i> , a novel Type I methanotroph with large cells and pale pink colour, isolated from an Indian rice field. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2473-2484.	0.7	28
385	Combined bacterial and fungal intestinal microbiota analyses: Impact of storage conditions and DNA extraction protocols. <i>PLoS ONE</i> , 2018, 13, e0201174.	1.1	41
386	On the maverick Planctomycetes. <i>FEMS Microbiology Reviews</i> , 2018, 42, 739-760.	3.9	210
387	Molecular Microbiome Analysis. , 2018, , 49-65.		0

#	ARTICLE	IF	CITATIONS
388	Thermophiles and Their Exploration for Thermostable Enzyme Production. <i>Microorganisms for Sustainability</i> , 2018, , 167-186.	0.4	0
389	<i>Labilibaculum manganireducens</i> gen. nov., sp. nov. and <i>Labilibaculum filiforme</i> sp. nov., Novel Bacteroidetes Isolated from Subsurface Sediments of the Baltic Sea. <i>Frontiers in Microbiology</i> , 2017, 8, 2614.	1.5	25
390	Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus <i>Mycobacterium</i> into an Emended Genus <i>Mycobacterium</i> and Four Novel Genera. <i>Frontiers in Microbiology</i> , 2018, 9, 67.	1.5	878
391	Metagenomic Approaches to Investigate the Contribution of the Vineyard Environment to the Quality of Wine Fermentation: Potentials and Difficulties. <i>Frontiers in Microbiology</i> , 2018, 9, 991.	1.5	90
392	Relationships between Substrate Promiscuity and Chiral Selectivity of Esterases from Phylogenetically and Environmentally Diverse Microorganisms. <i>Catalysts</i> , 2018, 8, 10.	1.6	11
393	Biocatalysis and Biotransformations. <i>Catalysts</i> , 2018, 8, 216.	1.6	3
394	Online Interactive Microbial Classification and Geospatial Distributional Analysis Using BioAtlas. <i>Methods in Molecular Biology</i> , 2018, 1807, 21-35.	0.4	2
395	Species classifier choice is a key consideration when analysing low-complexity food microbiome data. <i>Microbiome</i> , 2018, 6, 50.	4.9	65
396	Oxygen minimum zone cryptic sulfur cycling sustained by offshore transport of key sulfur oxidizing bacteria. <i>Nature Communications</i> , 2018, 9, 1729.	5.8	93
397	Hybridization capture reveals microbial diversity missed using current profiling methods. <i>Microbiome</i> , 2018, 6, 61.	4.9	34
398	Microbiomes of gall-inducing copepod crustaceans from the corals <i>Stylophora pistillata</i> (Scleractinia) and <i>Gorgonia ventalina</i> (Alcyonacea). <i>Scientific Reports</i> , 2018, 8, 11563.	1.6	13
399	Revision of the Synechococcales (Cyanobacteria) through recognition of four families including <i>Oculatellaceae</i> fam. nov. and <i>Trichocoleaceae</i> fam. nov. and six new genera containing 14 species. <i>Phytotaxa</i> , 2018, 365, 1.	0.1	99
400	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018, 36, 996-1004.	9.4	2,615
401	The Endosymbiotic <i>Wolbachia</i> and Host COI Gene Enables to Distinguish Between Two Invasive Palm Pests; Coconut Leaf Beetle, <i>Brontispa longissima</i> and Hispid Leaf Beetle, <i>Octodonta nipae</i> . <i>Journal of Economic Entomology</i> , 2018, 111, 2894-2902.	0.8	9
402	Genome Variation in the Model Halophilic Bacterium <i>Salinibacter ruber</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1499.	1.5	12
403	Whole genome sequencing and function prediction of 133 gut anaerobes isolated from chicken caecum in pure cultures. <i>BMC Genomics</i> , 2018, 19, 561.	1.2	108
404	Isolation and characterization of a novel 1-aminocyclopropane-1-carboxylate (ACC) deaminase producing plant growth promoting marine Gammaproteobacteria from crops grown in brackish environments. Proposal for <i>Pokkaliibacter plantistimulans</i> gen. nov., sp. nov., <i>Balneatrichaceae</i> fam. nov. in the order <i>Oceanospirillales</i> and an emended description of the genus <i>Balneatrix</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 570-580.	1.2	19
405	First description of a new uncultured purple sulfur bacterium colonizing marine mangrove sediment in the Caribbean: <i>Halochromatium</i> -like PSB from Guadeloupe. <i>Comptes Rendus - Biologies</i> , 2018, 341, 387-397.	0.1	6

#	ARTICLE	IF	CITATIONS
406	Inter-individual variability in copepod microbiomes reveals bacterial networks linked to host physiology. <i>ISME Journal</i> , 2018, 12, 2103-2113.	4.4	52
407	Bioinformatic, Molecular, and Genetic Tools for Exploring Genome-Wide Responses to Hydrocarbons. , 2018, , 127-135.		0
408	Exacerbation induces a microbiota shift in sputa of COPD patients. <i>PLoS ONE</i> , 2018, 13, e0194355.	1.1	34
409	<i>Paenibacillus albilobatus</i> sp. nov., isolated from acidic soil on Jeju Island. <i>Journal of Microbiology</i> , 2018, 56, 393-398.	1.3	1
410	Novel prosthecate bacteria from the candidate phylum Acetothermia. <i>ISME Journal</i> , 2018, 12, 2225-2237.	4.4	75
411	Description of three new <i>Peptoniphilus</i> species cultured in the vaginal fluid of a woman diagnosed with bacterial vaginosis: <i>Peptoniphilus pacaensis</i> sp. nov., <i>Peptoniphilus raoultii</i> sp. nov., and <i>Peptoniphilus vaginalis</i> sp. nov.. <i>MicrobiologyOpen</i> , 2019, 8, e00661.	1.2	20
412	Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. <i>Studies in Mycology</i> , 2019, 92, 135-154.	4.5	555
413	Conventional culture methods with commercially available media unveil the presence of novel culturable bacteria. <i>Gut Microbes</i> , 2019, 10, 77-91.	4.3	72
414	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , 2019, 42, 15-21.	1.2	149
415	Diversity and Dynamics of <i>Candidatus Endobugula</i> and Other Symbiotic Bacteria in Chinese Populations of the Bryozoan, <i>Bugula neritina</i> . <i>Microbial Ecology</i> , 2019, 77, 243-256.	1.4	4
416	The Hidden World of Rickettsiales Symbionts: <i>Candidatus Spectririckettsia obscura</i> , a Novel Bacterium Found in Brazilian and Indian <i>Paramecium caudatum</i> . <i>Microbial Ecology</i> , 2019, 77, 748-758.	1.4	42
417	The role of the microbiome in nonhealing diabetic wounds. <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 79-92.	1.8	79
418	Dialogue on the nomenclature and classification of prokaryotes. <i>Systematic and Applied Microbiology</i> , 2019, 42, 5-14.	1.2	41
419	Application of machine learning techniques for creating urban microbial fingerprints. <i>Biology Direct</i> , 2019, 14, 13.	1.9	29
420	High proportions of bacteria and archaea across most biomes remain uncultured. <i>ISME Journal</i> , 2019, 13, 3126-3130.	4.4	264
421	A pilot study to examine the association between human gut microbiota and the host's central obesity. <i>JGH Open</i> , 2019, 3, 480-487.	0.7	13
422	A Reverse Ecology Approach Based on a Biological Definition of Microbial Populations. <i>Cell</i> , 2019, 178, 820-834.e14.	13.5	118
423	Benchmarking Metagenomics Tools for Taxonomic Classification. <i>Cell</i> , 2019, 178, 779-794.	13.5	364

#	ARTICLE	IF	CITATIONS
424	Microdiversity ensures the maintenance of functional microbial communities under changing environmental conditions. <i>ISME Journal</i> , 2019, 13, 2969-2983.	4.4	121
425	Numerical analysis of phenotypic properties, genomic fingerprinting, and multilocus sequence analysis of <i>Bradyrhizobium</i> strains isolated from root nodules of <i>Lembotropis nigricans</i> of the tribe Genisteeae. <i>Annals of Microbiology</i> , 2019, 69, 1123-1134.	1.1	5
426	Perturbed Microbial Ecology in <i>Myasthenia Gravis</i> : Evidence from the Gut Microbiome and Fecal Metabolome. <i>Advanced Science</i> , 2019, 6, 1901441.	5.6	55
427	A Genomotaxonomy View of the <i>Bradyrhizobium</i> Genus. <i>Frontiers in Microbiology</i> , 2019, 10, 1334.	1.5	104
428	Primer-free FISH probes from metagenomics/metatranscriptomics data permit the study of uncharacterised taxa in complex microbial communities. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 17.	2.9	11
429	Impact of Antibiotic Gut Exposure on the Temporal Changes in Microbiome Diversity. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	35
430	Molecular techniques and their limitations shape our view of the holobiont. <i>Zoology</i> , 2019, 137, 125695.	0.6	5
431	Symbionts of the ciliate <i>Euplotes</i> : diversity, patterns and potential as models for bacteria-eukaryote endosymbioses. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190693.	1.2	73
432	DAIRYdb: a manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products. <i>BMC Genomics</i> , 2019, 20, 560.	1.2	48
433	<i>Streptococcus castoreus</i> , an uncommon group A <i>Streptococcus</i> in beavers. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1663-1673.	0.7	4
434	<i>Ilyomonas limi</i> gen. nov., sp. nov., a new member of the family Chitinophagaceae isolated from mud. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1715-1723.	0.7	8
435	Dynamics of the Pacific oyster pathobiota during mortality episodes in Europe assessed by 16S rRNA gene profiling and a new target enrichment next-generation sequencing strategy. <i>Environmental Microbiology</i> , 2019, 21, 4548-4562.	1.8	49
436	Phylogenetic Characterization of Mycobionts and Photobionts of Rock Tripe Lichen in East Antarctica. <i>Microorganisms</i> , 2019, 7, 203.	1.6	14
437	Amino Acids and Ribose: Drivers of Protein and RNA Fermentation by Ingested Bacteria of a Primitive Gut Ecosystem. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	5
438	Genomic ecology of Marine Group II, the most common marine planktonic Archaea across the surface ocean. <i>MicrobiologyOpen</i> , 2019, 8, e00852.	1.2	27
439	<i>Thermoanaerobacterium fractalcalcis</i> gen. nov. sp. nov., a Novel Fumarate-Fermenting Microorganism From a Deep Fractured Carbonate Aquifer of the US Great Basin. <i>Frontiers in Microbiology</i> , 2019, 10, 2224.	1.5	15
441	A collection of rumen bacteriome data from 334 mid-lactation dairy cows. <i>Scientific Data</i> , 2019, 6, 180301.	2.4	13
442	<i>Geomonas oryzae</i> gen. nov., sp. nov., <i>Geomonas edaphica</i> sp. nov., <i>Geomonas ferrireducens</i> sp. nov., <i>Geomonas terrae</i> sp. nov., Four Ferric-Reducing Bacteria Isolated From Paddy Soil, and Reclassification of Three Species of the Genus <i>Geobacter</i> as Members of the Genus <i>Geomonas</i> gen. nov.. <i>Frontiers in Microbiology</i> , 2019, 10, 2201.	1.5	54

#	ARTICLE	IF	CITATIONS
443	Microbial metabolisms in an abyssal ferromanganese crust from the Takuyo-Daigo Seamount as revealed by metagenomics. <i>PLoS ONE</i> , 2019, 14, e0224888.	1.1	14
444	<i>Nodosilinea signiensis</i> sp. nov. (Leptolyngbyaceae, Synechococcales), a new terrestrial cyanobacterium isolated from mats collected on Signy Island, South Orkney Islands, Antarctica. <i>PLoS ONE</i> , 2019, 14, e0224395.	1.1	15
445	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019, 10, 5029.	5.8	1,007
447	Anaerobic phenanthrene biodegradation with four kinds of electron acceptors enriched from the same mixed inoculum and exploration of metabolic pathways. <i>Frontiers of Environmental Science and Engineering</i> , 2019, 13, 1.	3.3	18
448	Introducing Murine Microbiome Database (MMDB): A Curated Database with Taxonomic Profiling of the Healthy Mouse Gastrointestinal Microbiome. <i>Microorganisms</i> , 2019, 7, 480.	1.6	19
449	Dynamics of dissolution for underwater compressed air energy storage. , 2019, , .		6
450	Description of a novel coccoid cyanobacterial genus and species <i>Sinocapsa zengkensis</i> gen. nov. sp. nov. (Sinocapsaceae, incertae sedis), with taxonomic notes on genera in Chroococciopsidales. <i>Phytotaxa</i> , 2019, 409, 146-160.	0.1	17
451	Phylogenetic complexities of the members of Rivulariaceae with the re-creation of the family Calotrichaceae and description of <i>Dulcicalothrix necridiiformans</i> gen nov., sp nov., and reclassification of <i>Calothrix desertica</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	16
452	Applications of sequencing technology in clinical microbial infection. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 7143-7150.	1.6	35
453	Distinction between <i>Borrelia</i> and <i>Borreliella</i> is more robustly supported by molecular and phenotypic characteristics than all other neighbouring prokaryotic genera: Response to Margos' et al. "The genus <i>Borrelia</i> reloaded" (<i>PLoS ONE</i> 13(12): e0208432). <i>PLoS ONE</i> , 2019, 14, e0221397.	1.1	64
454	Changes in Oral Microbial Ecology of C57BL/6 Mice at Different Ages Associated with Sampling Methodology. <i>Microorganisms</i> , 2019, 7, 283.	1.6	16
455	New genus-specific primers for PCR identification of <i>Rubrobacter</i> strains. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1863-1874.	0.7	7
456	Chlorinated ethene plume evolution after source thermal remediation: Determination of degradation rates and mechanisms. <i>Journal of Contaminant Hydrology</i> , 2019, 227, 103551.	1.6	12
457	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitrification anammox reactor using integrated multi-omics. <i>Microbiome</i> , 2019, 7, 122.	4.9	65
458	Rapid Inference of Direct Interactions in Large-Scale Ecological Networks from Heterogeneous Microbial Sequencing Data. <i>Cell Systems</i> , 2019, 9, 286-296.e8.	2.9	96
459	Nanoarray Digital Polymerase Chain Reaction with High-Resolution Melt for Enabling Broad Bacteria Identification and Phenotypic Molecular Antimicrobial Susceptibility Test. <i>Analytical Chemistry</i> , 2019, 91, 12784-12792.	3.2	63
460	<i>Phoenicibacter congongensis</i> gen. nov., sp. nov., a new genus isolated from the human gut and its description using a taxonogenomic approach. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 775-784.	0.7	2
461	<i>Edaphocola aurantiacus</i> gen. nov., sp. nov., a new member of the family Chitinophagaceae isolated from wetland soil in South Korea. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 687-694.	0.7	8

#	ARTICLE	IF	CITATIONS
462	Study of microbial dynamics during optimization of hydrogen production from food waste by using LCFA-rich agent. <i>Bioresource Technology Reports</i> , 2019, 5, 157-163.	1.5	6
463	Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. <i>MBio</i> , 2019, 10, .	1.8	60
464	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019, 68, 1781-1790.	6.1	73
465	Assessment of food microbiological indicators applied on poultry carcasses by culture combined MALDI-TOF MS identification and 16S rRNA amplicon sequencing. <i>Food Microbiology</i> , 2019, 82, 53-61.	2.1	28
466	Uncovering the Uncultivated Majority in Antarctic Soils: Toward a Synergistic Approach. <i>Frontiers in Microbiology</i> , 2019, 10, 242.	1.5	51
467	Anaerobic Degradation of Sulfated Polysaccharides by Two Novel <i>Kiritimatiellales</i> Strains Isolated From Black Sea Sediment. <i>Frontiers in Microbiology</i> , 2019, 10, 253.	1.5	56
468	Low molecular weight organic acids enhance the high molecular weight polycyclic aromatic hydrocarbons degradation by bacteria. <i>Chemosphere</i> , 2019, 222, 132-140.	4.2	52
469	Effects of growth conditions on siderophore producing bacteria and siderophore production from Indian Ocean sector of Southern Ocean. <i>Journal of Basic Microbiology</i> , 2019, 59, 412-424.	1.8	24
470	Microbial-Driven Butyrate Regulates Jejunal Homeostasis in Piglets During the Weaning Stage. <i>Frontiers in Microbiology</i> , 2018, 9, 3335.	1.5	40
471	In-situ dissolution rates of silicate minerals and associated bacterial communities in the critical zone (Strengbach catchment, France). <i>Geochimica Et Cosmochimica Acta</i> , 2019, 249, 95-120.	1.6	24
472	A double-blind randomized placebo-controlled trial of probiotics in systemic sclerosis associated gastrointestinal disease. <i>Seminars in Arthritis and Rheumatism</i> , 2019, 49, 411-419.	1.6	27
473	Metagenomics a modern approach to reveal the secrets of unculturable microbes. , 2019, , 177-195.		1
474	New Microbial Lineages Capable of Carbon Fixation and Nutrient Cycling in Deep-Sea Sediments of the Northern South China Sea. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	36
475	Evolutionary history constrains microbial traits across environmental variation. <i>Nature Ecology and Evolution</i> , 2019, 3, 1064-1069.	3.4	76
476	Paint particles are a distinct and variable substrate for marine bacteria. <i>Marine Pollution Bulletin</i> , 2019, 146, 117-124.	2.3	24
477	Diversity of <i>Ca. Micrarchaeota</i> in Two Distinct Types of Acidic Environments and Their Associations with <i>Thermoplasmatales</i> . <i>Genes</i> , 2019, 10, 461.	1.0	27
478	When Is A Lineage A Species? A Case Study In <i>Myxocorys</i> gen. nov. (<i>Synechococcales</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 2019, 55, 976-996.	1.0	51
479	Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 968-976.	15.2	748

#	ARTICLE	IF	CITATIONS
480	Specific inhibitors of lysozyme and peptidases inhibit the growth of the rumen protozoan <i>Entodinium caudatum</i> without decreasing feed digestion or fermentation <i>in vitro</i> . Journal of Applied Microbiology, 2019, 127, 670-682.	1.4	15
481	Anaerobic hydrocarbon degradation in candidate phylum <i>Atribacteria</i> ™ (JS1) inferred from genomics. ISME Journal, 2019, 13, 2377-2390.	4.4	63
482	First evidence of <i>Cardinium</i> (Sphingobacteria) in non-marine ostracods from Turkey. Journal of Crustacean Biology, 2019, 39, 547-551.	0.3	6
483	Metabolic versatility in a modern lineage of cyanobacteria from terrestrial hot springs. Free Radical Biology and Medicine, 2019, 140, 224-232.	1.3	20
484	Bioleaching of metal from waste stream using a native strain of <i>Acidithiobacillus</i> isolated from a coal mine drainage. Canadian Journal of Chemical Engineering, 2019, 97, 2920-2927.	0.9	9
485	Identifying the tick <i>Amblyomma javanense</i> (Acari: Ixodidae) from Chinese pangolin: generating species barcode, phylogenetic status and its implication in wildlife forensics. Experimental and Applied Acarology, 2019, 78, 461-467.	0.7	13
486	Position-Specific Metabolic Probing and Metagenomics of Microbial Communities Reveal Conserved Central Carbon Metabolic Network Activities at High Temperatures. Frontiers in Microbiology, 2019, 10, 1427.	1.5	12
487	Biogas upgrading and biochemical production from gas fermentation: Impact of microbial community and gas composition. Bioresource Technology, 2019, 286, 121413.	4.8	38
488	Organic substrate diffusibility governs microbial community composition, nutrient removal performance and kinetics of granulation of aerobic granular sludge. Water Research X, 2019, 4, 100033.	2.8	85
489	Relationship between Antimicrobial Susceptibility and Multilocus Sequence Type of <i>Mycoplasma bovis</i> Isolates and Development of a Method for Rapid Detection of Point Mutations Involved in Decreased Susceptibility to Macrolides, Lincosamides, Tetracyclines, and Spectinomycin. Applied and Environmental Microbiology, 2019, 85, .	1.4	23
490	A brief overview of the concepts, methods and computational tools used in phylogenetic tree construction and gene prediction. Meta Gene, 2019, 21, 100586.	0.3	8
491	Sulfate-Reducing Bacteria That Produce Exopolymers Thrive in the Calcifying Zone of a Hypersaline Cyanobacterial Mat. Frontiers in Microbiology, 2019, 10, 862.	1.5	54
492	Reading canonical and modified nucleobases in 16S ribosomal RNA using nanopore native RNA sequencing. PLoS ONE, 2019, 14, e0216709.	1.1	130
493	Enhancing anaerobic digestion of agricultural residues by microaerobic conditions. Biomass Conversion and Biorefinery, 2019, , 1.	2.9	6
494	Candidate Phyla Radiation Roizmanbacteria From Hot Springs Have Novel and Unexpectedly Abundant CRISPR-Cas Systems. Frontiers in Microbiology, 2019, 10, 928.	1.5	36
495	Asgard archaea capable of anaerobic hydrocarbon cycling. Nature Communications, 2019, 10, 1822.	5.8	165
496	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. Nature Biotechnology, 2019, 37, 632-639.	9.4	569
497	Predictive genomic traits for bacterial growth in culture versus actual growth in soil. ISME Journal, 2019, 13, 2162-2172.	4.4	66

#	ARTICLE	IF	CITATIONS
498	Spatial, Temporal, and Phylogenetic Scales of Microbial Ecology. <i>Trends in Microbiology</i> , 2019, 27, 662-669.	3.5	105
499	A bridge too far in naming species: a total evidence approach does not support recognition of four species in <i>Desertifilum</i> (Cyanobacteria). <i>Journal of Phycology</i> , 2019, 55, 898-911.	1.0	34
500	<i>Candidatus</i> <i>Syntrophosphaera thermopropionivorans</i> : a novel player in syntrophic propionate oxidation during anaerobic digestion. <i>Environmental Microbiology Reports</i> , 2019, 11, 558-570.	1.0	86
501	Rapid assessment of coral cover from environmental DNA in Hawai'i. <i>Environmental DNA</i> , 2019, 1, 40-53.	3.1	40
502	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	14
503	Neotypification of <i>Pleurocapsa fuliginosa</i> and epitypification of <i>P. minor</i> (Pleurocapsales): resolving a polyphyletic cyanobacterial genus. <i>Phytotaxa</i> , 2019, 392, 245.	0.1	9
504	Microbiota in Pouchitis and De Novo Crohn's Disease of the Ileal Pouch. , 2019, , 119-127.		0
505	PenSeq: coverage you can count on. <i>New Phytologist</i> , 2019, 221, 1177-1179.	3.5	1
506	Formate-removing inoculum dominated by <i>Methanobacterium congolense</i> supports succinate production from crude glycerol fermentation. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 625-634.	1.4	4
507	Expanding anaerobic alkane metabolism in the domain of Archaea. <i>Nature Microbiology</i> , 2019, 4, 595-602.	5.9	133
508	Taxonomic resolution of the genus <i>Cyanothece</i> (Chroococcales, Cyanobacteria), with a treatment on <i>Gloeothece</i> and three new genera, <i>Crocospaera</i> , <i>Rippkaea</i> , and <i>Zehria</i> . <i>Journal of Phycology</i> , 2019, 55, 578-610.	1.0	57
509	Integrating Soil Microbiology into Ecosystem Science. <i>Advances in Environmental Microbiology</i> , 2019, , 65-102.	0.1	1
510	Multilocus Sequence Analysis, a Rapid and Accurate Tool for Taxonomic Classification, Evolutionary Relationship Determination, and Population Biology Studies of the Genus <i>Shewanella</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13
511	Combination of a flow cytometric bead system with 16S rRNA-targeted oligonucleotide probes for bacteria detection. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 2161-2168.	1.9	8
512	A census-based estimate of Earth's bacterial and archaeal diversity. <i>PLoS Biology</i> , 2019, 17, e3000106.	2.6	139
513	<i>Ancrocorticija populigen</i> . nov., sp. nov, isolated from the symptomatic bark of <i>Populus</i> —Auramericanacanker. <i>MicrobiologyOpen</i> , 2019, 8, e792.	1.2	1
514	Overfeeding a High-Fat Diet Promotes Sex-Specific Alterations on the Gut Microbiota of the Zebrafish (<i>Danio rerio</i>). <i>Zebrafish</i> , 2019, 16, 268-279.	0.5	32
515	First description of two moderately halophilic and psychrotolerant <i>Mycoplasma</i> species isolated from cephalopods and proposal of <i>Mycoplasma marinum</i> sp. nov. and <i>Mycoplasma todarodis</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2019, 42, 457-467.	1.2	22

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516	Variation among human, veterinary and environmental <i>Mycobacterium chelonae-abscessus</i> complex isolates observed using core genome phylogenomic analysis, targeted gene comparison, and anti-microbial susceptibility patterns. <i>PLoS ONE</i> , 2019, 14, e0214274.	1.1	12
517	Marker genes as predictors of shared genomic function. <i>BMC Genomics</i> , 2019, 20, 268.	1.2	11
518	Description of <i>Janibacter massiliensis</i> sp. nov., cultured from the vaginal discharge of a patient with bacterial vaginosis. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1147-1159.	0.7	6
519	Manipulation of microbiota reveals altered callosal myelination and white matter plasticity in a model of Huntington disease. <i>Neurobiology of Disease</i> , 2019, 127, 65-75.	2.1	38
520	Dietary polysaccharides: fermentation potentials of a primitive gut ecosystem. <i>Environmental Microbiology</i> , 2019, 21, 1436-1451.	1.8	13
521	The Oral, Genital and Gut Microbiome in HIV Infection. , 2019, , 307-323.		2
522	Archaea, the tree of life, and cellular evolution in eukaryotes. <i>Science China Earth Sciences</i> , 2019, 62, 489-506.	2.3	5
523	Reliable identification of lactic acid bacteria by targeted and untargeted high-resolution tandem mass spectrometry. <i>Food Chemistry</i> , 2019, 285, 111-118.	4.2	13
524	Sequence and cultivation study of <i>Muribaculaceae</i> reveals novel species, host preference, and functional potential of this yet undescribed family. <i>Microbiome</i> , 2019, 7, 28.	4.9	481
525	Microbial Diversity and Organic Acid Production of Guinea Pig Faecal Samples. <i>Current Microbiology</i> , 2019, 76, 425-434.	1.0	2
526	Identification and evaluation of the microbiome in the female and male reproductive tracts. <i>Human Reproduction Update</i> , 2019, 25, 298-325.	5.2	115
527	Transmission in the Origins of Bacterial Diversity, From Ecotypes to Phyla. , 2019, , 311-343.		4
528	Changes in the Composition of the Gut Microbiota and the Blood Transcriptome in Preterm Infants at Less than 29 Weeks Gestation Diagnosed with Bronchopulmonary Dysplasia. <i>MSystems</i> , 2019, 4, .	1.7	23
529	DNA- and RNA-SIP Reveal <i>Nitrospira</i> spp. as Key Drivers of Nitrification in Groundwater-Fed Biofilters. <i>MBio</i> , 2019, 10, .	1.8	33
531	Meta-16S rRNA Gene Phylogenetic Reconstruction Reveals the Astonishing Diversity of Cosmopolitan <i>Myxobacteria</i> . <i>Microorganisms</i> , 2019, 7, 551.	1.6	10
532	Tephritid-microbial interactions to enhance fruit fly performance in sterile insect technique programs. <i>BMC Microbiology</i> , 2019, 19, 287.	1.3	39
534	<p>Neowollea manoromense gen. & sp. nov. (Nostocales, Cyanobacteria), a novel geosmin producer isolated from Thailand</p>. <i>Phytotaxa</i> , 2019, 424, 1-17.	0.1	7
535	The Compositionally Distinct Cyanobacterial Biocrusts From Brazilian Savanna and Their Environmental Drivers of Community Diversity. <i>Frontiers in Microbiology</i> , 2019, 10, 2798.	1.5	23

#	ARTICLE	IF	CITATIONS
536	In situ development of a methanotrophic microbiome in deep-sea sediments. <i>ISME Journal</i> , 2019, 13, 197-213.	4.4	61
537	Relevance of phenotypic information for the taxonomy of not-yet-cultured microorganisms. <i>Systematic and Applied Microbiology</i> , 2019, 42, 22-29.	1.2	34
538	<i>Candidatus</i> <i>Prosiliicoccus vernus</i> , a spring phytoplankton bloom associated member of the Flavobacteriaceae. <i>Systematic and Applied Microbiology</i> , 2019, 42, 41-53.	1.2	39
539	Microbial metal-sulfide oxidation in inactive hydrothermal vent chimneys suggested by metagenomic and metaproteomic analyses. <i>Environmental Microbiology</i> , 2019, 21, 682-701.	1.8	50
540	Repeated evolutionary transitions of flavobacteria from marine to non-marine habitats. <i>Environmental Microbiology</i> , 2019, 21, 648-666.	1.8	43
541	Decoding the ocean's microbiological secrets for marine enzyme biodiscovery. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	26
542	Microbial profiling during anaerobic digestion of cheese whey in reactors operated at different conditions. <i>Bioresource Technology</i> , 2019, 275, 375-385.	4.8	59
543	Inhibition Studies with 2-Bromoethanesulfonate Reveal a Novel Syntrophic Relationship in Anaerobic Oleate Degradation. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	30
544	Novel haloalkaliphilic methanotrophic bacteria: An attempt for enhancing methane bio-refinery. <i>Journal of Environmental Management</i> , 2019, 231, 1091-1099.	3.8	9
545	Elevational patterns and hierarchical determinants of biodiversity across microbial taxonomic scales. <i>Molecular Ecology</i> , 2019, 28, 86-99.	2.0	34
546	The morphology and metabolic potential of the Chloroflexi in full-scale activated sludge wastewater treatment plants. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	100
547	<i>Candidatus</i> <i>Hafkinia simulans</i> gen. nov., sp. nov., a Novel Holospora-Like Bacterium from the Macronucleus of the Rare Brackish Water Ciliate <i>Frontonia salmastra</i> (Oligohymenophorea), <i>Journal of Ecology</i> , 2019, 77, 1092-1106.	1.4	46
548	High-throughput identification and diagnostics of pathogens and pests: Overview and practical recommendations. <i>Molecular Ecology Resources</i> , 2019, 19, 47-76.	2.2	91
549	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	5.9	590
550	Fermenters in the earthworm gut: do transients matter?. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	18
551	Renaming of <i>Candidatus</i> <i>Methylocucumis oryzae</i> ™ as <i>Methylocucumis oryzae</i> gen. nov., sp. nov., a novel Type I methanotroph isolated from India. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 955-959.	0.7	22
552	Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermoprofundales (MBG-D archaea). <i>ISME Journal</i> , 2019, 13, 885-901.	4.4	92
553	Transmission in the Origins of Bacterial Diversity, From Ecotypes to Phyla. <i>Microbiology Spectrum</i> , 2017, 5, .	1.2	46

#	ARTICLE	IF	CITATIONS
554	Horizontal acquisition of a patchwork Calvin cycle by symbiotic and free-living Campylobacterota (formerly Epsilonproteobacteria). <i>ISME Journal</i> , 2020, 14, 104-122.	4.4	55
555	Root nodules of <i>Genista germanica</i> harbor <i>Bradyrhizobium</i> and <i>Rhizobium</i> bacteria exchanging <i>nodC</i> and <i>nodZ</i> genes. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126026.	1.2	6
556	Perspectives on Cultivation Strategies of Archaea. <i>Microbial Ecology</i> , 2020, 79, 770-784.	1.4	34
557	<i>Lactobacillus jinshani</i> sp. nov., isolated from solid-state vinegar culture of Zhenjiang aromatic vinegar. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 43-54.	0.7	24
558	Generating amplicon reads for microbial community assessment with next-generation sequencing. <i>Journal of Applied Microbiology</i> , 2020, 128, 330-354.	1.4	58
559	Biosorption of Cr(VI) by <i>Halomonas</i> sp. DK4, a halotolerant bacterium isolated from chrome electroplating sludge. <i>Environmental Science and Pollution Research</i> , 2020, 27, 27330-27344.	2.7	26
560	Three marine strains constitute the novel genus and species <i>Crateriforma conspicua</i> in the phylum Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1797-1809.	0.7	35
561	<i>Blastopirellula retiformator</i> sp. nov. isolated from the shallow-sea hydrothermal vent system close to Panarea Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1811-1822.	0.7	29
562	Description of the novel planctomycetal genus <i>Bremerella</i> , containing <i>Bremerella volcania</i> sp. nov., isolated from an active volcanic site, and reclassification of <i>Blastopirellula cremea</i> as <i>Bremerella cremea</i> comb. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1823-1837.	0.7	36
563	CAMITAX: Taxon labels for microbial genomes. <i>GigaScience</i> , 2020, 9, .	3.3	6
564	Description of three bacterial strains belonging to the new genus <i>Novipirellula</i> gen. nov., reclassification of <i>Rhodopirellula rosea</i> and <i>Rhodopirellula caenicola</i> and readjustment of the genus threshold of the phylogenetic marker <i>rpoB</i> for Planctomycetaceae. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1779-1795.	0.7	56
565	Bioinformatic strategies to address limitations of 16rRNA short-read amplicons from different sequencing platforms. <i>Journal of Microbiological Methods</i> , 2020, 169, 105811.	0.7	12
566	A diverse uncultivated microbial community is responsible for organic matter degradation in the Black Sea sulphidic zone. <i>Environmental Microbiology</i> , 2021, 23, 2709-2728.	1.8	47
567	Controversies in bacterial taxonomy: The example of the genus <i>Borrelia</i> . <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101335.	1.1	45
568	Physiological and genomic features of <i>Paraoceanicella profunda</i> gen. nov., sp. nov., a novel piezophile isolated from deep seawater of the Mariana Trench. <i>MicrobiologyOpen</i> , 2020, 9, e966.	1.2	21
569	Novel syntrophic bacteria in full-scale anaerobic digesters revealed by genome-centric metatranscriptomics. <i>ISME Journal</i> , 2020, 14, 906-918.	4.4	117
570	Multidomain ribosomal protein trees and the planctobacterial origin of neomura (eukaryotes). <i>Trends in Microbiology</i> , 2020, 28, 101-110.	1.0	50
571	<i>Rhodopirellula heiligendammensis</i> sp. nov., <i>Rhodopirellula pilleata</i> sp. nov., and <i>Rhodopirellula solitaria</i> sp. nov. isolated from natural or artificial marine surfaces in Northern Germany and California, USA, and emended description of the genus <i>Rhodopirellula</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1737-1750.	0.7	35

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572	<i>Alienimonas californiensis</i> gen. nov. sp. nov., a novel Planctomycete isolated from the kelp forest in Monterey Bay. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1751-1766.	0.7	40
573	Three novel <i>Rubripirellula</i> species isolated from plastic particles submerged in the Baltic Sea and the estuary of the river Warnow in northern Germany. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1767-1778.	0.7	41
574	<i>Reptodigitus Chapmanii</i> (Nostocales, Hapalosiphonaceae) Gen. Nov.: A Unique Nostocalean (Cyanobacteria) Genus Based on a Polyphasic Approach 1. <i>Journal of Phycology</i> , 2020, 56, 425-436.	1.0	18
575	<i>Rubinisphaera italica</i> sp. nov. isolated from a hydrothermal area in the Tyrrhenian Sea close to the volcanic island Panarea. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1727-1736.	0.7	38
576	Characterization of microbial communities in ethanol biorefineries. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2020, 47, 183-195.	1.4	6
577	Differences in foot skin microbiomes between patients with type 2 diabetes and healthy individuals. <i>Mycoses</i> , 2020, 63, 314-322.	1.8	9
578	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
579	<i>Paraflavitalea soli</i> gen. nov., sp. nov., isolated from greenhouse soil. <i>Journal of Microbiology</i> , 2020, 58, 17-23.	1.3	13
580	Analyses of the Bacterial Contamination on Belgian Broiler Carcasses at Retail Level. <i>Frontiers in Microbiology</i> , 2020, 11, 539540.	1.5	9
581	Sediment-associated bacterial community and predictive functionalities are influenced by choice of 16S ribosomal RNA hypervariable region(s): An amplicon-based diversity study. <i>Genomics</i> , 2020, 112, 4968-4979.	1.3	10
582	An effective culturomics approach to study the gut microbiota of mammals. <i>Research in Microbiology</i> , 2020, 171, 290-300.	1.0	9
583	Multimic features associated with mucosal healing and inflammation in paediatric Crohn's disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2020, 52, 1491-1502.	1.9	20
584	Combination of genetic tools to discern <i>Bacillus</i> species isolated from hot springs in South Africa. <i>African Journal of Microbiology Research</i> , 2020, 14, 447-464.	0.4	1
585	â€ˆCandidatus <i>Oscillochloris kuznetsovii</i> â€™ a novel mesophilic filamentous anoxygenic phototrophic Chloroflexales bacterium from Arctic coastal environments. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	8
586	<i>Oecophyllibacter saccharovorans</i> gen. nov. sp. nov., a bacterial symbiont of the weaver ant <i>Oecophylla smaragdina</i> . <i>Journal of Microbiology</i> , 2020, 58, 988-997.	1.3	14
587	Identification and classification of the <i>Tetrasphaera</i> genus in enhanced biological phosphorus removal process: a review. <i>Reviews in Environmental Science and Biotechnology</i> , 2020, 19, 699-715.	3.9	11
588	Evolutionary Timeline and Genomic Plasticity Underlying the Lifestyle Diversity in <i>Rhizobiales</i> . <i>MSystems</i> , 2020, 5, .	1.7	45
589	Metagenome analysis of gut microbial in both the caged and non-caged ducks. <i>Journal of Physics: Conference Series</i> , 2020, 1524, 012076.	0.3	0

#	ARTICLE	IF	CITATIONS
590	Sponge microbiome stability during environmental acquisition of highly specific photosymbionts. <i>Environmental Microbiology</i> , 2020, 22, 3593-3607.	1.8	20
591	Diversity and distribution of marine heterotrophic bacteria from a large culture collection. <i>BMC Microbiology</i> , 2020, 20, 207.	1.3	27
592	Groundwater <i>Elusimicrobia</i> are metabolically diverse compared to gut microbiome <i>Elusimicrobia</i> and some have a novel nitrogenase paralog. <i>ISME Journal</i> , 2020, 14, 2907-2922.	4.4	51
593	Updating the resolution for 16S rRNA OTUs clustering reveals the cryptic cyanobacterial genus and species. <i>Ecological Indicators</i> , 2020, 117, 106695.	2.6	6
595	<i>Caulifigura coniformis</i> gen. nov., sp. nov., a novel member of the family Planctomycetaceae isolated from a red biofilm sampled in a hydrothermal area. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1927-1937.	0.7	15
596	<i>Rosistilla oblonga</i> gen. nov., sp. nov. and <i>Rosistilla carotiformis</i> sp. nov., isolated from biotic or abiotic surfaces in Northern Germany, Mallorca, Spain and California, USA. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1939-1952.	0.7	20
597	Behind Taxonomic Variability: The Functional Redundancy in the Tick Microbiome. <i>Microorganisms</i> , 2020, 8, 1829.	1.6	25
598	Anti-Tick Microbiota Vaccine Impacts <i>Ixodes ricinus</i> Performance during Feeding. <i>Vaccines</i> , 2020, 8, 702.	2.1	53
599	Multistability and Reversibility of Aerobic Granular Sludge Microbial Communities Upon Changes From Simple to Complex Synthetic Wastewater and Back. <i>Frontiers in Microbiology</i> , 2020, 11, 574361.	1.5	21
600	Updates to the recently introduced family Lacipirellulaceae in the phylum Planctomycetes: isolation of strains belonging to the novel genera <i>Aeoliella</i> , <i>Botrimarina</i> , <i>Pirellulimonas</i> and <i>Pseudobythopirellula</i> and the novel species <i>Bythopirellula polymerisocia</i> and <i>Posidoniimonas corsicana</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1979-1997.	0.7	47
601	Colored Microbial Coatings in Show Caves from the Galapagos Islands (Ecuador): First Microbiological Approach. <i>Coatings</i> , 2020, 10, 1134.	1.2	15
602	Overlooked Diversity of Ultramicrobacterial Minorities at the Air-Sea Interface. <i>Atmosphere</i> , 2020, 11, 1214.	1.0	9
603	Genomic Characterization of a Novel <i>Tenericutes</i> Bacterium from Deep-Sea Holothurian Intestine. <i>Microorganisms</i> , 2020, 8, 1874.	1.6	22
604	SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis. <i>BMC Bioinformatics</i> , 2020, 21, 345.	1.2	41
605	Emergence of New Spoilage Microorganisms in the Brewing Industry and Development of Microbiological Quality Control Methods to Cope with This Phenomenon: A Review. <i>Journal of the American Society of Brewing Chemists</i> , 2020, 78, 245-259.	0.8	16
606	Method development for cross-study microbiome data mining: Challenges and opportunities. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2075-2080.	1.9	27
607	<i>Tenuifilum thalassicum</i> gen. nov., sp. nov., a novel moderate thermophilic anaerobic bacterium from a Kunashir Island shallow hot spring representing a new family <i>Tenuifilaceae</i> fam. nov. in the class <i>Bacteroidia</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126126.	1.2	22
608	Microbiomes and Specific Symbionts of Social Spiders: Compositional Patterns in Host Species, Populations, and Nests. <i>Frontiers in Microbiology</i> , 2020, 11, 1845.	1.5	20

#	ARTICLE	IF	CITATIONS
609	Symbiosis between nanohaloarchaeon and haloarchaeon is based on utilization of different polysaccharides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20223-20234.	3.3	49
610	Highly Reduced Genomes of Protist Endosymbionts Show Evolutionary Convergence. <i>Current Biology</i> , 2020, 30, 925-933.e3.	1.8	41
611	<i>Cryptosporidium parvum</i> Infection Depletes Butyrate Producer Bacteria in Goat Kid Microbiome. <i>Frontiers in Microbiology</i> , 2020, 11, 548737.	1.5	17
612	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020, 8, 1590.	1.6	23
613	phyloFlash: Rapid Small-Subunit rRNA Profiling and Targeted Assembly from Metagenomes. <i>MSystems</i> , 2020, 5, .	1.7	180
614	Metagenomic and Metatranscriptomic Analyses Revealed Uncultured Bacteroidales Populations as the Dominant Proteolytic Amino Acid Degradors in Anaerobic Digesters. <i>Frontiers in Microbiology</i> , 2020, 11, 593006.	1.5	57
615	Analysis of molecular diversity within single cyanobacterial colonies from environmental samples. <i>Scientific Reports</i> , 2020, 10, 18453.	1.6	5
616	Three Planctomycetes isolated from biotic surfaces in the Mediterranean Sea and the Pacific Ocean constitute the novel species <i>Symmachiella dynata</i> gen. nov., sp. nov. and <i>Symmachiella macrocystis</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1965-1977.	0.7	20
617	A preliminary study of the effect of total fishmeal replacement with different dietary sources on the gut microbiota of spotted rose snapper juvenile (<i>Lutjanus guttatus</i> Steindachner, 1869). <i>Aquaculture Research</i> , 2020, 51, 4771-4784.	0.9	2
618	Differential Gut Microbiota and Fecal Metabolites Related With the Clinical Subtypes of Myasthenia Gravis. <i>Frontiers in Microbiology</i> , 2020, 11, 564579.	1.5	19
620	Generation of Comprehensive Ecosystem-Specific Reference Databases with Species-Level Resolution by High-Throughput Full-Length 16S rRNA Gene Sequencing and Automated Taxonomy Assignment (AutoTax). <i>MBio</i> , 2020, 11, .	1.8	66
621	Cultural isolation of spore-forming bacteria in human feces using bile acids. <i>Scientific Reports</i> , 2020, 10, 15041.	1.6	13
622	A Novel Primer Mixture for GH48 Genes: Quantification and Identification of Truly Cellulolytic Bacteria in Biogas Fermenters. <i>Microorganisms</i> , 2020, 8, 1297.	1.6	3
623	Species-Level Analysis of Human Gut Microbiota With Metataxonomics. <i>Frontiers in Microbiology</i> , 2020, 11, 2029.	1.5	50
624	A ubiquitous subcuticular bacterial symbiont of a coral predator, the crown-of-thorns starfish, in the Indo-Pacific. <i>Microbiome</i> , 2020, 8, 123.	4.9	10
625	Community, Distribution, and Ecological Roles of Estuarine Archaea. <i>Frontiers in Microbiology</i> , 2020, 11, 2060.	1.5	24
626	<i>Stieleria varia</i> sp. nov., isolated from wood particles in the Baltic Sea, constitutes a novel species in the family Pirellulaceae within the phylum Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1953-1963.	0.7	14
627	Mud, Microbes, and Macrofauna: Seasonal Dynamics of the Iron Biogeochemical Cycle in an Intertidal Mudflat. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	6

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628	Using the Microbiome Amplification Preference Tool (MAPT) to Reveal <i>Medicago sativa</i> -Associated Eukaryotic Microbes. <i>Phytobiomes Journal</i> , 2020, 4, 340-350.	1.4	3
629	Diversity and Genomic Characterization of a Novel Parvarchaeota Family in Acid Mine Drainage Sediments. <i>Frontiers in Microbiology</i> , 2020, 11, 612257.	1.5	22
630	Cultivation-Independent Analysis of the Bacterial Community Associated With the Calcareous Sponge <i>Clathrina clathrus</i> and Isolation of <i>Poriferisphaera corsica</i> Gen. Nov., Sp. Nov., Belonging to the Barely Studied Class Phycisphaerae in the Phylum Planctomycetes. <i>Frontiers in Microbiology</i> , 2020, 11, 602250.	1.5	23
631	Genomic and Metabolic Insights into Two Novel Thiothrix Species from Enhanced Biological Phosphorus Removal Systems. <i>Microorganisms</i> , 2020, 8, 2030.	1.6	20
632	Recent development and new insight of diversification and symbiosis specificity of legume rhizobia: mechanism and application. <i>Journal of Applied Microbiology</i> , 2021, 131, 553-563.	1.4	29
633	Saccharibacteria as Organic Carbon Sinks in Hydrocarbon-Fueled Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 587782.	1.5	22
634	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	5.8	269
635	Additions to the genus <i>Gimesia</i> : description of <i>Gimesia alba</i> sp. nov., <i>Gimesia algae</i> sp. nov., <i>Gimesia aquarii</i> sp. nov., <i>Gimesia aquatilis</i> sp. nov., <i>Gimesia fumaroli</i> sp. nov. and <i>Gimesia panarensis</i> sp. nov., isolated from aquatic habitats of the Northern Hemisphere. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1999-2018.	0.7	41
637	Hydrocarbon seepage in the deep seabed links subsurface and seafloor biospheres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11029-11037.	3.3	33
638	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
639	Genome diversification in globally distributed novel marine Proteobacteria is linked to environmental adaptation. <i>ISME Journal</i> , 2020, 14, 2060-2077.	4.4	106
640	Stable and transient structural variation in lemur vaginal, labial and axillary microbiomes: patterns by species, body site, ovarian hormones and forest access. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	10
642	Ecological and genomic analyses of candidate phylum WPS bacteria in an unvegetated soil. <i>Environmental Microbiology</i> , 2020, 22, 3143-3157.	1.8	42
643	The wound microbiome. , 2020, , 237-258.		3
644	Multichannel bacterial discrimination based on recognition and disintegration disparity of short antimicrobial peptides. <i>Analytical Biochemistry</i> , 2020, 600, 113764.	1.1	5
645	Lipocalin2 Induced by Bacterial Flagellin Protects Mice against Cyclophosphamide Mediated Neutropenic Sepsis. <i>Microorganisms</i> , 2020, 8, 646.	1.6	6
646	<i>Calycomorphotria hydatis</i> gen. nov., sp. nov., a novel species in the family Planctomycetaceae with conspicuous subcellular structures. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1877-1887.	0.7	17
647	<i>Tautonia plasticadhaerens</i> sp. nov., a novel species in the family Isosphaeraceae isolated from an alga in a hydrothermal area of the Eolian Archipelago. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1889-1900.	0.7	19

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648	Draft Genome Sequences of 13 Isolates of <i>Adlercreutzia equolifaciens</i> , <i>Eggerthella lenta</i> , and <i>Gordonibacter urolithinifaciens</i> , Isolated from Human Fecal Samples in Karlsruhe, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
649	Culturomics-based genomics sheds light on the ecology of the new haloarchaeal genus <i>Halosegnis</i> . <i>Environmental Microbiology</i> , 2021, 23, 3418-3434.	1.8	25
650	Microbiology in Water-Miscible Metalworking Fluids. <i>Tribology Transactions</i> , 2020, 63, 1147-1171.	1.1	4
651	<i>Aequoribacter fuscus</i> gen. nov., sp. nov., a new member of the family Halieaceae, isolated from coastal seawater. <i>Journal of Microbiology</i> , 2020, 58, 463-471.	1.3	14
652	Towards Unraveling Macroecological Patterns in Rhizosphere Microbiomes. <i>Trends in Plant Science</i> , 2020, 25, 1017-1029.	4.3	42
653	Genome-centric microbiome analysis reveals solid retention time (SRT)-shaped species interactions and niche differentiation in food waste and sludge co-digesters. <i>Water Research</i> , 2020, 181, 115858.	5.3	37
654	MIDAS 3: An ecosystem-specific reference database, taxonomy and knowledge platform for activated sludge and anaerobic digesters reveals species-level microbiome composition of activated sludge. <i>Water Research</i> , 2020, 182, 115955.	5.3	175
655	Dataset supporting description of the new mussel species of genus <i>Gigantidas</i> (Bivalvia: Mytilidae) and metagenomic data of bacterial community in the host mussel gill tissue. <i>Data in Brief</i> , 2020, 30, 105651.	0.5	6
656	Novel cultivated endophytic Verrucomicrobia reveal deep-rooting traits of bacteria to associate with plants. <i>Scientific Reports</i> , 2020, 10, 8692.	1.6	30
657	Microbial Community Structure Along a Horizontal Oxygen Gradient in a Costa Rican Volcanic Influenced Acid Rock Drainage System. <i>Microbial Ecology</i> , 2020, 80, 793-808.	1.4	7
658	<i>Desulfolutivibrio sulfoxidireducens</i> gen. nov., sp. nov., isolated from a pyrite-forming enrichment culture and reclassification of <i>Desulfovibrio sulfodismutans</i> as <i>Desulfolutivibrio sulfodismutans</i> comb. nov. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126105.	1.2	26
659	One year cross-sectional study in adult and neonatal intensive care units reveals the bacterial and antimicrobial resistance genes profiles in patients and hospital surfaces. <i>PLoS ONE</i> , 2020, 15, e0234127.	1.1	18
660	Taxonomic and Functional Differences in Cervical Microbiome Associated with Cervical Cancer Development. <i>Scientific Reports</i> , 2020, 10, 9720.	1.6	37
661	Physiology of extremophiles. , 2020, , 13-22.		6
662	Engineered microbes and evolving plastic bioremediation technology. , 2020, , 417-443.		14
663	Spatial Compartmentalization of the Microbiome between the Lumen and Crypts Is Lost in the Murine Cecum following the Process of Surgery, Including Overnight Fasting and Exposure to Antibiotics. <i>MSystems</i> , 2020, 5, .	1.7	21
664	New Intranuclear Symbiotic Bacteria from Macronucleus of <i>Paramecium putrinum</i> "Candidatus <i>Gortzia Yakutica</i> ". <i>Diversity</i> , 2020, 12, 198.	0.7	19
665	Gut microbiome diversity detected by high-coverage 16S and shotgun sequencing of paired stool and colon sample. <i>Scientific Data</i> , 2020, 7, 92.	2.4	37

#	ARTICLE	IF	CITATIONS
666	The Landscape of Adaptive Evolution of a Gut Commensal Bacteria in Aging Mice. <i>Current Biology</i> , 2020, 30, 1102-1109.e5.	1.8	39
667	Molecular and morphological characterization of a novel dihydroanatoxin-a producing <i>Microcoleus</i> species (cyanobacteria) from the Russian River, California, USA. <i>Harmful Algae</i> , 2020, 93, 101767.	2.2	24
668	Microbiome Profile of Deep Endometriosis Patients: Comparison of Vaginal Fluid, Endometrium and Lesion. <i>Diagnostics</i> , 2020, 10, 163.	1.3	57
669	Potential of bacterial consortia obtained from different environments for bioremediation of paroxetine and bezafibrate. <i>Journal of Environmental Chemical Engineering</i> , 2020, 8, 103881.	3.3	16
670	Genomic and Transcriptomic Evidence Supports Methane Metabolism in <i>Archaeoglobi</i> . <i>MSystems</i> , 2020, 5, .	1.7	33
671	Benchmarking the MinION: Evaluating long reads for microbial profiling. <i>Scientific Reports</i> , 2020, 10, 5125.	1.6	34
672	A Genus Definition for <i>Bacteria</i> and <i>Archaea</i> Based on a Standard Genome Relatedness Index. <i>MBio</i> , 2020, 11, .	1.8	198
673	<i>Bradyrhizobia</i> associated with <i>Laburnum anagyroides</i> , an exotic legume grown in Poland. <i>Symbiosis</i> , 2020, 80, 245-255.	1.2	4
674	Impact of the gut microbiota on the m6A epitranscriptome of mouse cecum and liver. <i>Nature Communications</i> , 2020, 11, 1344.	5.8	59
675	Egyptian Mongoose (<i>Herpestes ichneumon</i>) Gut Microbiota: Taxonomical and Functional Differences across Sex and Age Classes. <i>Microorganisms</i> , 2020, 8, 392.	1.6	8
676	<i>Paradesulfovibrio onnuriensis</i> gen. nov., sp. nov., a chemolithoautotrophic sulfate-reducing bacterium isolated from the Onnuri vent field of the Indian Ocean and reclassification of <i>Desulfovibrio senegalensis</i> as <i>Paradesulfovibrio senegalensis</i> comb. nov.. <i>Journal of Microbiology</i> , 2020, 58, 252-259.	1.3	9
677	Species-specific genomic sequences for classification of bacteria. <i>Computers in Biology and Medicine</i> , 2020, 123, 103874.	3.9	6
678	Evaluation of groundwater bacterial community composition to inform waterborne pathogen vulnerability assessments. <i>Science of the Total Environment</i> , 2020, 743, 140472.	3.9	10
679	“ <i>Candidatus</i> <i>Mystax nordicus</i> ” Aggregates with Mitochondria of Its Host, the Ciliate <i>Paramecium nephridiatum</i> . <i>Diversity</i> , 2020, 12, 251.	0.7	9
680	Crosstalk Between Culturomics and Microbial Profiling of Egyptian Mongoose (<i>Herpestes ichneumon</i>) Gut Microbiome. <i>Microorganisms</i> , 2020, 8, 808.	1.6	5
681	Effect of solid waste fermentation substrate on wheat (<i>Triticum aestivum</i> L.) growth in closed artificial ecosystem. <i>Life Sciences in Space Research</i> , 2020, 26, 163-172.	1.2	1
682	A genomic view of trophic and metabolic diversity in clade-specific <i>Lamellodysidea</i> sponge microbiomes. <i>Microbiome</i> , 2020, 8, 97.	4.9	38
683	<i>Thalassoglobus polymorphus</i> sp. nov., a novel Planctomycete isolated close to a public beach of Mallorca Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1915-1926.	0.7	15

#	ARTICLE	IF	CITATIONS
684	Maoricimonas rarisocia gen. nov., sp. nov., a novel planctomycete isolated from marine sediments close to Mallorca Island. Antonie Van Leeuwenhoek, 2020, 113, 1901-1913.	0.7	17
685	The Microbiome of Posidonia oceanica Seagrass Leaves Can Be Dominated by Planctomycetes. Frontiers in Microbiology, 2020, 11, 1458.	1.5	40
686	A critical rebuttal of the proposed division of the genus Arcobacter into six genera using comparative genomic, phylogenetic, and phenotypic criteria. Systematic and Applied Microbiology, 2020, 43, 126108.	1.2	33
687	Design of targeted primers based on 16S rRNA sequences in meta-transcriptomic datasets and identification of a novel taxonomic group in the Asgard archaea. BMC Microbiology, 2020, 20, 25.	1.3	13
688	Core microbiomes: Characterization and identification. , 2020, , 43-84.		0
689	Microbial community analysis using high-throughput sequencing technology: a beginner's guide for microbiologists. Journal of Microbiology, 2020, 58, 176-192.	1.3	42
690	Modeling temperature response in bioenergy production: Novel solution to a common challenge of anaerobic digestion. Applied Energy, 2020, 263, 114646.	5.1	28
691	Nanopore sequencing of microbial communities reveals the potential role of sea lice as a reservoir for fish pathogens. Scientific Reports, 2020, 10, 2895.	1.6	24
692	Vibrio parahaemolyticus Infection in Mice Reduces Protective Gut Microbiota, Augmenting Disease Pathways. Frontiers in Microbiology, 2020, 11, 73.	1.5	9
693	A Multi-Omics Perspective of Quantitative Trait Loci in Precision Medicine. Trends in Genetics, 2020, 36, 318-336.	2.9	41
694	Polysaccharide niche partitioning of distinct <i>Polaribacter</i> clades during North Sea spring algal blooms. ISME Journal, 2020, 14, 1369-1383.	4.4	50
696	Community diversity and habitat structure shape the repertoire of extracellular proteins in bacteria. Nature Communications, 2020, 11, 758.	5.8	26
697	Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. Microbiome, 2020, 8, 16.	4.9	42
698	Reprint of: Manipulation of microbiota reveals altered callosal myelination and white matter plasticity in a model of Huntington disease. Neurobiology of Disease, 2020, 135, 104744.	2.1	7
699	Bacteria from the Midgut of Common Cockchafer (Melolontha melolontha L.) Larvae Exhibiting Antagonistic Activity Against Bacterial Symbionts of Entomopathogenic Nematodes: Isolation and Molecular Identification. International Journal of Molecular Sciences, 2020, 21, 580.	1.8	24
700	Epiphytic and Endophytic Bacteria on Olive Tree Phyllosphere: Exploring Tissue and Cultivar Effect. Microbial Ecology, 2020, 80, 145-157.	1.4	53
701	High-throughput cultivation of heterotrophic bacteria during a spring phytoplankton bloom in the North Sea. Systematic and Applied Microbiology, 2020, 43, 126066.	1.2	21
702	Tools for Analysis of the Microbiome. Digestive Diseases and Sciences, 2020, 65, 674-685.	1.1	70

#	ARTICLE	IF	CITATIONS
703	NG-Tax 2.0: A Semantic Framework for High-Throughput Amplicon Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 1366.	1.1	95
704	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
705	Diversity and metabolism of <i>Woeseiales</i> bacteria, global members of marine sediment communities. <i>ISME Journal</i> , 2020, 14, 1042-1056.	4.4	51
706	Putative novel <i>Bradyrhizobium</i> and <i>Phyllobacterium</i> species isolated from root nodules of <i>Chamaecytisus ruthenicus</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126056.	1.2	8
707	Effect of a Profound Feedstock Change on the Structure and Performance of Biogas Microbiomes. <i>Microorganisms</i> , 2020, 8, 169.	1.6	6
708	Combined bacterial and fungal targeted amplicon sequencing of respiratory samples: Does the DNA extraction method matter?. <i>PLoS ONE</i> , 2020, 15, e0232215.	1.1	16
709	Description of Three Novel Members in the Family Geobacteraceae, <i>Oryzomonas japonicum</i> gen. nov., sp. nov., <i>Oryzomonas sagensis</i> sp. nov., and <i>Oryzomonas ruber</i> sp. nov.. <i>Microorganisms</i> , 2020, 8, 634.	1.6	29
710	<i>Aureliella helgolandensis</i> gen. nov., sp. nov., a novel Planctomycete isolated from a jellyfish at the shore of the island Helgoland. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1839-1849.	0.7	19
711	Description of <i>Polystyrenella longa</i> gen. nov., sp. nov., isolated from polystyrene particles incubated in the Baltic Sea. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1851-1862.	0.7	14
712	<i>Lignipirellula cremea</i> gen. nov., sp. nov., a planctomycete isolated from wood particles in a brackish river estuary. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1863-1875.	0.7	15
713	Molecular analysis of the dominant lactic acid bacteria of chickpea liquid starters and doughs and propagation of chickpea sourdoughs with selected <i>Weissella confusa</i> . <i>Food Microbiology</i> , 2020, 91, 103490.	2.1	24
714	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 468.	1.5	1,537
715	Respiratory and Gut Microbiota in Commercial Turkey Flocks with Disparate Weight Gain Trajectories Display Differential Compositional Dynamics. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	22
716	<i>Alienimonas chondri</i> sp. nov., a novel planctomycete isolated from the biofilm of the red alga <i>Chondrus crispus</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126083.	1.2	17
717	Resistance of Tick Gut Microbiome to Anti-Tick Vaccines, Pathogen Infection and Antimicrobial Peptides. <i>Pathogens</i> , 2020, 9, 309.	1.2	28
718	<i>Pukyongia salina</i> gen. nov., sp. nov., a novel genus in the family Flavobacteriaceae. <i>Journal of Microbiology</i> , 2020, 58, 456-462.	1.3	11
719	A newly discovered <i>Gigantidas</i> bivalve mussel from the Onnuri Vent Field in the northern Central Indian Ridge. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 161, 103299.	0.6	17
720	The Composition of the Fungal and Oomycete Microbiome of <i>Rhododendron</i> Roots Under Varying Growth Conditions, Nurseries, and Cultivars. <i>Phytobiomes Journal</i> , 2020, 4, 156-164.	1.4	13

#	ARTICLE	IF	CITATIONS
721	On the Selection and Analysis of Clades in Comparative Evolutionary Studies. <i>Systematic Biology</i> , 2021, 70, 190-196.	2.7	4
722	Microbial Community-Driven Etiopathogenesis of Peri-Implantitis. <i>Journal of Dental Research</i> , 2021, 100, 21-28.	2.5	109
723	Freshwater phytoplankton diversity: models, drivers and implications for ecosystem properties. <i>Hydrobiologia</i> , 2021, 848, 53-75.	1.0	48
724	Phylogeny resolved, metabolism revealed: functional radiation within a widespread and divergent clade of sponge symbionts. <i>ISME Journal</i> , 2021, 15, 503-519.	4.4	24
725	A new boring toxin producer “ <i>Perforafilum tunnelli</i> gen. & sp. nov. (Oscillatoriales, Cyanobacteria) isolated from Laguna Madre, Texas, USA. <i>Phycologia</i> , 2021, 60, 10-24.	0.6	14
726	Sorption-desorption and biodegradation of sulfometuron-methyl and its effects on the bacterial communities in Amazonian soils amended with aged biochar. <i>Ecotoxicology and Environmental Safety</i> , 2021, 207, 111222.	2.9	16
727	A critical review on livestock manure biorefinery technologies: Sustainability, challenges, and future perspectives. <i>Renewable and Sustainable Energy Reviews</i> , 2021, 135, 110033.	8.2	176
728	<i>Marinomyxa</i> Gen. Nov. Accommodates Gall-Forming Parasites of the Tropical to Subtropical Seagrass Genus <i>Halophila</i> and Constitutes a Novel Deep-Branching Lineage Within Phytomyxea (Rhizaria) Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	1
729	Mining zebrafish microbiota reveals key community-level resistance against fish pathogen infection. <i>ISME Journal</i> , 2021, 15, 702-719.	4.4	49
730	Innovations to culturing the uncultured microbial majority. <i>Nature Reviews Microbiology</i> , 2021, 19, 225-240.	13.6	254
731	Mechanisms of the phytomicrobiome for enhancing soil fertility and health. , 2021, , 1-14.		5
732	<i>Koleobacter methoxysyntrophicus</i> gen. nov., sp. nov., a novel anaerobic bacterium isolated from deep subsurface oil field and proposal of <i>Koleobacteraceae</i> fam. nov. and <i>Koleobacterales</i> ord. nov. within the class <i>Clostridia</i> of the phylum <i>Firmicutes</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126154.	1.2	15
733	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	1.8	42
734	<i>Monilinema</i> gen. nov., a homocytous genus (Cyanobacteria, <i>Leptolyngbyaceae</i>) from saline-alkaline lakes of Pantanal wetlands, Brazil. <i>Journal of Phycology</i> , 2021, 57, 473-483.	1.0	3
735	Untangling filamentous marine cyanobacterial diversity from the coast of South Florida with the description of <i>Vermifilaceae</i> fam. nov. and three new genera: <i>Leptochromothrix</i> gen. nov., <i>Ophiophycus</i> gen. nov., and <i>Vermifilum</i> gen. nov.. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107010.	1.2	13
736	Wide distribution of <i>Phycisphaera</i> -like planctomycetes from <i>WD2101</i> soil group in peatlands and genome analysis of the first cultivated representative. <i>Environmental Microbiology</i> , 2021, 23, 1510-1526.	1.8	32
737	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. <i>Molecular Ecology</i> , 2021, 30, 1072-1085.	2.0	43
738	<i>Parakomarekiella sesnandensis</i> gen. et sp. nov. (Nostocales, Cyanobacteria) isolated from the Old Cathedral of Coimbra, Portugal (UNESCO World Heritage Site). <i>European Journal of Phycology</i> , 2021, 56, 301-315.	0.9	19

#	ARTICLE	IF	CITATIONS
739	Coadministration of metformin prevents olanzapine-induced metabolic dysfunction and regulates the gut-liver axis in rats. <i>Psychopharmacology</i> , 2021, 238, 239-248.	1.5	13
740	Comparing DNA Extraction and 16S rRNA Gene Amplification Methods for Plant-Associated Bacterial Communities. <i>Phytobiomes Journal</i> , 2021, 5, 190-201.	1.4	5
741	The assembly of methanotrophic communities regulated by soil pH in a mountain ecosystem. <i>Catena</i> , 2021, 196, 104883.	2.2	14
742	Revealing new sponge-associated cyanobacterial diversity: Novel genera and species. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106991.	1.2	20
743	The occurrence of <i>Affixifilum</i> gen. nov. and <i>Neolyngbya</i> (Oscillatoriaceae) in South Florida (USA), with the description of <i>A. floridanum</i> sp. nov. and <i>N. biscaynensis</i> sp. nov. <i>Journal of Phycology</i> , 2021, 57, 92-110.	1.0	12
744	Nanopore based sequencing enables easy and accurate identification of yeasts in breweries. <i>Journal of the Institute of Brewing</i> , 2021, 127, 160-166.	0.8	4
745	<i>Legionella septentrionalis</i> sp. nov., isolated from aquatic environments in the northern PR China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
746	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. <i>ISME Journal</i> , 2021, 15, 1810-1825.	4.4	74
747	Microbial genetics. , 2021, , 89-109.		1
748	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. <i>Nature Microbiology</i> , 2021, 6, 354-365.	5.9	109
749	Meta-Apo improves accuracy of 16S-amplicon-based prediction of microbiome function. <i>BMC Genomics</i> , 2021, 22, 9.	1.2	15
750	Newly discovered Asgard archaea <i>Hermodarchaeota</i> potentially degrade alkanes and aromatics via alkyl/benzyl-succinate synthase and benzoyl-CoA pathway. <i>ISME Journal</i> , 2021, 15, 1826-1843.	4.4	40
751	Genome-based phylogeny of the genera <i>Proteus</i> and <i>Cosenzaea</i> and description of <i>Proteus terrae</i> subsp. <i>terrae</i> subsp. nov. and <i>Proteus terrae</i> subsp. <i>cibarius</i> subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	16
752	The Isolate <i>Caproiciproducens</i> sp. 7D4C2 Produces n-Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 594524.	1.5	33
753	â€œCandidatus <i>Mesenet longicola</i> â€• Novel Endosymbionts of <i>Brontispa longissima</i> that Induce Cytoplasmic Incompatibility. <i>Microbial Ecology</i> , 2021, 82, 512-522.	1.4	14
755	<i>Geomonas silvestris</i> sp. nov., <i>Geomonas paludis</i> sp. nov. and <i>Geomonas limicola</i> sp. nov., isolated from terrestrial environments, and emended description of the genus <i>Geomonas</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	24
757	Analysis of the Conjunctival Microbiome in Patients with Atopic Keratoconjunctivitis and Healthy Individuals. <i>Annals of Dermatology</i> , 2021, 33, 163.	0.3	4
758	The effect of taxonomic classification by full-length 16S rRNA sequencing with a synthetic long-read technology. <i>Scientific Reports</i> , 2021, 11, 1727.	1.6	71

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759	Microdiversity and phylogeographic diversification of bacterioplankton in pelagic freshwater systems revealed through long-read amplicon sequencing. <i>Microbiome</i> , 2021, 9, 24.	4.9	17
760	Explorative Meta-Analysis of 417 Extant Archaeal Genomes to Predict Their Contribution to the Total Microbiome Functionality. <i>Microorganisms</i> , 2021, 9, 381.	1.6	2
761	Equivolumetric Protocol Generates Library Sizes Proportional to Total Microbial Load in 16S Amplicon Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 638231.	1.5	13
762	Vaginitypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
763	<i>Usitatibacter rugosus</i> gen. nov., sp. nov. and <i>Usitatibacter palustris</i> sp. nov., novel members of <i>Usitatibacteraceae</i> fam. nov. within the order <i>Nitrosomonadales</i> isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	47
764	<i>Microbacterium caowuchunii</i> sp. nov. and <i>Microbacterium lushaniae</i> sp. nov., isolated from plateau pika (<i>Ochotona curzoniae</i>) on the Qinghai-Tibet Plateau of PR China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	16
765	PPIT: an R package for inferring microbial taxonomy from <i>nifH</i> sequences. <i>Bioinformatics</i> , 2021, 37, 2289-2298.	1.8	13
766	Conducting research on diet-microbiome interactions: A review of current challenges, essential methodological principles, and recommendations for best practice in study design. <i>Journal of Human Nutrition and Dietetics</i> , 2021, 34, 631-644.	1.3	23
767	Bacterial shifts on broiler carcasses at retail upon frozen storage. <i>International Journal of Food Microbiology</i> , 2021, 340, 109051.	2.1	5
768	Transition from unclassified <i>Ktedonobacterales</i> to <i>Actinobacteria</i> during amorphous silica precipitation in a quartzite cave environment. <i>Scientific Reports</i> , 2021, 11, 3921.	1.6	12
769	<i>Heminiphilus faecis</i> gen. nov., sp. nov., a member of the family <i>Muribaculaceae</i> , isolated from mouse faeces and emended description of the genus <i>Muribaculum</i> . <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 275-286.	0.7	19
770	<i>Thiomicrothabodus sediminis</i> sp. nov. and <i>Thiomicrothabodus xiamenensis</i> sp. nov., novel sulfur-oxidizing bacteria isolated from coastal sediments and an emended description of the genus <i>Thiomicrothabodus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	15
771	Establishment and Application of Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry for Detection of <i>Shewanella</i> Genus. <i>Frontiers in Microbiology</i> , 2021, 12, 625821.	1.5	8
772	Potato extract inhibits lipase activity and ameliorates gut microbiome dysbiosis and weight gain in mice fed a high-fat diet. <i>Applied Biological Chemistry</i> , 2021, 64, .	0.7	5
774	Endophytic Bacteria From the Roots of the Medicinal Plant <i>Alkanna tinctoria</i> Tausch (Boraginaceae): Exploration of Plant Growth Promoting Properties and Potential Role in the Production of Plant Secondary Metabolites. <i>Frontiers in Microbiology</i> , 2021, 12, 633488.	1.5	48
775	Identification and characterization of potential compost degrading bacteria from agro-waste. <i>Malaysian Journal of Fundamental and Applied Sciences</i> , 2021, 17, 26-32.	0.4	0
776	Tumor-Associated Microbiome: Where Do We Stand?. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1446.	1.8	31
777	Phylogenomic Framework for Taxonomic Delineation of <i>Paracoccus</i> spp. and Exploration of Core-Pan Genome. <i>Indian Journal of Microbiology</i> , 2021, 61, 180-194.	1.5	3

#	ARTICLE	IF	CITATIONS
778	<i>Trichotorquatus</i> gen. nov. – a new genus of soil cyanobacteria discovered from American drylands. <i>Journal of Phycology</i> , 2021, 57, 886-902.	1.0	29
779	Isolation of Actinomycetes with Cellulolytic and Antimicrobial Activities from Soils Collected from an Urban Green Space in the Philippines. <i>International Journal of Microbiology</i> , 2021, 2021, 1-14.	0.9	10
780	<i>Iodimonas gelatinilytica</i> sp. nov., aerobic iodide-oxidizing bacteria isolated from brine water and surface seawater. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 625-631.	0.7	11
783	Phylogenetic Distribution of Polysaccharide-Degrading Enzymes in Marine Bacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 658620.	1.5	7
784	Survival strategies of ammonia-oxidizing archaea (AOA) in a full-scale WWTP treating mixed landfill leachate containing copper ions and operating at low-intensity of aeration. <i>Water Research</i> , 2021, 191, 116798.	5.3	39
785	The microbiome in obstructive sleep apnea. <i>Sleep</i> , 2021, 44, .	0.6	19
786	Filling the Gaps in the Cyanobacterial Tree of Life – Metagenome Analysis of <i>Stigonema ocellatum</i> DSM 106950, <i>Chlorogloea purpurea</i> SAG 13.99 and <i>Gomphosphaeria aponina</i> DSM 107014. <i>Genes</i> , 2021, 12, 389.	1.0	5
787	Novel Effects of Leonardite-Based Applications on Sugar Beet. <i>Frontiers in Plant Science</i> , 2021, 12, 646025.	1.7	11
788	Combining culturing and 16S rDNA sequencing to reveal seasonal and room variations of household airborne bacteria and correlative environmental factors in nanjing, southeast china. <i>Indoor Air</i> , 2021, 31, 1095-1108.	2.0	15
789	Evolution of rumen and oral microbiota in calves is influenced by age and time of weaning. <i>Animal Microbiome</i> , 2021, 3, 31.	1.5	20
790	<i>Caproicibacterium amylolyticum</i> gen. nov., sp. nov., a novel member of the family Oscillospiraceae isolated from pit clay used for making Chinese strong aroma-type liquor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	23
791	Description of <i>Candidatus Mesopelagibacter carboxydoxydans</i> and <i>Candidatus Anoxipelagibacter denitrificans</i> : Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126185.	1.2	14
792	High Diversity and Functional Potential of Undescribed – Acidobacteriota – in Danish Wastewater Treatment Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 643950.	1.5	56
793	Seasonal shifts of microbial methane oxidation in Arctic shelf waters above gas seeps. <i>Limnology and Oceanography</i> , 2021, 66, 1896-1914.	1.6	12
794	Location and Conformational Ensemble of Menaquinone and Menaquinol, and Protein – Lipid Modulations in Archaeal Membranes. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4714-4725.	1.2	10
795	OTUs and ASVs Produce Comparable Taxonomic and Diversity from Shrimp Microbiota 16S Profiles Using Tailored Abundance Filters. <i>Genes</i> , 2021, 12, 564.	1.0	23
796	Sequence and evolutionary analysis of bacterial ribosomal S1 proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1111-1124.	1.5	5
797	BEEexact: a Metataxonomic Database Tool for High-Resolution Inference of Bee-Associated Microbial Communities. <i>MSystems</i> , 2021, 6, .	1.7	20

#	ARTICLE	IF	CITATIONS
798	Characterizing the growing microorganisms at species level in 46 anaerobic digesters at Danish wastewater treatment plants: A six-year survey on microbial community structure and key drivers. <i>Water Research</i> , 2021, 193, 116871.	5.3	51
799	Development of a Rapid and Accurate Nanopore-based Sequencing Platform for on-Field Identification of Beer-Spoilage Bacteria in the Breweries. <i>Journal of the American Society of Brewing Chemists</i> , 2021, 79, 240-248.	0.8	4
800	Active Rumen Bacterial and Protozoal Communities Revealed by RNA-Based Amplicon Sequencing on Dairy Cows Fed Different Diets at Three Physiological Stages. <i>Microorganisms</i> , 2021, 9, 754.	1.6	10
801	<i>Croceimicrobium hydrocarbonivorans</i> gen. nov., sp. nov., a novel marine bacterium isolated from a bacterial consortium that degrades polyethylene terephthalate. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
802	Casting Light on the Adaptation Mechanisms and Evolutionary History of the Widespread <i>Sumerlaeota</i> . <i>MBio</i> , 2021, 12, .	1.8	12
803	“ <i>Candidatus Laterigemmans baculatus</i> ” gen. nov. sp. nov., the first representative of rod shaped planctomycetes with lateral budding in the family Pirellulaceae. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126188.	1.2	10
804	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <i>ISME Journal</i> , 2021, 15, 1879-1892.	4.4	87
805	Dissecting industrial fermentations of fine flavour cocoa through metagenomic analysis. <i>Scientific Reports</i> , 2021, 11, 8638.	1.6	16
807	Complete genome sequence of <i>Streptomyces cyanogenus</i> S136, producer of anticancer angucycline landomycin A. <i>3 Biotech</i> , 2021, 11, 282.	1.1	3
808	<i>Constrictifilum karadense</i> gen. et sp. nov., a new Nostoclean genus from Maharashtra, India. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	6
809	Microbiota profiling in aging-associated inflammation and liver degeneration. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151500.	1.5	11
810	New technologies for developing phage-based tools to manipulate the human microbiome. <i>Trends in Microbiology</i> , 2022, 30, 131-142.	3.5	20
811	<i>Butyribacter intestini</i> gen. nov., sp. nov., a butyric acid-producing bacterium of the family Lachnospiraceae isolated from human faeces, and reclassification of <i>Acetivibrio ethanolgignens</i> as <i>Acetanaerobacter ethanolgignens</i> gen. nov., comb. nov. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126201.	1.2	21
812	Recent advances and health implications of dietary fasting regimens on the gut microbiome. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 320, G847-G863.	1.6	16
813	Early-Life Immune System Maturation in Chickens Using a Synthetic Community of Cultured Gut Bacteria. <i>MSystems</i> , 2021, 6, .	1.7	68
814	Genome analysis reveals that the correct name of type strain <i>Adlercreutzia caecicola</i> DSM 22242T is <i>Parvibacter caecicola</i> Clavel et al. 2013. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
815	Organic farming: Does it contribute to contaminant-free produce and ensure food safety?. <i>Science of the Total Environment</i> , 2021, 769, 145079.	3.9	36
816	Effect of salinity on cable bacteria species composition and diversity. <i>Environmental Microbiology</i> , 2021, 23, 2605-2616.	1.8	23

#	ARTICLE	IF	CITATIONS
817	Phnomibacter ginsenosidimutans gen. nov., sp. nov., a novel glycoside hydrolase positive bacterial strain with ginsenoside hydrolysing activity. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
818	Automated analysis of genomic sequences facilitates high-throughput and comprehensive description of bacteria. ISME Communications, 2021, 1, .	1.7	228
819	Modulation of trypanosome establishment in Glossina palpalis palpalis by its microbiome in the Campo sleeping sickness focus, Cameroon. Infection, Genetics and Evolution, 2021, 90, 104763.	1.0	5
820	Bacteria Isolated From the Antarctic Sponge Iophon sp. Reveals Mechanisms of Symbiosis in Sporosarcina, Cellulophaga, and Nesterenkonia. Frontiers in Microbiology, 2021, 12, 660779.	1.5	5
821	Printing Microbial Dark Matter: Using Single Cell Dispensing and Genomics to Investigate the Patescibacteria/Candidate Phyla Radiation. Frontiers in Microbiology, 2021, 12, 635506.	1.5	14
822	Ecophysiology of the Cosmopolitan OM252 Bacterioplankton (<i>Gammaproteobacteria</i>). MSystems, 2021, 6, e0027621.	1.7	5
823	Probiotic Bacteria with High Alpha-Gal Content Protect Zebrafish against Mycobacteriosis. Pharmaceuticals, 2021, 14, 635.	1.7	14
824	Terrestrial dissolved organic matter inflow drives temporal dynamics of the bacterial community of a subarctic estuary (northern Baltic Sea). Environmental Microbiology, 2021, 23, 4200-4213.	1.8	19
825	Beating Naive Bayes at Taxonomic Classification of 16S rRNA Gene Sequences. Frontiers in Microbiology, 2021, 12, 644487.	1.5	12
826	First case of an invasive Bacteroides dorei infection detected in a patient with a mycotic aortic aneurysm raising a rebellion of major indigenous bacteria in humans: a case report and review. BMC Infectious Diseases, 2021, 21, 625.	1.3	6
829	Microbiological Aspects of Root Canal Infections and Disinfection Strategies: An Update Review on the Current Knowledge and Challenges. Frontiers in Oral Health, 2021, 2, 672887.	1.2	68
830	A synbiotic intervention modulates meta-omics signatures of gut redox potential and acidity in elective caesarean born infants. BMC Microbiology, 2021, 21, 191.	1.3	13
831	Reclassification of Facklamia ignava, Facklamia sourekii and Facklamia tabacinasalis as Falseniella ignava gen. nov., comb. nov., Hutsoniella sourekii gen. nov., comb. nov., and Ruoffia tabacinasalis gen. nov., comb. nov., and description of Ruoffia halotolerans sp. nov., isolated from hypersaline Inland Sea of Qatar. Antonie Van Leeuwenhoek, 2021, 114, 1181-1193.	0.7	28
832	Mass-immigration determines the assembly of activated sludge microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	48
833	A few dominant bacteria and their genomic basis in mediating distinct ecosystem functions. Environmental Microbiology, 2021, 23, 4478-4488.	1.8	2
834	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. Environmental Microbiology, 2021, 23, 4228-4245.	1.8	15
835	A Simple Culture Method Enhances the Recovery of Culturable Actinobacteria From Coastal Sediments. Frontiers in Microbiology, 2021, 12, 675048.	1.5	7
836	Marinobacterium alkalitolerans sp. nov., with nitrate reductase and urease activity isolated from green algal mat collected from a solar saltern. Antonie Van Leeuwenhoek, 2021, 114, 1117-1130.	0.7	3

#	ARTICLE	IF	CITATIONS
838	Methane-dependent selenate reduction by a bacterial consortium. ISME Journal, 2021, 15, 3683-3692.	4.4	17
840	Prevalence of <i>Campylobacter</i> spp. in Raccoon Dogs and Badgers in Miyazaki Prefecture, Japan. EcoHealth, 2021, 18, 241-249.	0.9	2
841	Immunohistochemical distribution of Immunoglobulin-A in relation to the intestinal microbiota of <i>Cairina moschata</i> (Muscovy) duck. Journal of Physics: Conference Series, 2021, 1918, 052004.	0.3	0
842	The Application of High-Throughput Technologies for the Study of Microbiome and Cancer. Frontiers in Genetics, 2021, 12, 699793.	1.1	13
843	Analysis of Microbiota and Mycobiota in Fungal Ball Rhinosinusitis: Specific Interaction between <i>Aspergillus fumigatus</i> and <i>Haemophilus influenzae</i> ?. Journal of Fungi (Basel, Switzerland), 2021, 7, 550.	1.5	9
844	' <i>Candidatus Xiphinematocola pachtaicus</i> ' gen. nov., sp. nov., an endosymbiotic bacterium associated with nematode species of the genus <i>Xiphinema</i> (Nematoda, Longidoridae). International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
845	<i>Aegicerativicinus sediminis</i> gen. nov., sp. nov., a novel carotenoid-producing marine bacterium in the family Flavobacteriaceae. Antonie Van Leeuwenhoek, 2021, 114, 1551-1563.	0.7	8
846	The bacterial and fungal nest microbiomes in populations of the social spider <i>Stegodyphus dumicola</i> . Systematic and Applied Microbiology, 2021, 44, 126222.	1.2	12
847	Identification and Genomic Characterization of Two Previously Unknown Magnetotactic Nitrospirae. Frontiers in Microbiology, 2021, 12, 690052.	1.5	7
848	Current Status of Mining, Modification, and Application of Cellulases in Bioactive Substance Extraction. Current Issues in Molecular Biology, 2021, 43, 687-703.	1.0	3
849	Study of factors involved in the behavior of biofilms formed by biohydrogen-producing microflora identified by molecular biology using dairy wastewater. International Journal of Hydrogen Energy, 2021, 46, 25965-25973.	3.8	4
850	Analysis of Bacterial Communities on North Sea Macroalgae and Characterization of the Isolated Planctomycetes <i>Adhaeritor mobilis</i> gen. nov., sp. nov., <i>Roseimaritima multifibrata</i> sp. nov., <i>Rosistilla ulvae</i> sp. nov. and <i>Rubripirellula lacrimiformis</i> sp. nov.. Microorganisms, 2021, 9, 1494.	1.6	34
851	<i>Ostreibacterium oceani</i> gen. nov., sp. nov., isolated from oyster, and description of <i>Ostreibacteriaceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
852	<i>Sandaracinobacteroides hominis</i> gen. nov., sp. nov., isolated from human skin. Archives of Microbiology, 2021, 203, 5067-5074.	1.0	12
854	Evidence for the existence of a new genus <i>Chlamydiifrater</i> gen. nov. inside the family Chlamydiaceae with two new species isolated from flamingo (<i>Phoenicopterus roseus</i>): <i>Chlamydiifrater phoenicopteri</i> sp. nov. and <i>Chlamydiifrater volucris</i> sp. nov.. Systematic and Applied Microbiology, 2021, 44, 126200.	1.2	24
855	Description of three new <i>Alteromonas</i> species <i>Alteromonas antoniana</i> sp. nov., <i>Alteromonas lipotrueae</i> sp. nov. and <i>Alteromonas lipotrueiana</i> sp. nov. isolated from marine environments, and proposal for reclassification of the genus <i>Salinimonas</i> as <i>Alteromonas</i> . Systematic and Applied Microbiology, 2021, 44, 126226.	1.2	39
856	<i>Miltoncostaea marina</i> gen. nov. sp. nov., and <i>Miltoncostaea oceani</i> sp. nov., a novel deep branching phylogenetic lineage within the class Thermoleophilia isolated from marine environments, and proposal of <i>Miltoncostaeaceae</i> fam. nov. and <i>Miltoncostaeales</i> ord. nov. Systematic and Applied Microbiology, 2021, 44, 126216.	1.2	22
857	Internal microbial zonation during the massive growth of marimo, a lake ball of <i>Aegagropila linnaei</i> in Lake Akan. IScience, 2021, 24, 102720.	1.9	3

#	ARTICLE	IF	CITATIONS
858	<i>Gelidibacter maritimus</i> sp. nov., isolated from marine sediment. Archives of Microbiology, 2021, 203, 5117-5122.	1.0	6
859	Holocene life and microbiome profiling in ancient tropical Lake Chalco, Mexico. Scientific Reports, 2021, 11, 13848.	1.6	8
860	Culture-Independent and Culture-Dependent Characterization of the Black Soldier Fly Gut Microbiome Reveals a Large Proportion of Culturable Bacteria with Potential for Industrial Applications. Microorganisms, 2021, 9, 1642.	1.6	23
861	Features of Bacterial Microbiota in the Wild Habitat of <i>Pulsatilla tongkangensis</i> , the Endangered <i>Long-Sepal Donggang Pasque-Flower</i> Plant, Endemic to Karst Topography of Korea. Frontiers in Microbiology, 2021, 12, 656105.	1.5	7
863	Heavy metals multi-tolerant <i>Bradyrhizobium</i> isolated from mercury mining region in Algeria. Journal of Environmental Management, 2021, 289, 112547.	3.8	12
864	Description of <i>Collinsella avium</i> sp. nov., a new member of the <i>Collinsella</i> genus isolated from the ceacum of feral chicken. New Microbes and New Infections, 2021, 42, 100902.	0.8	2
865	Microbial metabolism and adaptations in <i>Atribacteria</i> -dominated methane hydrate sediments. Environmental Microbiology, 2021, 23, 4646-4660.	1.8	20
866	Phytase Supplementation Effects on Amino Acid Digestibility in Broiler Chickens are Influenced by Dietary Calcium Concentrations but not by Acid-Binding Capacity. Current Developments in Nutrition, 2021, 5, nzab103.	0.1	7
867	Reciprocal effect of temperature and dietary lipids on metabolic performance and gut microbiota of Yellowtail kingfish (<i>Seriola lalandi</i>) juveniles. Aquaculture Research, 2021, 52, 6189-6204.	0.9	3
868	Proposal of <i>Carbonactinosporaceae</i> fam. nov. within the class Actinomycetia. Reclassification of <i>Streptomyces thermoautotrophicus</i> as <i>Carbonactinospira thermoautotrophica</i> gen. nov., comb. nov. Systematic and Applied Microbiology, 2021, 44, 126223.	1.2	20
869	Release LTP_12_2020, featuring a new ARB alignment and improved 16S rRNA tree for prokaryotic type strains. Systematic and Applied Microbiology, 2021, 44, 126218.	1.2	44
870	<i>Pelorhabdus rhamnosifermentans</i> gen. nov., sp. nov., a strictly anaerobic rhamnose degrader from freshwater lake sediment. Systematic and Applied Microbiology, 2021, 44, 126225.	1.2	8
871	Anti-Microbiota Vaccines Modulate the Tick Microbiome in a Taxon-Specific Manner. Frontiers in Immunology, 2021, 12, 704621.	2.2	38
872	Disturbed microbial ecology in Alzheimer's disease: evidence from the gut microbiota and fecal metabolome. BMC Microbiology, 2021, 21, 226.	1.3	38
873	<i>Candidatus</i> <i>Thiovulum</i> sp. strain imperiosus: the largest free-living Epsilonproteobacteriaeota <i>Thiovulum</i> strain lives in a marine mangrove environment. Canadian Journal of Microbiology, 2022, 68, 17-30.	0.8	4
874	Microbiome Analysis of the Rhizosphere from Wilt Infected Pomegranate Reveals Complex Adaptations in <i>Fusarium</i> A Preliminary Study. Agriculture (Switzerland), 2021, 11, 831.	1.4	9
875	<i>Nanchangia anserum</i> gen. nov., sp. nov., isolated from feces of greater white-fronted geese (<i>Anser</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	9
876	<i>Sinanaerobacter chloroacetimidivorans</i> gen. nov., sp. nov., an obligate anaerobic bacterium isolated from anaerobic sludge. Antonie Van Leeuwenhoek, 2021, 114, 1609-1617.	0.7	1

#	ARTICLE	IF	CITATIONS
878	Amplicon Sequence Variants Artificially Split Bacterial Genomes into Separate Clusters. <i>MSphere</i> , 2021, 6, e0019121.	1.3	76
879	Microbial Diversity and Function in Shallow Subsurface Sediment and Oceanic Lithosphere of the Atlantis Massif. <i>MBio</i> , 2021, 12, e0049021.	1.8	13
881	Phylogenetic insights into <i>Chroococcus</i> -like taxa (Chroococcales, Cyanobacteria), describing <i>Cryptochroococcus tibeticus</i> gen. nov. sp. nov. and <i>Limnococcus fonticola</i> sp. nov. from Qinghai-Tibet plateau. <i>Journal of Phycology</i> , 2021, 57, 1739-1748.	1.0	6
882	When will taxonomic saturation be achieved? A case study in <i>Nunduva</i> and <i>Kyrtuthrix</i> (Rivulariaceae, Cyanobacteria). <i>Journal of Phycology</i> , 2021, 57, 1699-1720.	1.0	17
883	Healthcare-Associated Infections-Related Bacteriome and Antimicrobial Resistance Profiling: Assessing Contamination Hotspots in a Developing Country Public Hospital. <i>Frontiers in Microbiology</i> , 2021, 12, 711471.	1.5	4
884	<i>Veronia nyctiphani</i> gen. nov., sp. nov., Isolated from the Stomach of the Euphausiid <i>Nyctiphanes simplex</i> (Hansen, 1911) in the Gulf of California, and Reclassification of <i>Enterovibrio pacificus</i> as <i>Veronia pacifica</i> comb. nov.. <i>Current Microbiology</i> , 2021, 78, 3782-3790.	1.0	16
885	Delineating virulence of <i>Vibrio campbellii</i> : a predominant luminescent bacterial pathogen in Indian shrimp hatcheries. <i>Scientific Reports</i> , 2021, 11, 15831.	1.6	17
886	Boron Mine Ponds: Metagenomic Insight to Bacterial Diversity. <i>Biological Diversity and Conservation</i> , 0, , 229-235.	0.3	3
887	Comprehensive Cultivation of the Swine Gut Microbiome Reveals High Bacterial Diversity and Guides Bacterial Isolation in Pigs. <i>MSystems</i> , 2021, 6, e0047721.	1.7	13
888	High-resolution microbiome analysis enabled by linking of 16S rRNA gene sequences with adjacent genomic contexts. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
889	Addressing the sublime scale of the microbial world: reconciling an appreciation of microbial diversity with the need to describe species. <i>New Microbes and New Infections</i> , 2021, 43, 100931.	0.8	14
890	Soy protein concentrate effects on gut microbiota structure and digestive physiology of <i>Totoaba macdonaldi</i> . <i>Journal of Applied Microbiology</i> , 2021, , .	1.4	6
891	<i>Clostridium chrysemydis</i> sp. nov., isolated from the faecal material of a painted turtle. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
892	Bacterial endosymbionts protect beneficial soil fungus from nematode attack. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	42
893	Description, Taxonomy, and Comparative Genomics of a Novel species, <i>Thermoleptolyngbya sichuanensis</i> sp. nov., Isolated From Hot Springs of Ganzi, Sichuan, China. <i>Frontiers in Microbiology</i> , 2021, 12, 696102.	1.5	14
894	Adaptability of a Caproate-Producing Bacterium Contributes to Its Dominance in an Anaerobic Fermentation System. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0120321.	1.4	27
895	Biocontrol potential of <i>Pseudomonas stutzeri</i> endophyte from <i>Withania somnifera</i> (Ashwagandha) seed extract against pathogenic <i>Fusarium oxysporum</i> and <i>Rhizoctonia solani</i> . <i>Archives of Phytopathology and Plant Protection</i> , 2022, 55, 1-18.	0.6	14
896	<i>Novisyntrophococcus fermenticellae</i> gen. nov., sp. nov., isolated from an anaerobic fermentation cellar of Chinese strong-flavour baijiu. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10

#	ARTICLE	IF	CITATIONS
897	Cultivation of particle-associated heterotrophic bacteria during a spring phytoplankton bloom in the North Sea. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126232.	1.2	4
898	Bioactivities of endophytic actinobacteria inhabiting <i>Artemisia herba-alba</i> emphasizing differences from free-living strains. <i>Folia Microbiologica</i> , 2022, 67, 81-89.	1.1	0
900	<i>Thermosynergistes pyruvatorans</i> gen. nov., sp. nov., an anaerobic, pyruvate-degrading bacterium from Shengli oilfield, and proposal of <i>Thermosynergistaceae</i> fam. nov. in the phylum <i>Synergistetes</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	15
901	A Novel Magnetotactic Alphaproteobacterium Producing Intracellular Magnetite and Calcium-Bearing Minerals. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0155621.	1.4	4
902	Reconstituting the genus <i>Mycobacterium</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	34
903	Surgical Menopause and Estrogen Therapy Modulate the Gut Microbiota, Obesity Markers, and Spatial Memory in Rats. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 702628.	1.8	18
904	Community and single cell analyses reveal complex predatory interactions between bacteria in high diversity systems. <i>Nature Communications</i> , 2021, 12, 5481.	5.8	14
905	Construction of a Fusellovirus with a Minimal Set of Genes. <i>ACS Synthetic Biology</i> , 2021, 10, 2617-2627.	1.9	1
906	<i>Oceaniferula marina</i> gen.nov., sp.nov., an anti-fluoroquinolone bacterium isolated from marine sediment. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1855-1865.	0.7	8
907	<i>Paradesulfitobacterium ferrireducens</i> gen. nov., sp. nov., a Fe(III)-reducing bacterium from petroleum-contaminated soil and reclassification of <i>Desulfitobacterium aromaticivorans</i> as <i>Paradesulfitobacterium aromaticivorans</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
908	Diversity of microbial communities and genes involved in nitrous oxide emissions in Antarctic soils impacted by marine animals as revealed by metagenomics and 100 metagenome-assembled genomes. <i>Science of the Total Environment</i> , 2021, 788, 147693.	3.9	12
909	Genome-Based Taxonomic Rearrangement of the Order Geobacterales Including the Description of <i>Geomonas azotofigans</i> sp. nov. and <i>Geomonas diazotrophica</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 737531.	1.5	59
910	Spare and repair the gut microbiota from antibiotic-induced dysbiosis: state-of-the-art. <i>Drug Discovery Today</i> , 2021, 26, 2159-2163.	3.2	15
911	<i>Perlalentimonas gracilis</i> gen. nov., sp. nov., a gliding aerotolerant anaerobe of the order <i>Bacteroidales</i> , isolated from a terrestrial mud volcano. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126245.	1.2	14
912	<i>Anaerocolumna chitinilytica</i> sp. nov., a chitin-decomposing anaerobic bacterium isolated from anoxic soil subjected to biological soil disinfestation. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
913	Phenogenomic Characterization of a Newly Domesticated and Novel Species from the Genus <i>Verrucosipora</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0132721.	1.4	2
914	Antibiotics and fecal transfaunation differentially affect microbiota recovery, associations, and antibiotic resistance in lemur guts. <i>Animal Microbiome</i> , 2021, 3, 65.	1.5	12
915	Application of MALDI-TOF analysis to reveal diversity and dynamics of winemaking yeast species in wild-fermented, organically produced, New Zealand Pinot Noir wine. <i>Food Microbiology</i> , 2021, 99, 103824.	2.1	10

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916	Conventional and conservation tillage practices affect soil microbial co-occurrence patterns and are associated with crop yields. <i>Agriculture, Ecosystems and Environment</i> , 2021, 319, 107534.	2.5	33
917	Role of <i>Bacillus</i> inoculation in rice straw composting and bacterial community stability after inoculation: Unite resistance or individual collapse. <i>Bioresource Technology</i> , 2021, 337, 125464.	4.8	44
918	Deciphering the phylogenetic affiliation of rhizobial strains recommended as chickpea inoculants in Argentina. <i>Applied Soil Ecology</i> , 2021, 166, 104069.	2.1	3
919	Adaptability to local conditions and phylogenetic differentiation of microsymbionts of TGx soybean genotypes in the semi-arid environments of Ghana and South Africa. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126264.	1.2	1
920	Description and functional testing of four species of the novel phototrophic genus <i>Chioneia</i> gen. nov., isolated from different East Antarctic environments. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126250.	1.2	26
921	Phylogenomics and molecular signatures support division of the order Neisseriales into emended families Neisseriaceae and Chromobacteriaceae and three new families Aquaspirillaceae fam. nov., Chitinibacteraceae fam. nov., and Leeiaceae fam. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126251.	1.2	46
922	Ex-situ biogas upgrading in thermophilic up-flow reactors: The effect of different gas diffusers and gas retention times. <i>Bioresource Technology</i> , 2021, 340, 125694.	4.8	22
923	Characterization of communities in a microalgae-bacteria system treating domestic wastewater reveals dominance of phototrophic and pigmented bacteria. <i>Algal Research</i> , 2021, 59, 102447.	2.4	21
924	Wildlife-borne microorganisms and strategies to prevent and control emerging infectious diseases. <i>Journal of Biosafety and Biosecurity</i> , 2021, 3, 67-71.	1.4	5
925	<i>Tenebriella</i> gen. nov. “The dark twin of <i>Oscillatoria</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107293.	1.2	11
926	Microbial community redundancy in biomethanation systems lead to faster recovery of methane production rates after starvation. <i>Science of the Total Environment</i> , 2022, 804, 150073.	3.9	12
927	“ <i>Candidatus</i> <i>Sarmatiella mevalonica</i> ”™ endosymbiont of the ciliate <i>Paramecium</i> provides insights on evolutionary plasticity among <i>Rickettsiales</i> . <i>Environmental Microbiology</i> , 2021, 23, 1684-1701.	1.8	20
928	Artisanal Fresco cheese from Sonora: Physicochemical composition, microbial quality, and bacterial characterization by high-throughput sequencing. <i>International Journal of Dairy Technology</i> , 2021, 74, 359-370.	1.3	10
929	Comparative Genomics Provides Insights into the Taxonomy of <i>Azoarcus</i> and Reveals Separate Origins of <i>Nif</i> Genes in the Proposed <i>Azoarcus</i> and <i>Aromatoleum</i> Genera. <i>Genes</i> , 2021, 12, 71.	1.0	16
930	Use of Corn Husk Meal in the Development of a Functional Diet for Nile tilapia (<i>Oreochromis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Waste and Biomass Valorization, 2021, 12, 4355.	1.8	4
931	16S rRNA Gene Amplicon Sequencing of Gut Microbiota in Three Species of Deep-Sea Fish in Suruga Bay, Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	10
932	Modern Bioremediation Approaches for Clean and Green Environment. , 2021, , 221-237.		0
934	Efficient dilution-to-extinction isolation of novel virus“host model systems for fastidious heterotrophic bacteria. <i>ISME Journal</i> , 2021, 15, 1585-1598.	4.4	26

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935	<i>Clostridium fessum</i> sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
936	<i>Veillonella nakazawae</i> sp. nov., an anaerobic Gram-negative coccus isolated from the oral cavity of Japanese children. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	21
937	Aspirin Positively Contributes to <i>Drosophila</i> Intestinal Homeostasis and Delays Aging through Targeting Imd. , 2021, 12, 1821.		17
939	Functionalization and Modification of Hydrocarbon-Like Molecules Guided by Metagenomics: Enzymes Most Requested at the Industrial Scale for Chemical Synthesis as Study Cases. , 2016, , 1-21.		1
940	Biodiversity of "Non-model" Rickettsiales and Their Association with Aquatic Organisms. , 2016, , 59-91.		31
941	Towards a Microbial Conservation Perspective in High Mountain Lakes. Advances in Global Change Research, 2017, , 157-180.	1.6	10
942	Microbial Diversity and Possible Activity in Nitrate- and Radionuclide-Contaminated Groundwater. , 2020, , 35-66.		2
943	History of Rhizobial Taxonomy. , 2019, , 23-39.		3
944	<i>Hankyongella ginsenosidimutans</i> gen. nov., sp. nov., isolated from mineral water with ginsenoside covering activity. Antonie Van Leeuwenhoek, 2020, 113, 719-727.	0.7	2
945	<i>Candidatus Abditibacter</i> , a novel genus within the Cryomorphaceae, thriving in the North Sea. Systematic and Applied Microbiology, 2020, 43, 126088.	1.2	21
946	Superior resolution characterisation of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing. Water Research, 2020, 178, 115815.	5.3	40
947	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. Nature Biotechnology, 2019, 37, 179-185.	9.4	402
948	A human gut bacterial genome and culture collection for improved metagenomic analyses. Nature Biotechnology, 2019, 37, 186-192.	9.4	420
949	Microbial dark matter coming to light: challenges and opportunities. National Science Review, 2021, 8, nwa280.	4.6	86
950	<i>Planctomicrobium piriforme</i> gen. nov., sp. nov., a stalked planctomycete from a littoral wetland of a boreal lake. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 1659-1665.	0.8	38
951	<i>Halovulum dunhuangense</i> gen. nov., sp. nov., isolated from a saline terrestrial spring. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 2810-2816.	0.8	18
952	Genome-based taxonomic framework for the class Negativicutes: division of the class Negativicutes into the orders Selenomonadales emend., Acidaminococcales ord. nov. and Veillonellales ord. nov.. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3203-3215.	0.8	75
953	<i>Anaerobium acetethylicum</i> gen. nov., sp. nov., a strictly anaerobic, gluconate-fermenting bacterium isolated from a methanogenic bioreactor. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3289-3296.	0.8	33

#	ARTICLE	IF	CITATIONS
954	<i>Deinococcus metalli</i> sp. nov., isolated from an abandoned lead-zinc mine. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3457-3461.	0.8	9
955	<i>Rarimicrobium hominis</i> gen. nov., sp. nov., representing the fifth genus in the phylum Synergistetes that includes human clinical isolates. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3965-3970.	0.8	12
956	<i>Aliikangiella marina</i> gen. nov., sp. nov., a marine bacterium from the culture broth of <i>Picochlorum</i> sp. 122, and proposal of <i>Kangiellaceae</i> fam. nov. in the order <i>Oceanospirillales</i> . International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4488-4494.	0.8	36
957	<i>Pyruvatibacter mobilis</i> gen. nov., sp. nov., a marine bacterium from the culture broth of <i>Picochlorum</i> sp. 122. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 184-188.	0.8	16
958	<i>Paludisphaera borealis</i> gen. nov., sp. nov., a hydrolytic planctomycete from northern wetlands, and proposal of <i>Isosphaeraceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 837-844.	0.8	53
959	Multilocus sequence analysis supports the taxonomic position of <i>Astragalus glycyphyllos</i> symbionts based on DNA-DNA hybridization. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1906-1912.	0.8	5
960	<i>Alkalispirochaeta cellulovorans</i> gen. nov., sp. nov., a cellulose-hydrolysing, alkaliphilic, halotolerant bacterium isolated from the gut of a wood-eating cockroach (<i>Cryptocercus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td (p). International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1612-1619.	0.8	40
961	<i>Longimicrobium terrae</i> gen. nov., sp. nov., an oligotrophic bacterium of the under-represented phylum <i>Gemmatimonadetes</i> isolated through a system of miniaturized diffusion chambers. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1976-1985.	0.8	53
962	Modest proposals to expand the type material for naming of prokaryotes. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2108-2112.	0.8	84
963	<i>Corynebacterium guangdongense</i> sp. nov., isolated from a contaminated plate. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3201-3206.	0.8	6
964	<i>Brevitalea aridisoli</i> , <i>B. deliciosa</i> and <i>Arenimicrobium luteum</i> , three novel species of <i>Acidobacteria</i> subdivision 4 (class <i>Blastocatellia</i>) isolated from savanna soil and description of the novel family <i>Pyrinomonadaceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3355-3366.	0.8	58
965	<i>Anaerospromusa subterranea</i> gen. nov., sp. nov., a spore-forming anaerobe belonging to the class <i>Negativicutes</i> isolated from saprolite. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3848-3854.	0.8	14
966	<i>Pseudodesulfovibrio indicus</i> gen. nov., sp. nov., a piezophilic sulfate-reducing bacterium from the Indian Ocean and reclassification of four species of the genus <i>Desulfovibrio</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3904-3911.	0.8	71
967	<i>Streptococcus halotolerans</i> sp. nov. isolated from the respiratory tract of <i>Marmota himalayana</i> in Qinghai-Tibet Plateau of China. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4211-4217.	0.8	16
968	<i>Streptococcus marmotae</i> sp. nov., isolated from the respiratory tract of <i>Marmota himalayana</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4315-4322.	0.8	15
969	<i>Wukongibacter baidiensis</i> gen. nov., sp. nov., an anaerobic bacterium isolated from hydrothermal sulfides, and proposal for the reclassification of the closely related <i>Clostridium halophilum</i> and <i>Clostridium caminithermale</i> within <i>Maledivibacter</i> gen. nov. and <i>Paramaledivibacter</i> gen. nov., respectively. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4355-4361.	0.8	37
970	<i>Akkermansia glycaniphila</i> sp. nov., an anaerobic mucin-degrading bacterium isolated from reticulated python faeces. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4614-4620.	0.8	68
971	Isolation and characterization of <i>Acidobacterium ailaaui</i> sp. nov., a novel member of <i>Acidobacteria</i> subdivision 1, from a geothermally heated Hawaiian microbial mat. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5328-5335.	0.8	60

#	ARTICLE	IF	CITATIONS
972	Description of <i>Candidatus Marispirochaeta associata</i> TM and reclassification of <i>Spirochaeta bajacaliforniensis</i> , <i>Spirochaeta smaragdinae</i> and <i>Spirochaeta sinaica</i> to a new genus <i>Sediminispirochaeta</i> gen. nov. as <i>Sediminispirochaeta bajacaliforniensis</i> comb. nov., <i>Sediminispirochaeta smaragdinae</i> comb. nov. and <i>Sediminispirochaeta sinaica</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5506-5513.	0.8	44
973	Phylogenomic analysis of the family Peptoclostridaceae (Clostridium cluster XI) and proposal for reclassification of <i>Clostridium litorale</i> (Fendrich et al. 1991) and <i>Eubacterium acidaminophilum</i> (Zindel et al. 1989) as <i>Peptoclostridium litorale</i> gen. nov. comb. nov. and <i>Peptoclostridium acidaminophilum</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5506-5513.	0.8	77
974	<i>Raineyella antarctica</i> gen. nov., sp. nov., a psychrotolerant, d-amino-acid-utilizing anaerobe isolated from two geographic locations of the Southern Hemisphere. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5529-5536.	0.8	26
975	<i>Fimbrigiobus ruber</i> gen. nov., sp. nov., a Gemmata-like planctomycete from Sphagnum peat bog and the proposal of <i>Gemmataceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 218-224.	0.8	56
976	<i>Micropepsis pineolensis</i> gen. nov., sp. nov., a mildly acidophilic alphaproteobacterium isolated from a poor fen, and proposal of <i>Micropepsaceae</i> fam. nov. within <i>Micropepsales</i> ord. nov.. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 839-844.	0.8	27
977	Defining the taxonomic status of described subdivision 3 Acidobacteria: proposal of <i>Bryobacteraceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 498-501.	0.8	59
978	<i>Anaeromicrobium sediminis</i> gen. nov., sp. nov., a fermentative bacterium isolated from deep-sea sediment. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1462-1467.	0.8	15
979	Reclassification of <i>Bacillus saliphilus</i> as <i>Alkalicoccus saliphilus</i> gen. nov., comb. nov., and description of <i>Alkalicoccus halolimnae</i> sp. nov., a moderately halophilic bacterium isolated from a salt lake. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1557-1563.	0.8	26
980	<i>Niveitalea solisilvae</i> gen. nov., sp. nov., isolated from forest soil and emended description of the genus <i>Flavihumibacter</i> Zhang et al. 2010. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1374-1380.	0.8	15
981	Description of two novel members of the family <i>Erysipelotrichaceae</i> : <i>Ileibacterium valens</i> gen. nov., sp. nov. and <i>Dubosiella newyorkensis</i> , gen. nov., sp. nov., from the murine intestine, and emendation to the description of <i>Faecalibacterium rodentium</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1247-1254.	0.8	81
982	<i>Rectinema cohabitans</i> gen. nov., sp. nov., a rod-shaped spirochaete isolated from an anaerobic naphthalene-degrading enrichment culture. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1288-1295.	0.8	35
983	<i>Fournierella massiliensis</i> gen. nov., sp. nov., a new human-associated member of the family <i>Ruminococcaceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1393-1399.	0.8	33
984	An evaluation of <i>Thiomicrospira</i> , <i>Hydrogenovibrio</i> and <i>Thioalkalimicrobium</i> : reclassification of four species of <i>Thiomicrospira</i> to each <i>Thiomicrospira</i> gen. nov. and <i>Hydrogenovibrio</i> , and reclassification of all four species of <i>Thioalkalimicrobium</i> to <i>Thiomicrospira</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1140-1151.	0.8	118
985	<i>Actinomyces liubingyangii</i> sp. nov. isolated from the vulture <i>Gypaetus barbatus</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1873-1879.	0.8	21
986	Reclassification of <i>Thiobacillus aquaesulis</i> (Wood & Kelly, 1995) as <i>Annwoodia aquaesulis</i> gen. nov., comb. nov., transfer of <i>Thiobacillus</i> (Beijerinck, 1904) from the <i>Hydrogenophilales</i> to the <i>Nitrosomonadales</i> , proposal of <i>Hydrogenophilalia</i> class. nov. within the <i>Proteobacteria</i> TM , and four new families within the orders <i>Nitrosomonadales</i> and <i>Rhodocyclales</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1191-1205.	0.8	124
987	Isolation and characterization of <i>Kingella negevensis</i> sp. nov., a novel <i>Kingella</i> species detected in a healthy paediatric population. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2370-2376.	0.8	34
988	<i>Silvanigrella aquatica</i> gen. nov., sp. nov., isolated from a freshwater lake, description of <i>Silvanigrellaceae</i> fam. nov. and <i>Silvanigrellales</i> ord. nov., reclassification of the order <i>Bdellovibrionales</i> in the class <i>Oligoflexia</i> , reclassification of the families <i>Bacteriovoracaceae</i> and <i>Halobacteriovoracaceae</i> in the new order <i>Bacteriovoracales</i> ord. nov., and reclassification of the family <i>Pseudobacteriovoracaceae</i> in the order <i>Oligoflexales</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2555-2568.	0.8	76
989	<i>Merdimonas faecis</i> gen. nov., sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2430-2435.	0.8	18

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990	Proposal for the reclassification of obligately purine-fermenting bacteria <i>Clostridium acidurici</i> (Barker 1938) and <i>Clostridium purinilyticum</i> (D'Arre et al. 1981) as <i>Gottschalkia acidurici</i> gen. nov. comb. nov. and <i>Gottschalkia purinilytica</i> comb. nov. and of <i>Eubacterium angustum</i> (Beuscher and Tj ETQq0 0 0 rgBTsOverlook 10 Tf 50		
991	International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2711-2719. <i>Swionibacillus sediminis</i> gen. nov., sp. nov., a member of the family Bacillaceae isolated from ocean sediment. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3440-3445.	0.8	9
992	<i>Lactobacillus cerevisiae</i> sp. nov., isolated from a spoiled brewery sample. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3452-3457.	0.8	18
993	<i>Croceivirga radices</i> gen. nov., sp. nov., isolated from a rotten tropical mangrove root. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3733-3738.	0.8	15
994	<i>Agaribacterium haliotis</i> gen. nov., sp. nov., isolated from abalone faeces. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3819-3823.	0.8	11
995	<i>Lactobacillus curtus</i> sp. nov., isolated from beer in Finland. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3899-3906.	0.8	13
996	Reclassification of <i>Halothiobacillus hydrothermalis</i> and <i>Halothiobacillus halophilus</i> to <i>Guyparkeria</i> gen. nov. in the Thioalkalibacteraceae fam. nov., with emended descriptions of the genus <i>Halothiobacillus</i> and family Halothiobacillaceae. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3919-3928.	0.8	52
997	<i>Williamwhitmania taraxaci</i> gen. nov., sp. nov., a proteolytic anaerobe with a novel type of cytology from Lake Untersee in Antarctica, description of <i>Williamwhitmaniaceae</i> fam. nov., and emendation of the order Bacteroidales Krieg 2012. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4132-4145.	0.8	32
998	Description of <i>Anaerotignum aminivorans</i> gen. nov., sp. nov., a strictly anaerobic, amino-acid-decomposing bacterium isolated from a methanogenic reactor, and reclassification of <i>Clostridium propionicum</i> , <i>Clostridium neopropionicum</i> and <i>Clostridium lactatifermentans</i> as species of the genus <i>Anaerotignum</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4146-4153.	0.8	66
999	Reclassification of <i>Thiomicrospira hydrogeniphila</i> (Watsuji et al. 2016) to <i>Thiomicrospira hydrogeniphila</i> comb. nov., with emended description of <i>Thiomicrospira</i> (Boden et al., 2017). International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4205-4209.	0.8	18
1000	<i>Desertibacillus haloalkaliphilus</i> gen. nov., sp. nov., isolated from a saline desert. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4435-4442.	0.8	29
1001	<i>Floriccoccus tropicus</i> gen. nov., sp. nov. and <i>Floriccoccus penangensis</i> sp. nov. isolated from fresh flowers of durian tree and hibiscus. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4979-4985.	0.8	12
1002	<i>Bacillus marinesedimentorum</i> sp. nov., isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 198-203.	0.8	6
1003	<i>Xylanibacillus composti</i> gen. nov., sp. nov., isolated from compost. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 698-702.	0.8	12
1004	<i>Natronolimnobius aegyptiacus</i> sp. nov., an extremely halophilic alkalithermophilic archaeon isolated from the athalassohaline Wadi An Natrun, Egypt. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 498-506.	0.8	15
1005	<i>Aminipila butyrica</i> gen. nov., sp. nov., a strictly anaerobic, arginine-decomposing bacterium isolated from a methanogenic reactor of cattle waste. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 443-448.	0.8	16
1006	<i>Marivivens niveibacter</i> sp. nov., isolated from the seawater of tropical mangrove. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 570-574.	0.8	7
1007	<i>Proteiniborus indolifex</i> sp. nov., isolated from a thermophilic industrial-scale biogas plant. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 824-828.	0.8	21

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1008	<i>Desulfothermobacter acidiphilus</i> gen. nov., sp. nov., a thermoacidophilic sulfate-reducing bacterium isolated from a terrestrial hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 871-875.	0.8	14
1009	<i>Roseisolibacter agri</i> gen. nov., sp. nov., a novel slow-growing member of the under-represented phylum Gemmatimonadetes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1028-1036.	0.8	38
1010	<i>Veillonella infantium</i> sp. nov., an anaerobic, Gram-stain-negative coccus isolated from tongue biofilm of a Thai child. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1101-1106.	0.8	29
1011	<i>Methylomusa anaerophila</i> gen. nov., sp. nov., an anaerobic methanol-utilizing bacterium isolated from a microbial fuel cell. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1118-1122.	0.8	17
1012	<i>Saccharolobus caldissimus</i> gen. nov., sp. nov., a facultatively anaerobic iron-reducing hyperthermophilic archaeon isolated from an acidic terrestrial hot spring, and reclassification of <i>Sulfolobus solfataricus</i> as <i>Saccharolobus solfataricus</i> comb. nov. and <i>Sulfolobus shibatae</i> as <i>Saccharolobus shibatae</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1271-1278.	0.8	80
1013	<i>Camelliibacillus cellulolyticus</i> gen. nov., sp. nov., a cellulose-degrading bacterium isolated from tea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1867-1873.	0.8	11
1014	Evaluation of the genus <i>Thiothrix</i> Winogradsky 1888 (Approved Lists 1980) emend. Aruga et al. 2002: reclassification of <i>Thiothrix disciformis</i> to <i>Thiolinea disciformis</i> gen. nov., comb. nov., and of <i>Thiothrix flexilis</i> to <i>Thiofilum flexile</i> gen. nov., comb. nov., with emended description of <i>Thiothrix</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2226-2239.	0.8	36
1015	<i>Vicinamibacteraceae</i> fam. nov., the first described family within the subdivision 6 Acidobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2331-2334.	0.8	51
1016	Review of the genus <i>Methylobacterium</i> and closely related organisms: a proposal that some <i>Methylobacterium</i> species be reclassified into a new genus, <i>Methylorubrum</i> gen. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2727-2748.	0.8	212
1017	<i>Clostridium beihaiense</i> sp. nov., an anaerobic bacterium isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2789-2793.	0.8	8
1018	<i>Ruegeria kandeliae</i> sp. nov., isolated from the rhizosphere soil of a mangrove plant <i>Kandelia candel</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2653-2658.	0.8	16
1019	<i>Winogradskyella tangerina</i> sp. nov., a member of the Flavobacteriaceae isolated from coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2832-2837.	0.8	7
1020	Review of <i>Desulfotomaculum</i> species and proposal of the genera <i>Desulfallas</i> gen. nov., <i>Desulfofundulus</i> gen. nov., <i>Desulfofarcimen</i> gen. nov. and <i>Desulfohalotomaculum</i> gen. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2891-2899.	0.8	150
1021	Reclassification of <i>Eubacterium combesii</i> and discrepancies in the nomenclature of botulinum neurotoxin-producing clostridia: Challenging Opinion 69. Request for an Opinion. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3068-3075.	0.8	12
1022	<i>Petroclostridium xylanilyticum</i> gen. nov., sp. nov., a xylan-degrading bacterium isolated from an oilfield, and reclassification of clostridial cluster III members into four novel genera in a new Hungateclostridiaceae fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3197-3211.	0.8	182
1023	<i>Blautia argi</i> sp. nov., a new anaerobic bacterium isolated from dog faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 33-38.	0.8	25
1024	<i>Catenibacillus scindens</i> gen. nov., sp. nov., a C-deglycosylating human intestinal representative of the Lachnospiraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3356-3361.	0.8	12
1025	Refining the taxonomic structure of the phylum Acidobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3796-3806.	0.8	101

#	ARTICLE	IF	CITATIONS
1026	<i>Clostridium composti</i> sp. nov., a new anaerobic bacteria isolated from compost. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3869-3873.	0.8	9
1027	<i>Thioflexithrix pseukupensis</i> gen. nov., sp. nov., a filamentous gliding sulfur bacterium from the family Beggiatoaceae. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 798-804.	0.8	12
1028	<i>Clostridium fermenticellae</i> sp. nov., isolated from the mud in a fermentation cellar for the production of the Chinese liquor, baijiu. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 859-865.	0.8	29
1029	Ming et al. 2016, <i>Meiothermus terrae</i> Yu et al. 2014 and <i>Meiothermus timidus</i> Pires et al. 2005, to <i>Calidithermus</i> gen. nov., as <i>Calidithermus chliarophilus</i> comb. nov., <i>Calidithermus roseus</i> comb. nov., <i>Calidithermus terrae</i> comb. nov. and <i>Calidithermus timidus</i> comb. nov., respectively, and emended description of the genus <i>Meiothermus</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1123-1129.	0.8	28
1030	Comparative genomics of <i>Parolsenella catena</i> and <i>Libanicoccus massiliensis</i> : Reclassification of <i>Libanicoccus massiliensis</i> as <i>Parolsenella massiliensis</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1123-1129.	0.8	11
1031	<i>Citroniella saccharovorans</i> gen. nov. sp. nov., a member of the family Peptoniphilaceae isolated from a human fecal sample from a coastal traditional community member. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1142-1148.	0.8	12
1032	<i>Roseithermus sacchariphilus</i> gen. nov., sp. nov. and proposal of <i>Salisaetaceae</i> fam. nov., representing new family in the order Rhodothermales. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1213-1219.	0.8	24
1033	Genome-based classification of two halotolerant extreme acidophiles, <i>Acidihalobacter prosperus</i> V6 (=DSM 14174 =JCM 32253) and ' <i>Acidihalobacter ferrooxidans</i> ' V8 (=DSM 14175 =JCM 32254) as two new species, <i>Acidihalobacter aeolianus</i> sp. nov. and <i>Acidihalobacter ferrooxydans</i> sp. nov., respectively. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1557-1565.	0.8	25
1034	<i>Suicoccus acidiformans</i> gen. nov., sp. nov., isolated from a sick pig. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1443-1451.	0.8	14
1035	Minimal standards for the description of new genera and species of rhizobia and agrobacteria. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1852-1863.	0.8	170
1036	<i>Faecalibacillus intestinalis</i> gen. nov., sp. nov. and <i>Faecalibacillus faecis</i> sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2120-2128.	0.8	18
1037	<i>Staphylococcus debuckii</i> sp. nov., a coagulase-negative species from bovine milk. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2239-2249.	0.8	10
1038	<i>Vagococcus bubulae</i> sp. nov., isolated from ground beef, and <i>Vagococcus vulneris</i> sp. nov., isolated from a human foot wound. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2268-2276.	0.8	26
1039	<i>Lactococcus allomyrinae</i> sp. nov., isolated from gut of larvae of <i>Allomyrina dichotoma</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3682-3688.	0.8	13
1040	<i>Roseomonas wenyumeiae</i> sp. nov., isolated from faeces of Tibetan antelopes (<i>Pantholops hodgsonii</i>) on the Qinghai-Tibet Plateau. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2979-2986.	0.8	10
1041	<i>Streptococcus hillyeri</i> sp. nov., isolated from equine trachea. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3009-3013.	0.8	7
1042	<i>Gordonibacter faecihominis</i> is a later heterotypic synonym of <i>Gordonibacter urolithinifaciens</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2527-2532.	0.8	10
1043	Reclassification of ' <i>Polyangium brachysporum</i> ' DSM 7029 as <i>Schlegelella brevitalea</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2877-2883.	0.8	30

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1044	<i>Cohaesibacter intestini</i> sp. nov., isolated from the intestine of abalone, <i>Haliotis discus hannai</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3202-3206.	0.8	10
1045	<i>Schaedlerella arabinosiphila</i> gen. nov., sp. nov., a D-arabinose-utilizing bacterium isolated from faeces of C57BL/6J mice that is a close relative of <i>Clostridium</i> species ASF 502. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3616-3622.	0.8	12
1046	Reclassification of the <i>Clostridium clostridioforme</i> and <i>Clostridium sphenoides</i> clades as <i>Enterocloster</i> gen. nov. and <i>Lacrimispora</i> gen. nov., including reclassification of 15 taxa. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 23-34.	0.8	131
1047	Description of <i>Biomabacter acetigenes</i> gen. nov., sp. nov., and proposal of <i>Thermosediminibacterales</i> ord. nov. containing two novel families of <i>Tepidanaerobacteraceae</i> fam. nov. and <i>Thermosediminibacteraceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3891-3902.	0.8	26
1048	<i>Gudongella oleilytica</i> gen. nov., sp. nov., an aerotolerant bacterium isolated from Shengli oilfield and validation of family <i>Tissierellaceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 951-957.	0.8	24
1049	<i>Paenibacillus protaetiae</i> sp. nov., isolated from gut of larva of <i>Protaetia brevitarsis seulensis</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 989-994.	0.8	9
1050	<i>Thermaurantimonas aggregans</i> gen. nov., sp. nov., a moderately thermophilic heterotrophic aggregating bacterium isolated from microbial mats at a terrestrial hot spring. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1117-1121.	0.8	11
1051	<i>Anaerohalosphaera lusitana</i> gen. nov., sp. nov., and <i>Limihaloglobus sulfuriphilus</i> gen. nov., sp. nov., isolated from solar saltern sediments, and proposal of <i>Anaerohalosphaeraceae</i> fam. nov. within the order <i>Sedimentisphaerales</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1321-1330.	0.8	36
1052	<i>Fluviispira multicolorata</i> gen. nov., sp. nov. and <i>Silvanigrella paludirubra</i> sp. nov., isolated from freshwater habitats. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1630-1638.	0.8	18
1053	<i>Hymenobacter sediminis</i> sp. nov., isolated from lake sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1895-1902.	0.8	10
1054	<i>Calorimonas adulescens</i> gen. nov., sp. nov., an anaerobic thermophilic bacterium utilizing methoxylated benzoates. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2066-2071.	0.8	9
1055	<i>Georgenia wutianyii</i> sp. nov. and <i>Georgenia yuyongxinii</i> sp. nov. isolated from plateau pika (<i>Ochotona</i>) Tj ETQq1 1 0.784314 rgBT /Over International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2318-2324.	0.8	10
1056	Cultivation and description of <i>Duncaniella dubosii</i> sp. nov., <i>Duncaniella freteri</i> sp. nov. and emended description of the species <i>Duncaniella muris</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3105-3110.	0.8	23
1057	<i>Denitrobaculum tricleocarpae</i> gen. nov., sp. nov., a marine bacterium from coralline algae <i>Tricleocarpa</i> sp. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3335-3339.	0.8	10
1058	<i>Zhaonella formicivorans</i> gen. nov., sp. nov., an anaerobic formate-utilizing bacterium isolated from Shengli oilfield, and proposal of four novel families and <i>Moorellales</i> ord. nov. in the phylum <i>Firmicutes</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3361-3373.	0.8	27
1059	Proposal to reclassify the proteobacterial classes <i>Deltaproteobacteria</i> and <i>Oligoflexia</i> , and the phylum <i>Thermodesulfobacteria</i> into four phyla reflecting major functional capabilities. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5972-6016.	0.8	830
1060	<i>Actinomarinicola tropica</i> gen. nov. sp. nov., a new marine actinobacterium of the family <i>lamiaceae</i> , isolated from South China Sea sediment environments. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3852-3858.	0.8	18
1061	<i>Patiriisocius marinistellae</i> gen. nov., sp. nov., isolated from the starfish <i>Patiria pectinifera</i> , and reclassification of <i>Ulvibacter marinus</i> as a member of the genus <i>Patiriisocius</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4119-4129.	0.8	17

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1062	<i>Ningiella ruwaisensis</i> gen. nov., sp. nov., a member of the family Alteromonadaceae isolated from marine water of the Arabian Gulf. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4130-4138.	0.8	22
1063	<i>Halobacterium bonnevilliei</i> sp. nov., <i>Halobaculum saliterrae</i> sp. nov. and <i>Halovenus carboxidivorans</i> sp. nov., three novel carbon monoxide-oxidizing Halobacteria from saline crusts and soils. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4261-4268.	0.8	24
1064	<i>Caproicibacter fermentans</i> gen. nov., sp. nov., a new caproate-producing bacterium and emended description of the genus <i>Caproiciproducens</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4269-4279.	0.8	49
1065	<i>Gimesia benthica</i> sp. nov., a planctomycete isolated from a deep-sea water sample of the Northwest Indian Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4384-4389.	0.8	14
1066	<i>Muribaculum gordoncarteri</i> sp. nov., an anaerobic bacterium from the faeces of C57BL/6J mice. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4725-4729.	0.8	19
1067	<i>Sphaerochaeta halotolerans</i> sp. nov., a novel spherical halotolerant spirochete from a Russian heavy oil reservoir, emended description of the genus <i>Sphaerochaeta</i> , reclassification of <i>Sphaerochaeta coccoides</i> to a new genus <i>Parasphaerochaeta</i> gen. nov. as <i>Parasphaerochaeta coccoides</i> comb. nov. and proposal of <i>Sphaerochaetaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4748-4759.	0.8	30
1068	<i>Terricaulis silvestris</i> gen. nov., sp. nov., a novel prosthecate, budding member of the family Caulobacteraceae isolated from forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4966-4977.	0.8	14
1069	<i>Tichowtungia aerotolerans</i> gen. nov., sp. nov., a novel representative of the phylum Kiritimatiellaeota and proposal of <i>Tichowtungiaceae</i> fam. nov., <i>Tichowtungiales</i> ord. nov. and <i>Tichowtungia</i> class. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5001-5011.	0.8	27
1070	<i>Oceanipulchritudo coccoides</i> gen. nov., sp. nov., isolated from marine sediment within the family Puniceicoccaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5654-5664.	0.8	11
1071	Genome-based classification of <i>Acidihalobacter prosperus</i> F5 (=DSM 105917=JCM 32255) as <i>Acidihalobacter yilgarnensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6226-6234.	0.8	13
1072	Description of <i>Oceanispirochaeta crateris</i> sp. nov. and reclassification of <i>Spirochaeta perfilievii</i> as <i>Thiospirochaeta perfilievii</i> gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6373-6380.	0.8	14
1073	<i>Aquipluma nitroreducens</i> gen. nov. sp. nov., a novel facultatively anaerobic bacterium isolated from a freshwater lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6408-6413.	0.8	10
1114	Individuality, phenotypic differentiation, dormancy and "persistence"™ in culturable bacterial systems: commonalities shared by environmental, laboratory, and clinical microbiology. <i>F1000Research</i> , 2015, 4, 179.	0.8	46
1115	Individuality, phenotypic differentiation, dormancy and "persistence"™ in culturable bacterial systems: commonalities shared by environmental, laboratory, and clinical microbiology. <i>F1000Research</i> , 2015, 4, 179.	0.8	49
1116	"Candidatus <i>Fokinia solitaria</i> ", a Novel "Stand-Alone" Symbiotic Lineage of Midichloriaceae (Rickettsiales). <i>PLoS ONE</i> , 2016, 11, e0145743.	1.1	44
1117	Characterising the Canine Oral Microbiome by Direct Sequencing of Reverse-Transcribed rRNA Molecules. <i>PLoS ONE</i> , 2016, 11, e0157046.	1.1	38
1118	Unraveling the Physiological Roles of the Cyanobacterium <i>Geitlerinema</i> sp. BBD and Other Black Band Disease Community Members through Genomic Analysis of a Mixed Culture. <i>PLoS ONE</i> , 2016, 11, e0157953.	1.1	13
1119	K-shuff: A Novel Algorithm for Characterizing Structural and Compositional Diversity in Gene Libraries. <i>PLoS ONE</i> , 2016, 11, e0167634.	1.1	8

#	ARTICLE	IF	CITATIONS
1120	The functional microbiome of arthropods. <i>PLoS ONE</i> , 2017, 12, e0176573.	1.1	101
1121	Highly divergent 16S rRNA sequences in ribosomal operons of <i>Scytonema hyalinum</i> (Cyanobacteria). <i>PLoS ONE</i> , 2017, 12, e0186393.	1.1	67
1122	Gut-derived Flavonifractor species variants are differentially enriched during in vitro incubation with quercetin. <i>PLoS ONE</i> , 2020, 15, e0227724.	1.1	6
1123	<i>Nitrosophilus alvini</i> gen. nov., sp. nov., a hydrogen-oxidizing chemolithoautotroph isolated from a deep-sea hydrothermal vent in the East Pacific Rise, inferred by a genome-based taxonomy of the phylum "Campylobacterota". <i>PLoS ONE</i> , 2020, 15, e0241366.	1.1	22
1124	First Molecular Identification of Symbiotic Archaea in a Sponge Collected from the Persian Gulf, Iran. <i>Open Microbiology Journal</i> , 2018, 12, 323-332.	0.2	4
1125	Production and Characterization of L-Asparaginases of <i>Streptomyces</i> Isolated from the Arauca Riverbank (Colombia). <i>Open Microbiology Journal</i> , 2019, 13, 204-215.	0.2	4
1126	Characterization of mid-intestinal microbiota of farmed Chinook salmon using 16S rRNA gene metabarcoding. <i>Archives of Biological Sciences</i> , 2019, 71, 577-587.	0.2	22
1127	Relating next-generation sequencing and bioinformatics concepts to routine microbiological testing. <i>Electronic Journal of General Medicine</i> , 2019, 16, em136.	0.3	4
1128	Recent Progress of Microbiological Quality Control Methods in Unpasteurized Beer Production. <i>Journal of the Japanese Society for Food Science and Technology</i> , 2020, 67, 411-423.	0.1	5
1129	Microbiota intestinal benéfica e prejudicial na avicultura: Revisão. <i>Research, Society and Development</i> , 2020, 9, e43973667.	0.0	1
1130	Marine mammals are natural hosts of <i>Oceanivirga salmonicida</i> , a bacterial pathogen of Atlantic salmon. <i>Diseases of Aquatic Organisms</i> , 2020, 139, 161-174.	0.5	7
1131	Microbial Communities in Vermiculation Deposits from an Alpine Cave. <i>Frontiers in Earth Science</i> , 2020, 8, .	0.8	27
1132	Effects on the Ileal Microbiota of Phosphorus and Calcium Utilization, Bird Performance, and Gender in Japanese Quail. <i>Animals</i> , 2020, 10, 885.	1.0	21
1133	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. <i>Microorganisms</i> , 2020, 8, 131.	1.6	26
1134	Next-generation sequencing reveals the diversity of benthic diatoms in tidal flats. <i>Algae</i> , 2018, 33, 167-180.	0.9	16
1135	Ancient DNA Research in Maritime and Underwater Archaeology: Pitfalls, Promise, and Future Directions. <i>Open Quaternary</i> , 2020, 6, .	0.5	7
1136	<i>Komarekiella atlantica</i> gen. et sp. nov. (Nostocaceae, Cyanobacteria): a new subaerial taxon from the Atlantic Rainforest and Kauai, Hawaii. <i>Fottea</i> , 2017, 17, 178-190.	0.4	52
1137	<i>Nunduva</i> , a new marine genus of Rivulariaceae (Nostocales, Cyanobacteria) from marine rocky shores. <i>Fottea</i> , 2018, 18, 86-105.	0.4	33

#	ARTICLE	IF	CITATIONS
1138	Molecular characterization of <i>Geitleria appalachiana</i> sp. nov. (Nostocales, Cyanobacteria) and formation of Geitleriaceae fam. nov.. <i>Fottea</i> , 2018, 18, 150-163.	0.4	11
1139	<i>Lagosinema tenuis</i> gen. et sp. nov. (Prochlorotrichaceae, Cyanobacteria): a new brackish water genus from Tropical Africa. <i>Fottea</i> , 2019, 19, 1-12.	0.4	11
1140	Phylogeny and taxonomy of <i>Synechococcus</i> -like cyanobacteria. <i>Fottea</i> , 2020, 20, 171-191.	0.4	59
1141	<i>Johannesbaptistia floridana</i> sp. nov. (Chroococcales, Cyanobacteria), a novel marine cyanobacterium from coastal South Florida (USA). <i>Fottea</i> , 2020, 20, 152-159.	0.4	5
1142	Two new <i>Oculatella</i> (Oculatellaceae, Cyanobacteria) species in soil crusts from tropical semi-arid uplands of MÃ©xico. <i>Fottea</i> , 2020, 20, 160-170.	0.4	14
1143	Consistent and correctable bias in metagenomic sequencing experiments. <i>ELife</i> , 2019, 8, .	2.8	263
1144	Description of a new member of the family <i>Erysipelotrichaceae</i> : <i>Dakotella fusiforme</i> gen. nov., sp. nov., isolated from healthy human feces. <i>PeerJ</i> , 2020, 8, e10071.	0.9	6
1145	Accuracy of taxonomy prediction for 16S rRNA and fungal ITS sequences. <i>PeerJ</i> , 2018, 6, e4652.	0.9	223
1146	Viromes of one year old infants reveal the impact of birth mode on microbiome diversity. <i>PeerJ</i> , 2018, 6, e4694.	0.9	103
1147	Improved taxonomic assignment of rumen bacterial 16S rRNA sequences using a revised SILVA taxonomic framework. <i>PeerJ</i> , 2019, 7, e6496.	0.9	82
1148	Novel and Conventional Isolation Techniques to Obtain Planctomycetes from Marine Environments. <i>Microorganisms</i> , 2021, 9, 2078.	1.6	12
1149	<i>Aerofilum fasciculatum</i> gen. nov., sp. nov. (Oculatellaceae) and <i>Euryhalinema pallustris</i> sp. nov. (Prochlorotrichaceae) isolated from an Indian mangrove forest. <i>Phytotaxa</i> , 2021, 522, 165-186.	0.1	6
1151	<i>Rhodocaloribacter litoris</i> gen. nov., sp. nov., isolated from an intertidal hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
1153	Fecal biomarkers of environmental enteric dysfunction and the gut microbiota of rural Malawian children: An observational study. <i>Heliyon</i> , 2021, 7, e08194.	1.4	6
1154	Methanogenesis and Salt Tolerance Genes of a Novel Halophilic Methanosarcinaceae Metagenome-Assembled Genome from a Former Solar Saltern. <i>Genes</i> , 2021, 12, 1609.	1.0	10
1155	Microbial communities in an anammox reactor treating municipal wastewater at mainstream conditions: Practical implications of different molecular approaches. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 106622.	3.3	15
1156	Microbiome Clusters Disclose Physiologic Variances in Dairy Cows Challenged by Calving and Lipopolysaccharides. <i>MSystems</i> , 2021, 6, e0085621.	1.7	6
1158	Phylogenomics of Haloarchaea: The Controversy of the Genera <i>Natrinema</i> - <i>Haloterrigena</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 740909.	1.5	66

#	ARTICLE	IF	CITATIONS
1159	Metagenomic Sequencing of Multiple Soil Horizons and Sites in Close Vicinity Revealed Novel Secondary Metabolite Diversity. <i>MSystems</i> , 2021, 6, e0101821.	1.7	16
1160	Activities and metabolic versatility of distinct anammox bacteria in a full-scale wastewater treatment system. <i>Water Research</i> , 2021, 206, 117763.	5.3	42
1161	CRISPR/Cas12a-assisted rapid identification of key beer spoilage bacteria. <i>Innovative Food Science and Emerging Technologies</i> , 2021, 74, 102854.	2.7	10
1164	Metagenomic Mining of Enzyme Diversity. , 2016, , 1-25.		1
1165	Catheter-Related Bacteremia Due to <i>Gordonia sputi</i> in a Patient with Acute Lymphocytic Leukemia: a Case Report. <i>Japanese Journal of Infectious Diseases</i> , 2016, 69, 342-343.	0.5	3
1167	<i>Jiulongibacter sediminis</i> gen. nov., sp. nov., a new member of the family Cytophagaceae, isolated from the surface sediment of the Jiulong River in China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2347-2353.	0.8	10
1168	<i>Marinomonas gallaica</i> sp. nov. and <i>Marinomonas atlantica</i> sp. nov., isolated from reared clams (<i>Ruditapes decussatus</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3183-3188.	0.8	14
1169	Molecular Taxonomy of Environmental Prokaryotes. , 2016, , 3-35.		0
1170	Hot Cell-Direct PCR Aimed at Specific Cell Detection. , 0, , .		0
1172	Bioinformatic, Molecular, and Genetic Tools for Exploring Genome-Wide Responses to Hydrocarbons. , 2017, , 1-9.		0
1173	Identification of Antibiotic Producing Bacteria from Soil Samples of Dhaka, Bangladesh. <i>Journal of Microbiology & Experimentation</i> , 2017, 4, .	0.1	2
1177	<i>Streptococcus azizii</i> sp. nov., isolated from naïve weanling mice. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5032-5037.	0.8	5
1178	Novel 'Housekeeping' Genes and an Unusually Heterogeneous Distribution of Transporter Expression Profiles in Human Tissues and Cell Lines, Assessed Using the Gini Coefficient. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1179	<i>Oleiharenicola alkalitolerans</i> gen. nov., sp. nov., a new member of the phylum Verrucomicrobia isolated from an oilsands tailings pond. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1078-1084.	0.8	11
1181	<i>Neptunicella marina</i> gen. nov., sp. nov., isolated from surface seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1423-1428.	0.8	7
1183	<i>Chryseomicrobium excrementi</i> sp. nov., a Gram-stain-positive rod-shaped bacterium isolated from an earthworm (<i>Eisenia fetida</i>) cast. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2165-2171.	0.8	4
1185	Isolation and Molecular Identification of Food Grade Lactic Acid Bacteria and Their Antifungal Activity. <i>Journal of Biological Sciences</i> , 2018, 18, 260-269.	0.1	4
1187	Genetic variability in <i>Acidithiobacillus</i> spp. â€“ a working horse of environmental biotechnologies. <i>Nova Biotechnologica Et Chimica</i> , 2018, 17, 125-131.	0.1	1

#	ARTICLE	IF	CITATIONS
1191	Genome-based reclassification of <i>Paenibacillus dauci</i> as a later heterotypic synonym of <i>Paenibacillus shenyangensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 177-182.	0.8	6
1193	<i>Kistimonas alittae</i> sp. nov., a gammaproteobacterium isolated from the marine annelid <i>Alitta succinea</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 235-240.	0.8	12
1194	Determining Difference in Evolutionary Variation of Bacterial RecA proteins vs 16SrRNA Genes by using 16s_Toxonomy Tree. <i>Iranian Journal of Medical Microbiology</i> , 2019, 13, 32-43.	0.1	0
1195	<i>Streptococcus chenjunshii</i> sp. nov. isolated from feces of Tibetan antelopes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1237-1243.	0.8	7
1196	Proposal of <i>Parashewanella</i> gen. nov. to accommodate <i>Parashewanella curva</i> sp. nov. and <i>Parashewanella spongiae</i> comb. nov. in the <i>Shewanellaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1259-1264.	0.8	16
1197	<i>Aerophototrophica crusticola</i> gen. nov., sp. nov., isolated from desert biocrusts. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	9
1199	<i>Criibacterium bergeronii</i> gen. nov., sp. nov., a new member of the family <i>Peptostreptococcaceae</i> , isolated from human clinical samples. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	9
1206	La microbiota del tracto digestivo de camarones peneidos: una perspectiva histÃ³rica y estado del arte//The gut microbiota of penaeid shrimp: a historical perspective and state of the art. <i>Biocencia</i> , 2019, 22, 5-16.	0.1	0
1208	Microbial Omics: Role in Ecological Studies and Environmental Control Measures. <i>Environmental Chemistry for A Sustainable World</i> , 2020, , 173-196.	0.3	1
1211	Systematic review of descriptions of novel bacterial species: evaluation of the twenty-first century taxonomy through text mining. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2925-2936.	0.8	2
1212	<i>Exilibacterium tricleocarpae</i> gen. nov., sp. nov., a marine bacterium from coralline algae <i>Tricleocarpa</i> sp.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3427-3432.	0.8	10
1215	<i>Parapseudoflavitalea muciniphila</i> gen. nov., sp. nov., a member of the family <i>Chitinophagaceae</i> isolated from a human peritoneal tumour and reclassification of <i>Pseudobacter ginsenosidimutans</i> as <i>Pseudoflavitalea ginsenosidimutans</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3639-3646.	0.8	17
1216	<i>Mesohalobacter halotolerans</i> gen. nov., sp. nov., isolated from a marine solar saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3588-3596.	0.8	7
1217	<i>Amedibacterium intestinale</i> gen. nov., sp. nov., isolated from human faeces, and reclassification of <i>Eubacterium dolichum</i> Moore et al. 1976 (Approved Lists 1980) as <i>Amedibacillus dolichus</i> gen. nov., comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3656-3664.	0.8	18
1218	<i>Haloflavibacter putidus</i> gen. nov., sp. nov., isolated from coastal seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3740-3748.	0.8	6
1219	<i>Aeromicrobium chenweiae</i> sp. nov. and <i>Aeromicrobium yanjieii</i> sp. nov., isolated from Tibetan antelope (<i>Pantholops hodgsonii</i>) and plateau pika (<i>Ochotona curzoniae</i>), respectively. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4683-4690.	0.8	16
1221	<i>Fundicoccus ignavus</i> gen. nov., sp. nov., a novel genus of the family <i>Aerococcaceae</i> isolated from bulk tank milk. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4774-4781.	0.8	10
1222	ORPER: A Workflow for Constrained SSU rRNA Phylogenies. <i>Genes</i> , 2021, 12, 1741.	1.0	2

#	ARTICLE	IF	CITATIONS
1223	Venatorbacter cucullus gen. nov sp. nov a novel bacterial predator. Scientific Reports, 2021, 11, 21393.	1.6	3
1224	Distribution of RecBCD and AddAB recombination-associated genes among bacteria in 33 phyla. Microbiology (United Kingdom), 2020, 166, 1047-1064.	0.7	5
1225	Bacterial Succession through the Artisanal Process and Seasonal Effects Defining Bacterial Communities of Raw-Milk Adobera Cheese Revealed by High Throughput DNA Sequencing. Microorganisms, 2021, 9, 24.	1.6	10
1227	New Insights into the Ecology and Physiology of Methanomassiliicoccales from Terrestrial and Aquatic Environments. Microorganisms, 2021, 9, 30.	1.6	23
1228	Mixed Infection of Cytomegalovirus and Pulmonary Nocardiosis Caused by <i>Nocardia elegans</i> Diagnosed Using Nanopore Sequencing Technology: A Case Report. Internal Medicine, 2022, , .	0.3	4
1229	First characterization of the gut microbiome associated with <i>Mytilus chilensis</i> collected at a mussel farm and from a natural environment in Chile. Aquaculture, 2022, 548, 737644.	1.7	10
1230	Testing the effects of processing on donor human Milk: Analytical methods. Food Chemistry, 2022, 373, 131413.	4.2	5
1234	Analysis of residual sludge stored in UASB of a WWT in Petrolina-PE-Brazil. Revista Eletrônica Em GestÃO EducaÇÃO E Tecnologia Ambiental, 0, 24, 10.	0.0	0
1235	Biology of Wood Deteriogens. , 2020, , 99-176.		0
1236	Microbes: The Next-Generation Bioenergy Producers. , 2020, , 29-60.		0
1237	Metagenome Mining. , 2020, , 50-89.		0
1238	The Microbiome in Food Allergy and Eosinophilic Esophagitis. , 2020, , 147-160.		0
1239	Molekulare Struktur und Regulation prokaryotischer Gene. , 2020, , 131-201.		0
1242	Anaerosphaera multitolerans sp. nov., a salt-tolerant member of the family Peptoniphilaceae isolated from a mesophilically operated biogas fermenter fed with maize silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1217-1223.	0.8	6
1244	Rariglobus hedericola gen. nov., sp. nov., belonging to the Verrucomicrobia, isolated from a temperate freshwater habitat. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1830-1836.	0.8	9
1245	Mumia zhuanghunii sp. nov., isolated from the intestinal contents of plateau pika (<i>Ochotona</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Microbiology, 2020, 70, 2233-2238.	0.8	8
1247	RESCRIPT: Reproducible sequence taxonomy reference database management. PLoS Computational Biology, 2021, 17, e1009581.	1.5	277
1248	Screening and Molecular Identification of Bacteria from the Midgut of Amphimallon solstitialis Larvae Exhibiting Antagonistic Activity against Bacterial Symbionts of Entomopathogenic Nematodes. International Journal of Molecular Sciences, 2021, 22, 12005.	1.8	4

#	ARTICLE	IF	CITATIONS
1249	<i>Desulfomarina profunda</i> gen. nov., sp. nov., a novel mesophilic, hydrogen-oxidizing, sulphate-reducing chemolithoautotroph isolated from a deep-sea hydrothermal vent chimney. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
1250	Terrestrial-type nitrogen-fixing symbiosis between seagrass and a marine bacterium. <i>Nature</i> , 2021, 600, 105-109.	13.7	48
1253	<i>Vaginimicrobium propionicum</i> gen. nov., sp. nov., a novel propionic acid bacterium derived from human vaginal discharge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4091-4097.	0.8	11
1254	<i>Agriterribacter humi</i> gen. nov., sp. nov., a novel bacterium of the family Chitinophagaceae isolated from soil of a farming field. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5123-5130.	0.8	15
1255	<i>Poritiphilus flavus</i> gen. nov., sp. nov., a member of the family Flavobacteriaceae isolated from coral <i>Porites lutea</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5620-5626.	0.8	8
1256	<i>Aliikangiella coralliicola</i> sp. nov., a bacterium isolated from coral <i>Porites lutea</i> , and proposal of Pleioneaceae fam. nov. to accommodate <i>Pleionea</i> and <i>Aliikangiella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5880-5887.	0.8	13
1257	Impact of water content and dietary organic carbon richness on gut bacteria in the earthworm <i>Lumbricus terrestris</i> . <i>FEMS Microbes</i> , 2020, 1, .	0.8	1
1259	Treatment of dairy industry wastewater using bacterial biomass isolated from eutrophic lake sediments for the production of agricultural water. <i>Bioresource Technology Reports</i> , 2022, 17, 100891.	1.5	3
1260	<i>Ilocasia fonsfrigidiae</i> NS-1 gen. nov., sp. nov., a Novel Deep-Sea Bacterium Possessing Diverse Carbohydrate Metabolic Pathways. <i>Frontiers in Microbiology</i> , 2021, 12, 725159.	1.5	2
1261	<i>Sphingobacterium hungaricum</i> sp. nov. a novel species on the borderline of the genus <i>Sphingobacterium</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	5
1262	<i>Paralysiella testudinis</i> gen. nov., sp. nov., isolated from the cloaca of a toad-headed turtle (<i>Mesoclemmys nasuta</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
1263	Identification of a gut microbiota member that ameliorates DSS-induced colitis in intestinal barrier enhanced <i>Dusp6</i> -deficient mice. <i>Cell Reports</i> , 2021, 37, 110016.	2.9	35
1265	<i>Arcobacter vandammei</i> sp. nov., isolated from the rectal mucus of a healthy pig. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
1266	<i>Candidatus Gromoviella agglomerans</i> ™, a novel intracellular <i>Holosporaceae</i> parasite of the ciliate <i>Paramecium</i> showing marked genome reduction. <i>Environmental Microbiology Reports</i> , 2022, 14, 34-49.	1.0	9
1267	Paradox of complex diversity: Challenges in the diagnosis and management of bacterial keratitis. <i>Progress in Retinal and Eye Research</i> , 2022, 88, 101028.	7.3	16
1268	Soil Bacteria in Urban Community Gardens Have the Potential to Disseminate Antimicrobial Resistance Through Horizontal Gene Transfer. <i>Frontiers in Microbiology</i> , 2021, 12, 771707.	1.5	3
1270	Clean room microbiome complexity impacts planetary protection bioburden. <i>Microbiome</i> , 2021, 9, 238.	4.9	11
1271	16S rRNA gene sequences of <i>Candidatus Methylumidiphilus</i> (<i>Methylococcales</i>), a putative methanotrophic genus in lakes and ponds. <i>Aquatic Microbial Ecology</i> , 2022, 88, 25-30.	0.9	0

#	ARTICLE	IF	CITATIONS
1272	Bacterial Gut Microbiota and Infections During Early Childhood. <i>Frontiers in Microbiology</i> , 2021, 12, 793050.	1.5	11
1273	Recognizing novel cyanobacterial diversity in marine benthic mats, with the description of <i>Sirenicapillariaceae</i> fam. nov., two new genera, <i>Sirenicapillaria</i> gen. nov. and <i>Tigrinifilum</i> gen. nov., and seven new species. <i>Phycologia</i> , 2022, 61, 146-165.	0.6	10
1274	A review on the application of bioinformatics tools in food microbiome studies. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
1275	Cyanobacterial diversity and taxonomic uncertainty: polyphasic pathways to improved resolution. , 2022, , 7-45.		0
1276	Continuous-mode acclimation and operation of lignocellulosic sulfate-reducing bioreactors for enhanced metal immobilization from acidic mining-influenced water. <i>Journal of Hazardous Materials</i> , 2022, 425, 128054.	6.5	7
1277	Deep nasal sinus cavity microbiota dysbiosis in Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2021, 7, 111.	2.5	11
1278	Promising bioactive compounds from the marine environment and their potential effects on various diseases. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 14.	1.5	71
1279	<i>Caproicibacterium lactatifermentans</i> sp. nov., isolated from pit clay used for the production of Chinese strong aroma-type liquor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	18
1280	GAL08, an Uncultivated Group of Acidobacteria, Is a Dominant Bacterial Clade in a Neutral Hot Spring. <i>Frontiers in Microbiology</i> , 2021, 12, 787651.	1.5	1
1281	<i>Thainema</i> gen. nov. (Leptolyngbyaceae, Synechococcales): A new genus of simple trichal cyanobacteria isolated from a solar saltern environment in Thailand. <i>PLoS ONE</i> , 2022, 17, e0261682.	1.1	8
1282	Gut Microbial Signatures for Glycemic Responses of GLP-1 Receptor Agonists in Type 2 Diabetic Patients: A Pilot Study. <i>Frontiers in Endocrinology</i> , 2021, 12, 814770.	1.5	23
1283	Dietary shifts and social interactions drive temporal fluctuations of the gut microbiome from wild redfronted lemurs. <i>ISME Communications</i> , 2022, 2, .	1.7	16
1284	<i>Sulfuriroseicoccus oceanibius</i> gen. nov., sp. nov., a representative of the phylum Verrucomicrobia with a special cytoplasmic membrane. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 337-352.	0.7	0
1285	The ecological assembly of bacterial communities in Antarctic wetlands varies across levels of phylogenetic resolution. <i>Environmental Microbiology</i> , 2022, , .	1.8	1
1286	Description of two nitrogen-fixing bacteria, <i>Geomonas fuzhouensis</i> sp. nov. and <i>Geomonas agri</i> sp. nov., isolated from paddy soils. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 435-444.	0.7	7
1287	Past, present and future of the boundaries of the <i>Pseudomonas</i> genus: Proposal of <i>Stutzerimonas</i> gen. Nov. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126289.	1.2	103
1288	Microbiome analyses of 12 psyllid species of the family Psyllidae identified various bacteria including <i>Fukatsuia</i> and <i>Serratia symbiotica</i> , known as secondary symbionts of aphids. <i>BMC Microbiology</i> , 2022, 22, 15.	1.3	17
1289	A qRT-PCR Method Capable of Quantifying Specific Microorganisms Compared to NGS-Based Metagenome Profiling Data. <i>Microorganisms</i> , 2022, 10, 324.	1.6	6

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1291	Comparative Genomics Reveal the Animal-Associated Features of the Acanthopleuribacteraceae Bacteria, and Description of <i>Sulfidibacter corallicola</i> gen. nov., sp., nov.. <i>Frontiers in Microbiology</i> , 2022, 13, 778535.	1.5	1
1292	The Planctomycetia: an overview of the currently largest class within the phylum Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 169-201.	0.7	24
1293	<i>Mucisphaera caldilacus</i> gen. nov., sp. nov., a novel planctomycete of the class Phycisphaerae isolated in the shallow sea hydrothermal system of the Lipari Islands. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 407.	0.7	8
1295	Soil microbiomes in three farming systems more affected by depth than farming system. <i>Applied Soil Ecology</i> , 2022, 173, 104396.	2.1	4
1296	Revolution in microbial bioprospecting via the development of omics-based technologies. , 2022, , 27-46.		1
1297	<i>Salsipaludibacter albus</i> gen. nov., sp. nov., a novel actinobacterial strain isolate from a Portuguese solar saltern and proposal of <i>Salsipaludibacteraceae</i> fam. nov. and <i>Salsipaludibacterales</i> ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
1298	Drivers of gut microbiome variation within and between groups of a wild Malagasy primate. <i>Microbiome</i> , 2022, 10, 28.	4.9	19
1299	Development of an efficient antimicrobial susceptibility testing method with species identification by Nanopore sequencing of 16S rRNA amplicons. <i>PLoS ONE</i> , 2022, 17, e0262912.	1.1	4
1300	Introducing <i>Petrachlorosaceae</i> fam. nov., <i>Petrachloros</i> gen. nov. and <i>Petrachloros mirabilis</i> sp. nov. (<i>Synechococcales</i> , <i>Cyanobacteria</i>) isolated from a Portuguese UNESCO monument. <i>Journal of Phycology</i> , 2022, , .	1.0	0
1301	Genome Analysis and Description of Three Novel Diazotrophs <i>Geomonas</i> Species Isolated From Paddy Soils. <i>Frontiers in Microbiology</i> , 2021, 12, 801462.	1.5	26
1303	Roots alter soil microbial diversity and interkingdom interactions in diversified agricultural landscapes. <i>Oikos</i> , 2023, 2023, .	1.2	6
1305	Alterations in Intestinal Microbiota Composition in Mice Treated With Vitamin D3 or Cathelicidin. <i>Frontiers in Oncology</i> , 2021, 11, 700038.	1.3	3
1306	An investigation of canine leptospiral antibodies in Tokyo and Yokohama. Comparison of Canine Positive rates between rapid microscopic agglutination test and SchÃ¼ffner-Mochtar test. <i>International Journal of Zoonoses</i> , 1974, 1, 82-90.	0.0	0
1307	<i>Desulfovolcanus ferrireducens</i> gen. nov., sp. nov., a thermophilic autotrophic iron and sulfate-reducing bacterium from subseafloor basalt that grows on akaganÃ©ite and lepidocrocite minerals. <i>Extremophiles</i> , 2022, 26, 13.	0.9	2
1308	Characterization of <i>Alistipes montrealensis</i> sp. nov., Isolated from Human Feces of a Patient with Metastatic Melanoma Treated with Immune Checkpoint Inhibitors. <i>Microbiology Research</i> , 2022, 13, 140-151.	0.8	1
1309	Niche partitioning of the ubiquitous and ecologically relevant NS5 marine group. <i>ISME Journal</i> , 2022, 16, 1570-1582.	4.4	11
1310	Effects of production system on the gut microbiota diversity and IgA distribution of Kampong chickens, Indonesia. <i>Biodiversitas</i> , 2022, 23, .	0.2	0
1311	A Bacterial Genome and Culture Collection of Gut Microbial in Weanling Piglet. <i>Microbiology Spectrum</i> , 2022, 10, e0241721.	1.2	3

#	ARTICLE	IF	CITATIONS
1312	The novel genus, <i>Candidatus</i> Phosphoribacter TM , previously identified as <i>Tetrasphaera</i> , is the dominant polyphosphate accumulating lineage in EBPR wastewater treatment plants worldwide. ISME Journal, 2022, 16, 1605-1616.	4.4	41
1313	Microbial communities across activated sludge plants show recurring species-level seasonal patterns. ISME Communications, 2022, 2, .	1.7	18
1314	Cultivation and metabolic insights of an uncultured clade, Bacteroidetes <i>Candidatus</i> Sulfidibacteriales ord. nov.), from deep-sea hydrothermal vents. Environmental Microbiology, 2022, 24, 2484-2501.	1.8	7
1315	Biannual Administrations of Azithromycin and the Gastrointestinal Microbiome of Malawian Children: A Nested Cohort Study Within a Randomized Controlled Trial. Frontiers in Public Health, 2022, 10, 756318.	1.3	1
1318	Disentangle genus microdiversity within a complex microbial community by using a multi-distance long-read binning method: example of <i>Candidatus</i> Accumulibacter. Environmental Microbiology, 2022, 24, 2136-2156.	1.8	4
1319	Acetate Degradation at Low pH by the Moderately Acidophilic Sulfate Reducer <i>Acididesulfobacillus</i> acetoxydans gen. nov. sp. nov.. Frontiers in Microbiology, 2022, 13, 816605.	1.5	6
1320	Epitheliocystis in Greater Amberjack: Evidence of a Novel Causative Agent, Pathology, Immune Response and Epidemiological Findings. Microorganisms, 2022, 10, 627.	1.6	2
1321	Anti-Microbiota Vaccine Reduces Avian Malaria Infection Within Mosquito Vectors. Frontiers in Immunology, 2022, 13, 841835.	2.2	18
1322	Harnessing taxonomically diverse and metabolically versatile genus <i>Paracoccus</i> for bioplastic synthesis and xenobiotic biodegradation. Journal of Applied Microbiology, 2022, 132, 4208-4224.	1.4	10
1323	Discovery of the non-cosmopolitan lineages in <i>Candidatus</i> Thermoprofundales. Environmental Microbiology, 2022, 24, 3063-3080.	1.8	3
1324	Translational multi-omics microbiome research for strategies to improve cattle production and health. Emerging Topics in Life Sciences, 2022, , .	1.1	3
1325	Pathogenicity and Its Implications in Taxonomy: The <i>Brucella</i> and <i>Ochrobactrum</i> Case. Pathogens, 2022, 11, 377.	1.2	19
1326	Characterization of the First Cultured Representative of <i>Candidatus</i> Thermofonsia Clade 2 within <i>Chloroflexi</i> Reveals Its Phototrophic Lifestyle. MBio, 2022, 13, e0028722.	1.8	8
1327	Composition of the ileum microbiota is a mediator between the host genome and phosphorus utilization and other efficiency traits in Japanese quail (<i>Coturnix japonica</i>). Genetics Selection Evolution, 2022, 54, 20.	1.2	6
1328	<i>Thiomicrobacter heinhorstiae</i> sp. nov. and <i>Thiomicrobacter cannonii</i> sp. nov.: novel sulphur-oxidizing chemolithoautotrophs isolated from the chemocline of Hospital Hole, an anchialine sinkhole in Spring Hill, Florida, USA. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	13
1330	Comparative analysis of the oral microbiome of burning mouth syndrome patients. Journal of Oral Microbiology, 2022, 14, 2052632.	1.2	7
1331	Expansion of the Beta-Proteobacterial Genus <i>Ca. Ichthyocystis</i> : A Case Report of Epitheliocystis in the Pompano <i>Trachinotus ovatus</i> . Pathogens, 2022, 11, 421.	1.2	2
1332	Bacterial community structure and metabolic potential in microbialite-forming mats from South Australian saline lakes. Geobiology, 2022, 20, 546-559.	1.1	3

#	ARTICLE	IF	CITATIONS
1333	Photobacterium halophilum sp. nov. and a Salt-Loving Bacterium Isolated from Marine Sediment. Diversity, 2022, 14, 188.	0.7	0
1334	Amazonocrinis thailandica sp. nov. (Nostocales, Cyanobacteria), a novel species of the previously monotypic Amazonocrinis genus from Thailand. Algae, 2022, 37, 1-14.	0.9	4
1336	Protocol to assess the impact of early-life antibiotic exposure on murine longevity. STAR Protocols, 2022, 3, 101220.	0.5	1
1337	Anaerobic single-cell dispensing facilitates the cultivation of human gut bacteria. Environmental Microbiology, 2022, 24, 3861-3881.	1.8	15
1338	A comparative whole-genome approach identifies bacterial traits for marine microbial interactions. Communications Biology, 2022, 5, 276.	2.0	18
1339	Development of a device for cultivation and isolation of microbes using a specialized cellulose film. Journal of Microbiological Methods, 2022, 195, 106450.	0.7	1
1340	Synergistic interaction of gut microbiota enhances the growth of nematode through neuroendocrine signaling. Current Biology, 2022, 32, 2037-2050.e4.	1.8	8
1341	Unraveling the microbiota of the fish parasite Pseudoterranova decipiens in codfish (Gadus morhua) reveals a fish-related bacterial community. International Journal of Food Microbiology, 2022, 367, 109591.	2.1	2
1342	MiDAS 4: A global catalogue of full-length 16S rRNA gene sequences and taxonomy for studies of bacterial communities in wastewater treatment plants. Nature Communications, 2022, 13, 1908.	5.8	114
1343	Impact of the Gastrointestinal Tract Microbiota on Cardiovascular Health and Pathophysiology. Journal of Cardiovascular Pharmacology, 2022, Publish Ahead of Print, .	0.8	1
1344	Prospective Comparison Between Shotgun Metagenomics and Sanger Sequencing of the 16S rRNA Gene for the Etiological Diagnosis of Infections. Frontiers in Microbiology, 2022, 13, 761873.	1.5	13
1345	Ex-situ biogas upgrading in thermophilic trickle bed reactors packed with micro-porous packing materials. Chemosphere, 2022, 296, 133987.	4.2	18
1346	Tracking the diversity and interaction of methanogens in the energy recovery process of a full-scale wastewater treatment plant. Environmental Research, 2022, 211, 113010.	3.7	2
1347	Biogeography of culturable marine bacteria from both poles reveals that "everything is not everywhere"™ at the genomic level. Environmental Microbiology, 2022, 24, 98-109.	1.8	5
1348	The Role of Genital Tract Microbiome in Fertility: A Systematic Review. International Journal of Molecular Sciences, 2022, 23, 180.	1.8	36
1349	Interplay between microbial community composition and chemodiversity of dissolved organic matter throughout the Black Sea water column redox gradient. Limnology and Oceanography, 2022, 67, 329-347.	1.6	8
1350	Pinibacter aurantiacus gen. nov., sp. nov., isolated from rhizospheric soil of a pine tree. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
1351	The Archaeal Transcription Termination Factor aCPSF1 is a Robust Phylogenetic Marker for Archaeal Taxonomy. Microbiology Spectrum, 2021, 9, e0153921.	1.2	5

#	ARTICLE	IF	CITATIONS
1353	What Does 16S rRNA Gene-Targeted Next Generation Sequencing Contribute to the Study of Infective Endocarditis in Heart-Valve Tissue?. <i>Pathogens</i> , 2022, 11, 34.	1.2	6
1354	The Succession of Bacterial Community Attached on Biodegradable Plastic Mulches During the Degradation in Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 785737.	1.5	25
1355	<i>Paraneptunicella aestuarii</i> gen. nov., sp. nov., a member of the family Alteromonadaceae isolated from seawater in East China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
1356	<i>Phosphitispora fastidiosa</i> gen. nov. sp. nov., a new dissimilatory phosphite-oxidizing anaerobic bacterium isolated from anaerobic sewage sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14
1357	Omic Technologies and Cold Adaptations. , 2022, , 253-284.		1
1359	<i>Roseococcus microcystis</i> sp. nov., isolated from a <i>Microcystis aeruginosa</i> culture sample. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
1360	Revealing microbial species diversity using sequence capture by hybridization. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
1361	Rapid Detection of <i>Staphylococcus aureus</i> and <i>Streptococcus pneumoniae</i> by Real-Time Analysis of Volatile Metabolites. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1362	Amplicon Sequencing of Single-Copy Protein-Coding Genes Reveals Accurate Diversity for Sequence-Discrete Microbiome Populations. <i>Microbiology Spectrum</i> , 2022, 10, e0210521.	1.2	0
1363	New insights into the energy metabolism and taxonomy of <i>Deferribacteres</i> revealed by the characterization of a new isolate from a hypersaline microbial mat. <i>Environmental Microbiology</i> , 2022, 24, 2543-2575.	1.8	26
1364	Geosmin-producing <i>Scytonema foetidum</i> sp. nov. (Scytonemataceae, Cyanobacteria): morphology and molecular phylogeny. <i>Fottea</i> , 2022, 22, 78-92.	0.4	1
1365	Exploring the Gut Microbiome in Myasthenia Gravis. <i>Nutrients</i> , 2022, 14, 1647.	1.7	17
1366	Comparative Genomics Reveals Genetic Diversity and Metabolic Potentials of the Genus <i>Qipengyuania</i> and Suggests Fifteen Novel Species. <i>Microbiology Spectrum</i> , 2022, 10, e0126421.	1.2	55
1367	Cultivation and Functional Characterization of a Deep-Sea <i>Lentisphaerae</i> Representative Reveals Its Unique Physiology and Ecology. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	1
1368	Short- and long-read metabarcoding of the eukaryotic rRNA operon: Evaluation of primers and comparison to shotgun metagenomics sequencing. <i>Molecular Ecology Resources</i> , 2022, 22, 2304-2318.	2.2	16
1369	Comparative Genomics of Members of the Genus <i>Defluviicoccus</i> With Insights Into Their Ecophysiological Importance. <i>Frontiers in Microbiology</i> , 2022, 13, 834906.	1.5	8
1526	Revision of the <i>Candidatus Phytoplasma</i> ™ species description guidelines. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	119
1527	Organic waste separation with microbial inoculants as an effective tool for horticulture. , 2022, , 369-397.		0

#	ARTICLE	IF	CITATIONS
1528	Enhanced Cultured Diversity of the Mouse Gut Microbiota Enables Custom-Made Synthetic Communities. SSRN Electronic Journal, 0, , .	0.4	1
1529	Functional Insights of Salinity Stress-Related Pathways in Metagenome-Resolved <i>Methanotrix</i> Genomes. Applied and Environmental Microbiology, 2022, 88, e0244921.	1.4	8
1530	Gut microbiota of ring-tailed lemurs (<i>Lemur catta</i>) vary across natural and captive populations and correlate with environmental microbiota. Animal Microbiome, 2022, 4, 29.	1.5	24
1531	<i>Sideroxyarcus emersonii</i> gen. nov. sp. nov., a neutrophilic, microaerobic iron- and thiosulfate-oxidizing bacterium isolated from iron-rich wetland sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	12
1532	Litter Management Strategies and Their Impact on the Environmental and Respiratory Microbiome Might Influence Health in Poultry. Microorganisms, 2022, 10, 878.	1.6	1
1533	Opportunities and challenges of using metagenomic data to bring uncultured microbes into cultivation. Microbiome, 2022, 10, 76.	4.9	59
1534	<i>Nodosilinea hunanensis</i> sp. nov. (Prochlorotrichaceae, Synechococcales) from a Freshwater Pond in China Based on a Polyphasic Approach. Diversity, 2022, 14, 364.	0.7	4
1535	Intracellular silicification by early-branching magnetotactic bacteria. Science Advances, 2022, 8, eabn6045.	4.7	11
1536	<i>Tannockella kyphosi</i> gen. nov., sp. nov., a member of the family Erysipelotrichaceae, isolated from the hindgut of the marine herbivorous fish <i>Kyphosus sydneyanus</i> . International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	9
1537	Exploring the microbial influence on seasonal nitrous oxide concentration in a full-scale wastewater treatment plant using metagenome assembled genomes. Water Research, 2022, 219, 118563.	5.3	5
1538	Assessment of the Safety and Efficacy of an Oral Probiotic-Based Vaccine Against <i>Aspergillus</i> Infection in Captive-Bred Humboldt Penguins (<i>Spheniscus humboldti</i>). Frontiers in Immunology, 2022, 13, .	2.2	5
1539	<i>Copranaerobaculum intestinale</i> gen. nov., sp. nov., a novel anaerobic bacterium isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
1541	<i>Undibacter mobilis</i> gen. nov., sp. nov. isolated from an artificial wetland in Okcheon, Korea. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	10
1542	<i>Streptomyces benahoarensis</i> sp. nov. Isolated From a Lava Tube of La Palma, Canary Islands, Spain. Frontiers in Microbiology, 2022, 13, .	1.5	3
1545	Archaeal communities perform an important role in maintaining microbial stability under long term continuous cropping systems. Science of the Total Environment, 2022, 838, 156413.	3.9	5
1546	A new family for æ termite gut treponemesæ™: description of Breznariellaceae fam. nov., Gracilinema caldarium gen. nov., comb. nov., Leadbetteria azotonutricia gen. nov., comb. nov., Helmutkoenigia isopterocolens gen. nov., comb. nov., and Zuelzera stenostrepta gen. nov., comb. nov., and proposal of Rectinemataceae fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	35
1547	Microbiota in Tumors: From Understanding to Application. Advanced Science, 2022, 9, .	5.6	26
1548	Reclassification of <i>Brevibacterium frigoritolerans</i> as <i>Peribacillus frigoritolerans</i> comb. nov. based on phylogenomics and multiple molecular synapomorphies. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	14

#	ARTICLE	IF	CITATIONS
1549	Description of <i>Prasinibacter corallicola</i> gen. nov., sp. nov., a zeaxanthin-producing bacterium isolated from stony coral <i>Porites lutea</i> . <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	0
1551	Characterization of Microbial Shifts during the Production and Ripening of Raw Ewe Milk-Derived Idiazabal Cheese by High-Throughput Sequencing. <i>Biology</i> , 2022, 11, 769.	1.3	4
1552	Culturing the uncultured microbial majority in activated sludge: A critical review. <i>Critical Reviews in Environmental Science and Technology</i> , 2023, 53, 601-624.	6.6	13
1553	Meroterpenoids Possibly Produced by a Bacterial Endosymbiont of the Tropical Basidiomycete <i>Echinochaete brachypora</i> . <i>Biomolecules</i> , 2022, 12, 755.	1.8	2
1554	<i>Sessilibacter corallicola</i> gen. nov., sp. nov., a sessile bacterium isolated from coral <i>Porites lutea</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
1555	A Microbiota-Dependent Response to Anticancer Treatment in an In Vitro Human Microbiota Model: A Pilot Study With Hydroxycarbamide and Daunorubicin. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	0
1556	Microbial community diversity changes during voltage reversal repair in a 12-unit microbial fuel cell. <i>Chemical Engineering Journal</i> , 2022, 446, 137334.	6.6	9
1557	Biofilm formation, antimicrobial assay, and toxin-genotypes of <i>Clostridium perfringens</i> type C isolates cultured from a neonatal Yangtze finless porpoise. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	1
1558	<i>Rubinisphaera margarita</i> sp. nov., a novel planctomycete isolated from marine sediments collected in the Portuguese north coast. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	7
1559	Four new members of the family Cytophagaceae: <i>Chryseosolibacter histidini</i> gen. nov., sp. nov., <i>Chryseosolibacter indicus</i> gen. nov., sp. nov., <i>Dawidia cretensis</i> , gen. nov., sp. nov., and <i>Dawidia soli</i> , gen. nov., sp. nov. isolated from diverse habitat. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1059-1072.	0.7	1
1560	Cultured Bacteria Provide Insight into the Functional Potential of the Coral-Associated Microbiome. <i>MSystems</i> , 2022, 7, .	1.7	14
1562	A Survey of Statistical Methods for Microbiome Data Analysis. <i>Frontiers in Applied Mathematics and Statistics</i> , 0, 8, .	0.7	5
1563	Dynamic Variations in Rumen Fermentation Characteristics and Bacterial Community Composition during In Vitro Fermentation. <i>Fermentation</i> , 2022, 8, 276.	1.4	11
1564	Microbial Forensics: A Present to Future Perspective on Genomic Targets, Bioinformatic Challenges, and Applications. <i>Forensic Genomics</i> , 2022, 2, 42-64.	0.3	3
1565	<i>Candidatus</i> Nitrosopolaris, a genus of putative ammonia-oxidizing archaea with a polar/alpine distribution. <i>FEMS Microbes</i> , 2022, 3, .	0.8	10
1567	Identification of sulfate-reducing magnetotactic bacteria via a group-specific 16S rDNA primer and correlative fluorescence and electron microscopy: Strategy for culture-independent study. <i>Environmental Microbiology</i> , 2022, 24, 5019-5038.	1.8	5
1568	Isolation, diversity and antimicrobial activity of planctomycetes from the Tejo river estuary (Portugal). <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	8
1569	Holistic Approach to the Restoration of a Vandalized Monument: The Cross of the Inquisition, Seville City Hall, Spain. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 6222.	1.3	1

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1570	Genotypic and symbiotic diversity studies of rhizobia nodulating <i>Acacia saligna</i> in Tunisia reveal two novel symbiovars within the <i>Rhizobium leguminosarum</i> complex and <i>Bradyrhizobium</i> . <i>Systematic and Applied Microbiology</i> , 2022, 45, 126343.	1.2	2
1571	HiLi-chip: A high-throughput library construction chip for comprehensive profiling of environmental microbial communities. <i>Environmental Research</i> , 2022, 213, 113650.	3.7	1
1574	Climate dictates microbial community composition and diversity in Australian biological soil crusts (biocrusts). <i>Environmental Microbiology</i> , 2022, 24, 5467-5482.	1.8	6
1575	Ecosystem-specific microbiota and microbiome databases in the era of big data. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	9
1576	High-throughput Method for Novel Medium Development for Culture of Anaerobic Gut Bacteria. <i>Current Protocols</i> , 2022, 2, .	1.3	3
1577	Within-community variation of interspecific divergence patterns in passerine gut microbiota. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	2
1578	Expanding the phylogenetic distribution of cytochrome <i>b</i> -containing methanogenic archaea sheds light on the evolution of methanogenesis. <i>ISME Journal</i> , 2022, 16, 2373-2387.	4.4	12
1579	Urbanization promotes specific bacteria in freshwater microbiomes including potential pathogens. <i>Science of the Total Environment</i> , 2022, 845, 157321.	3.9	12
1580	Uptake of Phytoplankton-Derived Carbon and Cobalamins by Novel <i>Acidobacteria</i> Genera in <i>Microcystis</i> Blooms Inferred from Metagenomic and Metatranscriptomic Evidence. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	7
1581	Fluctuating selection on bacterial iron regulation in the mammalian gut. <i>Current Biology</i> , 2022, , .	1.8	5
1582	<i>Sala cibi</i> gen. nov., sp. nov., an extremely halophilic archaeon isolated from solar salt. <i>Journal of Microbiology</i> , 0, , .	1.3	5
1583	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
1584	Phylogenetic Diversity of Bacteria Associated with Speleothems of a Silicate Cave in a Guiana Shield Tepui. <i>Microorganisms</i> , 2022, 10, 1395.	1.6	4
1585	Antibiotic-induced gut dysbiosis and autoimmune disease: A systematic review of preclinical studies. <i>Autoimmunity Reviews</i> , 2022, 21, 103140.	2.5	8
1586	iChip-Inspired Isolation, Bioactivities and Dereplication of Actinomycetota from Portuguese Beach Sediments. <i>Microorganisms</i> , 2022, 10, 1471.	1.6	7
1587	Okra Growth, Yield and Rhizosphere Microbiome Responses to the Encapsulated Bioinoculant Application under Reduced Fertilization Regime. <i>Biology</i> , 2022, 11, 1107.	1.3	0
1588	<i>Rickettsia helvetica</i> infection is associated with microbiome modulation in <i>Ixodes ricinus</i> collected from humans in Serbia. <i>Scientific Reports</i> , 2022, 12, .	1.6	10
1589	Coastal Transient Niches Shape the Microdiversity Pattern of a Bacterioplankton Population with Reduced Genomes. <i>MBio</i> , 2022, 13, .	1.8	1

#	ARTICLE	IF	CITATIONS
1590	Composition and functionality of bacterioplankton communities in marine coastal zones adjacent to finfish aquaculture. <i>Marine Pollution Bulletin</i> , 2022, 182, 113957.	2.3	0
1591	Gastrointestinal microbiome in the context of <i>Helicobacter pylori</i> infection in stomach and gastroduodenal diseases. <i>Progress in Molecular Biology and Translational Science</i> , 2022, , 53-95.	0.9	1
1592	Phytoplasma Taxonomy: Nomenclature, Classification, and Identification. <i>Biology</i> , 2022, 11, 1119.	1.3	33
1593	Phylogenomic analysis and metabolic role reconstruction of mutualistic <i>Rhizobiales</i> hindgut symbionts of <i>Acromyrmex</i> leaf-cutting ants. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	1
1594	Molecular Markers: An Overview of Data Published for Fungi over the Last Ten Years. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 803.	1.5	15
1595	Insight into bacterial community profiles of oil shale and sandstone in ordos basin by culture-dependent and culture-independent methods. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2022, 57, 723-735.	0.9	2
1596	Differential richness inference for 16S rRNA marker gene surveys. <i>Genome Biology</i> , 2022, 23, .	3.8	5
1598	Digging deeper into the taxonomy of <i>Cylindrospermum</i> and description of <i>Johanseniella tripurensis</i> gen. et sp. nov. from India. <i>FEMS Microbiology Letters</i> , 2022, 369, .	0.7	3
1599	Life barcoded by DNA barcodes. <i>Conservation Genetics Resources</i> , 2022, 14, 351-365.	0.4	12
1600	<i>Parvicella tangerina</i> gen. nov., sp. nov. (Parvicellaceae fam. nov., Flavobacteriales), first cultured representative of the marine clade UBA10066, and <i>Lysobacter luteus</i> sp. nov., from activated sludge of a seawater-processing wastewater treatment plant. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	2
1601	Phylogenomics and comparative genomic analyses support the creation of the novel family Ignatzschineriaceae fam. nov. comprising the genera Ignatzschineria and Wohlfahrtiimonas within the order Cardiobacteriales. <i>Research in Microbiology</i> , 2023, 174, 103988.	1.0	7
1602	Taxonomic revision of the genus Amphritea supported by genomic and in silico chemotaxonomic analyses, and the proposal of Aliamphritea gen. nov.. <i>PLoS ONE</i> , 2022, 17, e0271174.	1.1	7
1603	Water Physicochemical Parameters and Microbial Composition Distinguish <i>Anopheles</i> and <i>Culex</i> Mosquito Breeding Sites: Potential as Ecological Markers for Larval Source Surveillance. <i>Journal of Medical Entomology</i> , 0, , .	0.9	3
1604	Detection of interphylum transfers of the magnetosome gene cluster in magnetotactic bacteria. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
1606	Transfer of <i>Bacillus</i> <i>atepidiphilus</i> Narsing Rao et al. 2021 to the genus <i>Peribacillus</i> as <i>Peribacillus tepidiphilus</i> comb. nov.. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	4
1607	Meta-analysis of larvae of the black soldier fly (<i>Hermetia illucens</i>) microbiota based on 16S rRNA gene amplicon sequencing. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	8
1608	The Genus Iodidimonas: From Its Discovery to Potential Applications. <i>Microorganisms</i> , 2022, 10, 1661.	1.6	4
1609	Rapid evolution of a novel protective symbiont into keystone taxon in <i>Caenorhabditis elegans</i> microbiota. <i>Scientific Reports</i> , 2022, 12, .	1.6	8

#	ARTICLE	IF	CITATIONS
1610	Characterization of <i>Marinilongibacter aquaticus</i> gen. nov., sp. nov., a unique marine bacterium harboring four CRISPR-Cas systems in the phylum Bacteroidota. <i>Journal of Microbiology</i> , 2022, 60, 905-915.	1.3	4
1611	Vaginal Microbiome in Reproductive Medicine. <i>Diagnostics</i> , 2022, 12, 1948.	1.3	9
1612	Microbiomic Analysis of Bacteria Associated with Rock Tripe Lichens in Continental and Maritime Antarctic Regions. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 817.	1.5	5
1613	Impacts of bioturbation on iron biogeochemistry and microbial communities in coastal sediment mesocosms under varying degrees of hypoxia. <i>Estuarine, Coastal and Shelf Science</i> , 2022, 276, 108032.	0.9	3
1614	Larval gut microbiome of <i>Pelidnota luridipes</i> (Coleoptera: Scarabaeidae): high bacterial diversity, different metabolic profiles on gut chambers and species with probiotic potential. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	1.7	3
1615	Rapid detection of <i>Staphylococcus aureus</i> and <i>Streptococcus pneumoniae</i> by real-time analysis of volatile metabolites. <i>IScience</i> , 2022, 25, 105080.	1.9	6
1616	<i>Rhodopirellula aestuarii</i> sp. nov., a novel member of the genus <i>Rhodopirellula</i> isolated from brackish sediments collected in the Tagus River estuary, Portugal. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126360.	1.2	3
1617	Genome-based taxonomic classification of the closest-to-Comamonadaceae group supports a new family Sphaerotilaceae fam. nov. and taxonomic revisions. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126352.	1.2	12
1618	Methods of DNA introduction for the engineering of commensal microbes. <i>Engineering Microbiology</i> , 2022, 2, 100048.	2.2	6
1619	Archaea: A Goldmine for Molecular Biologists and Evolutionists. <i>Methods in Molecular Biology</i> , 2022, , 1-21.	0.4	3
1620	Functional characterization of prokaryotic dark matter: the road so far and what lies ahead. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100159.	1.4	2
1621	RiboTaxa: combined approaches for rRNA genes taxonomic resolution down to the species level from metagenomics data revealing novelties. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	4
1622	Dust-Associated Bacterial and Fungal Communities in Indoor Multiple-Use and Public Transportation Facilities. <i>Atmosphere</i> , 2022, 13, 1373.	1.0	3
1623	Meta-Analysis and Validation of a Colorectal Cancer Risk Prediction Model Using Deep Sequenced Fecal Metagenomes. <i>Cancers</i> , 2022, 14, 4214.	1.7	3
1625	Comparative Study of Different Diagnostic Routine Methods for the Identification of <i>Acinetobacter</i> radioresistens. <i>Microorganisms</i> , 2022, 10, 1767.	1.6	1
1626	Metabolomic analysis of halotolerant endophytic bacterium <i>Salinivibrio costicola</i> isolated from <i>Suaeda maritima</i> (L.) dumort. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
1629	Genome analysis of a new sulphur disproportionating species <i>Thermosulfurimonas</i> strain F29 and comparative genomics of sulfur-disproportionating bacteria from marine hydrothermal vents. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
1630	Improving environmental monitoring of <i>Vibrionaceae</i> in coastal ecosystems through 16S rRNA gene amplicon sequencing. <i>Environmental Science and Pollution Research</i> , 2022, 29, 67466-67482.	2.7	5

#	ARTICLE	IF	CITATIONS
1631	Discovery of a new genus of anaerobic ammonium oxidizing bacteria with a mechanism for oxygen tolerance. <i>Water Research</i> , 2022, 226, 119165.	5.3	19
1632	Uncovering Lasonolide A Biosynthesis Using Genome-Resolved Metagenomics. <i>MBio</i> , 2022, 13, .	1.8	7
1633	â€œ <i>Candidatus</i> Euplotechlamydia quinta,â€•a novel chlamydiaâ€•like bacterium hosted by the ciliate <i>Euplotes octocarinatus</i> (Ciliophora, Spirotrichea). <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	2
1635	Untangling the link between the human gut microbiota composition and the severity of the symptoms of the <sc>COVID</sc>â€•19 infection. <i>Environmental Microbiology</i> , 2022, 24, 6453-6462.	1.8	6
1636	<i>Shewanella</i> infection in humans: Epidemiology, clinical features and pathogenicity. <i>Virulence</i> , 2022, 13, 1515-1532.	1.8	16
1637	Reduced gut microbiota diversity in patients with congenital generalized lipodystrophy. <i>Diabetology and Metabolic Syndrome</i> , 2022, 14, .	1.2	2
1638	Review of the Cyanobacterial Genus Phormidesmis (Leptolyngbyaceae) with the Description of <i>Apatinema</i> gen. nov.. <i>Diversity</i> , 2022, 14, 731.	0.7	4
1639	The active core microbiota of two high-yielding laying hen breeds fed with different levels of calcium and phosphorus. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	5
1640	Insights into the microbial life in silica-rich subterranean environments: microbial communities and ecological interactions in an orthoquartzite cave (ImawarÃ Yeuta, Auyan Tepui, Venezuela). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1641	The species-level microbiota of healthy eyes revealed by the integration of metataxonomics with culturomics and genome analysis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
1643	Comment on â€œBiodegradation of Polystyrene by <i>Pseudomonas</i> sp. Isolated from the Gut of Superworms (Larvae of <i>Zophobas atratus</i>)â€•. <i>Environmental Science & Technology</i> , 2022, 56, 14214-14215.	4.6	0
1645	High genomic differentiation and limited gene flow indicate recent cryptic speciation within the genus <i>Laspinema</i> (cyanobacteria). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
1646	Enhanced cultured diversity of the mouse gut microbiota enables custom-made synthetic communities. <i>Cell Host and Microbe</i> , 2022, 30, 1630-1645.e25.	5.1	26
1648	Connectivity and divergence of symbiotic bacteria of deep-sea hydrothermal vent mussels in relation to the structure and dynamics of mid-ocean ridges. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
1649	Bacterial community diversity on the surface of Chinese wolfberry fruit and its potential for biological control. <i>Food Science and Technology</i> , 0, 42, .	0.8	1
1650	Description of <i>Halosolutus amylolyticus</i> gen. nov., sp. nov., <i>Halosolutus halophilus</i> sp. nov. and <i>Halosolutus gelatinilyticus</i> sp. nov., and genome-based taxonomy of genera <i>Natribaculum</i> and <i>Halovarius</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
1651	<i>Neocylindrospermum variakineticum</i> gen</i>. & <i>sp. nov</i>. (Nostocales, Cyanobacteria), a novel genus separated from <i>Cylindrospermum</i> using a polyphasic method. <i>Phycologia</i> , 2022, 61, 653-668.	0.6	1
1652	Harnessing the Power of Model Organisms To Unravel Microbial Functions in the Coral Holobiont. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, .	2.9	22

#	ARTICLE	IF	CITATIONS
1655	Distribution and Molecular Characteristics of <i>Vibrio</i> Species Isolated from Aquatic Environments in China, 2020. <i>Microorganisms</i> , 2022, 10, 2007.	1.6	2
1656	Polyphasic evaluation and cytotoxic investigation of isolated cyanobacteria with an emphasis on potent activities of a <i>Scytonema</i> strain. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1657	Phycological exploration of the global biodiversity hotspots of Northeast India: discovery of a new species of soil-dwelling cyanobacteria, <i>Desikacharya kailashaharensis</i> sp. nov. <i>FEMS Microbiology Letters</i> , 2022, 369, .	0.7	3
1658	Gut microbiome insights from 16S rRNA analysis of 17-year periodical cicadas (Hemiptera: Magicicada) TJ ETQq1 1 0.784314 rpgBT / Over	1.6	1
1659	<i>Stieleria sedimenti</i> sp. nov., a Novel Member of the Family Pirellulaceae with Antimicrobial Activity Isolated in Portugal from Brackish Sediments. <i>Microorganisms</i> , 2022, 10, 2151.	1.6	3
1661	Comparative Genomic Insights into the Evolution of <i>Halobacteria</i> -Associated <i>Candidatus</i> <i>Nanohaloarchaeota</i> . <i>MSystems</i> , 2022, 7, .	1.7	6
1662	Description of a moderately acidotolerant and aerotolerant anaerobic bacterium <i>Acidilutibacter cellobiosedens</i> gen. nov., sp. nov. within the family Acidilutibacteraceae fam. nov., and proposal of <i>Sporanaerobacteraceae</i> fam. nov. and <i>Tepidimicrobiaceae</i> fam. nov.. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126376.	1.2	5
1663	Application of ecosystem-specific reference databases for increased taxonomic resolution in soil microbial profiling. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1664	Lab- and pilot-scale anaerobic digestion of municipal bio-waste and potential of digestate for biogas upgrading sustained by microbial analysis. <i>Renewable Energy</i> , 2022, 201, 344-353.	4.3	6
1665	Isolation and characterization of a thermophilic chain elongating bacterium that produces the high commodity chemical n-caproate from polymeric carbohydrates. <i>Bioresource Technology</i> , 2023, 367, 128170.	4.8	5
1666	Microbial community shifts induced by plastic and zinc as substitutes of tire abrasion. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1667	A Metabolomics-Based Toolbox to Assess and Compare the Metabolic Potential of Unexplored, Difficult-to-Grow Bacteria. <i>Marine Drugs</i> , 2022, 20, 713.	2.2	0
1668	<i>Aestuarium zhoushanense</i> is a later heterotypic synonym of <i>Marivivens donghaensis</i> , and transfer of <i>Paradonghicola geojensis</i> to the genus <i>Marivivens</i> as <i>Marivivens geojensis</i> comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1
1669	Cow's microbiome from antepartum to postpartum: A long-term study covering two physiological challenges. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1670	<i>Paracrocinitomix mangrovi</i> gen. nov., sp. nov., isolated from a mangrove sediment: proposal of two new families, <i>Phaeocystidibacteraceae</i> fam. nov. and <i>Owenweeksaceae</i> fam. nov., and emended description of the family <i>Schleiferiaceae</i> . <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 171-184.	0.7	2
1671	Diversity of rhizobia, symbiotic effectiveness, and potential of inoculation in <i>Acacia mearnsii</i> seedling production. <i>Brazilian Journal of Microbiology</i> , 0, , .	0.8	1
1672	Is There a Universal Endurance Microbiota?. <i>Microorganisms</i> , 2022, 10, 2213.	1.6	2
1673	<i>Moorella sulfireducens</i> sp. nov., a thermophilic anaerobic bacterium isolated from a terrestrial thermal spring. <i>Extremophiles</i> , 2022, 26, .	0.9	2

#	ARTICLE	IF	CITATIONS
1675	Low diversity and microdiversity of comammox bacteria in wastewater systems suggest specific adaptations within the Ca. Nitrospira nitrosa cluster. <i>Water Research</i> , 2023, 229, 119497.	5.3	8
1676	High-resolution Microbiome Analyses of Nine Psyllid Species of the Family Triozidae Identified Previously Unrecognized but Major Bacterial Populations, including <i>Liberibacter</i> and <i>Wolbachia</i> of Supergroup O. <i>Microbes and Environments</i> , 2022, 37, n/a.	0.7	6
1677	Alterations of the fecal microbiota in relation to acute COVID-19 infection and recovery. <i>Molecular Biomedicine</i> , 2022, 3, .	1.7	11
1680	Targeted 16S rRNA Gene Capture by Hybridization and Bioinformatic Analysis. <i>Methods in Molecular Biology</i> , 2023, , 187-208.	0.4	0
1681	Characteristics of rhizosphere and endogenous bacterial community of Ulleung-sanmaneul, an endemic plant in Korea: application for alleviating salt stress. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1682	A Novel Microcystin-Producing Cyanobacterial Species from the Genus <i>Desmonostoc</i> , <i>Desmonostoc alborizicum</i> sp. nov., Isolated from a Water Supply System of Iran. <i>Current Microbiology</i> , 2023, 80, .	1.0	5
1683	Plant microbiomes harbor potential to promote nutrient turnover in impoverished substrates of a Brazilian biodiversity hotspot. <i>ISME Journal</i> , 2023, 17, 354-370.	4.4	14
1684	<i>Bdellovibrio reynosensis</i> sp. nov., from a Mexico soil sample. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	2
1685	<i>Hominibacterium faecale</i> gen. nov., sp. nov., an anaerobic l-arginine-degrading bacterium isolated from human feces. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	1
1686	Insights into the phylogenetic inconsistencies of the genus <i>Amazonocrinis</i> and description of epilithic <i>Amazonocrinis malviyae</i> sp. nov. (Cyanobacteria, Nostocales) from Jammu and Kashmir, India. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	2
1687	<i>Anaeropeptidovorans aminofermentans</i> gen. nov., sp. nov., a mesophilic proteolytic salt-tolerant bacterium isolated from a laboratory-scale biogas fermenter, and emended description of <i>Clostridium colinum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 72, .	0.8	3
1688	Assessing the drivers of gut microbiome composition in wild redfronted lemurs via longitudinal metacommunity analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
1689	<i>Vulcanimicrobium alpinus</i> gen. nov. sp. nov., the first cultivated representative of the candidate phylum "Eremiobacterota", is a metabolically versatile aerobic anoxygenic phototroph. <i>ISME Communications</i> , 2022, 2, .	1.7	8
1690	Disproportionation of Inorganic Sulfur Compounds by Mesophilic Chemolithoautotrophic <i>Campylobacterota</i> . <i>MSystems</i> , 2023, 8, .	1.7	5
1691	Assessment of diversity of archaeal communities in Algerian chott. <i>Extremophiles</i> , 2023, 27, .	0.9	2
1692	Wheat genome architecture influences interactions with phytobeneficial microbial functional groups in the rhizosphere. <i>Plant, Cell and Environment</i> , 2023, 46, 1018-1032.	2.8	2
1693	<i>Nitrosophilus kaiyonis</i> sp. nov., a hydrogen-, sulfur- and thiosulfate-oxidizing chemolithoautotroph within "Campylobacterota" isolated from a deep-sea hydrothermal vent in the Mid-Okina Trough. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	2
1694	Genome-based taxonomic rearrangement of Oceanobacter-related bacteria including the description of <i>Thalassolituus hydrocarbonoclasticus</i> sp. nov. and <i>Thalassolituus pacificus</i> sp. nov. and emended description of the genus <i>Thalassolituus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4

#	ARTICLE	IF	CITATIONS
1695	Volatiles of the Apicomplexan Alga <i>Chromera velia</i> and Associated Bacteria. <i>ChemBioChem</i> , 2023, 24, .	1.3	0
1696	Biogeochemical impacts of fish farming on coastal sediments: Insights into the functional role of cable bacteria. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1697	Physiological and comparative proteomic characterization of <i>Desulfolithobacter dissulfuricans</i> gen. nov., sp. nov., a novel mesophilic, sulfur-disproportionating chemolithoautotroph from a deep-sea hydrothermal vent. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
1698	<i>Trichotorquatus salinus</i> sp. nov. (Oculatellaceae, Cyanobacteria) from a Saltern of Gomso, Republic of Korea. <i>Diversity</i> , 2023, 15, 65.	0.7	0
1699	Taxonomic Assignment-Based Genome Reconstruction from Apical Periodontal Metagenomes to Identify Antibiotic Resistance and Virulence Factors. <i>Life</i> , 2023, 13, 194.	1.1	2
1700	The role of the gut microbiota in patients with Kleefstra syndrome. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 0, , .	1.1	0
1701	<i>Allobaculum mucilyticum</i> sp. nov. and <i>Allobaculum fili</i> sp. nov., isolated from the human intestinal tract. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
1703	Current Progress of Bioinformatics for Human Health. <i>Translational Bioinformatics</i> , 2023, , 145-162.	0.0	0
1704	Phylogenomic analysis of the genus <i>Alcanivorax</i> : proposal for division of this genus into the emended genus <i>Alcanivorax</i> and two novel genera <i>Alloalcanivorax</i> gen. nov. and <i>Isoalcanivorax</i> gen. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
1705	<i>Escherichia Coli</i> : What Is and Which Are? <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	5
1706	Microbial rewilding in the gut microbiomes of captive ring-tailed lemurs (<i>Lemur catta</i>) in Madagascar. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
1707	Exploring Uncultured Thermophilic Archaea Hidden in Terrestrial Hot Springs. <i>Journal of Geography (Chigaku Zasshi)</i> , 2022, 131, 647-663.	0.1	2
1708	Atlantic Salmon (<i>Salmo salar</i>) Transfer to Seawater by Gradual Salinity Changes Exhibited an Increase in The Intestinal Microbial Abundance and Richness. <i>Microorganisms</i> , 2023, 11, 76.	1.6	4
1709	Out of the blue: the independent activity of sulfur-oxidizers and diatoms mediate the sudden color shift of a tropical river. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	0
1710	Thermophilic Carboxylesterases from Hydrothermal Vents of the Volcanic Island of Ischia Active on Synthetic and Biobased Polymers and Mycotoxins. <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	2
1711	<i>Anaeromicropila herbilytica</i> gen. nov., sp. nov., a plant polysaccharide-decomposing anaerobic bacterium isolated from anoxic soil subjected to reductive soil disinfestation, and reclassification of <i>Clostridium populeti</i> as <i>Anaeromicropila populeti</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	3
1712	<i>Chrysoosporium ovalisporum</i> is synonymous with the true branching cyanobacterium <i>Umezakia natans</i> (Nostocales/Aphanizomenonaceae). <i>Journal of Phycology</i> , 2023, 59, 326-341.	1.0	1
1713	Development of microbial inspection for beer industry. <i>Journal of the Japanese Society for Food Science and Technology</i> , 2023, , .	0.1	0

#	ARTICLE	IF	CITATIONS
1714	Terrestrial Species of <i>Drouetiella</i> (Cyanobacteria, Oculatellaceae) from the Russian Arctic and Subarctic Regions and Description of <i>Drouetiella ramosa</i> sp. nov.. <i>Diversity</i> , 2023, 15, 132.	0.7	3
1715	Phylogenetic of <i>Microhyla</i> from Malang water sources (East Java), based on 16S rRNA gene. <i>AIP Conference Proceedings</i> , 2023, , .	0.3	0
1716	Reclassification of <i>Clostridium cocleatum</i> , <i>Clostridium ramosum</i> , <i>Clostridium spiroforme</i> and <i>Clostridium saccharogumia</i> as <i>Thomasclavelia cocleata</i> gen. nov., comb. nov., <i>Thomasclavelia ramosa</i> comb. nov., gen. nov., <i>Thomasclavelia spiroformis</i> comb. nov. and <i>Thomasclavelia saccharogumia</i> comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	5
1717	Microbial biotechnology for wastewater treatment into circular economy. , 2023, , 333-354.		0
1718	Ecophysiology and genomics of the brackish water adapted SAR11 subclade IIIa. <i>ISME Journal</i> , 2023, 17, 620-629.	4.4	10
1719	Distribution of Bacterial Endosymbionts of the <i>Cardinium</i> Clade in Plant-Parasitic Nematodes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2905.	1.8	0
1720	Microbiota Phenotype Promotes Anastomotic Leakage in a Model of Rats with Ischemic Colon Resection. <i>Microorganisms</i> , 2023, 11, 680.	1.6	2
1721	Structural differences in the gut microbiome of bats using terrestrial vs. aquatic feeding resources. <i>BMC Microbiology</i> , 2023, 23, .	1.3	3
1722	<i>Natronogravilivirga saccharolytica</i> gen. nov., sp. nov. and <i>Cyclonatronum proteinivorum</i> gen. nov., sp. nov., haloalkaliphilic organotrophic bacteroidetes from hypersaline soda lakes forming a new family <i>Cyclonatronaceae</i> fam. nov. in the order <i>Balneolales</i> . <i>Systematic and Applied Microbiology</i> , 2023, 46, 126403.	1.2	3
1723	Unraveling prevalence of homoacetogenesis and methanogenesis pathways due to inhibitors addition. <i>Bioresource Technology</i> , 2023, 376, 128922.	4.8	0
1724	Phylogenomics reveals insights into the functional evolution of the genus <i>Agrobacterium</i> and enables the description of <i>Agrobacterium divergens</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126420.	1.2	2
1725	The power of DNA based methods in probiotic authentication. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
1726	Comparison of overwintering potential of seeds in laboratory and field conditions for the risk assessment of transgenic plants: a sunflower case study. <i>Journal of Ecology and Environment</i> , 0, 47, .	1.6	1
1727	Composition, Succession and Key Species of Microbiota in Strong Aroma-Type Baijiu Production. , 2023, , 473-501.		0
1729	A novel sulfate-reducing and nitrogen-fixing bacterium <i>Fundidesulfovibrio soli</i> sp. nov., isolated from paddy soils. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	1
1730	<i>Aminithiophilus ramosus</i> gen. nov., sp. nov., a sulphur-reducing bacterium isolated from a pyrite-forming enrichment culture, and taxonomic revision of the family <i>Synergistaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	2
1731	<i>Khargia</i> gen. nov., a new genus of simple trichal Cyanobacteria from the Persian Gulf. <i>Fottea</i> , 2023, 23, 49-61.	0.4	1
1732	Impact of 16S rRNA Gene Redundancy and Primer Pair Selection on the Quantification and Classification of Oral Microbiota in Next-Generation Sequencing. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0

#	ARTICLE	IF	CITATIONS
1733	Variation of butyrate production in the gut microbiome in type 2 diabetes patients. <i>International Microbiology</i> , 2023, 26, 601-610.	1.1	7
1734	Host metabolome and faecal microbiome shows potential interactions impacted by age and weaning times in calves. <i>Animal Microbiome</i> , 2023, 5, .	1.5	5
1735	Genomic diversity in <i>Fructobacillus</i> spp. isolated from fructose-rich niches. <i>PLoS ONE</i> , 2023, 18, e0281839.	1.1	3
1736	Description of <i>Fervidibacillus</i> gen. nov. with Two Species, <i>Fervidibacillus albus</i> sp. nov., and <i>Fervidibacillus halotolerans</i> sp. nov., Isolated from Tidal Flat Sediments and Emendation of Misclassified Taxa in the Genus <i>Caldibacillus</i> . <i>Journal of Microbiology</i> , 2023, 61, 175-187.	1.3	1
1737	Genome-centric metagenomic insights into the role of Chloroflexi in anammox, activated sludge and methanogenic reactors. <i>BMC Microbiology</i> , 2023, 23, .	1.3	18
1739	Fine-scale evaluation of two standard 16S rRNA gene amplicon primer pairs for analysis of total prokaryotes and archaeal nitrifiers in differently managed soils. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
1740	Introducing <i>Cyanodorina</i> gen. nov. and <i>Cyanodorina ovale</i> sp. nov. (Microcystaceae, Chroococcales), a Novel Coccoid Cyanobacterium Isolated from Caohai Lake in China Based on a Polyphasic Approach. <i>Diversity</i> , 2023, 15, 329.	0.7	0
1741	Avian Malaria Parasites Modulate Gut Microbiome Assembly in Canaries. <i>Microorganisms</i> , 2023, 11, 563.	1.6	4
1742	Genomic characterization and molecular dating of the novel bacterium <i>Permianibacter aggregans</i> HW001T, which originated from Permian ground water. <i>Marine Life Science and Technology</i> , 2023, 5, 12-27.	1.8	0
1743	<i>Cartusia hunanesis</i> sp. nov. (Oculatellaceae, Oculatellales) from a Stream in China Based on Polyphasic Approach. <i>Diversity</i> , 2023, 15, 350.	0.7	0
1744	Australian soil microbiome: A first sightseeing regional prediction driven by cycles of soil temperature and pedogenic variations. <i>Molecular Ecology</i> , 2023, 32, 6243-6259.	2.0	5
1745	Use of modified ichip for the cultivation of thermo-tolerant microorganisms from the hot spring. <i>BMC Microbiology</i> , 2023, 23, .	1.3	2
1747	Community response of soil microorganisms to combined contamination of polycyclic aromatic hydrocarbons and potentially toxic elements in a typical coking plant. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
1748	Infectious Agents: From the Red Queen Paradigm to Some of Their Genuine Traits. , 2023, , 47-107.		0
1750	Metabolic Versatility of the Family <i>Haliaceae</i> Revealed by the Genomics of Novel Cultured Isolates. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
1751	Combing fecal microbial community data to identify consistent obesity-specific microbial signatures and shared metabolic pathways. <i>IScience</i> , 2023, 26, 106476.	1.9	4
1753	Estradiol-mediated protection against high-fat diet induced anxiety and obesity is associated with changes in the gut microbiota in female mice. <i>Scientific Reports</i> , 2023, 13, .	1.6	7
1754	The microbial dark matter and "wanted list" in worldwide wastewater treatment plants. <i>Microbiome</i> , 2023, 11, .	4.9	10

#	ARTICLE	IF	CITATIONS
1755	Geographical subdivision of Alviniconcha snail populations in the Indian Ocean hydrothermal vent regions. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	2
1756	Problematic Cannabis Use Is Associated with Reduced Rectal Microbial Species Richness and Diversity Among a Pilot Sample of Young Sexual and Gender Minorities. <i>AIDS Research and Human Retroviruses</i> , 2024, 40, 1-6.	0.5	0
1757	<i>Rathayibacter rubneri</i> sp. nov. isolated from <i>Allium cepa</i> var. Rijnsburger, an onion landrace. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	2
1758	<i>Paraflavisolibacter caeni</i> gen. nov., sp. nov., a novel taxon within the family Chitinophagaceae isolated from sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
1759	Signatures of HIV and Major Depressive Disorder in the Plasma Microbiome. <i>Microorganisms</i> , 2023, 11, 1022.	1.6	1
1760	<i>Enterocloster alcoholdehydrogenati</i> sp. nov., a Novel Bacterial Species Isolated from the Feces of a Patient with Alcoholism. <i>Current Microbiology</i> , 2023, 80, .	1.0	1
1761	<i>Aeoliella straminimaris</i> sp. nov., a novel member of the phylum Planctomycetota with an unusual filamentous structure. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
1764	<i>Maliibacterium massiliense</i> gen. nov. sp. nov., Isolated from Human Feces and Proposal of <i>Maliibacteriaceae</i> fam. nov.. <i>Current Microbiology</i> , 2023, 80, .	1.0	0
1778	Targeted Enrichment of Low-Abundance and Uncharacterized Taxon Members in Complex Microbial Community with Primer-Free FISH Probes—Designed from Next Generation Sequencing Dataset. <i>Methods in Molecular Biology</i> , 2023, , 303-315.	0.4	0
1819	Interactions of Pathogenic <i>Escherichia coli</i> with Gut Microbiota. , 2023, , 277-294.		0
1837	A Review on Microbial Species for Forensic Body Fluid Identification in Healthy and Diseased Humans. <i>Current Microbiology</i> , 2023, 80, .	1.0	1
1880	Impact of the microbiome in fertility. , 2024, , 313-323.		0
1940	Antimicrobial activity of <i>Chondromyces</i> spp. isolated from Indonesian mangrove. <i>AIP Conference Proceedings</i> , 2023, , .	0.3	0
1971	Symbionts of Ciliates and Ciliates as Symbionts. <i>Indian Journal of Microbiology</i> , 0, , .	1.5	0
1984	Microbiome Testing in Female Infertility. , 2023, , 133-144.		0